

SEQUENCE LISTING

<110> SpyBiotech Limited

<120> Vaccine composition

<130> P9800wo1

<160> 60

<170> PatentIn version 3.5

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Leu Asp

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Glu Ala Ala Ala Lys
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<222> (2215)..(2232)

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<223> Signal peptide

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<400> 14
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<210> 15
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<210> 16
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<220>
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<222> (91)..(834)
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<222> (835)..(837)
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<210> 17
<211> 702
<212> DNA
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<223> Ectodomain

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<222> (643)..(687)

<223> Linker

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<222> (688)..(699)

<223> C-tag

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<222> (700)..(702)

<223> Stop codon

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gtggaagacg ccaagatatt tggagcgcac atggtgcca agcagaccaa gctgctacgc 480

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<223> Signal peptide

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<222> (76)..(642)

<223> Ectodomain

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tggtctaaac tgacgtattc caaacgcgat gacgcggcga cgttttactg tccttttctc 180

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cccagatgtc gcaacgagac cctgtatctg ctgtacaacc gggaaggcca gaccttggtg 300

gagagaagct ccacctgggt gaaaaagggt atctggtacc tgagcggctg gaaccaaacc 360

atctccaac ggatgccccg aacggcttcg aaaccgagcg acggaaacgt gcagatcagc 420

gtggaagacg ccaagatfff tggagcgcac atggtgccca agcagaccaa gctgctacgc 480

ttcgtcgtca acgatggcac acgttatcag atgtgtgtga tgaagctgga gagctgggct 540

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<212> DNA

<213> Artificial Sequence

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<213> Human cytomegalovirus

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<223> T>C mutation at position 634

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<222> (543)..(756)
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<222> (757)..(759)
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gaacgctggt acgatttcaa aatgtgcaat cgcttcaccg tcgcgtacgt attttcatga 180

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ccgtaagtct cttctgagg gccttacagc ctatgggaga gtaagacaga gagggacaaa 480

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aggttatacc tcgaagctga cgggcgaata cgctgcggca aagtaaacga caaggcgcag 600

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<222> (55)..(236)
<223> Ectodomain

<220>
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<222> (237)..(344)

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<222> (345)..(495)
<223> Ectodomain

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<222> (496)..(498)
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tctcgcgcgc tgcccgacca aaccggttac aagtatgtgg aacagctcgt ggacctcacg 180

ttgaactacc actacgatgc gagccacggc ttggacaact ttgacgtgct caagaggtga 240

gggtacgcgc taaagatgca tgacaacggg aaggttaagg cgaacgggta acgggtaagt 300

aaccgcatgg ggtatgaaat gacgttcgga acctgtgctt gcagaatcaa cgtgaccgag 360

gtgtcgttgc tcatcagcga ctttagacgt cagaaccgtc gcggcggcac caacaaaagg 420

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<222> (277)..(303)
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<222> (304)..(315)
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<222> (316)..(993)
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<222> (1006)..(1008)
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<220>
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<210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flexible linker from SpyCatcher-HBsAg

<400> 24
 ggttctggtg gatctggtgg ttccggt 27

<210> 25
 <211> 12
 <212> DNA

<213> Artificial Sequence

<220>

<223> PVTN linker from SpyCatcher-HbsAg

<400> 25

ccagttacta at 12

<210> 26

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> HBsAg

<400> 26

atggaaaaca tcactccgg ttcttgggt ccttgttgg tttgcaggc tggattctc 60
ttgttgacta gaacttgac tatccacag tcctgggact ctgtgtggac ttcctgaac 120
ttcttgggtg gttccccagt ttgttgggt caaaactctc aatcccaac ttccaaccac 180
tcccaacat ctgtccacc aattgtctc gggtacagat ggatgtgtt gagaagattc 240
atcattttct tggtcatctt gttgttgtt ttgatcttct tgttggttt gttggactac 300
cagggtatgt tgccagttg tccattgatc ccagggtcca ctactacaa cactgggtcca 360
tgtaagactt gtactactcc agctcagggt aactccatgt tccctcatg ttgtgtact 420
aagccaactg acggtactg tactgtatc ccaattccat cctcctgggc ttctgctaag 480
tactgtggg aatgggcttc cgtagattc tctggttgt cctgttggt tccattcgtt 540
cagtgggtcg ttggtttgc cccaactgtt tgggtgtccg ctatttgat gatgtgttac 600
tggtgtccat cctgtactc tatcgttcc ccattcatcc cttgtgtcc aatcttctc 660
tggtgtggg ttacatc 678

<210> 27

<211> 744

<212> PRT

<213> Artificial Sequence

<220>

<223> gH-SpyTag-His

<220>

<221> misc_feature

<222> (1)..(23)

<223> Signal peptide

<220>

<221> misc_feature

<222> (24)..(717)

<223> Ectodomain

<220>

<221> misc_feature

<222> (718)..(719)

<223> Transmembrane domain (truncated)

<220>

<221> misc_feature

<222> (720)..(725)

<223> Linker

<220>

<221> misc_feature

<222> (726)..(738)

<223> Spytag

<220>

<221> misc_feature

<222> (739)..(744)

<223> 6x His tag

<400> 27

Met Arg Pro Gly Leu Pro Ser Tyr Leu Ile Ile Leu Ala Val Cys Leu
1 5 10 15

Phe Ser His Leu Leu Ser Ser Arg Tyr Gly Ala Glu Ala Val Ser Glu
20 25 30

Pro Leu Asp Lys Ala Phe His Leu Leu Asn Thr Tyr Gly Arg Pro
35 40 45

Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser Ser
50 55 60

Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn Phe
65 70 75 80

Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys Leu
85 90 95

Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu Thr
100 105 110

Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val
115 120 125

Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys Ala
130 135 140

Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro Ile Asp
145 150 155 160

Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His Gly
165 170 175

Trp Thr Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe Asn
180 185 190

Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr Val
195 200 205

Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu Leu Arg Tyr
210 215 220

Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser Ile
225 230 235 240

Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg Val
245 250 255

Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln Thr
260 265 270

Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln Leu Asn Arg
275 280 285

His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala Leu Asp Phe
290 295 300

Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg Tyr
305 310 315 320

Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg Arg

325 330 335

Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala Ala
340 345 350

Arg Gln Glu Glu Ala Gly Ala Gln Val Ser Val Pro Arg Ala Leu Asp
355 360 365

Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys Leu
370 375 380

Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala Val
385 390 395 400

Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asn Gln Ile Thr Asp Ile
405 410 415

Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln Gln
420 425 430

His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala Leu
435 440 445

Lys Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala Arg
450 455 460

Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val His
465 470 475 480

Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys Ser
485 490 495

Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His His
500 505 510

Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg Arg
515 520 525

Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr Val
530 535 540

Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln Pro
545 550 555 560

Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly Glu
565 570 575

Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Ile Val Thr
580 585 590

Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr Val
595 600 605

Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys Cys
610 615 620

Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Val Ala Leu
625 630 635 640

Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu Glu
645 650 655

Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp Ser
660 665 670

Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val Ser
675 680 685

Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val Leu
690 695 700

Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu Gly
705 710 715 720

Ser Gly Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro
725 730 735

Thr Lys His His His His His His
740

<210> 28

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> gH with truncated transmembrane domain

<220>

<221> misc_feature

<222> (1)..(23)

<223> Signal peptide

<220>

<221> misc_feature

<222> (24)..(717)

<223> Ectodomain

<220>

<221> misc_feature

<222> (718)..(719)

<223> Transmembrane domain (truncated)

