

eolf-seq1
SEQUENCE LISTING

<110> ECOLE POLYTECHNIQUE FEDERALE DE LAUSANNE (EPFL)

<120> ENGINEERED ANTIGEN PRESENTING CELLS AND USES THEREOF

<130> P1995PC00

<150> EP16153966.3

<151> 2016-02-02

<160> 136

<170> PatentIn version 3.3

<210> 1

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of anti-HER2 scFv CHA21

<400> 1

ggggatattg tcctcacaca gactcccagc tccctgcctg tgtccgtcgg agagaaagtg	60
accatgacat gcaagtctag tcagacactg ctctactcta acaatcagaa gaactacctc	120
gcatggtatc agcagaaacc aggacagagc cccaagctgc tcatctcctg ggctttcacc	180
cggaaatccg ggggtgcctga ccgcttcaca ggtagcggct ccggaactga ttttactctg	240
accattggat ctgtgaaggc agaggacctc gccgtctact attgccagca gtacagtaat	300
tatccatgga cttttggcgg agggaccagg ctggaaatca agagaggtgg aggaggggtcc	360
ggtaggaggag ggtctgggtg aggagggagt ggtggaggag ggtcagaggt gcagctgcag	420
cagtctggcc ccgaagtggc caaaactgga gcttcagtca aaatcagctg taaggcatct	480
gggtacagct tcaccggcta cttcatcaac tgggtgaaga aaaattcagg gaagagccct	540
gagtggatcg gccacatttc aagctcctac gccacaagca cttacaacca gaagttcaaa	600
aataaggccg cttttaccgt ggacacatct agttcaaccg ctttcatgca gctgaactcc	660
ctcacatctg aagatagtcg tgtgtactat tgtgtcagga gcggcaacta cgaagaatat	720

eolf-seql
gctatggatt actgggggca ggggacctcc gtgactgtct caagc 765

<210> 2
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of IgK domain

<400> 2
atggattttc aggtccagat tttctccttc ctctcattt cagccagcgt cattatgtct 60
cgg 63

<210> 3
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of S5_BamHI_Kozak

<400> 3
ggatccgcca cc 12

<210> 4
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of S3_BamHI_AgeI_MluI_SalI_stop_XhoI

<400> 4
accggtacgc gtgtcgactg actcgag 27

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of S5_FCgRIIIa_BamHI_Kozak.start_AgeI

eolf-seql

<400> 5
ggatccgcca ccatgaccgg t 21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of S3_FCgRIIIa_MluI_SalI_stop_XhoI

<400> 6
acgcgtgtcg actgactcga g 21

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of dLNGFR_Fw_AgeI

<400> 7
aaaaaacggg tcttctgggg gtgtcccttg 30

<210> 8
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of dLNGFR_Rv_MluI

<400> 8
aaaaaacgcg tagttagcct ccccatctc c 31

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of FLT3_Fw_AgeI

eolf-seql

<400> 9
aaaaaacggg tccaggcccc ttccctttca tc 32

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of FLT3_Rv_XhoI

<400> 10
aaaaactcga gagaggcgag gctaattcttg g 31

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Tlr4_Fw_AgeI

<400> 11
aaaaaacggg tcagctgtat tccctcagca ct 32

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Tlr4_Rv_SalI

<400> 12
aaaaagtcga ctgggttttag gccccagagt t 31

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Ccr2_Fw_AgeI

eolf-seql

<400> 13
aaaaaacgg tatggaagac aataatatgt tacctc 36

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Ccr2_Rv_MluI

<400> 14
aaaaaacgcg tatgtacaaa ctgctccctc c 31

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Itgb2_Fw_AgeI

<400> 15
aaaaaacgg taatgcacgg ctggtagagt g 31

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Itgb2_Rv_MluI

<400> 16
aaaaaacgcg tgggggtcac atctgcttga t 31

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Csf2rb_Fw_AgeI

eolf-seql

<400> 17
aaaaaacgg tactcagaag atggcttact cattca 36

<210> 18
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Csf2rb_Rv_MluI

<400> 18
aaaaaacgcg ttggtgagat tgggaggaga c 31

<210> 19
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Ccr1_Fw_AgeI

<400> 19
aaaaaacgg tactccatgc caaaagactg ct 32

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Ccr1_Rv_MluI

<400> 20
aaaaaacgcg taccttcctt ggttgacacc tatg 34

<210> 21
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Ccr5_Fw_AgeI

eolf-seq1

<400> 21
 aaaaaaccgg tatgtcagca ccctgccaaa aa 32

<210> 22
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of Ccr5_Rv_MluI

<400> 22
 aaaaaacgcg tcattcctac tccaagctg cat 33

<210> 23
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of Cxcr4_Fw_XmaI

<400> 23
 aaaaacccgg gttccgggat gaaaacgtcc a 31

<210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of Cxcr4_Rv_MluI

<400> 24
 aaaaaacgcg ttgcataagt gtagctgga gtg 33

<210> 25
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of Selplg_Fw_AgeI

eolf-seql

<400> 25
aaaaaacggg tattgccacc actgacccta 30

<210> 26
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of Selp1g_Rv_MluI

<400> 26
aaaaaacgcg tgcaaaggctc tcgcttaggt g 31

<210> 27
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of anti-HER2 CHA21

<400> 27

Asp Ile Val Leu Thr Gln Thr Pro Ser Ser Leu Pro Val Ser Val Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Thr Leu Leu Tyr Ser
20 25 30

Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe Thr Arg Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Gly Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln

eolf-seql

85

90

95

Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
130 135 140

Val Val Lys Thr Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
145 150 155 160

Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp Val Lys Lys Asn Ser Gly
165 170 175

Lys Ser Pro Glu Trp Ile Gly His Ile Ser Ser Ser Tyr Ala Thr Ser
180 185 190

Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala Ala Phe Thr Val Asp Thr
195 200 205

Ser Ser Ser Thr Ala Phe Met Gln Leu Asn Ser Leu Thr Ser Glu Asp
210 215 220

Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly Asn Tyr Glu Glu Tyr Ala
225 230 235 240

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
245 250

<210> 28

<211> 250

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Amino acid sequence of anti-HER2 trastuzumab-based scFv

<220>

<221> misc_feature

<222> (250)..(250)

<223> Xaa can be any naturally occurring amino acid

<400> 28

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Ser Thr
100 105 110

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp

eolf-seql

145	150	155	160
Val Arg Gln Ala	Pro Gly Lys Gly Leu	Glu Trp Val Ala Arg	Ile Tyr
	165	170	175
Pro Thr Asn Gly Tyr Thr Arg Tyr	Ala Asp Ser Val Lys Gly	Arg Phe	
	180	185	190
Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr	Leu Gln Met Asn		
	195	200	205
Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	Ser Arg Trp Gly		
	210	215	220
Gly Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val			
225	230	235	240
Thr Val Ser Ser Gly Thr Gly Thr Arg Xaa			
	245	250	

<210> 29
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of anti-HER2 pertuzumab-based scFv

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly			
1	5	10	15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ile Gly			
20	25	30	
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile			
35	40	45	

eolf-seql

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 130 135 140
 Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 145 150 155 160
 Thr Phe Thr Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys
 165 170 175
 Gly Leu Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile
 180 185 190
 Tyr Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser
 195 200 205
 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 210 215 220
 Ala Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp
 225 230 235 240

eolf-seql

Tyr Trp

<210> 30
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of anti-HER2 FRP5-based scFv

<220>
 <221> misc_feature
 <222> (243)..(243)
 <223> Xaa can be any naturally occurring amino acid

<400> 30

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu
1			5					10						15	

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

Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Lys	Trp	Met
	35					40						45			

Gly	Trp	Ile	Asn	Thr	Ser	Thr	Gly	Glu	Ser	Thr	Phe	Ala	Asp	Asp	Phe
50					55						60				

Lys	Gly	Arg	Phe	Asp	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Asn	Thr	Ala	Tyr
65				70					75					80	

Leu	Gln	Ile	Asn	Asn	Leu	Lys	Ser	Glu	Asp	Met	Ala	Thr	Tyr	Phe	Cys
			85					90						95	

Ala	Arg	Trp	Glu	Val	Tyr	His	Gly	Tyr	Val	Pro	Tyr	Trp	Gly	Gln	Gly
			100				105						110		

eolf-seql

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe
130 135 140

Leu Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Asp Val Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val
180 185 190

Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr
195 200 205

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
210 215 220

His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg Xaa

<210> 31

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of proteinic domain derived from dLNGFR

<400> 31

Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly

eolf-seql

1	5	10	15
Leu Tyr Thr	His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu		
	20	25	30
Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys			
	35	40	45
Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys			
	50	55	60
Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys			
	65	70	75
Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln			
	85	90	95
Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly			
	100	105	110
Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu			
	115	120	125
Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro			
	130	135	140
Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu			
	145	150	155
Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp			
	165	170	175
Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser			
	180	185	190
Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr			

eolf-seql

195

200

205

Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val
210 215 220

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

Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg Trp
245 250 255

Asn Arg Gly Ile Leu
260

<210> 32
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of proteinic domain derived from FcgRIIIA

<400> 32

His Glu Asn Ser Glu Leu Leu Ile Pro Lys Ala Thr His Asn Asp Ser
1 5 10 15

Gly Ser Tyr Phe Cys Arg Gly Leu Ile Gly His Asn Asn Lys Ser Ser
20 25 30

Ala Ser Phe Arg Ile Ser Leu Gly Asp Pro Gly Ser Pro Ser Met Phe
35 40 45

Pro Pro Trp His Gln Ile Thr Phe Cys Leu Leu Ile Gly Leu Leu Phe
50 55 60

Ala Ile Asp Thr Val Leu Tyr Phe Ser Val Arg Arg Gly Leu Gln Ser
65 70 75 80

eolf-seql

Pro Val Ala Asp Tyr Glu Glu Pro Lys Ile Gln Trp Ser Lys Glu Pro
85 90 95

Gln Asp Lys Thr Arg Val Asp
100

<210> 33

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of proteinic domain derived from FLT3

<400> 33

Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Phe Tyr Ala Thr
1 5 10 15

Ile Gly Leu Cys Leu Pro Phe Ile Val Val Leu Ile Val Leu Ile Cys
20 25 30

His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Ile
35 40 45

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

Asp Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu
65 70 75 80

Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Arg Val Met Asn Ala
85 90 95

Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val
100 105 110

Lys Met Leu Lys Glu Lys Ala Asp Ser Cys Glu Lys Glu Ala Leu Met

eolf-seql

115

120

125

Ser Glu Leu Lys Met Met Thr His Leu Gly His His Asp Asn Ile Val
130 135 140

Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Val Tyr Leu Ile Phe
145 150 155 160

Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu Arg Ser Lys Arg
165 170 175

Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu His Asn Phe
180 185 190

Ser Phe Tyr Pro Thr Phe Gln Ala His Ser Asn Ser Ser Met Pro Gly
195 200 205

Ser Arg Glu Val Gln Leu His Pro Pro Leu Asp Gln Leu Ser Gly Phe
210 215 220

Asn Gly Asn Leu Ile His Ser Glu Asp Glu Ile Glu Tyr Glu Asn Gln
225 230 235 240

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

Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu Phe
260 265 270

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

Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu Ala
290 295 300

Arg Asp Ile Leu Ser Asp Ser Ser Tyr Val Val Arg Gly Asn Ala Arg

eolf-seql

<220>

<223> Amino acid sequence of proteinic domain derived from TLR4

<400> 34

Gln Leu Tyr Ser Leu Ser Thr Leu Asp Cys Ser Phe Asn Arg Ile Glu
1 5 10 15

Thr Ser Lys Gly Ile Leu Gln His Phe Pro Lys Ser Leu Ala Phe Phe
20 25 30

Asn Leu Thr Asn Asn Ser Val Ala Cys Ile Cys Glu His Gln Lys Phe
35 40 45

Leu Gln Trp Val Lys Glu Gln Lys Gln Phe Leu Val Asn Val Glu Gln
50 55 60

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

Phe Asn Asn Ser Thr Cys Tyr Met Tyr Lys Thr Ile Ile Ser Val Ser
85 90 95

Val Val Ser Val Ile Val Val Ser Thr Val Ala Phe Leu Ile Tyr His
100 105 110

Phe Tyr Phe His Leu Ile Leu Ile Ala Gly Cys Lys Lys Tyr Ser Arg
115 120 125

Gly Glu Ser Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asn Glu
130 135 140

Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro
145 150 155 160

Arg Phe His Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala
165 170 175

eolf-seql

Ile Ala Ala Asn Ile Ile Gln Glu Gly Phe His Lys Ser Arg Lys Val
180 185 190

Ile Val Val Val Ser Arg His Phe Ile Gln Ser Arg Trp Cys Ile Phe
195 200 205

Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ser Gly
210 215 220

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

Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp
245 250 255

Glu Asp Asn Pro Leu Gly Arg His Ile Phe Trp Arg Arg Leu Lys Asn
260 265 270

Ala Leu Leu Asp Gly Lys Ala Ser Asn Pro Glu Gln Thr Ala Glu Glu
275 280 285

Glu Gln Glu Thr Ala Thr Trp Thr
290 295

<210> 35
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of proteinic domain derived from CCR2

<400> 35

Met Glu Asp Asn Asn Met Leu Pro Gln Phe Ile His Gly Ile Leu Ser
1 5 10 15

Thr Ser His Ser Leu Phe Thr Arg Ser Ile Gln Glu Leu Asp Glu Gly

eolf-seql

20

25

30

Ala Thr Thr Pro Tyr Asp Tyr Asp Asp Gly Glu Pro Cys His Lys Thr
35 40 45

Ser Val Lys Gln Ile Gly Ala Trp Ile Leu Pro Pro Leu Tyr Ser Leu
50 55 60

Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Ile Ile Leu
65 70 75 80

Ile Gly Cys Lys Lys Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn
85 90 95

Leu Ala Ile Ser Asp Leu Leu Phe Leu Leu Thr Leu Pro Phe Trp Ala
100 105 110

His Tyr Ala Ala Asn Glu Trp Val Phe Gly Asn Ile Met Cys Lys Val
115 120 125

Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile
130 135 140

Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
145 150 155 160

Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Ile Thr Ser Val Val
165 170 175

Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr
180 185 190

Lys Ser Lys Gln Asp Asp His His Tyr Thr Cys Gly Pro Tyr Phe Thr
195 200 205

Gln Leu Trp Lys Asn Phe Gln Thr Ile Met Arg Asn Ile Leu Ser Leu

eolf-seql

210

215

220

Ile Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu His
225 230 235 240

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

Leu Ile Phe Ala Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr
260 265 270

Asn Ile Val Leu Phe Leu Thr Thr Phe Gln Glu Ser Leu Gly Met Ser
275 280 285

Asn Cys Val Ile Asp Lys His Leu Asp Gln Ala Met Gln Val Thr Glu
290 295 300

Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Val Ile Tyr Ala Phe
305 310 315 320

Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Ile Phe Phe Arg Lys His
325 330 335

Ile Ala Lys Arg Leu Cys Lys Gln Cys Pro Val Phe Tyr Arg Glu Thr
340 345 350

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

Val Ser Val Gly Leu
370

<210> 36

<211> 187

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Amino acid sequence of proteinic domain derived from ITGB2

<400> 36

Asn	Ala	Arg	Leu	Val	Glu	Cys	Ser	Gly	Arg	Gly	His	Cys	Gln	Cys	Asn
1				5					10				15		

Arg	Cys	Ile	Cys	Asp	Glu	Gly	Tyr	Gln	Pro	Pro	Met	Cys	Glu	Asp	Cys
			20					25					30		

Pro	Ser	Cys	Gly	Ser	His	Cys	Arg	Asp	Asn	His	Thr	Ser	Cys	Ala	Glu
		35					40					45			

Cys	Leu	Lys	Phe	Asp	Lys	Gly	Pro	Phe	Glu	Lys	Asn	Cys	Ser	Val	Gln
	50					55					60				

Cys	Ala	Gly	Met	Thr	Leu	Gln	Thr	Ile	Pro	Leu	Lys	Lys	Lys	Pro	Cys
65					70					75					80

Lys	Glu	Arg	Asp	Ser	Glu	Gly	Cys	Trp	Ile	Thr	Tyr	Thr	Leu	Gln	Gln
				85					90					95	

Lys	Asp	Gly	Arg	Asn	Ile	Tyr	Asn	Ile	His	Val	Glu	Asp	Ser	Leu	Glu
			100					105					110		

Cys	Val	Lys	Gly	Pro	Asn	Val	Ala	Ala	Ile	Val	Gly	Gly	Thr	Val	Val
		115					120					125			

Gly	Val	Val	Leu	Ile	Gly	Val	Leu	Leu	Leu	Val	Ile	Trp	Lys	Ala	Leu
	130					135					140				

Thr	His	Leu	Thr	Asp	Leu	Arg	Glu	Tyr	Arg	Arg	Phe	Glu	Lys	Glu	Lys
145					150					155					160

Leu	Lys	Ser	Gln	Trp	Asn	Asn	Asp	Asn	Pro	Leu	Phe	Lys	Ser	Ala	Thr
				165					170					175	

eolf-seql

Thr Thr Val Met Asn Pro Lys Phe Ala Glu Ser
180 185

<210> 37

<211> 533

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of proteinic domain derived from CSF2RB

<400> 37

Thr Gln Lys Met Ala Tyr Ser Phe Ile Glu His Thr Phe Gln Val Gln
1 5 10 15

Tyr Lys Lys Lys Ser Asp Ser Trp Glu Asp Ser Lys Thr Glu Asn Leu
20 25 30

Asp Arg Ala His Ser Met Asp Leu Ser Gln Leu Glu Pro Asp Thr Ser
35 40 45

Tyr Cys Ala Arg Val Arg Val Lys Pro Ile Ser Asn Tyr Asp Gly Ile
50 55 60

Trp Ser Lys Trp Ser Glu Glu Tyr Thr Trp Lys Thr Asp Trp Val Met
65 70 75 80

Pro Thr Leu Trp Ile Val Leu Ile Leu Val Phe Leu Ile Leu Thr Leu
85 90 95

Leu Leu Ile Leu Arg Phe Gly Cys Val Ser Val Tyr Arg Thr Tyr Arg
100 105 110

Lys Trp Lys Glu Lys Ile Pro Asn Pro Ser Lys Ser Leu Leu Phe Gln
115 120 125

Asp Gly Gly Lys Gly Leu Trp Pro Pro Gly Ser Met Ala Ala Phe Ala

eolf-seql

130

135

140

Thr Lys Asn Pro Ala Leu Gln Gly Pro Gln Ser Arg Leu Leu Ala Glu
145 150 155 160

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

Leu Thr Ile Glu Asp Pro Asn Ile Ile Arg Val Pro Pro Ser Gly Pro
180 185 190

Asp Thr Thr Pro Ala Ala Ser Ser Glu Ser Thr Glu Gln Leu Pro Asn
195 200 205

Val Gln Val Glu Gly Pro Thr Pro Asn Arg Pro Arg Lys Gln Leu Pro
210 215 220

Ser Phe Asp Phe Asn Gly Pro Tyr Leu Gly Pro Pro Gln Ser His Ser
225 230 235 240

Leu Pro Asp Leu Pro Asp Gln Leu Gly Ser Pro Gln Val Gly Gly Ser
245 250 255

Leu Lys Pro Ala Leu Pro Gly Ser Leu Glu Tyr Met Cys Leu Pro Pro
260 265 270

Gly Gly Gln Ala Gln Leu Val Pro Leu Ser Gln Val Met Gly Gln Gly
275 280 285

Gln Ala Met Asp Val Gln Cys Gly Ser Ser Leu Glu Thr Ser Gly Ser
290 295 300

Pro Ser Val Glu Pro Lys Glu Asn Pro Pro Val Glu Leu Ser Met Glu
305 310 315 320

Glu Gln Glu Ala Arg Asp Asn Pro Val Thr Leu Pro Ile Ser Ser Gly

eof-seq1

325

330

335

Gly Pro Glu Gly Ser Met Met Ala Ser Asp Tyr Val Thr Pro Gly Asp
340 345 350

Pro Val Leu Thr Leu Pro Thr Gly Pro Leu Ser Thr Ser Leu Gly Pro
355 360 365

Ser Leu Gly Leu Pro Ser Ala Gln Ser Pro Arg Leu Cys Leu Lys Leu
370 375 380

Pro Arg Val Pro Ser Gly Ser Pro Ala Leu Gly Pro Pro Gly Phe Glu
385 390 395 400

Asp Tyr Val Glu Leu Pro Pro Ser Val Ser Gln Ala Ala Lys Ser Pro
405 410 415

Pro Gly His Pro Ala Pro Pro Val Ala Ser Ser Pro Thr Val Ile Pro
420 425 430

Gly Glu Pro Arg Glu Glu Val Gly Pro Ala Ser Pro His Pro Glu Gly
435 440 445

Leu Leu Val Leu Gln Gln Val Gly Asp Tyr Cys Phe Leu Pro Gly Leu
450 455 460

Gly Pro Gly Ser Leu Ser Pro His Ser Lys Pro Pro Ser Pro Ser Leu
465 470 475 480

Cys Ser Glu Thr Glu Asp Leu Val Gln Asp Leu Ser Val Lys Lys Phe
485 490 495

Pro Tyr Gln Pro Met Pro Gln Ala Pro Ala Ile Gln Phe Phe Lys Ser
500 505 510

Leu Lys His Gln Asp Tyr Leu Ser Leu Pro Pro Trp Asp Asn Ser Gln

eolf-seql

515

520

525

Ser Gly Lys Val Cys
530

<210> 38

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of proteinic domain derived from CCR1

<400> 38

Thr Pro Cys Gln Lys Thr Ala Val Arg Ala Phe Gly Ala Gly Leu Leu
1 5 10 15

Pro Pro Leu Tyr Ser Leu Val Phe Ile Ile Gly Val Val Gly Asn Val
20 25 30

Leu Val Ile Leu Val Leu Met Gln His Arg Arg Leu Gln Ser Met Thr
35 40 45

Ser Ile Tyr Leu Phe Asn Leu Ala Val Ser Asp Leu Val Phe Leu Phe
50 55 60

Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys Asp Asp Trp Ile Phe
65 70 75 80

Gly Asp Ala Met Cys Lys Leu Leu Ser Gly Phe Tyr Tyr Leu Gly Leu
85 90 95

Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
100 105 110

Ala Ile Val His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr Phe
115 120 125

eolf-seql

Gly Ile Ile Thr Ser Ile Ile Thr Trp Ala Leu Ala Ile Leu Ala Ser
130 135 140

Met Pro Ala Leu Tyr Phe Phe Lys Ala Gln Trp Glu Phe Thr His Arg
145 150 155 160

Thr Cys Ser Pro His Phe Pro Tyr Lys Ser Leu Lys Gln Trp Lys Arg
165 170 175

Phe Gln Ala Leu Lys Leu Asn Leu Leu Gly Leu Ile Leu Pro Leu Leu
180 185 190

Val Met Ile Ile Cys Tyr Ala Gly Ile Ile Arg Ile Leu Leu Arg Arg
195 200 205

Pro Ser Glu Lys Lys Val Lys Ala Val Arg Leu Ile Phe Ala Ile Thr
210 215 220

Leu Leu Phe Phe Leu Leu Trp Thr Pro Tyr Asn Leu Ser Val Phe Val
225 230 235 240

Ser Ala Phe Gln Asp Val Leu Phe Thr Asn Gln Cys Glu Gln Ser Lys
245 250 255

Gln Leu Asp Leu Ala Met Gln Val Thr Glu Val Ile Ala Tyr Thr His
260 265 270

Cys Cys Val Asn Pro Ile Ile Tyr Val Phe Val Gly Glu Arg Phe Trp
275 280 285

Lys Tyr Leu Arg Gln Leu Phe Gln Arg His Val Ala Ile Pro Leu Ala
290 295 300

Lys Trp Leu Pro Phe Leu Ser Val Asp Gln Leu Glu Arg Thr Ser Ser
305 310 315 320

eolf-seql

Ile Ser Pro Ser Thr Gly Glu His Glu Leu Ser Ala Gly Phe
 325 330

<210> 39

<211> 337

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of proteinic domain derived from CCR5