<400> 28

Met Arg Pro Gly Leu Pro Ser Tyr Leu Ile Ile Leu Ala Val Cys Leu
1 5 10 15

Phe Ser His Leu Leu Ser Ser Arg Tyr Gly Ala Glu Ala Val Ser Glu
20 25 30

Pro Leu Asp Lys Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg Pro
35 40 45

Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser Ser
50 55 60

Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn Phe
65 70 75 80

Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys Leu
85 90 95

Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu Thr
100 105 110

Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val
115 120 125

Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys Ala
130 135 140

Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro Ile Asp
145 150 155 160

Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His Gly
165 170 175

Trp Thr Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe Asn
180 185 190

Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr Val
195 200 205

Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu Leu Arg Tyr
210 215 220

Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser Ile
225 230 235 240

Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg Val
245 250 255

Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln Thr
260 265 270

Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln Leu Asn Arg
275 280 285

His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala Leu Asp Phe
290 295 300

Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg Tyr
305 310 315 320

Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg Arg
325 330 335

Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala Ala
340 345 350

Arg Gln Glu Glu Ala Gly Ala Gln Val Ser Val Pro Arg Ala Leu Asp
355 360 365

Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys Leu
370 375 380

Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala Val
385 390 395 400

Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asn Gln Ile Thr Asp Ile
405 410 415

Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln Gln
420 425 430

His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala Leu
435 440 445

Lys Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala Arg
450 455 460

Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val His
465 470 475 480

Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys Ser
485 490 495

Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His His
500 505 510

Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg Arg
515 520 525

Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr Val
530 535 540

Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln Pro
545 550 555 560

Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly Glu
565 570 575

Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Ile Val Thr
580 585 590

Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr Val
595 600 605

Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys Cys
610 615 620

Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Val Ala Leu
625 630 635 640

Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu Glu
645 650 655

Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp Ser
660 665 670

Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val Ser
675 680 685

Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val Leu
690 695 700

Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu
705 710 715

<210> 29

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker from gH construct

<400> 29

Gly Ser Gly Gly Ser Gly
1 5

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Spytag

<400> 30

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

<210> 31

<211> 278

<212> PRT

<213> Human cytomegalovirus

<220>

<221> misc_feature

<222> (1)..(30)

<223> Signal peptide

<220>

<221> misc_feature

<222> (31)..(278)

<223> Ectodomain

<400> 31

Met Cys Arg Arg Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro Val
1 5 10 15

Ile Leu Leu Trp Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Ala Ala
20 25 30

Val Ser Val Ala Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys Pro
35 40 45

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

Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Gly Arg Asp Gly
65 70 75 80

Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala Ala
85 90 95

Asn Ser Val Leu Leu Asp Glu Ala Phe Leu Asp Thr Leu Ala Leu Leu
100 105 110

Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser Ser
115 120 125

Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu Cys
130 135 140

Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys Arg
145 150 155 160

Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr Glu
165 170 175

His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val Val
180 185 190

Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg Leu
195 200 205

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

Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp Pro
225 230 235 240

Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro Glu
245 250 255

Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly Pro
260 265 270

Gln Ala Val Asp Ala Arg
275

<210> 32

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> UL130 - C-tag

<220>
<221> misc_feature
<222> (1)..(25)
<223> Signal peptide

<220>
<221> misc_feature
<222> (26)..(214)
<223> Ectodomain

<220>
<221> misc_feature
<222> (215)..(229)
<223> Linker

<220>
<221> misc_feature
<222> (230)..(233)
<223> C-tag

<400> 32

Met Leu Arg Leu Leu Leu Arg His His Phe His Cys Leu Leu Leu Cys
1 5 10 15

Ala Val Trp Ala Thr Pro Cys Leu Ala Ser Pro Trp Ser Thr Leu Thr
20 25 30

Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser Lys
35 40 45

Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser Pro
50 55 60

Pro Arg Ser Pro Leu Gln Phe Ser Gly Phe Gln Arg Val Ser Thr Gly
65 70 75 80

Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu Gly
85 90 95

Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val Ile Trp
100 105 110

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

Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu Asp Ala

130 135 140

Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu Leu Arg
145 150 155 160

Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met Lys Leu
 165 170 175

Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe Gln Val
 180 185 190

Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys Thr
 195 200 205

His Pro Asn Leu Ile Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 210 215 220

Gly Gly Gly Gly Ser Glu Pro Glu Ala
225 230

<210> 33

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> UL130 (signal sequence and ectodomain)

<220>

<221> misc_feature

<222> (1)..(25)

<223> Signal peptide

<220>

<221> misc_feature

<222> (26)..(214)

<223> Ectodomain

<400> 33

Met Leu Arg Leu Leu Leu Arg His His Phe His Cys Leu Leu Leu Cys
1 5 10 15

Ala Val Trp Ala Thr Pro Cys Leu Ala Ser Pro Trp Ser Thr Leu Thr
 20 25 30

Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser Lys
35 40 45

Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser Pro
50 55 60

Pro Arg Ser Pro Leu Gln Phe Ser Gly Phe Gln Arg Val Ser Thr Gly
65 70 75 80

Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu Gly
85 90 95

Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val Ile Trp
100 105 110

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

Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu Asp Ala
130 135 140

Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu Leu Arg
145 150 155 160

Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met Lys Leu
165 170 175

Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe Gln Val
180 185 190

Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys Thr
195 200 205

His Pro Asn Leu Ile Val
210

<210> 34

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker from UL130 construct

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 35

<211> 171

<212> PRT

<213> Human cytomegalovirus

<220>

<221> misc_feature

<222> (1)..(27)

<223> Signal peptide

<220>

<221> misc_feature

<222> (28)..(171)

<223> Ectodomain

<400> 35

Met Ser Pro Lys Asp Leu Thr Pro Phe Leu Thr Ala Leu Trp Leu Leu
1 5 10 15

Leu Gly His Ser Arg Val Pro Arg Val Arg Ala Glu Glu Cys Cys Glu
20 25 30

Phe Ile Asn Val Asn His Pro Pro Glu Arg Cys Tyr Asp Phe Lys Met
35 40 45

Cys Asn Arg Phe Thr Val Ala Leu Arg Cys Pro Asp Gly Glu Val Cys
50 55 60

Tyr Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr Met
65 70 75 80

Thr His Ser Leu Thr Arg Gln Val Val His Asn Lys Leu Thr Ser Cys
85 90 95

Asn Tyr Asn Pro Leu Tyr Leu Glu Ala Asp Gly Arg Ile Arg Cys Gly
100 105 110

Lys Val Asn Asp Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser Val

115 120 125

Pro Tyr Arg Trp Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg Ile Val
130 135 140

Gly Leu Asp Gln Tyr Leu Glu Ser Val Lys Lys His Lys Arg Leu Asp
145 150 155 160

Val Cys Arg Ala Lys Met Gly Tyr Met Leu Gln
165 170

<210> 36
<211> 129
<212> PRT
<213> Human cytomegalovirus

<220>
<221> misc_feature
<222> (1)..(18)
<223> Signal peptide

<220>
<221> misc_feature
<222> (19)..(129)
<223> Ectodomain

<400> 36

Met Arg Leu Cys Arg Val Trp Leu Ser Val Cys Leu Cys Ala Val Val
1 5 10 15

Leu Gly Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr Arg
20 25 30

Val Pro His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln Thr
35 40 45

Arg Tyr Lys Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr His
50 55 60

Tyr Asp Ala Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg Ile
65 70 75 80

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

Arg Arg Gly Gly Thr Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly Ser
100 105 110