<400> 39

Met Ser Ala Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Gln
 1 5 10 15

Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly
 20 25 30

Asn Met Met Val Phe Leu Ile Leu Ile Ser Cys Lys Lys Leu Lys Ser
 35 40 45

Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe
 50 55 60

Leu Leu Thr Leu Pro Phe Trp Ala His Tyr Ala Ala Asn Glu Trp Val
 65 70 75 80

Phe Gly Asn Ile Met Cys Lys Val Phe Thr Gly Leu Tyr His Ile Gly
 85 90 95

Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr
 100 105 110

Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Val Arg Thr Val Asn
 115 120 125

Phe Gly Val Ile Thr Ser Val Val Thr Trp Ala Val Ala Val Phe Ala

eolf-seql

130

135

140

Ser Leu Pro Glu Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Phe His
145 150 155 160

Tyr Thr Cys Ser Pro His Phe Pro His Thr Gln Tyr His Phe Trp Lys
165 170 175

Ser Phe Gln Thr Leu Lys Met Val Ile Leu Ser Leu Ile Leu Pro Leu
180 185 190

Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu His Thr Leu Phe Arg
195 200 205

Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Ala
210 215 220

Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Leu
225 230 235 240

Leu Leu Thr Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser
245 250 255

Ser Asn Arg Leu Asp Gln Ala Met Gln Ala Thr Glu Thr Leu Gly Met
260 265 270

Thr His Cys Cys Leu Asn Pro Val Ile Tyr Ala Phe Val Gly Glu Lys
275 280 285

Phe Arg Ser Tyr Leu Ser Val Phe Phe Arg Lys His Ile Val Lys Arg
290 295 300

Phe Cys Lys Arg Cys Ser Ile Phe Gln Gln Asp Asn Pro Asp Arg Ala
305 310 315 320

Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu His Glu Val Ser Thr Gly

325 eolf-seql 330 335

Leu

<210> 40
 <211> 329
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of proteinic domain derived from CXCR4
 <400> 40

Phe Arg Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile
 1 5 10 15

Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
 20 25 30

Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr
 35 40 45

Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro
 50 55 60

Phe Trp Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu
 65 70 75 80

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

Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His
 100 105 110

Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val
 115 120 125

eolf-seql

Tyr Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe
130 135 140

Ile Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg
145 150 155 160

Tyr Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe
165 170 175

Gln Phe Gln His Ile Met Val Gly Leu Val Leu Pro Gly Ile Val Ile
180 185 190

Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly
195 200 205

His Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala
210 215 220

Phe Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser
225 230 235 240

Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile
245 250 255

Val His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys
260 265 270

Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser
275 280 285

Ser Ala Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys
290 295 300

Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu
305 310 315 320

eolf-seql

Ser Glu Ser Ser Ser Phe His Ser Ser
325

<210> 41

<211> 297

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of proteinic domain derived from SELPLG

<400> 41

Ile Ala Thr Thr Asp Pro Thr Ala Pro Gly Thr Gly Gly Thr Ala Val
1 5 10 15

Gly Met Leu Ser Thr Asp Ser Ala Thr Gln Trp Ser Leu Thr Ser Val
20 25 30

Glu Thr Val Gln Pro Ala Ser Thr Glu Val Glu Thr Ser Gln Pro Ala
35 40 45

Pro Met Glu Ala Glu Thr Ser Gln Pro Ala Pro Met Glu Ala Glu Thr
50 55 60

Ser Gln Pro Ala Pro Met Glu Ala Asp Thr Ser Lys Pro Ala Pro Thr
65 70 75 80

Glu Ala Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala Glu Thr Ser Gln
85 90 95

Pro Ala Pro Asn Glu Ala Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala
100 105 110

Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala Glu Thr Thr Gln Leu Pro
115 120 125

Arg Ile Gln Ala Val Lys Thr Leu Phe Thr Thr Ser Ala Ala Thr Glu

eolf-seql

130

135

140

Val Pro Ser Thr Glu Pro Thr Thr Met Glu Thr Ala Ser Thr Glu Ser
145 150 155 160

Asn Glu Ser Thr Ile Phe Leu Gly Pro Ser Val Thr His Leu Pro Asp
165 170 175

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

Pro Thr Leu Pro Gly Ser Ser Asp Leu Ile Pro Val Lys Gln Cys Leu
195 200 205

Leu Ile Ile Leu Ile Leu Ala Ser Leu Ala Thr Ile Phe Leu Val Cys
210 215 220

Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Thr His Met Tyr Pro
225 230 235 240

Val Arg Asn Tyr Ser Pro Thr Glu Met Ile Cys Ile Ser Ser Leu Leu
245 250 255

Pro Glu Gly Gly Asp Gly Ala Pro Val Thr Ala Asn Gly Gly Leu Pro
260 265 270

Lys Val Gln Asp Leu Lys Thr Glu Pro Ser Gly Asp Arg Asp Gly Asp
275 280 285

Asp Leu Thr Leu His Ser Phe Leu Pro
290 295

<210> 42

<211> 22

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Amino acid sequence of IgK domain

<400> 42

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly
20

<210> 43

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from dLNGFR

<400> 43

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cttctggggg tgtcccttgg aggtgccaag gaggcatgcc ccacaggcct gtacacacac      60
agcgggtgagt gctgcaaagc ctgcaacctg ggcgagggtg tggcccagcc ttgtggagcc    120
aaccagaccg tgtgtgagcc ctgcctggac agcgtgacgt tctccgacgt ggtgagcgcg      180
accgagccgt gcaagccgtg caccgagtgc gtggggctcc agagcatgtc ggcgccgtgc      240
gtggaggccg acgacgccgt gtgccgtgc gcctacggct actaccagga tgagacgact      300
gggcgctgcg aggcgtgccg cgtgtgagag gcgggctcgg gcctcgtgtt ctcctgccag      360
gacaagcaga acaccgtgtg cgaggagtgc cccgacggca cgtattccga cgaggccaac      420
cacgtggacc cgtgcctgcc ctgcaccgtg tgcgaggaca ccgagcgcca gctccgcgag      480
tgcacacgct gggccgacgc cgagtgcgag gagatccctg gccgttggat tacacgggtcc      540
acacccccag agggctcgga cagcacagcc cccagcacc aggagcctga ggcacctcca      600
gaacaagacc tcatagccag cacggtggca ggtgtggtga ccacagtgat gggcagctcc      660
cagcccgtgg tgacccgagg caccaccgac aacctcatcc ctgtctattg ctccatcctg      720
gctgctgtgg ttgtgggcct tgtggcctac atagccttca agaggtggaa cagggggatc      780
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ctctag

786

<210> 44

<211> 312

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from FcgRIIIA

<400> 44

cacgagaact ccgaactgct gattcctaag gcaactcaca acgactccgg ctctattttc 60

tgtagagggc tgattggaca taacaacaag agctccgcct cattcaggat tagcctgggc 120

gacccagggt ctcccagtat gttccccct tggcaccaga tcaccttttg cctgctgatt 180

ggactgctgt tcgctatcga tacagtgtg tacttttctg tccggagagg cctgcagtca 240

cccgtggcag attacgaaga acccaagatt cagtggagca aggagcccca ggataagacg 300

cgtgtcgact ga 312

<210> 45

<211> 1407

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from FLT3

<400> 45

ccaggcccct tccctttcat ccaagacaac atctccttct atgcgaccat tgggctctgt 60

ctcccccttca ttgttgttct cattgtgttg atctgccaca aatacaaaaa gcaatttagg 120

tacgagagtc agctgcagat gatccagggtg actggccccc tggataacga gtacttctac 180

gttgacttca gggactatga atatgacctt aagtgggagt tcccagagaga gaacttagag 240

tttgggaagg tcctggggtc tggcgctttc gggagggtga tgaacgccac ggcctatggc 300

attagtaaaa cgggagtctc aattcagggtg gcggtgaaga tgctaaaaga gaaagctgac 360

agctgtgaaa aagaagctct catgtcggag ctcaaaatga tgacccacct gggacaccat 420

eolf-seq1

gacaacatcg tgaatctgct gggggcatgc acactgtcag ggccagtgtta cttgattttt	480
gaatattgtt gctatggtga cctcctcaac tacctaagaa gtaaaagaga gaagtttcac	540
aggacatgga cagagatttt taaggaacat aatttcagtt tttaccctac tttccaggca	600
cattcaaatt ccagcatgcc tggttcacga gaagttcagt tacacccgcc cttggatcag	660
ctctcagggt tcaatgggaa ttttaattcat tctgaagatg agattgaata tgaaaaccag	720
aagaggctgg cagaagaaga ggaggaagat ttgaacgtgc tgacgtttga agacctcctt	780
tgctttgcgt accaagtggc caaaggcatg gaattcctgg agttcaagtc gtgtgtccac	840
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ctgccggtga agtggatggc acctgagagc ttatttgaag ggatctacac aatcaagagt	1020
gacgtctggt cctacggcat ctttctctgg gagatatttt cactgggtgt gaacccttac	1080
cctggcattc ctgtcgacgc taacttctat aaactgattc agagtggatt taaaatggag	1140
cagccattct atgccacaga agggatatac tttgtaatgc aatcctgctg ggcttttgac	1200
tcaaggaagc ggccatcctt cccaacctg acttcatttt taggatgtca gctggcagag	1260
gcagaagaag cgatgtatca gaacatgggt ggcaacgtcc cagaacatcc atccatctac	1320
caaaacaggc ggccccctcag cagagaggca ggctcagagc cgccatcgcc acaggcccag	1380
gtgaagattc acggagaaaag aagtttag	1407

<210> 46

<211> 891

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from TLR4

<400> 46

cagctgtatt ccctcagcac tcttgattgc agtttcaatc gcatagagac atctaaagga	60
atactgcaac attttccaaa gagtctagcc ttcttcaatc ttactaacia ttctgttgct	120

eolf-seq1

tgtatatgtg aacatcagaa attcctgcag tgggtcaagg aacagaagca gttcttggtg	180
aatgttgaac aaatgacatg tgcaacacct gtagagatga atacctcctt agtgttggat	240
tttaataatt ctacctgtta tatgtacaag acaatcatca gtgtgtcagt ggtcagtggtg	300
attgtggat ccactgtagc atttctgata taccacttct attttcacct gatacttatt	360
gctggctgta aaaagtacag cagaggagaa agcatctatg atgcatttgt gatctactcg	420
agtcagaatg aggactgggt gagaaatgag ctggtaaaga atttagaaga aggagtgtccc	480
cgctttcacc tctgccttca ctacagagac tttattcctg gtgtagccat tgctgccaac	540
atcatccagg aaggcttcca caagagccgg aaggttattg tggtagtgct tagacacttt	600
attcagagcc gttgggtgtat ctttgaatat gagattgctc aaacatggca gtttctgagc	660
agccgctctg gcatcatctt cattgtcctt gagaagggtg agaagtccct gctgaggcag	720
caggtggaat tgtatcgctt tcttagcaga aacacctacc tggaatggga ggacaatcct	780
ctggggaggc acatcttctg gagaagactt aaaaatgtccc tattggatgg aaaagcctcg	840
aatcctgagc aaacagcaga ggaagaacaa gaaacggcaa cttggacctg a	891

<210> 47

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from CCR2

<400> 47

atggaagaca ataatatgtt acctcagttc atccatggca tactatcaac atctcattct	60
ctattttacac gaagtatcca agagcttgat gaaggggcca ccacaccgta tgactacgat	120
gatggtgagc cttgtcataa aaccagtgtg aagcaaattg gagcttggat cctgcctcca	180
ctctactccc tggatttcat ctttggtttt gtgggcaaca tgttgggtcat tataattctg	240
ataggctgta aaaagctgaa gagcatgact gatattctatc tgctcaacct ggccatctct	300
gacctgctct tcctgctcac attaccattc tgggctcact atgctgcaaa tgagtgggtc	360

eolf-seq1

tttgggaata taatgtgtaa agtattcaca gggctctatc acattgggta ttttggtgga	420
atctttttca ttatcctcct gacaattgat aggtacttgg ctattgttca tgctgtgttt	480
gctttaaaag ccaggacagt tacctttggg gtgataacaa gtgtagtcac ttgggtgggtg	540
gctgtgtttg cctctctacc aggaatcata ttactaaat ccaaacaaga tgatcaccat	600
tacacctgtg gcccttattt tacacaacta tggaagaatt tccaacaat aatgagaaat	660
atcttgagcc tgatcctgcc tctacttgtc atggatcatct gctactcagg aattctccac	720
accctgtttc gctgtaggaa tgagaagaag aggcacaggg ctgtgaggct catctttgcc	780
atcatgattg tctactttct cttctggact ccatacaata ttgttctctt cttgaccacc	840
ttccaggaat ccttggggaat gagtaactgt gtgattgaca agcacttaga ccaggccatg	900
caggtgacag agactcttgg aatgacacac tgctgcatta atcctgtcat ttatgccttt	960
gttgagagaga agttccgaag gtatctctcc atatttttca gaaagcacat tgctaaacgt	1020
ctctgcaaac agtgcccagt tttctatagg gagacagcag atcgagtgag ctctacattc	1080
actccttcca ctggggagca agaggtctcg gttgggttgt aa	1122