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

Asn

<210> 37
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> SpyCatcher-HBsAg

<220>
<221> misc_feature
<222> (1)..(92)
<223> SpycatcherDeltaN1

<220>
<221> misc_feature
<222> (93)..(101)
<223> Flexible Linker

<220>
<221> misc_feature
<222> (102)..(105)
<223> PVTN linker

<220>
<221> misc_feature
<222> (106)..(331)
<223> HBsAg

<220>
<221> misc_feature
<222> (332)..(335)
<223> C-tag

<400> 37

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

Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp Ser Ser Gly Lys Thr

20

25

30

Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp Phe Tyr Leu Tyr
35 40 45

Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro Asp Gly Tyr Glu
50 55 60

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

Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His Ile Gly Ser Gly Gly
85 90 95

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

Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr
115 120 125

Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu
130 135 140

Asn Phe Leu Gly Gly Ser Pro Val Cys Leu Gly Gln Asn Ser Gln Ser
145 150 155 160

Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly
165 170 175

Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu
180 185 190

Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met
195 200 205

Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Thr Thr Thr Asn Thr Gly
210 215 220

Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn Ser Met Phe Pro
225 230 235 240

Ser Cys Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro
245 250 255

Ile Pro Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Glu Trp Ala Ser
260 265 270

Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe
275 280 285

Val Gly Leu Ser Pro Thr Val Trp Leu Ser Ala Ile Trp Met Met Trp
290 295 300

Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Val Ser Pro Phe Ile Pro Leu
305 310 315 320

Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile Glu Pro Glu Ala
325 330 335

<210> 38

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> SpyCatcherDeltaN1

<400> 38

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

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

Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp Phe Tyr Leu Tyr
35 40 45

Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro Asp Gly Tyr Glu
50 55 60

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

Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His Ile

<210> 39

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Flexible linker from SpyCatcher-HBsAg

<400> 39

Gly Ser Gly Gly Ser Gly Gly Ser Gly

1 5

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> PVTN linker from SpyCatcher-HBsAg

<400> 40

Pro Val Thr Asn

1

<210> 41

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> HBsAg

<400> 41

Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln

1 5 10 15

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu

20 25 30

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser Pro Val Cys

35 40 45

Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser

50 55 60

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Thr Thr Thr Asn Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala
115 120 125

Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys
145 150 155 160

Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
195 200 205

Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 42

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<223> gH-(GSG)2-SpyTag-His (without introns) optimised for CHO expression

<220>
<221> misc_feature
<222> (1)..(69)
<223> gH signal peptide

<220>
<221> misc_feature
<222> (70)..(2151)
<223> gH ectodomain

<220>
<221> misc_feature
<222> (2152)..(2157)
<223> gH truncated transmembrane domain

<220>
<221> misc_feature
<222> (2158)..(2175)
<223> (GSG)2 linker

<220>
<221> misc_feature
<222> (2176)..(2214)
<223> Spytag

<220>
<221> misc_feature
<222> (2215)..(2232)
<223> Histag

<220>
<221> misc_feature
<222> (2233)..(2235)
<223> Stop codon

<400> 42
atgaggcctg gcctgccttc ttatctgac atcctggccg tgtgcctgtt ctcccatctg 60

ctgtcctcta gatacggcgc cgaggctgtg tctgagcctc tggataaggc ctttcatctg 120

ctgtctgaaca cctacggcag acctatccgg ttctgcgcg agaacaccac acagtgcacc 180

tacaactcca gcctgcggaa ctccacagtc gtgcgggaaa acgcatctc ttcaacttt 240

ttccagtct acaaccagta ctatgtgtc cacatgcctc gctgcctgtt cgctggacct 300

ctggctgagc agttcctgaa ccagggtggac ctgaccgaga cactggaaag ataccagcag 360

cggctgaaca catatgcctt ggtgtctaag gacctggcct cctacagatc cttcagccag 420

cagctgaagg ctcaggactc tctgggagag cagcctacaa cagtgcctcc tcctatcgac 480

ctgtctatcc ctacgtgtg gatgcctcca cagaccacac ctcatggctg gaccgagtct 540

cataccacct ctggcctgca cgggcctcac ttcaaccaga cctgcatcct gttcgacggc 600

cacgacctgc tgttctccac cgtgacacca tgtctgcacc agggcttcta cctgatcgac 660
 gagctgagat acgtgaagat taccctgaca gaggacttct tcgtggtcac cgtgtccatc 720
 gacgacgaca ccctatgct gctgatcttc ggccatctgc ctcggtgct gttcaaggcc 780
 ccttaccagc gggacaactt catcctgaga cagaccgaga agcacgagct gctggtgctg 840
 gtcaagaagg accagctgaa ccggcactcc tacctgaagg accctgactt cctggacgcc 900
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 gccgtggacg tgctgaagtc tggcagatgc cagatgctgg acagacggac cgtggaaatg 1020
 gccttcgctt acgccctggc tctgtttgcc gccgctagac aagaagaggc tggcgcccaa 1080
 gtgtccgtgc ctgagcact ggatagacaa gccgctctgc tgcagatcca agagttcatg 1140
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 gatctggcca agagggctct gtggaccct aaccagatca ccgacatcac atccctcgtg 1260
 cggctgggtg acatcctgtc caagcagaac cagcagcatc tgatccctca gtgggccctg 1320
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 agctaccccg tgccacaac cgtcgttggc cagagcctga tcatacca gaccgactct 1860
 cagaccaagt gcgagctgac ccggaacatg cacacaacc actccatcac cgtggctctg 1920
 aacatctccc tggaaaactg cgccttctgc cagtctgcc tgctggaata cgatgacacc 1980
 cagggcgtga tcaacatcat gtatatgcac gactccgacg acgtgctgtt tgccctggat 2040
 cctfacaacg aggtgggtgt gtctagcccc agaacacact acctgatgct gctcaagaac 2100
 ggcaccgtgc tggaagtgc cgacgtggtg tggacgcca ccgattctag attgctcggc 2160
 tctggtggct ccggcgtca tatcgtgatg gtggatgctt acaagccac caagcaccat 2220

<210> 43

<211> 837

<212> DNA

<213> Artificial Sequence

<220>

<223> gL (without introns) optimised for CHO expression

<220>

<221> misc_feature

<222> (1)..(90)

<223> gL signal peptide

<220>

<221> misc_feature

<222> (91)..(834)

<223> gL ectodomain

<220>

<221> misc_feature

<222> (835)..(837)

<223> Stop codon

<400> 43

atgtgcagaa ggcctgactg cggcttctcc ttctctcccg gacctgtgat cctgctgtgg 60

tgctgtctgc tgctgccat cgtttctcc gccgctgtgt ctgtggctcc taccgtgct 120

gaaaaggtgc cagctgagtg tcccagactg accagaagat gtctgctggg cgaagtgttc 180

gagggcgata agtacgagtc ttggctgcgg cctctggta acgtgaccgg aagagatgga 240

cccctgagcc agctgatccg gtacagacct gtgacacctg aggccgcaa ttccgtgctg 300

ctggatgagg ccttctgga cacttgccc ctgctgtaca acaacccga tcagctgaga 360

gccctgctga cctgctgtc ctctgatacc gctcctagat ggatgaccgt gatgcggggc 420

tactctgagt gcggagatgg aagcccagcc gtgtacacct gtgtggacga tctgtgcaga 480

ggctacgacc tgaccagact gtctacggc cggccatct ttaccgagca tgtgtgggc 540

tttgagctgg tgccctctag cctgttcaat gtgggtgggg ccatccggaa tgaggccacc 600

agaacaaata gagccgtgcg gctgcctgtg tctacagctg ctgctcctga gggcatcacc 660

ctgttctacg gcctgtacaa cgccgtgaaa gaggctgcc tgagacacca gctggaccct 720

ccactgctga ggcacctgga taagtactac gctggcctgc ctctgagct gaagcagacc 780

agagtgaacc tgcctgtca ctccagatac ggcctcagg ctgtggacgc cagataa 837

<210> 44
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> UL128 (without introns) optimised for CHO expression