<210> 48

<211> 564

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from ITGB2

<400> 48

aatgcacggc tggtagagtg cagtggccgt ggccactgcc aatgcaacag gtgcatatgt	60
gacgaaggct accagccacc gatgtgtgag gattgtccca gctgtggctc gactgcagg	120
gacaaccaca cctcttgtgc cgagtgcctg aagtttgata agggcccttt tgagaagaac	180
tgtagtgttc agtgtgctgg tatgacgctg cagactatcc ctttgaagaa aaagccctgc	240
aaggagaggg actcgggaagg ctgttggata acttacactt tgcagcagaa ggacggaagg	300
aacatttaca acatccatgt ggaggacagt ctagagtgtg tgaagggcc caatgtggct	360

eolf-seql

gccatcgtag ggggcaccgt ggtagggtgtc gtactgattg gtgtcctcct cctgggtcatc 420
 tggaaggccc tgaccacact gactgacctc agggagtaca ggcgctttga gaaggagaaa 480
 ctcaagtccc aatggaacaa tgacaacccc ctcttcaaga gtgctacgac aacgggtcatg 540
 aacccaagt ttgctgaaag ctag 564

<210> 49

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from CSF2RB

<400> 49

actcagaaga tggcttactc attcattgag cacacattcc aggtccagta caagaagaaa 60
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 tcccagctgg agccagacac ctcatctgc gccagggtga gggtaagcc catctctaac 180
 tacgatggga tctggagcaa gtggagcgaa gactacactt ggaagactga ctgggtgatg 240
 cccacgctgt ggatagtcct catcctgggtc tttctcatcc tcaccttgct cctgatcctt 300
 cgctttggct gtgtctctgt atacaggacg tacaggaagt ggaaggaaaa gatccccaac 360
 cccagcaaga gcctcctgtt ccaggatgga ggtaaagggtc tctggcctcc tggcagcatg 420
 gcagccttcg ccactaagaa ccccgctctc caggggccac agagcagggt tcttgctgag 480
 caacaggggg agtcatatgc acatttgga gacaacaacg tgtcacctct cactatagag 540
 gaccctaata taattcgagt tccaccatcc gggcctgata caacccagc tgcctcatcc 600
 gaatccacag agcaacttcc caatgttcaa gtagagggtac caactcctaa cagacctagg 660
 aagcaattac ccagctttga cttcaatggg ccctacctgg ggcctcccca atcccactct 720
 ctgcctgatc tcccagacca gctgggttcc cccaggtgg gtgggagcct gaagccagca 780
 ctgccagggt ccttgagta catgtgtctg cccctggag gtcaagcgca actggttcca 840
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eolf-seq1

acctcaggga gcccttctgt ggagccaaag gagaaccctc cagttgagct gagcatggag 960
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 agtatgatgg cctctgatta tgtcactcct ggagatccgg tgctcactct gcccacaggg 1080
 cccctgtcta cctctctggg cccctctcta gggttgccct cagcccaaag ccccggtctc 1140
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 gactatgtgg agctgcctcc aagtgtgagc caggctgcca agtccccctcc aggccatcct 1260
 gtcctcctg tggcaagcag cccacagtg atcccaggag agcccaggga ggaagtgggc 1320
 ccagcatccc cacatcccga aggcctcctt gttcttcagc aggttgggga ctactgcttc 1380
 ctccctggcc tgggacctgg ctccctctca ccacacagta agccaccctc tccaagtctg 1440
 tgttctgaga ctgaggacct agtccaggac ttgtctgtca aaaagtttcc ctatcagccc 1500
 atgccccagg cgccagccat tcagtttttc aagtcctaa agcatcagga ctacctgtcc 1560
 ctgccccctt gggacaatag ccagtctggg aagggtgtgct ga 1602

<210> 50

<211> 1005

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from CCR1

<400> 50

actccatgcc aaaagactgc tgtaagagcc tttggggctg gactcctgcc cccctgtat 60
 tctctagtgt tcatcattgg agtgggtggc aatgtcctag tgattctggt gtcacatgcag 120
 cataggaggc ttcaaagcat gaccagcatc tacctgttca acctggctgt ctctgatctg 180
 gtcttccttt tcactttacc tttctggatt gactacaagt tgaaagacga ctggattttt 240
 ggtgatgcca tgtgcaagct tctctctggg ttttattacc tgggtttata cagtgaatc 300
 ttctttatca tcctgttgac gattgacaga tacctggcca ttgtccatgc tgtgtttgcc 360
 ctgaggggccc gaactgttac ttttggcatc atcaccagta ttatcacctg ggccctagcc 420

eolf-seql

atcttagctt ccatgcctgc cttatacttt ttttaaggccc agtgggagtt cactcaccgt	480
acctgtagcc ctcatthccc ctacaagagc ctgaagcagt ggaagagggt tcaagctcta	540
aagctaaacc ttcttggact aattttgcct ctgttagtca tgataatctg ctatgcaggg	600
atcatcagaa ttctgctcag aagaccaggt gagaagaagg tcaaagccgt gcgtctgata	660
tttgctatta ctcttctatt cttcctcctc tggacccccct acaatctgag tgtatttggt	720
tctgctttcc aagatgttct attcaccaat cagtgtgagc agagtaagca actggacctg	780
gcatgcagg tgactgaggt gattgcctac acccactgtt gtgtcaaccc aatcatttat	840
gtttttgtgg gtgaacgggt ctggaagtac cttcggcagc tgtttcaaag gcatgtggct	900
ataccactgg caaaatggct gcccttcctc tctgtggacc aactagaaaag gaccagttct	960
atatctccat ccacaggaga acatgagctc tctgctggct tctga	1005

<210> 51

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from CCR5

<400> 51

atgtcagcac cctgccaaaa aatcaatgtg aaacaaattg cggctcagct cctgccccca	60
ctctactccc tgggtattcat ctttggtttt gtgggtaaca tgatgggtctt cctcatcttg	120
ataagctgca aaaagctgaa gagcgtgact gatattctacc tgctcaacct ggccatctct	180
gacctgctct tcctgctcac actaccattc tgggctcact atgctgcaaa tgagtgggtc	240
tttgggaaca taatgtgtaa agtattcaca gggctctatc acattgggta ttttggtgga	300
atcttcttca ttatcctcct gacaattgat aggtacttgg ctattgtcca tgctgtgttt	360
gctttaaaag tcagaacgggt caactttggg gtgataacaa gtgtagtcac ttgggcgggtg	420
gctgtgtttg cctctctccc agaaataatc tttaccagat ctcagaaaaga aggttttcat	480
tatacatgca gtcctcattt tccacacact cagtatcatt tctggaagag tttccaaaca	540

eolf-seq1

ttaaagatgg	tcatcttgag	cctgatacctg	cctctacttg	tcatgggcat	ctgctactca	600
ggaattctcc	acaccctggt	tcgctgtagg	aatgagaaga	agaggcacag	ggctgtgagg	660
ctcatctttg	ccatcatgat	tgtctacttt	ctcttctgga	ctccctacaa	cattgtcctc	720
ctcctgacca	ccttccagga	attctttgga	ctgaataact	gcagtagttc	taatagacta	780
gaccaggcca	tgcaggcaac	agagactctt	ggaatgacac	actgctgcct	aaaccctgtc	840
atctatgcct	ttgttggaga	gaagttccgg	agttatctct	cagtgttctt	ccgaaaacac	900
attgtcaaac	gcttttgcaa	acggtgttca	attttccagc	aagacaatcc	tgatcgtgca	960
agctcagtct	atacccgatc	cacaggagaa	catgaagttt	ctactggttt	atga	1014

<210> 52

<211> 990

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from CXCR4

<400> 52

ttccgggatg	aaaacgtcca	tttcaatagg	atcttcctgc	ccaccatcta	cttcatcatc	60
ttcttgactg	gcatagtcgg	caatggattg	gtgatacctg	tcatgggtta	ccagaagaag	120
ctaaggagca	tgacggacaa	gtaccggctg	cacctgtcag	tggctgacct	cctctttgtc	180
atcacactcc	ccttctgggc	agttgatgcc	atggctgact	ggtacttttg	gaaatttttg	240
tgtaaggctg	tccatatcat	ctacactgtc	aacctctaca	gcagcgttct	catcctggcc	300
ttcatcagcc	tggaccggta	cctcgctatt	gtccacgcca	ccaacagtca	gaggccaagg	360
aaactgctgg	ctgaaaaggc	agtctatgtg	ggcgtctgga	tcccagccct	cctcctgact	420
atacctgact	tcatctttgc	cgacgtcagc	cagggggaca	tcagtcaggg	ggatgacagg	480
tacatctgtg	accgccttta	ccccgatagc	ctgtggatgg	tggtgtttca	attccagcat	540
ataatggtgg	gtctcgtcct	gcccggcatc	gtcatcctct	cctgttactg	catcatcatc	600
tctaagctgt	cacactccaa	gggccaccag	aagcgcaagg	ccctcaagac	gacagtcata	660

eolf-seq1

ctcatcctag ctttctttgc ctgctggctg ccatattatg tggggatcag catcgactcc	720
ttcacccctt tgggggtcat caagcaagga tgtgacttcg agagcatcgt gcacaagtgg	780
atctccatca cagaggccct cgccttcttc cactgttgcc tgaaccccat cctctatgcc	840
ttcctcgggg ccaagttcaa aagctctgcc cagcatgcac tcaactccat gagcagaggc	900
tccagcctca agatcctttc caaaggaaag cggggtggac actcttccgt ctccacggag	960
tcagaatcct ccagttttca ctccagctaa	990

<210> 53

<211> 894

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of proteinic domain derived from SELPLG

<400> 53

attgccacca ctgaccctac tgccccaggt acaggaggga cagctgttgg gatgctgagc	60
acagactctg ccacacagtg gagtctaacc tcagtagaga ccgtccaacc agcatccaca	120
gaggtagaga cctcgcagcc agcaccatg gaggcagaga cctcgcagcc agcaccatg	180
gaggcagaga cctcgcagcc agcaccatg gaggcagaca cctcaaagcc agcaccacg	240
gaggcagaga cctcaaagcc agcaccacg gaggcagaga cctctcagcc agcaccac	300
gaggcagaga cctcaaaacc agcaccacg gaggcagaga cctcaaaacc agcaccacg	360
gaggcagaga ccaccagct tcccaggatt caggctgtaa aaactctgtt tacaacgtct	420
gcagccaccg aagtcccttc cacagaacct accaccatgg agacggcgtc cacagagtct	480
aacgagtcta ccatcttcct tgggccatcc gtgactcact tacctgacag cggcctgaag	540
aaagggtga ttgtgacccc tgggaattca cctgccccaa ccctgccagg gagttcagat	600
ctcatcccgg tgaagcaatg tctgtgatt atcctcatct tggcttctct ggccaccatc	660
ttcctcgtgt gcacagtggg gctggcggtc cgtctgtccc gtaagacca catgtacca	720
gtgcggaact actccccac ggagatgatc tgcattctgt ccctgctacc tgagggggga	780

eolf-seql

gacggggccc ctgtcacagc caatgggggc ctgccaagg tccaggacct gaagacagag 840

cccagtgggg accgggatgg ggacgacctc accctgcaca gcttcctccc ttag 894

<210> 54

<211> 539

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-N

<400> 54

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly

eolf-seql

130

135

140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

Thr Val Ser Ser Thr Gly Leu Leu Gly Val Ser Leu Gly Gly Ala Lys
275 280 285

Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys
290 295 300

Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln
305 310 315 320

Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val

eolf-seql

325

330

335

Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln
 340 345 350

Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys
 355 360 365

Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys
 370 375 380

Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys
 385 390 395 400

Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu
 405 410 415

Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr
 420 425 430

Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu
 435 440 445

Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser
 450 455 460

Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln
 465 470 475 480

Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly
 485 490 495

Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro
 500 505 510

Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr

eolf-seql

515

520

525

Ile Ala Phe Lys Arg Trp Asn Arg Gly Ile Leu
530 535

<210> 55

<211> 381

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-G

<400> 55

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

eolf-seql

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

Thr Val Ser Ser Thr Gly His Glu Asn Ser Glu Leu Leu Ile Pro Lys
275 280 285

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

His Asn Asn Lys Ser Ser Ala Ser Phe Arg Ile Ser Leu Gly Asp Pro
305 310 315 320

eolf-seql

Gly Ser Pro Ser Met Phe Pro Pro Trp His Gln Ile Thr Phe Cys Leu
 325 330 335

Leu Ile Gly Leu Leu Phe Ala Ile Asp Thr Val Leu Tyr Phe Ser Val
 340 345 350

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

Gln Trp Ser Lys Glu Pro Gln Asp Lys Thr Arg Val Asp
 370 375 380

<210> 56
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of EVIR-F

<400> 56

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
 20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
 50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
 65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly

eolf-seql

85

90

95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
 115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
 165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
 180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
 195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
 210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
 225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
 245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
 260 265 270

Thr Val Ser Ser Thr Gly Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn

eolf-seql

275

280

285

Ile Ser Phe Tyr Ala Thr Ile Gly Leu Cys Leu Pro Phe Ile Val Val
 290 295 300

Leu Ile Val Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu
 305 310 315 320

Ser Gln Leu Gln Met Ile Gln Val Thr Gly Pro Leu Asp Asn Glu Tyr
 325 330 335

Phe Tyr Val Asp Phe Arg Asp Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
 340 345 350

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 355 360 365

Gly Arg Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 370 375 380

Ser Ile Gln Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Cys
 385 390 395 400

Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Met Met Thr His Leu Gly
 405 410 415

His His Asp Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly
 420 425 430

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

Tyr Leu Arg Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile
 450 455 460

Phe Lys Glu His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ala His Ser

eolf-seql

465		470		475		480									
Asn	Ser	Ser	Met	Pro	Gly	Ser	Arg	Glu	Val	Gln	Leu	His	Pro	Pro	Leu
			485						490					495	
Asp	Gln	Leu	Ser	Gly	Phe	Asn	Gly	Asn	Leu	Ile	His	Ser	Glu	Asp	Glu
			500					505					510		
Ile	Glu	Tyr	Glu	Asn	Gln	Lys	Arg	Leu	Ala	Glu	Glu	Glu	Glu	Glu	Asp
		515					520					525			
Leu	Asn	Val	Leu	Thr	Phe	Glu	Asp	Leu	Leu	Cys	Phe	Ala	Tyr	Gln	Val
		530					535					540			
Ala	Lys	Gly	Met	Glu	Phe	Leu	Glu	Phe	Lys	Ser	Cys	Val	His	Arg	Asp
545					550					555					560
Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	His	Gly	Lys	Val	Val	Lys	Ile
				565					570					575	
Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Leu	Ser	Asp	Ser	Ser	Tyr	Val
			580					585						590	
Val	Arg	Gly	Asn	Ala	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser
		595					600					605			
Leu	Phe	Glu	Gly	Ile	Tyr	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Tyr	Gly
		610					615				620				
Ile	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Val	Asn	Pro	Tyr	Pro	Gly
625					630					635					640
Ile	Pro	Val	Asp	Ala	Asn	Phe	Tyr	Lys	Leu	Ile	Gln	Ser	Gly	Phe	Lys
				645					650					655	
Met	Glu	Gln	Pro	Phe	Tyr	Ala	Thr	Glu	Gly	Ile	Tyr	Phe	Val	Met	Gln

eolf-seql

660

665

670

Ser Cys Trp Ala Phe Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu
675 680 685

Thr Ser Phe Leu Gly Cys Gln Leu Ala Glu Ala Glu Glu Ala Met Tyr
690 695 700

Gln Asn Met Gly Gly Asn Val Pro Glu His Pro Ser Ile Tyr Gln Asn
705 710 715 720

Arg Arg Pro Leu Ser Arg Glu Ala Gly Ser Glu Pro Pro Ser Pro Gln
725 730 735

Ala Gln Val Lys Ile His Gly Glu Arg Ser
740 745

<210> 57
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of EVIR-T

<400> 57

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

eolf-seql

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

eolf-seql

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

Thr Val Ser Ser Thr Gly Gln Leu Tyr Ser Leu Ser Thr Leu Asp Cys
275 280 285

Ser Phe Asn Arg Ile Glu Thr Ser Lys Gly Ile Leu Gln His Phe Pro
290 295 300

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

Cys Glu His Gln Lys Phe Leu Gln Trp Val Lys Glu Gln Lys Gln Phe
325 330 335

Leu Val Asn Val Glu Gln Met Thr Cys Ala Thr Pro Val Glu Met Asn
340 345 350

Thr Ser Leu Val Leu Asp Phe Asn Asn Ser Thr Cys Tyr Met Tyr Lys
355 360 365

Thr Ile Ile Ser Val Ser Val Val Ser Val Ile Val Val Ser Thr Val
370 375 380

Ala Phe Leu Ile Tyr His Phe Tyr Phe His Leu Ile Leu Ile Ala Gly
385 390 395 400

Cys Lys Lys Tyr Ser Arg Gly Glu Ser Ile Tyr Asp Ala Phe Val Ile
405 410 415

Tyr Ser Ser Gln Asn Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn
420 425 430

Leu Glu Glu Gly Val Pro Arg Phe His Leu Cys Leu His Tyr Arg Asp
435 440 445

eolf-seql

Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile Gln Glu Gly Phe
 450 455 460

His Lys Ser Arg Lys Val Ile Val Val Val Ser Arg His Phe Ile Gln
 465 470 475 480

Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe
 485 490 495

Leu Ser Ser Arg Ser Gly Ile Ile Phe Ile Val Leu Glu Lys Val Glu
 500 505 510

Lys Ser Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg
 515 520 525

Asn Thr Tyr Leu Glu Trp Glu Asp Asn Pro Leu Gly Arg His Ile Phe
 530 535 540

Trp Arg Arg Leu Lys Asn Ala Leu Leu Asp Gly Lys Ala Ser Asn Pro
 545 550 555 560

Glu Gln Thr Ala Glu Glu Glu Gln Glu Thr Ala Thr Trp Thr
 565 570

<210> 58
 <211> 651
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of EVIR-C2

<400> 58

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser

eolf-seql

20

25

30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala

eolf-seql

210

215

220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
 225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
 245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
 260 265 270