<220>
<221> misc_feature
<222> (1)..(81)
<223> UL128 signal peptide

<220>
<221> misc_feature
<222> (82)..(513)
<223> UL128 ectodomain

<220>
<221> misc_feature
<222> (514)..(516)
<223> Stop codon

<400> 44
atgtccccta aggatctgac cccttctctg accgctctgt ggctgctgct gggccattct 60

agagtgcccta gagtcagagc cgaggaatgc tgcgagttca tcaacgtgaa ccatectcca 120

gagcgggtgct acgacttcaa gatgtgcaac agattcaccg tggctctgcg gtgccctgat 180

ggcgaagtgt gctactcccc tgaaaagacc gccgagatca gaggcacgtg gaccaccatg 240

acacactccc tgaccagaca ggtgggtgcac aacaagctga ccagctgcaa ctacaaccct 300

ctgtacctgg aagccgacgg cagaatcaga tgcggcaaag tgaacgacaa ggcccagtac 360

ctgttgggcg ctgctggctc tgtgccctac agatggatca acctggaata cgacaagatc 420

acccggatcg tcggcctgga ccagtatctg gaatccgtga agaagcaca gcggtctggac 480

gtgtgcagag ccaagatggg ctatatgctg cagtaa 516

<210> 45
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> UL130-(G4S)3 - C-tag (without introns) optimised for CHO expression

<220>
<221> misc_feature
<222> (1)..(75)
<223> UL130 signal peptide

<220>
<221> misc_feature
<222> (76)..(642)
<223> UL130 ectodomain

<220>
<221> misc_feature
<222> (643)..(687)
<223> (G4S)3 linker

<220>
<221> misc_feature
<222> (688)..(699)
<223> C-tag

<220>
<221> misc_feature
<222> (700)..(702)
<223> Stop codon

<400> 45
atgctgagac tgctgctgag acaccacttc cactgcctgc tgctgtgtgc cgtttgggct 60
acaccttgtc tggcctctcc atggtctacc ctgaccgcca accagaatcc ttctccacct 120
tggtccaagc tgacctactc caagcctcac gatgccgcta cttctactg cccctttctg 180
taccatctc cacctcggag ccctctgcag ttctctggct tccagagagt gtccaccgga 240
cctgagtgcc ggaacgagac actgtacctg ctgtacaacc gcgagggcca gacactggtg 300
gaaagatcct ctacctgggt caagaaagt atctgggtatc tgagcggccg gaaccagacc 360
atcctgcaga gaatgcctcg gaccgcctct aagccttctg acggcaacgt gcagatctcc 420
gtggaagatg ccaagatctt cggcgcccac atggtgccca agcagaccaa actgctgaga 480
ttcgtggtca acgacggcac ccgctaccag atgtgcgtga tgaagctgga aagctgggcc 540
cacgtgttc gggattactc cgtgtcttcc caagtgcggc tgaccttcac cgaggccaac 600
aaccagacct acaccttctg caccatctct aacctgatcg tcggaggcgg aggatctggc 660
ggaggtggaa gtggcggagg cggatctgag cccgaggcct aa 702

<210> 46
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> UL131A (without introns) optimised for CHO expression

<220>
<221> misc_feature
<222> (1)..(54)
<223> UL131 signal peptide

<220>
<221> misc_feature
<222> (55)..(387)
<223> UL131 ectodomain

<220>
<221> misc_feature
<222> (388)..(390)
<223> Stop codon

<400> 46
atgagactgt gcagagtgtg gctgtccgtg tgcctgtgtg ctgtggttct gggccagtgc 60
cagagagaga cagccgagaa gaacgactac tacagagtgc cccactactg ggacgcctgc 120
agtagagctt tgcccgatca gaccgcgtac aaatacgtgg aacagctggt ggatctgacc 180
ctgaactacc actacgacgc ctctcacggc ctggacaact tcgacgtgct gaagcggatc 240
aacgtgaccg aggtgtccct gctgatctct gacttcgggc ggcagaatag aagaggcggc 300
accaacaagc ggaccacctt taatgctgcc ggctctctgg ctccccacgc cagatctctg 360
gaattttccg tgcggctgtt cgccaactaa 390

<210> 47
<211> 1587
<212> DNA
<213> Artificial Sequence

<220>
<223> RSV-F-SpyTag-Ctag

<220>
<221> misc_feature
<222> (1)..(75)
<223> Signal peptide

<220>
<221> misc_feature
<222> (1435)..(1515)
<223> Foldon domain

<220>
<221> misc_feature
<222> (1516)..(1533)
<223> (GSG)2 linker

<220>
<221> misc_feature
<222> (1534)..(1572)
<223> Spytag

<220>
<221> misc_feature
<222> (1573)..(1584)
<223> Ctag

<220>
<221> misc_feature
<222> (1585)..(1587)
<223> Stop codon

<400> 47
atggaactgc tgaacctgaa ggccaacgcc atcaccacca tcctgaccgc cgtgaccttc 60
tgcttcgcca gcggccagaa catcaccgag gaattctacc agagcacctg cagcgccgtg 120
agcaagggct acctgagcgc cctgcggacc ggctgggtaca ccagcgtgat caccatcgag 180
ctgtccaaca tcaaagaaaa caagtgaac ggaccgcagc ccaaagtga gctgatcaag 240
caggaactgg acaagtacaa gaacgccgtg accgagctgc agctgctgat gcagagcacc 300
cccgccaccg gatctggcag cgccatttgc agcggcgtgg ccgtgtgtaa agtgctgcac 360
ctggaaggcg aagtgaacaa gatcaagtcc gccctgctgt ccaccaacaa ggccgtgggtg 420
tccttgagca acggcgtgag cgtgctgacc ttcaaggtgc tggatctgaa gaactacatc 480
gacaagcagc tgctgcccac cctgaacaag cagagctgca gcatcagcaa catcgagaca 540
gtgatcgagt tccagcagaa gaacaaccgg ctgctggaaa tcaccgggga gttcagcgtg 600
aacgccggag tgaccacccc cgtgtccacc tacatgctga ccaacagcga gctgctgtcc 660
ctgatcaatg acatgcccac caccaacgac cagaaaaagc tgatgagcaa caacgtgcag 720
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gtgggtgcagc tgcccctgta cggcgtgatc gacccccct gctggaagct gcacaccagc 840
cccctgtgca caaccaacac caaagagggc agcaacatct gcctgaccgc gaccgaccgg 900
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 accaagtga cgcagcaaa caagaacaga ggcatcatca agaccttcag caacggctgc 1200
 gactacgtgt ccaataaggg cgtggacacc gtgtccgtgg gcaacacact gtactgcgtg 1260
 aataagcagg aaggcaagag cctgtacgtg aaggcgagc ccatcatcaa cttctacgac 1320
 cccctggtgt tccccagca cgagttcgac gctagcatca gccaggtgaa cgagaagatc 1380
 aaccagagcc tggccttcac cagaaagagc gacgaactgc tgtccgcat cggcggctac 1440
 atccccgagg cccccagaga tggccaggcc tacgtgcgga aggacggcga gtgggtgctg 1500
 ctgtctacat ttctgggaag cggaggctct ggtgccata tcgtgatggt ggacgcctac 1560
 aagcctacca aagagccga ggcctaa 1587

<210> 48
 <211> 1515
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sc9-10 DS-Cav1 A149C Y458C (RSV-F)