Thr Val Ser Ser Thr Gly Met Glu Asp Asn Asn Met Leu Pro Gln Phe
 275 280 285

Ile His Gly Ile Leu Ser Thr Ser His Ser Leu Phe Thr Arg Ser Ile
 290 295 300

Gln Glu Leu Asp Glu Gly Ala Thr Thr Pro Tyr Asp Tyr Asp Asp Gly
 305 310 315 320

Glu Pro Cys His Lys Thr Ser Val Lys Gln Ile Gly Ala Trp Ile Leu
 325 330 335

Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met
 340 345 350

Leu Val Ile Ile Ile Leu Ile Gly Cys Lys Lys Leu Lys Ser Met Thr
 355 360 365

Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Leu
 370 375 380

Thr Leu Pro Phe Trp Ala His Tyr Ala Ala Asn Glu Trp Val Phe Gly
 385 390 395 400

Asn Ile Met Cys Lys Val Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe

eolf-seql

405

410

415

Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala
420 425 430

Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly
435 440 445

Val Ile Thr Ser Val Val Thr Trp Val Val Ala Val Phe Ala Ser Leu
450 455 460

Pro Gly Ile Ile Phe Thr Lys Ser Lys Gln Asp Asp His His Tyr Thr
465 470 475 480

Cys Gly Pro Tyr Phe Thr Gln Leu Trp Lys Asn Phe Gln Thr Ile Met
485 490 495

Arg Asn Ile Leu Ser Leu Ile Leu Pro Leu Leu Val Met Val Ile Cys
500 505 510

Tyr Ser Gly Ile Leu His Thr Leu Phe Arg Cys Arg Asn Glu Lys Lys
515 520 525

Arg His Arg Ala Val Arg Leu Ile Phe Ala Ile Met Ile Val Tyr Phe
530 535 540

Leu Phe Trp Thr Pro Tyr Asn Ile Val Leu Phe Leu Thr Thr Phe Gln
545 550 555 560

Glu Ser Leu Gly Met Ser Asn Cys Val Ile Asp Lys His Leu Asp Gln
565 570 575

Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn
580 585 590

Pro Val Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser

eolf-seql

595

600

605

Ile Phe Phe Arg Lys His Ile Ala Lys Arg Leu Cys Lys Gln Cys Pro
610 615 620

Val Phe Tyr Arg Glu Thr Ala Asp Arg Val Ser Ser Thr Phe Thr Pro
625 630 635 640

Ser Thr Gly Glu Gln Glu Val Ser Val Gly Leu
645 650

<210> 59

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-I

<400> 59

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

eolf-seql

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

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

eolf-seql

Gly His Cys Gln Cys Asn Arg Cys Ile Cys Asp Glu Gly Tyr Gln Pro
290 295 300

Pro Met Cys Glu Asp Cys Pro Ser Cys Gly Ser His Cys Arg Asp Asn
305 310 315 320

His Thr Ser Cys Ala Glu Cys Leu Lys Phe Asp Lys Gly Pro Phe Glu
325 330 335

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

Leu Lys Lys Lys Pro Cys Lys Glu Arg Asp Ser Glu Gly Cys Trp Ile
355 360 365

Thr Tyr Thr Leu Gln Gln Lys Asp Gly Arg Asn Ile Tyr Asn Ile His
370 375 380

Val Glu Asp Ser Leu Glu Cys Val Lys Gly Pro Asn Val Ala Ala Ile
385 390 395 400

Val Gly Gly Thr Val Val Gly Val Val Leu Ile Gly Val Leu Leu Leu
405 410 415

Val Ile Trp Lys Ala Leu Thr His Leu Thr Asp Leu Arg Glu Tyr Arg
420 425 430

Arg Phe Glu Lys Glu Lys Leu Lys Ser Gln Trp Asn Asn Asp Asn Pro
435 440 445

Leu Phe Lys Ser Ala Thr Thr Thr Val Met Asn Pro Lys Phe Ala Glu
450 455 460

Ser
465

eolf-seql

<210> 60

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-C

<400> 60

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

eolf-seql

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

eolf-seql

340

345

350

Lys Thr Asp Trp Val Met Pro Thr Leu Trp Ile Val Leu Ile Leu Val
355 360 365

Phe Leu Ile Leu Thr Leu Leu Leu Ile Leu Arg Phe Gly Cys Val Ser
370 375 380

Val Tyr Arg Thr Tyr Arg Lys Trp Lys Glu Lys Ile Pro Asn Pro Ser
385 390 395 400

Lys Ser Leu Leu Phe Gln Asp Gly Gly Lys Gly Leu Trp Pro Pro Gly
405 410 415

Ser Met Ala Ala Phe Ala Thr Lys Asn Pro Ala Leu Gln Gly Pro Gln
420 425 430

Ser Arg Leu Leu Ala Glu Gln Gln Gly Glu Ser Tyr Ala His Leu Glu
435 440 445

Asp Asn Asn Val Ser Pro Leu Thr Ile Glu Asp Pro Asn Ile Ile Arg
450 455 460

Val Pro Pro Ser Gly Pro Asp Thr Thr Pro Ala Ala Ser Ser Glu Ser
465 470 475 480

Thr Glu Gln Leu Pro Asn Val Gln Val Glu Gly Pro Thr Pro Asn Arg
485 490 495

Pro Arg Lys Gln Leu Pro Ser Phe Asp Phe Asn Gly Pro Tyr Leu Gly
500 505 510

Pro Pro Gln Ser His Ser Leu Pro Asp Leu Pro Asp Gln Leu Gly Ser
515 520 525

Pro Gln Val Gly Gly Ser Leu Lys Pro Ala Leu Pro Gly Ser Leu Glu

eolf-seql

530

535

540

Tyr Met Cys Leu Pro Pro Gly Gly Gln Ala Gln Leu Val Pro Leu Ser
 545 550 555 560

Gln Val Met Gly Gln Gly Gln Ala Met Asp Val Gln Cys Gly Ser Ser
 565 570 575

Leu Glu Thr Ser Gly Ser Pro Ser Val Glu Pro Lys Glu Asn Pro Pro
 580 585 590

Val Glu Leu Ser Met Glu Glu Gln Glu Ala Arg Asp Asn Pro Val Thr
 595 600 605

Leu Pro Ile Ser Ser Gly Gly Pro Glu Gly Ser Met Met Ala Ser Asp
 610 615 620

Tyr Val Thr Pro Gly Asp Pro Val Leu Thr Leu Pro Thr Gly Pro Leu
 625 630 635 640

Ser Thr Ser Leu Gly Pro Ser Leu Gly Leu Pro Ser Ala Gln Ser Pro
 645 650 655

Arg Leu Cys Leu Lys Leu Pro Arg Val Pro Ser Gly Ser Pro Ala Leu
 660 665 670

Gly Pro Pro Gly Phe Glu Asp Tyr Val Glu Leu Pro Pro Ser Val Ser
 675 680 685

Gln Ala Ala Lys Ser Pro Pro Gly His Pro Ala Pro Pro Val Ala Ser
 690 695 700

Ser Pro Thr Val Ile Pro Gly Glu Pro Arg Glu Glu Val Gly Pro Ala
 705 710 715 720

Ser Pro His Pro Glu Gly Leu Leu Val Leu Gln Gln Val Gly Asp Tyr

eolf-seql

725

730

735

Cys Phe Leu Pro Gly Leu Gly Pro Gly Ser Leu Ser Pro His Ser Lys
740 745 750

Pro Pro Ser Pro Ser Leu Cys Ser Glu Thr Glu Asp Leu Val Gln Asp
755 760 765

Leu Ser Val Lys Lys Phe Pro Tyr Gln Pro Met Pro Gln Ala Pro Ala
770 775 780

Ile Gln Phe Phe Lys Ser Leu Lys His Gln Asp Tyr Leu Ser Leu Pro
785 790 795 800

Pro Trp Asp Asn Ser Gln Ser Gly Lys Val Cys
805 810

<210> 61

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-C1

<400> 61

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

eolf-seql

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

eolf-seql

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

Thr Val Ser Ser Thr Gly Thr Pro Cys Gln Lys Thr Ala Val Arg Ala
275 280 285

Phe Gly Ala Gly Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Ile
290 295 300

Gly Val Val Gly Asn Val Leu Val Ile Leu Val Leu Met Gln His Arg
305 310 315 320

Arg Leu Gln Ser Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Val Ser
325 330 335

Asp Leu Val Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu
340 345 350

Lys Asp Asp Trp Ile Phe Gly Asp Ala Met Cys Lys Leu Leu Ser Gly
355 360 365

Phe Tyr Tyr Leu Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu
370 375 380

Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg
385 390 395 400

Ala Arg Thr Val Thr Phe Gly Ile Ile Thr Ser Ile Ile Thr Trp Ala
405 410 415

Leu Ala Ile Leu Ala Ser Met Pro Ala Leu Tyr Phe Phe Lys Ala Gln
420 425 430

Trp Glu Phe Thr His Arg Thr Cys Ser Pro His Phe Pro Tyr Lys Ser
435 440 445

eolf-seql

Leu Lys Gln Trp Lys Arg Phe Gln Ala Leu Lys Leu Asn Leu Leu Gly
 450 455 460

Leu Ile Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Ala Gly Ile Ile
 465 470 475 480

Arg Ile Leu Leu Arg Arg Pro Ser Glu Lys Lys Val Lys Ala Val Arg
 485 490 495

Leu Ile Phe Ala Ile Thr Leu Leu Phe Phe Leu Leu Trp Thr Pro Tyr
 500 505 510

Asn Leu Ser Val Phe Val Ser Ala Phe Gln Asp Val Leu Phe Thr Asn
 515 520 525

Gln Cys Glu Gln Ser Lys Gln Leu Asp Leu Ala Met Gln Val Thr Glu
 530 535 540

Val Ile Ala Tyr Thr His Cys Cys Val Asn Pro Ile Ile Tyr Val Phe
 545 550 555 560

Val Gly Glu Arg Phe Trp Lys Tyr Leu Arg Gln Leu Phe Gln Arg His
 565 570 575

Val Ala Ile Pro Leu Ala Lys Trp Leu Pro Phe Leu Ser Val Asp Gln
 580 585 590

Leu Glu Arg Thr Ser Ser Ile Ser Pro Ser Thr Gly Glu His Glu Leu
 595 600 605

Ser Ala Gly Phe
 610

<210> 62
 <211> 615
 <212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-C5

<400> 62

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser
20 25 30

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

Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe
65 70 75 80

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile

eolf-seq1

165

170

175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

Thr Val Ser Ser Thr Gly Met Ser Ala Pro Cys Gln Lys Ile Asn Val
275 280 285

Lys Gln Ile Ala Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
290 295 300

Ile Phe Gly Phe Val Gly Asn Met Met Val Phe Leu Ile Leu Ile Ser
305 310 315 320

Cys Lys Lys Leu Lys Ser Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala
325 330 335

Ile Ser Asp Leu Leu Phe Leu Leu Thr Leu Pro Phe Trp Ala His Tyr
340 345 350

Ala Ala Asn Glu Trp Val Phe Gly Asn Ile Met Cys Lys Val Phe Thr

eolf-seql

355

360

365

Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu
370 375 380

Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu
385 390 395 400

Lys Val Arg Thr Val Asn Phe Gly Val Ile Thr Ser Val Val Thr Trp
405 410 415

Ala Val Ala Val Phe Ala Ser Leu Pro Glu Ile Ile Phe Thr Arg Ser
420 425 430

Gln Lys Glu Gly Phe His Tyr Thr Cys Ser Pro His Phe Pro His Thr
435 440 445

Gln Tyr His Phe Trp Lys Ser Phe Gln Thr Leu Lys Met Val Ile Leu
450 455 460

Ser Leu Ile Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile
465 470 475 480

Leu His Thr Leu Phe Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
485 490 495

Val Arg Leu Ile Phe Ala Ile Met Ile Val Tyr Phe Leu Phe Trp Thr
500 505 510

Pro Tyr Asn Ile Val Leu Leu Leu Thr Thr Phe Gln Glu Phe Phe Gly
515 520 525

Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Ala
530 535 540

Thr Glu Thr Leu Gly Met Thr His Cys Cys Leu Asn Pro Val Ile Tyr

eolf-seql

Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
85 90 95

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

Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly
115 120 125

Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
145 150 155 160

Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile
165 170 175

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp
180 185 190

Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser
195 200 205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

eolf-seql

Thr Val Ser Ser Thr Gly Phe Arg Asp Glu Asn Val His Phe Asn Arg
275 280 285

Ile Phe Leu Pro Thr Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val
290 295 300

Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg
305 310 315 320

Ser Met Thr Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu
325 330 335

Phe Val Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp Trp
340 345 350

Tyr Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
355 360 365

Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg
370 375 380

Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
385 390 395 400

Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro Ala Leu Leu
405 410 415

Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser Gln Gly Asp Ile
420 425 430

Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg Leu Tyr Pro Asp Ser
435 440 445

Leu Trp Met Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Val
450 455 460

eolf-seql

Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys
465 470 475 480

Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr Thr
485 490 495

Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr Val
500 505 510

Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Gly Val Ile Lys Gln Gly
515 520 525

Cys Asp Phe Glu Ser Ile Val His Lys Trp Ile Ser Ile Thr Glu Ala
530 535 540

Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu
545 550 555 560

Gly Ala Lys Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met Ser
565 570 575

Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly His
580 585 590

Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
595 600 605

<210> 64

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-S

<400> 64

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

eolf-seql

1	5	10	15
Val Ile Met Ser Arg Gly Asp Ile Val Leu Thr Gln Thr Pro Ser Ser	20	25	30
Leu Pro Val Ser Val Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser	35	40	45
Gln Thr Leu Leu Tyr Ser Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr	50	55	60
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Trp Ala Phe	65	70	75
Thr Arg Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly	85	90	95
Thr Asp Phe Thr Leu Thr Ile Gly Ser Val Lys Ala Glu Asp Leu Ala	100	105	110
Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Trp Thr Phe Gly Gly	115	120	125
Gly Thr Arg Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly	130	135	140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu	145	150	155
Gln Gln Ser Gly Pro Glu Val Val Lys Thr Gly Ala Ser Val Lys Ile	165	170	175
Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Phe Ile Asn Trp	180	185	190
Val Lys Lys Asn Ser Gly Lys Ser Pro Glu Trp Ile Gly His Ile Ser			

eolf-seql

195

200

205

Ser Ser Tyr Ala Thr Ser Thr Tyr Asn Gln Lys Phe Lys Asn Lys Ala
210 215 220

Ala Phe Thr Val Asp Thr Ser Ser Ser Thr Ala Phe Met Gln Leu Asn
225 230 235 240

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Ser Gly
245 250 255

Asn Tyr Glu Glu Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
260 265 270

Thr Val Ser Ser Thr Gly Ile Ala Thr Thr Asp Pro Thr Ala Pro Gly
275 280 285

Thr Gly Gly Thr Ala Val Gly Met Leu Ser Thr Asp Ser Ala Thr Gln
290 295 300

Trp Ser Leu Thr Ser Val Glu Thr Val Gln Pro Ala Ser Thr Glu Val
305 310 315 320

Glu Thr Ser Gln Pro Ala Pro Met Glu Ala Glu Thr Ser Gln Pro Ala
325 330 335

Pro Met Glu Ala Glu Thr Ser Gln Pro Ala Pro Met Glu Ala Asp Thr
340 345 350

Ser Lys Pro Ala Pro Thr Glu Ala Glu Thr Ser Lys Pro Ala Pro Thr
355 360 365

Glu Ala Glu Thr Ser Gln Pro Ala Pro Asn Glu Ala Glu Thr Ser Lys
370 375 380

Pro Ala Pro Thr Glu Ala Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala

eolf-seql

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385              390              395              400

Glu Thr Thr Gln Leu Pro Arg Ile Gln Ala Val Lys Thr Leu Phe Thr
      405              410              415

Thr Ser Ala Ala Thr Glu Val Pro Ser Thr Glu Pro Thr Thr Met Glu
      420              425              430

Thr Ala Ser Thr Glu Ser Asn Glu Ser Thr Ile Phe Leu Gly Pro Ser
      435              440              445

Val Thr His Leu Pro Asp Ser Gly Leu Lys Lys Gly Leu Ile Val Thr
      450              455              460

Pro Gly Asn Ser Pro Ala Pro Thr Leu Pro Gly Ser Ser Asp Leu Ile
465              470              475              480

Pro Val Lys Gln Cys Leu Leu Ile Ile Leu Ile Leu Ala Ser Leu Ala
      485              490              495

Thr Ile Phe Leu Val Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg
      500              505              510

Lys Thr His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Ile
      515              520              525

Cys Ile Ser Ser Leu Leu Pro Glu Gly Gly Asp Gly Ala Pro Val Thr
      530              535              540

Ala Asn Gly Gly Leu Pro Lys Val Gln Asp Leu Lys Thr Glu Pro Ser
545              550              555              560

Gly Asp Arg Asp Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
      565              570              575

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<210> 65

eolf-seql

<211> 1620
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of EVIR-N

<400> 65
 atggattttc aggtccagat tttctccttc ctctcattt cagccagcgt cattatgtct 60
 cgggggggata ttgtcctcac acagactccc agctccctgc ctgtgtccgt cggagagaaa 120
 gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac 180
 ctcgcatggg atcagcagaa accaggacag agccccaagc tgctcatctc ctgggctttc 240
 acccggaat cgggggtgcc tgaccgcttc acaggtagcg gctccggaac tgattttact 300
 ctgaccattg gatctgtgaa ggcagaggac ctcgccgtct actattgcca gcagtacagt 360
 aattatccat ggacttttgg cggaggggacc aggctggaaa tcaagagagg tggaggaggg 420
 tccggtggag gagggtctgg tggaggaggg agtggtggag gagggtcaga ggtgcagctg 480
 cagcagtctg gccccgaagt ggtcaaaact ggagcttcag tcaaaatcag ctgtaaggca 540
 tctgggtaca gcttcaccgg ctacttcatc aactgggtga agaaaaattc agggaagagc 600
 cctgagtgga tcggccacat ttcaagctcc tacgccacaa gcacttacaa ccagaagttc 660
 aaaaataagg ccgcttttac cgtggacaca tctagttcaa ccgccttcac gcagctgaac 720
 tccctcacat ctgaagatag tgctgtgtac tattgtgtca ggagcggcaa ctacgaagaa 780
 tatgctatgg attactgggg gcaggggacc tccgtgactg tctcaagcac cggctcttctg 840
 ggggtgtccc ttggaggtgc caaggaggca tgccccacag gcctgtacac acacagcggg 900
 gagtgctgca aagcctgcaa cctgggcgag ggtgtggccc agccttgtgg agccaaccag 960
 accgtgtgtg agccctgcct ggacagcgtg acgttctccg acgtgggtgag cgcgaccgag 1020
 ccgtgcaagc cgtgcaccga gtgcgtgggg ctccagagca tgcggcgcc gtgcgtggag 1080
 gccgacgacg ccgtgtgccg ctgcgcctac ggctactacc aggatgagac gactgggcgc 1140
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eolf-seql

cagaacaccg tgtgcgagga gtgccccgac ggcacgtatt ccgacgaggc caaccacgtg	1260
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<210> 66

<211> 1146

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-G

<400> 66

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gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
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aattatccat ggacttttgg cggaggggacc aggctggaaa tcaagagagg tggaggaggg	420
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cagcagtctg gccccgaagt ggtcaaaact ggagcttcag tcaaaatcag ctgtaaggca	540
tctgggtaca gcttcaccgg ctacttcatc aactgggtga agaaaaattc agggagagc	600
cctgagtggg tcggccacat ttcaagctcc tacgccacaa gcacttacaa ccagaagttc	660
aaaaataagg ccgctttttac cgtggacaca tctagttcaa ccgccttcat gcagctgaac	720

eolf-seq1

tccctcacat ctgaagatag tgctgtgtac tattgtgtca ggagcggcaa ctacgaagaa	780
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gggtctccca gtatgttccc cccttggcac cagatcacct tttgcctgct gattggactg	1020
ctgttcgcta tcgatacagt gctgtacttt tctgtccgga gaggcctgca gtcacccgtg	1080
gcagattacg aagaacccaa gattcagtgg agcaaggagc cccaggataa gacgcgtgtc	1140
gactga	1146

<210> 67
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of EVIR-F

<400> 67	
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gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
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cagcagtctg gccccgaagt ggtcaaaact ggagcttcag tcaaaatcag ctgtaaggca	540
tctgggtaca gcttcaccgg ctacttcatt aactgggtga agaaaaattc aggggaagagc	600
cctgagtgga tcggccacat ttcaagctcc tacgccacaa gcacttacaa ccagaagttc	660

eolf-seq1

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ttctatgcca cagaagggat atactttgta atgcaatcct gctgggcttt tgactcaagg	2040
aagcggccat ccttcccca cctgacttca tttttaggat gtcagctggc agaggcagaa	2100

eolf-seq1

gaagcgatgt atcagaacat ggggtggcaac gtcccagaac atccatccat ctacaaaaac	2160
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<210> 68
 <211> 1725
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of EVIR-T

<400> 68	
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gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
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caacattttc caaagagtct agccttcttc aatcttacta acaattctgt tgcttgata	960

eolf-seq1

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gaacaaatga catgtgcaac acctgtagag atgaataacct ccttagtggt ggattttaat	1080
aattctacct gttatatgta caagacaatc atcagtgtgt cagtggtcag tgtgattgtg	1140
gtatccactg tagcatttct gatataccac ttctattttc acctgatact tattgctggc	1200
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<210> 69

<211> 1956

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-C2

<400> 69

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gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
ctcgcattgg atcagcagaa accaggacag agccccaagc tgctcatctc ctgggctttc	240
acccggaaaat ccgggggtgcc tgaccgcttc acaggtagcg gctccggaac tgattttact	300
ctgaccattg gatctgtgaa ggcagaggac ctcgccgtct actattgcca gcagtacagt	360

eolf-seq1

aattatccat ggacttttgg cggaggggacc aggctggaaa tcaagagagg tggaggaggg	420
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cagcagtctg gccccgaagt ggtcaaaact ggagcttcag tcaaaatcag ctgtaaggca	540
tctgggtaca gcttcaccgg ctacttcatc aactgggtga agaaaaattc aggggaagagc	600
cctgagtgga tcggccacat ttcaagctcc tacgccacaa gcacttacaa ccagaagttc	660
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gaatccttgg gaatgagtaa ctgtgtgatt gacaagcact tagaccaggc catgcagggtg	1740
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eolf-seql

gagaagttcc gaaggatatct ctccatatatt ttcagaaaagc acattgctaa acgtctctgc 1860
 aaacagtgcc cagtttttcta tagggagaca gcagatcgag tgagctctac attcactcct 1920
 tccactggggg agcaagaggt ctcggttggg ttgttaa 1956

<210> 70

<211> 1398

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-I

<400> 70

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eolf-seq1

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<210> 71

<211> 2436

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-C

<400> 71

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eolf-seq1

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eolf-seq1

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<210> 72

<211> 1839

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-C1

<400> 72

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eolf-seq1

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aaccttcttg gactaatttt gcctctgtta gtcatgataa tctgctatgc agggatcatc	1440
agaattctgc tcagaagacc cagtgagaag aagg tcaaag ccgtgcgtct gatatttgct	1500
attactcttc tattcttcct cctctggacc ccctacaatc tgagtgtatt tgtttctgct	1560
ttccaagatg ttctattcac caatcagtgt gagcagagta agcaactgga cctggccatg	1620
caggtgactg aggtgattgc ctacaccac tgttgtgtca acccaatcat ttatgttttt	1680
gtgggtgaac ggctctggaa gtaccttcgg cagctgtttc aaaggcatgt ggctatacca	1740
ctggcaaaat ggctgccctt cctctctgtg gaccaactag aaaggaccag ttctatatct	1800
ccatccacag gagaacatga gctctctgct ggcttctga	1839

<210> 73
 <211> 1848
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of EVIR-C5

<400> 73
 atggattttc aggtccagat tttctccttc ctctcatctt cagccagcgt cattatgtct 60

eolf-seq1

cggggggata ttgtcctcac acagactccc agctccctgc ctgtgtccgt cggagagaaa	120
gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
ctcgcacatgg atcagcagaa accaggacag agccccaagc tgctcatctc ctgggctttc	240
acccggaaat ccgggggtgcc tgaccgcttc acaggtagcg gctccggaac tgattttact	300
ctgaccattg gatctgtgaa ggcagaggac ctcgccgtct actattgcca gcagtacagt	360
aattatccat ggacttttgg cggaggggacc aggctggaaa tcaagagagg tggaggaggg	420
tccggtggag gagggctctgg tggaggaggg agtggtggag gagggtcaga ggtgcagctg	480
cagcagtctg gccccgaagt ggtcaaaact ggagcttcag tcaaaatcag ctgtaaggca	540
tctgggtaca gcttcaccgg ctacttcatc aactgggtga agaaaaattc agggagagc	600
cctgagtgga tcggccacat ttcaagctcc tacgccacaa gcacttaca ccagaagttc	660
aaaaataagg ccgcttttac cgtggacaca tctagttcaa ccgccttcac gcagctgaac	720
tccctcacat ctgaagatag tgctgtgtac tattgtgtca ggagcggcaa ctacgaagaa	780
tatgctatgg attactgggg gcaggggacc tccgtgactg tctcaagcac cggtatgtca	840
gcaccctgcc aaaaaatcaa tgtgaaacaa attgcggctc agctcctgcc cccactctac	900
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aacataatgt gtaaagtatt cacagggctc tatcacattg gttattttgg tggaatcttc	1140
ttcattatcc tcctgacaat tgataggtag ttggctattg tccatgctgt gtttgcttta	1200
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tgagtcctc attttccaca cactcagtat ctttctgga agagtttcca aacattaaag	1380
atggctcatct tgagcctgat cctgcctcta cttgtcatgg tcatctgcta ctcaggaatt	1440
ctccacaccc tgtttcgctg taggaatgag aagaagaggc acagggctgt gaggctcatc	1500

eolf-seq1

tttgccatca tgattgtcta ctttctcttc tggactccct acaacattgt cctcctcctg	1560
accaccttcc aggaattctt tggactgaat aactgcagta gttctaata tagactagaccag	1620
gccatgcagg caacagagac tcttggaatg acacactgct gcctaaaccc tgtcatctat	1680
gcctttgttg gagagaagtt ccggagttat ctctcagtgt tcttccgaaa acacattgtc	1740
aaacgctttt gcaaacgggtg ttcaattttc cagcaagaca atcctgatcg tgcaagctca	1800
gtctataccc gatccacagg agaacatgaa gtttctactg gtttatga	1848

<210> 74

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-CX

<400> 74

atggattttc aggtccagat tttctccttc ctctcattt cagccagcgt cattatgtct	60
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gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
ctcgcattgg atcagcagaa accaggacag agccccaagc tgctcatctc ctgggctttc	240
acccggaaaat ccgggggtgcc tgaccgcttc acaggtagcg gctccggaac tgattttact	300
ctgaccattg gatctgtgaa ggacagaggac ctgcccgtct actattgcca gcagtacagt	360
aattatccat ggacttttgg cggaggggacc aggttggaat tcaagagagg tggaggaggg	420
tccggtggag gaggggtctgg tggaggaggg agtggtggag gagggtcaga ggtgcagctg	480
cagcagtctg gccccgaagt ggtcaaaaact ggagcttcag tcaaaatcag ctgtaaggca	540
tctgggtaca gcttcaccgg ctacttcatt aactgggtga agaaaaattc agggagagagc	600
cctgagtggg tcggccacat ttcaagctcc tacgccacaa gcacttacaa ccagaagttc	660
aaaaataagg ccgctttttac cgtggacaca tctagttcaa ccgccttcat gcagctgaac	720
tccctcacat ctgaagatag tgctgtgtac tattgtgtca ggagcggcaa ctacgaagaa	780

eolf-seq1

tatgctatgg attactgggg gcaggggacc tccgtgactg tctcaagcac cgggttccgg	840
gatgaaaacg tccatttcaa taggatcttc ctgcccacca tctacttcat catcttcttg	900
actggcatag tcggcaatgg attggtgatc ctgggtcatgg gttaccagaa gaagctaagg	960
agcatgacgg acaagtaccg gctgcacctg tcagtggctg acctcctctt tgtcatcaca	1020
ctcccccttct gggcagttga tgccatggct gactgggtact ttgggaaatt tttgtgtaag	1080
gctgtccata tcatctacac tgtcaacctc tacagcagcg ttctcatcct ggccttcatc	1140
agcctggacc ggtacctcgc tattgtccac gccaccaaca gtcagaggcc aaggaaactg	1200
ctggctgaaa aggcagtcta tgtgggcgtc tggatcccag ccctcctcct gactatacct	1260
gacttcatct ttgccgacgt cagccagggg gacatcagtc agggggatga caggtacatc	1320
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gtgggtctcg tcctgcccgg catcgtcatc ctctcctggt actgcatcat catctctaag	1440
ctgtcacact ccaagggccca ccagaagcgc aaggccctca agacgacagt catcctcatc	1500
ctagctttct ttgcctgctg gctgccatat tatgtgggga tcagcatcga ctcccttcatc	1560
cttttggggg tcatcaagca aggatgtgac ttcgagagca tcgtgcacaa gtggatctcc	1620
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ggggccaagt tcaaaaagtc tgcccagcat gcactcaact ccatgagcag aggctccagc	1740
ctcaagatcc tttccaaagg aaagcggggg ggacactctt ccgtctccac ggagtcagaa	1800
tcctccagtt ttcactccag ctaa	1824