<220>
 <221> misc_feature
 <222> (1)..(75)
 <223> Signal peptide

<220>
 <221> misc_feature
 <222> (1435)..(1515)
 <223> Foldon domain

<400> 48
 atggaactgc tgatcctgaa ggccaacgcc atcaccacca tcctgaccgc cgtgaccttc 60
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 caggaactgg acaagtacaa gaacgccgtg accgagctgc agctgctgat gcagagcacc 300
 cccgccaccg gatctggcag cgccatttgc agcggcgtgg ccgtgtgtaa agtgctgcac 360
 ctggaaggcg aagtgaacaa gatcaagtcc gccctgctgt ccaccaacaa ggccgtggtg 420

tcctgagca acggcgtgag cgtgctgacc ttcaaggtgc tggatctgaa gaactacatc 480
 gacaagcagc tgctgcccac cctgaacaag cagagctgca gcatcagcaa catcgagaca 540
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 aacgccggag tgaccacccc cgtgtccacc tacatgctga ccaacagcga gctgctgtcc 660
 ctgatcaatg acatgcccac caccaacgac cagaaaaagc tgatgagcaa caacgtgcag 720
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 gtggtgcagc tgcccctgta cggcgtgac gacaccccct gctggaagct gcacaccagc 840
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 aacctgtgca acgtggacat ctcaacccc aagtacgact gcaagatcat gacctcaag 1080
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 gactacgtgt ccaataaggg cgtggacacc gtgtccgtgg gcaacacact gtactgcgtg 1260
 aataagcagg aaggcaagag cctgtacgtg aaggcgagc ccatcatcaa cttctacgac 1320
 cccctggtgt tcccagcga cgagttcgac gctagcatca gccaggtgaa cgagaagatc 1380
 aaccagagcc tggccttcat cagaaagagc gacgaactgc tgtccgcat cggcggtac 1440
 atccccgagg cccccagaga tggccaggcc tacgtgcgga aggacggcga gtgggtgctg 1500
 ctgtctacat ttctg 1515

<210> 49

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Sc-9-10 DS-Cav1 A149C Y458C (RSV-F) without the signal peptide

<220>

<221> misc_feature

<222> (1360)..(1440)

<223> Foldon domain

<400> 49

cagaacatca ccgaggaatt ctaccagagc acctgcagcg ccgtgagcaa gggctacctg 60

agcgccctgc ggaccggctg gtacaccagc gtgatcacca tcgagctgtc caacatcaaa 120
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 gtgagcgtgc tgacctcaa ggtgctggat ctgaagaact acatcgacaa gcagctgctg 420
 cccatcctga acaagcagag ctgcagcatc agcaacatcg agacagtgat cgagttccag 480
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 accccctgtt ccactcatg gctgaccaac agcgagctgc tgtccctgat caatgacatg 600
 cccatcacca acgaccagaa aaagctgatg agcaacaacg tgcagatcgt gcggcagcag 660
 agctactcca tcattgtcat catcaaagaa gaggtgctgg cctacgtggt gcagctgccc 720
 ctgtacggcg tgatcgacac cccctgctgg aagctgcaca ccagccccct gtgcacaacc 780
 aacaccaaag agggcgacaa catctgcctg acccggaccg accggggctg gtactgacg 840
 aacgccggca gctgtcctt cttccacag gccgagacat gcaaggtgca gagcaaccgg 900
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 agcaacaaga acagaggcat catcaagacc ttacgaacg gctgcgacta cgtgtccaat 1140
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 agcgacgagt tcgacgctag catcagccag gtgaacgaga agatcaacca gagcctggcc 1320
 ttcatcagaa agagcgacga actgctgtcc gccatggcg gctacatccc cgaggcccc 1380
 agagatggcc aggcctacgt gcggaaggac ggcgagtggg tgctgctgtc tacatttctg 1440

<210> 50

<211> 528

<212> PRT

<213> Artificial Sequence

<220>

<223> RSV-F-SpyTag-Ctag

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> Signal peptide

<220>
<221> MISC_FEATURE
<222> (479)..(505)
<223> Foldon domain

<220>
<221> MISC_FEATURE
<222> (506)..(511)
<223> (GSG)2 linker

<220>
<221> MISC_FEATURE
<222> (512)..(524)
<223> Spytag

<220>
<221> MISC_FEATURE
<222> (525)..(527)
<223> Ctag

<400> 50

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

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

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

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
100 105 110

Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
115 120 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
130 135 140

Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile
145 150 155 160

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser
165 170 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
180 185 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
195 200 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
210 215 220

Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln
225 230 235 240

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
245 250 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
260 265 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
275 280 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
290 295 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305 310 315 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu

325 330 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
340 345 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
355 360 365

Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr
370 375 380

Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys
385 390 395 400

Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr
405 410 415

Leu Tyr Cys Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly
420 425 430

Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu
435 440 445

Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu
450 455 460

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Ser Ala Ile Gly Gly Tyr
465 470 475 480

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly
485 490 495

Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Ser Gly Gly Ser Gly Ala
500 505 510

His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Glu Pro Glu Ala
515 520 525

<210> 51

<211> 1010

<212> PRT

<213> Artificial Sequence

<220>

<223> Sc-9-10 DS-Cav1 A149C Y458C (RSV-F)

<220>

<221> MISC_FEATURE

<222> (1)..(25)

<223> Signal peptide

<220>

<221> MISC_FEATURE

<222> (479)..(505)

<223> Foldon domain

<400> 51

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

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

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

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

Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile Cys Ser Gly
100 105 110

Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
115 120 125

Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
130 135 140

Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile
145 150 155 160

Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser
165 170 175

Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu
180 185 190

Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val
195 200 205

Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp
210 215 220

Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln
225 230 235 240

Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu
245 250 255

Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr
260 265 270

Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys
275 280 285

Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys
290 295 300

Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys
305 310 315 320

Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Arg Thr Leu
325 330 335

Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr
340 345 350

Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile
355 360 365

Thr Ser Leu Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr

370 375 380

Ile Leu Thr Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr
385 390 395 400

Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu
 405 410 415

Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu
 420 425 430

Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys
 435 440 445

Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu
 450 455 460

Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Gly Ser Gly Ser Ala Ile
465 470 475 480

Cys Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
 485 490 495

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
 500 505 510

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
 515 520 525

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
 530 535 540

Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn
545 550 555 560

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
 565 570 575

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
 580 585 590

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
595 600 605

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
610 615 620

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
625 630 635 640

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
645 650 655

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
660 665 670

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu
675 680 685

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser
690 695 700

Arg Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn
705 710 715 720

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
725 730 735

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
740 745 750

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
755 760 765

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
770 775 780

Gly Asn Thr Leu Tyr Cys Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
785 790 795 800

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
805 810 815

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
820 825 830

Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu Ser Ala Ile
835 840 845

Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
850 855 860

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Ala Ile Val
865 870 875 880

Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly
885 890 895

Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly
900 905 910

Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Cys Val Asn Lys Gln
915 920 925

Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr
930 935 940

Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln
945 950 955 960

Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp
965 970 975

Glu Leu Leu Ser Ala Ile Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp
980 985 990

Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr
995 1000 1005

Phe Leu
1010

<211> 480
<212> PRT
<213> Artificial Sequence

<220>

<223> sc9-10 DS-Cav1 A149C Y458C (RSV-F) without the signal peptide

<220>

<221> MISC_FEATURE

<222> (454)..(480)

<223> Foldon domain

<400> 52

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

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

Gly Ser Ala Ile Cys Ser Gly Val Ala Val Cys Lys Val Leu His Leu
85 90 95

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
115 120 125

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
130 135 140

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
145 150 155 160

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
165 170 175

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
180 185 190

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
195 200 205

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
210 215 220

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
225 230 235 240

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
245 250 255

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
260 265 270

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
275 280 285

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
290 295 300

Thr Met Asn Ser Arg Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
305 310 315 320

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
325 330 335

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
340 345 350

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
355 360 365

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
370 375 380

Thr Val Ser Val Gly Asn Thr Leu Tyr Cys Val Asn Lys Gln Glu Gly
385 390 395 400

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
 405 410 415

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
 420 425 430

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
 435 440 445

Leu Ser Ala Ile Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
 450 455 460

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
465 470 475 480

<210> 53

<211> 1704

<212> DNA

<213> Artificial Sequence

<220>

<223> RSV-F DS-Cav1-SpyTag-Ctag

<220>

<221> misc_feature

<222> (1)..(75)

<223> Signal peptide

<220>

<221> misc_feature

<222> (1552)..(1632)

<223> Foldon domain

<220>

<221> misc_feature

<222> (1633)..(1650)

<223> (GSG)₂ linker

<220>

<221> misc_feature

<222> (1651)..(1689)

<223> Spytag

<220>
<221> misc_feature
<222> (1690)..(1701)
<223> Ctag

<220>
<221> misc_feature
<222> (1702)..(1704)
<223> Stop codon

<400> 53

atggaactgc tgatcctgaa ggccaacgcc atcaccacca tcctgaccgc cgtgaccttc	60
tgcttcgcca gcgccagaa catcaccgag gaattctacc agagcacctg cagcgccgtg	120
agcaagggct acctgagcgc cctgcggacc ggctgggtaca ccagcgtgat caccatcgag	180
ctgtccaaca tcaaagaaaa caagtgaac ggcaccgacg ccaaagtga gctgatcaag	240
caggaaactgg acaagtacaa gaacgccgtg accgagctgc agctgctgat gcagagcacc	300
cccgccacca acaacagagc cagaagagag ctgccccggg tcatgaacta caccctgaac	360
aacgccaaga aaaccaacgt gacctgagc aagaagagaa agagaagatt cctgggcttc	420
ctgctgggcg tgggcagcgc cattgccagc ggcgtggccg tgtgtaaagt gctgcacctg	480
gaaggcgaag tgaacaagat caagtccgcc ctgctgtcca ccaacaaggc cgtggtgtcc	540
ctgagcaacg gcgtgagcgt gctgaccttc aagggtctgg atctgaagaa ctacatcgac	600
aagcagctgc tgcccatcct gaacaagcag agctgcagca tcagcaacat cgagacagtg	660
atcgagtcc agcagaagaa caaccggctg ctggaaatca cccgggagtt cagcgtgaac	720
gccggagtga ccacccccgt gtccacctac atgctgacca acagcgagct gctgtccctg	780
atcaatgaca tgcccatcac caacgaccag aaaaagctga tgagcaacaa cgtgcagatc	840
gtgcggcagc agagctactc catcatgtgc atcatcaaag aagaggtgct ggcctacgtg	900
gtgcagctgc ccctgtacgg cgtgatcgac acccctgct ggaagtgca caccagcccc	960
ctgtgcacaa ccaacaccaa agagggcagc aacatctgcc tgaccgggac cgaccggggc	1020
tggtactgcg acaacgccgg cagcgtgtcc ttctttccac aggccgagac atgcaaggtg	1080
cagagcaacc ggggtgtctg cgacacatg aacagcctga ccctgccctc cgaagtgaac	1140
ctgtgcaacg tggacatctt caacccaag tacgactgca agatcatgac ctccaagacc	1200
gacgtgtcca gtcctgat caccctcctg ggcgccatcg tgtcctgcta cggcaagacc	1260
aagtgacccg ccagcaacaa gaacagaggc atcatcaaga cttcagcaa cggctgcgac	1320

tacgtgtcca ataagggcgt ggacaccgtg tccgtgggca acacactgta ctacgtgaat 1380
aagcaggaag gcaagagcct gtacgtgaag ggcgagccca tcatcaactt ctacgacccc 1440
ctggtgttcc ccagcgacga gttcgacgcc agcatcagcc aggtgaacga gaagatcaac 1500
cagagcctgg ccttcatcag aaagagcgac gaactgctgt ccgccatcgg cggctacatc 1560
cccgaggccc ccagagatgg ccaggcctac gtgcggaagg acggcgagtg ggtgctgctg 1620
tctacatttc tgggaagcgg aggctctggt gcccatatcg tgatggtgga cgcctacaag 1680
cctaccaaag agcccgaggc ctaa 1704

<210> 54
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> RSV-F DS-Cav1

<220>
<221> misc_feature
<222> (1)..(75)
<223> Signal peptide

<220>
<221> misc_feature
<222> (1552)..(1632)
<223> Foldon domain

<400> 54
atggaactgc tgatcctgaa ggccaacgcc atcaccacca tctgaccgc cgtgaccttc 60
tgcttcgcca gcgccagaa catcaccgag gaattctacc agagcacctg cagcgccgtg 120
agcaagggtt acctgagcgc cctgcggacc ggctggtaca ccagcgtgat caccatcgag 180
ctgtccaaca tcaaagaaaa caagtgaac ggcaccgacg ccaaagtga gctgatcaag 240
caggaaactgg acaagtacaa gaacgccgtg accgagctgc agctgctgat gcagagcacc 300
cccgccacca acaacagagc cagaagagag ctgccccggt tcatgaacta caccctgaac 360
aacgccaaga aaaccaactg gaccctgagc aagaagagaa agagaagatt cctgggcttc 420
ctgctgggcg tgggcagcgc cattgccagc ggcgtggccg tgtgtaaagt gctgcacctg 480
gaaggcgaag tgaacaagat caagtcgcc ctgctgtcca ccaacaaggc cgtggtgtcc 540
ctgagcaacg gcgtgagcgt gctgaccttc aaggtgctgg atctgaagaa ctacatcgac 600

aagcagctgc tgcccatcct gaacaagcag agctgcagca tcagcaacat cgagacagtg 660
atcgagttcc agcagaagaa caaccggctg ctggaaatca cccgggagtt cagcgtgaac 720
gccggagtga ccacccccgt gtccacctac atgtgacca acagcgagct gctgtccctg 780
atcaatgaca tgcccatcac caacgaccag aaaaagctga tgagcaaaa cgtgcagatc 840
gtgcggcagc agagctactc catcatgtgc atcatcaaag aagagggtgct ggcctacgtg 900
gtgcagctgc ccctgtacgg cgtgatcgac accccctgct ggaagctgca caccagcccc 960
ctgtgcacaa ccaacaccaa agagggcagc aacatctgcc tgacccggac cgaccggggc 1020
tggtactgcg acaacgccgg cagcgtgtcc ttctttccac aggccgagac atgcaagtg 1080
cagagcaacc ggggtgttctg cgacacatg aacagcctga ccctgccctc cgaagtgaac 1140
ctgtgcaacg tggacatctt caacccaag tacgactgca agatcatgac ctccaagacc 1200
gacgtgtcca gtcctgtgat cacctccctg ggcgccatcg tgtcctgcta cggcaagacc 1260
aagtcaccg ccagcaaaa gaacagaggc atcatcaaga cttcagcaa cggctgcgac 1320
tacgtgtcca ataagggcgt ggacaccgtg tccgtgggca acacactgta ctacgtgaat 1380
aagcaggaag gcaagagcct gtacgtgaag ggcgagccca tcatcaactt ctacgacccc 1440
ctggtgttcc ccagcgacga gttcgacgcc agcatcagcc aggtgaacga gaagatcaac 1500
cagagcctgg cttcatcag aaagagcgac gaactgctgt ccgccatcgg cggctacatc 1560
cccaggcccc ccagagatgg ccaggcctac gtgcggaagg acggcgagtg ggtgctgctg 1620
tctacatttc tg 1632

<210> 55

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> RSV-F DS-Cav1 without the signal peptide

<220>

<221> misc_feature

<222> (1477)..(1557)

<223> Foldon domain

<400> 55

cagaacatca ccgaggaatt ctaccagagc acctgcagcg ccgtgagcaa gggctacctg 60

agcgccctgc ggaccggctg gtacaccagc gtgatcacca tcgagctgtc caacatcaaa 120

gaaaacaagt gcaacggcac cgacgcaaaa gtgaagctga tcaagcagga actggacaag 180
 tacaagaacg ccgtgaccga gctgcagctg ctgatgcaga gcacccccgc caccaacaac 240
 agagccagaa gagagctgcc ccggttcattg aactacaccc tgaacaacgc caagaaaacc 300
 aacgtgaccc tgagcaagaa gagaaagaga agattcctgg gcttcctgct gggcgtgggc 360
 agcgccattg ccagcggcgt ggccgtgtgt aaagtgtgc acctggaagg cgaagtgaac 420
 aagatcaagt ccgccctgct gtccaccaac aaggccgtgg tgtccctgag caacggcgtg 480
 agcgtgctga ctttaaggt gctggatctg aagaactaca tcgacaagca gctgctgccc 540
 atcctgaaca agcagagctg cagcatcagc aacatcgaga cagtgatcga gttccagcag 600
 aagaacaacc ggctgctgga aatcacccgg gagttcagcg tgaacgccgg agtgaccacc 660
 cccgtgtcca cctacatgct gaccaacagc gagctgctgt ccctgatcaa tgacatgccc 720
 atcaccaacg accagaaaaa gctgatgagc aacaacgtgc agatcgtgcg gcagcagagc 780
 tactccatca tgtgcatcat caaagaagag gtgctggcct acgtggtgca gctgccctg 840
 tacggcgtga tcgacacccc ctgctggaag ctgcacacca gcccctgtg cacaaccaac 900
 accaaagagg gcagcaacat ctgcctgacc cggaccgacc ggggctggta ctgcgacaac 960
 gccggcagcg tgtcttctt tccacaggcc gagacatgca aggtgcagag caaccgggtg 1020
 ttctgcgaca ccatgaacag cctgaccctg cctccgaag tgaacctgtg caacgtggac 1080
 atcttaacc ccaagtacga ctgcaagatc atgacctca agaccgacgt gtccagctcc 1140
 gtgatcacct cctggggcgc catcgtgtcc tgctacggca agaccaagtg caccgccagc 1200
 aacaagaaca gaggcatcat caagacctc agcaacggct gcgactacgt gtccaataag 1260
 ggcgtggaca ccgtgtccgt gggcaacaca ctgtactacg tgaataagca ggaaggcaag 1320
 agcctgtacg tgaagggcga gcccatcatc aactctacg accccctggg gttccccagc 1380
 gacgagttcg acgccagcat cagccagggtg aacgagaaga tcaaccagag cctggccttc 1440
 atcagaaaaga gcgacgaact gctgtccgcc atcggcggct acatccccga ggccccaga 1500
 gatggccagg cctacgtgcg gaaggacggc gagtgggtgc tgctgtctac atttctg 1557

<210> 56

<211> 567

<212> PRT

<213> Artificial Sequence

<220>
<223> RSV-F DS-Cav1-SpyTag-Ctag

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> Signal peptide

<220>
<221> MISC_FEATURE
<222> (518)..(544)
<223> Foldon domain

<220>
<221> MISC_FEATURE
<222> (545)..(550)
<223> Linker

<220>
<221> MISC_FEATURE
<222> (551)..(563)
<223> Spytag

<220>
<221> MISC_FEATURE
<222> (564)..(567)
<223> Ctag

<400> 56

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

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

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

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
165 170 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

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

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
245 250 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

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

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
530 535 540

Gly Ser Gly Gly Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys
545 550 555 560

Pro Thr Lys Glu Pro Glu Ala
565

<210> 57
<211> 544
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV-F DS-Cav1

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> Signal peptide

<220>
<221> MISC_FEATURE
<222> (518)..(544)
<223> Foldon domain

<400> 57

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

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

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

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
165 170 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

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

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
245 250 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

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

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
530 535 540

<210> 58
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV-F DS-Cav1 without the signal peptide

<220>
<221> MISC_FEATURE
<222> (493)..(519)
<223> Foldon domain

<400> 58

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

145 150 155 160

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
 165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
 180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
 195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
 210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

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

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
 260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
 275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
 290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
 325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser
 340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
 355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Lys Ser Asp Glu Leu Leu Ser Ala Ile Gly Gly Tyr Ile Pro
485 490 495

Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp
500 505 510

Val Leu Leu Ser Thr Phe Leu
515

<210> 59

<211> 2088

<212> DNA

<213> Artificial Sequence

<220>

<223> gH without the signal peptide

<220>

<221> misc_feature

<222> (1077)..(1077)

<223> C>A mutation at position 1077

<220>

<221> misc_feature

<222> (1)..(2082)
<223> Ectodomain

<220>
<221> misc_feature
<222> (2083)..(2088)
<223> Transmembrane domain (truncated)

<400> 59
cgatatggcg cagaagccgt atccgaaccg ctggacaaag cgtttcacct actgctcaac 60
acctacggga gacctatccg cttcctgcgt gaaaatacca cccagtgtac ctacaacagc 120
agcctccgta acagcacggg cgtcagggaa aacgccatca gtttcaactt ttccaaagc 180
tataatcaat actatgtatt ccatatgcct cgatgtcttt ttgcgggtcc tctggcggag 240
cagtttctga accaggtaga tctgaccgaa accctggaaa gataccaaca gagacttaac 300
acttacgcgc tggatatcaa agacctggcc agctaccgat cttttcgca gcagctaaag 360
gcacaagaca gcctaggtag acagcccacc actgtgccac cgcccattga cctgtcaata 420
cctcacgttt ggatgccacc gcaaaccact ccacacggct ggacagaatc acataccacc 480
tcaggactac accgaccaca cttaaccag acctgtatcc tctttgatgg acacgatcta 540
ctattcagca ccgtcacacc ttgttgcac caaggctttt acctcatcga cgaactacgt 600
tacgttaaaa taacactgac cgaggacttc ttcgtagtta cgggtgccat agacgacgac 660
acacccatgc tgcttatctt cgccatctt ccacgcgtac tttcaaagc gccctatcaa 720
cgcgacaact ttatactacg acaaactgaa aaacacgagc tcttgggtgct agttaagaaa 780
gatcaactga accgtcactc ttatctcaaa gaccgggact ttcttgacgc cgcacttgac 840
ttcaactacc tagacctcag cgcactacta cgtaacagct ttcaccgtta cgccgtggat 900
gtactcaaga gcggtcgatg tcagatgctg gaccgccgca cggtagaaat ggccttcgcc 960
tacgcattag cactgttcgc agcagcccga caagaagagg ccggcgccca agtctccgtc 1020
ccacggggccc tagaccgcca ggccgcactc ttacaaatac aagaatttat gatcacatgc 1080
cttcacaaa caccaccag caccacgttg ctgctgtatc ccacggccgt ggacctggcc 1140
aaacgagccc tttggacacc gaatcagatc accgacatca ccagcctcgt acgcctggtc 1200
tacatactct ctaaacagaa tcagcaacat ctcatcccc aatgggcact acgacagatc 1260
gccgactttg ccctaaaact acacaaaacg cacctggcct cttttcttc agccttcgca 1320
cgccaagaac tctacctcat gggcagcctc gtccactcca tgctgggtaca tacgacggag 1380

agacgcgaaa tcttcacgt agaaacgggc ctctgttcat tggccgagct atcacacttt 1440
 acgcagttgt tagtcatcc acaccagaa tacctcagcg acctgtacac accctgttcc 1500
 agtagcgggc gacgcgatca ctgctcgaa cgcctcacgc gtctcttccc cgatgccacc 1560
 gtccccgcta ccgttcccgc cgcctctcc atcctatcta ccatgcaacc aagcacgctg 1620
 gaaaccttc ccgacctgt ttgcttgccg ctggcggaat ccttctccgc gctgaccgtc 1680
 tccgaacacg tcagttatat cgtaacaaac cagtacctga tcaaaggat ctctaccct 1740
 gtctccacca ccgtcgtagg ccagagcctc atcatcacc agacggacag tcaaactaaa 1800
 tgcgaactga cgcgcaacat gcataccaca cacagcatca cagtggcgct caacatttcg 1860
 ctagaaaact gcgccttttg ccaaagcgcc ctgctagaat acgacgacac gcaaggcgtc 1920
 atcaacatca tgtacatgca cgactcggac gacgtcctt tcgccctgga tcctacaac 1980
 gaagtgggtg tctcatctcc gcgaactcac tacctcatgc ttttgaaaaa cggtagcgta 2040
 ctagaagtaa ctgacgtcgt cgtggacgcc accgacagtc gtctcctc 2088

<210> 60
 <211> 696
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gH without the signal peptide

<220>
 <221> MISC_FEATURE
 <222> (1)..(694)
 <223> Ectodomain

<220>
 <221> MISC_FEATURE
 <222> (694)..(696)
 <223> Transmembrane domain (truncated)

<400> 60

Arg Tyr Gly Ala Glu Ala Val Ser Glu Pro Leu Asp Lys Ala Phe His
 1 5 10 15

Leu Leu Leu Asn Thr Tyr Gly Arg Pro Ile Arg Phe Leu Arg Glu Asn
 20 25 30

Thr Thr Gln Cys Thr Tyr Asn Ser Ser Leu Arg Asn Ser Thr Val Val
35 40 45

Arg Glu Asn Ala Ile Ser Phe Asn Phe Phe Gln Ser Tyr Asn Gln Tyr
50 55 60

Tyr Val Phe His Met Pro Arg Cys Leu Phe Ala Gly Pro Leu Ala Glu
65 70 75 80

Gln Phe Leu Asn Gln Val Asp Leu Thr Glu Thr Leu Glu Arg Tyr Gln
85 90 95

Gln Arg Leu Asn Thr Tyr Ala Leu Val Ser Lys Asp Leu Ala Ser Tyr
100 105 110

Arg Ser Phe Ser Gln Gln Leu Lys Ala Gln Asp Ser Leu Gly Glu Gln
115 120 125

Pro Thr Thr Val Pro Pro Pro Ile Asp Leu Ser Ile Pro His Val Trp
130 135 140

Met Pro Pro Gln Thr Thr Pro His Gly Trp Thr Glu Ser His Thr Thr
145 150 155 160

Ser Gly Leu His Arg Pro His Phe Asn Gln Thr Cys Ile Leu Phe Asp
165 170 175

Gly His Asp Leu Leu Phe Ser Thr Val Thr Pro Cys Leu His Gln Gly
180 185 190

Phe Tyr Leu Ile Asp Glu Leu Arg Tyr Val Lys Ile Thr Leu Thr Glu
195 200 205

Asp Phe Phe Val Val Thr Val Ser Ile Asp Asp Asp Thr Pro Met Leu
210 215 220

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

Arg Asp Asn Phe Ile Leu Arg Gln Thr Glu Lys His Glu Leu Leu Val
245 250 255

Leu Val Lys Lys Asp Gln Leu Asn Arg His Ser Tyr Leu Lys Asp Pro
260 265 270

Asp Phe Leu Asp Ala Ala Leu Asp Phe Asn Tyr Leu Asp Leu Ser Ala
275 280 285

Leu Leu Arg Asn Ser Phe His Arg Tyr Ala Val Asp Val Leu Lys Ser
290 295 300

Gly Arg Cys Gln Met Leu Asp Arg Arg Thr Val Glu Met Ala Phe Ala
305 310 315 320

Tyr Ala Leu Ala Leu Phe Ala Ala Ala Arg Gln Glu Glu Ala Gly Ala
325 330 335

Gln Val Ser Val Pro Arg Ala Leu Asp Arg Gln Ala Ala Leu Leu Gln
340 345 350

Ile Gln Glu Phe Met Ile Thr Cys Leu Ser Gln Thr Pro Pro Arg Thr
355 360 365

Thr Leu Leu Leu Tyr Pro Thr Ala Val Asp Leu Ala Lys Arg Ala Leu
370 375 380

Trp Thr Pro Asn Gln Ile Thr Asp Ile Thr Ser Leu Val Arg Leu Val
385 390 395 400

Tyr Ile Leu Ser Lys Gln Asn Gln Gln His Leu Ile Pro Gln Trp Ala
405 410 415

Leu Arg Gln Ile Ala Asp Phe Ala Leu Lys Leu His Lys Thr His Leu
420 425 430

Ala Ser Phe Leu Ser Ala Phe Ala Arg Gln Glu Leu Tyr Leu Met Gly
435 440 445

Ser Leu Val His Ser Met Leu Val His Thr Thr Glu Arg Arg Glu Ile
450 455 460

Phe Ile Val Glu Thr Gly Leu Cys Ser Leu Ala Glu Leu Ser His Phe
465 470 475 480

Thr Gln Leu Leu Ala His Pro His His Glu Tyr Leu Ser Asp Leu Tyr
485 490 495

Thr Pro Cys Ser Ser Ser Gly Arg Arg Asp His Ser Leu Glu Arg Leu
500 505 510

Thr Arg Leu Phe Pro Asp Ala Thr Val Pro Ala Thr Val Pro Ala Ala
515 520 525

Leu Ser Ile Leu Ser Thr Met Gln Pro Ser Thr Leu Glu Thr Phe Pro
530 535 540

Asp Leu Phe Cys Leu Pro Leu Gly Glu Ser Phe Ser Ala Leu Thr Val
545 550 555 560

Ser Glu His Val Ser Tyr Ile Val Thr Asn Gln Tyr Leu Ile Lys Gly
565 570 575

Ile Ser Tyr Pro Val Ser Thr Thr Val Val Gly Gln Ser Leu Ile Ile
580 585 590

Thr Gln Thr Asp Ser Gln Thr Lys Cys Glu Leu Thr Arg Asn Met His
595 600 605

Thr Thr His Ser Ile Thr Val Ala Leu Asn Ile Ser Leu Glu Asn Cys
610 615 620

Ala Phe Cys Gln Ser Ala Leu Leu Glu Tyr Asp Asp Thr Gln Gly Val
625 630 635 640

Ile Asn Ile Met Tyr Met His Asp Ser Asp Asp Val Leu Phe Ala Leu
645 650 655

Asp Pro Tyr Asn Glu Val Val Val Ser Ser Pro Arg Thr His Tyr Leu
660 665 670

Met Leu Leu Lys Asn Gly Thr Val Leu Glu Val Thr Asp Val Val Val
675 680 685

Asp Ala Thr Asp Ser Arg Leu Leu

690

695