<210> 75

<211> 1728

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-S

<400> 75

atggattttc aggtccagat tttctccttc ctctcatctt cagccagcgt cattatgtct	60
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eolf-seq1

cggggggata ttgtcctcac acagactccc agctccctgc ctgtgtccgt cggagagaaa	120
gtgaccatga catgcaagtc tagtcagaca ctgctctact ctaacaatca gaagaactac	180
ctcgcacatgg atcagcagaa accaggacag agccccaagc tgctcatctc ctgggctttc	240
acccggaaat ccgggggtgcc tgaccgcttc acaggtagcg gctccggaac tgattttact	300
ctgaccattg gatctgtgaa ggcagaggac ctcgccgtct actattgcca gcagtacagt	360
aattatccat ggacttttgg cggaggggacc aggctggaaa tcaagagagg tggaggaggg	420
tccggtggag gagggctctgg tggaggaggg agtggtggag gagggtcaga ggtgcagctg	480
cagcagtctg gccccgaagt ggtcaaaact ggagcttcag tcaaaatcag ctgtaaggca	540
tctgggtaca gcttcaccgg ctacttcac taaactgggtga agaaaaattc aggggaagagc	600
cctgagtgga tcggccacat ttcaagctcc tacgccacaa gcacttacaa ccagaagttc	660
aaaaataagg ccgctttttac cgtggacaca tctagttcaa ccgccttcac gcagctgaac	720
tccctcacat ctgaagatag tgctgtgtac tattgtgtca ggagcggcaa ctacgaagaa	780
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gagacctcgc agccagcacc catggaggca gagacctcgc agccagcacc catggaggca	1020
gagacctcgc agccagcacc catggaggca gacacctcaa agccagcacc cacggaggca	1080
gagacctcaa agccagcacc cacggaggca gagacctctc agccagcacc caacgaggca	1140
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gagaccaccc agcttcccag gattcaggct gtaaaaaactc tgttttacaac gtctgcagcc	1260
accgaagtcc cttccacaga acctaccacc atggagacgg cgtccacaga gtctaacgag	1320
tctaccatct tccttgggcc atccgtgact cacttacctg acagcggcct gaagaaaggg	1380
ctgattgtga cccctgggaa ttcacctgcc ccaaccctgc caggaggttc agatctcatc	1440
ccggtgaagc aatgtctgct gattatcctc atcttggctt ctctggccac catcttcctc	1500

eolf-seq1

gtgtgcacag tgggtgctggc ggtccgtctg tcccgtgaaga cccacatgta cccagtgcgg 1560
aactactccc ccacggagat gatctgcatc tcgtccctgc tacctgaggg gggagacggg 1620
gcccctgtca cagccaatgg gggcctgccc aagggtccagg acctgaagac agagcccagt 1680
ggggaccggg atggggacga cctcacctg cacagcttcc tcccttag 1728

<210> 76

<211> 748

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of anti-HER2 scFv Trastuzumab

<400> 76

gatattcaga tgacccagtc ccccagctcc ctgtcagcaa gcgtgggcga ccgagtcact 60
atcacctgcc gagctagcca ggatgtgaac accgcagtcg cctggtacca gcagaagcca 120
gggaaagcac ccaagctgct catctactcc gcctctttcc tgtattcagg agtgccaagc 180
aggttttagtg gctcaagaag cggaactgac ttcacactga ctatctctag tctccagccc 240
gaggattttg caacctacta ttgccagcag cactatacca cacccttac cttcggtcag 300
ggcacaaaag tggaaattaa gcggaccggc tccacatctg gaagtgggaa gcccggttcc 360
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agtctgaggc tctcatgtgc cgctagcggc ttcaacatca aagacacata cattcattgg 480
gtgcgccagg ctcttgggaa gggctctggaa tgggtcgcac gaatctatcc aactaatggg 540
tacacccgat atgctgactc tgtgaaaggc aggttcacaa tttccgccga tacatctaag 600
aacactgctt acctgcagat gaatagtctc agagctgagg atactgcagt ctactattgt 660
agccgggtggg gaggggatgg cttctatgct atggatgtct gggggcaggg gactctggtg 720
actgtctcaa gtggtaccgg tacgcgtg 748

<210> 77

<211> 726

<212> DNA

eolf-seql

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of anti-HER2 scFv Pertuzumab

<400> 77

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ggaaaagctc ctaagctgct catctattcc gcatcttaca ggtacacagg cgtgccctct	180
cgcttcagtg gttcaggcag cggaactgac tttactctga ccatttctag tctccagcct	240
gaggatttcg caacctacta ttgtcagcag tactatatct acccatatac ctttgggcag	300
ggtacaaaag tggaaattaa gagaacagtc gcagctccag gaggaggagg tagcggagga	360
gggggttccg gcggaggggg ttctggcgga gggggtagtg aggtgcagct ggtcgaaagc	420
ggaggaggac tcgtgcagcc tgggtggcagc ctgagactct cctgcgcagc ctctggcttc	480
accttcaccg actacaccat ggattgggtg cggcaggcac caggaaaggg actggagtgg	540
gtggcagacg tcaaccccaa ttccggaggg tctatctaca accagagggtt caaaggaagg	600
ttcaccctga gtgtggatcg atcaaagaac accctgtatc tccagatgaa ttccctgagg	660
gccgaagata cagccgtcta ttattgtgca agaaacctgg gtccatcatt ttattttgac	720
tattgg	726

<210> 78

<211> 727

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of anti-HER2 scFv FRP5

<400> 78

caggtccagc tccagcagtc aggtccagaa ctcaagaagc caggggaaac agtcaaaatc	60
tcatgtaaag cctcaggata cccattcact aactatggga tgaattgggt gaagcaggca	120
cctggccagg gactgaaatg gatgggttgg atcaacacta gcaccgggga gtccacattc	180

eolf-seql

gccgacgatt ttaagggccg gttcgacttt tctctcgaaa ccagtgc aaa tacagcctat 240
ctgcagatta acaatctcaa atccgaggat atggccacct acttctgcgc tcgctgggaa 300
gtgtaccacg gatatgtccc atactggggg cagggtacca cagtgcagc cagctccgga 360
ggaggagggt caggaggagg aggtagcgga ggaggagggt ccgacatcca gctgacacag 420
tctcataagt ttctctccac ttctgtgggc gacagggtct ctattacctg taaagctagt 480
caggatgtgt ataacgccgt cgcttggtac cagcagaagc ccggccagag ccctaaactg 540
ctcatctata gcgcctctag taggtacact ggagtgccaa gcagattcac cggcagtgga 600
tcaggccccg acttcacctt caccatttca agcgtgcagg ctgaggatct ggcagtctac 660
ttttgccagc agcattttcg caccctttc acctttggaa gcgggactaa actggagatt 720
aagagga 727

<210> 79

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of hinge domain derived from dLNGFR

<400> 79

Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly
1 5 10 15

Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu
20 25 30

Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys
35 40 45

Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys
50 55 60

Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys

eolf-seql																		
65						70						75						80
Val	Glu	Ala	Asp	Asp	Ala	Val	Cys	Arg	Cys	Ala	Tyr	Gly	Tyr	Tyr	Gln			
				85					90					95				
Asp	Glu	Thr	Thr	Gly	Arg	Cys	Glu	Ala	Cys	Arg	Val	Cys	Glu	Ala	Gly			
				100					105					110				
Ser	Gly	Leu	Val	Phe	Ser	Cys	Gln	Asp	Lys	Gln	Asn	Thr	Val	Cys	Glu			
				115					120					125				
Glu	Cys	Pro	Asp	Gly	Thr	Tyr	Ser	Asp	Glu	Ala	Asn	His	Val	Asp	Pro			
				130					135					140				
Cys	Leu	Pro	Cys	Thr	Val	Cys	Glu	Asp	Thr	Glu	Arg	Gln	Leu	Arg	Glu			
145					150					155					160			
Cys	Thr	Arg	Trp	Ala	Asp	Ala	Glu	Cys	Glu	Glu	Ile	Pro	Gly	Arg	Trp			
				165					170					175				
Ile	Thr	Arg	Ser	Thr	Pro	Pro	Glu	Gly	Ser	Asp	Ser	Thr	Ala	Pro	Ser			
				180					185					190				
Thr	Gln	Glu	Pro	Glu	Ala	Pro	Pro	Glu	Gln	Asp	Leu	Ile	Ala	Ser	Thr			
				195					200					205				
Val	Ala	Gly	Val	Val	Thr	Thr	Val	Met	Gly	Ser	Ser	Gln	Pro	Val	Val			
				210					215					220				
Thr	Arg	Gly	Thr	Thr	Asp	Asn												
225					230													

<210> 80
 <211> 22
 <212> PRT
 <213> Artificial Sequence

eolf-seql

<220>

<223> Amino acid sequence of a transmembrane domain derived from dLNGFR

<400> 80

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

Val Ala Tyr Ile Ala Phe
20

<210> 81

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an intracellular domain derived from dLNGFR

<400> 81

Lys Arg Trp Asn Arg Gly Ile Leu
1 5

<210> 82

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of hinge domain derived from FcgRIIIA

<400> 82

His Glu Asn Ser Glu Leu Leu Ile Pro Lys Ala Thr His Asn Asp Ser
1 5 10 15

Gly Ser Tyr Phe Cys Arg Gly Leu Ile Gly His Asn Asn Lys Ser Ser
20 25 30

Ala Ser Phe Arg Ile Ser Leu Gly Asp Pro Gly Ser Pro Ser Met Phe
35 40 45

eolf-seql

Pro Pro
50

<210> 83
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a transmembrane domain derived from
FcγRIIIA

<400> 83

Trp His Gln Ile Thr Phe Cys Leu Leu Ile Gly Leu Leu Phe Ala Ile
1 5 10 15

Asp Thr Val Leu Tyr Phe
20

<210> 84
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of an intracellular domain derived from
FcγRIIIA

<400> 84

Ser Val Arg Arg Gly Leu Gln Ser Pro Val Ala Asp Tyr Glu Glu Pro
1 5 10 15

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

<210> 85
<211> 10
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> Amino acid sequence of hinge domain derived from FLT3

<400> 85

Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn
1 5 10

<210> 86

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a transmembrane domain derived from FLT3

<400> 86

Ile Ser Phe Tyr Ala Thr Ile Gly Leu Cys Leu Pro Phe Ile Val Val
1 5 10 15

Leu Ile Val Leu Ile Cys
20

<210> 87

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an intracellular domain derived from FLT3

<400> 87

His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Ile
1 5 10 15

Gln Val Thr Gly Pro Leu Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg
20 25 30

Asp Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu
35 40 45

eolf-seql

Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Arg Val Met Asn Ala
50 55 60

Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val
65 70 75 80

Lys Met Leu Lys Glu Lys Ala Asp Ser Cys Glu Lys Glu Ala Leu Met
85 90 95

Ser Glu Leu Lys Met Met Thr His Leu Gly His His Asp Asn Ile Val
100 105 110

Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Val Tyr Leu Ile Phe
115 120 125

Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu Arg Ser Lys Arg
130 135 140

Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu His Asn Phe
145 150 155 160

Ser Phe Tyr Pro Thr Phe Gln Ala His Ser Asn Ser Ser Met Pro Gly
165 170 175

Ser Arg Glu Val Gln Leu His Pro Pro Leu Asp Gln Leu Ser Gly Phe
180 185 190

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

Lys Arg Leu Ala Glu Glu Glu Glu Glu Asp Leu Asn Val Leu Thr Phe
210 215 220

Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu Phe
225 230 235 240

eolf-seql

Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
245 250 255

Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu Ala
260 265 270

Arg Asp Ile Leu Ser Asp Ser Ser Tyr Val Val Arg Gly Asn Ala Arg
275 280 285

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile Tyr
290 295 300

Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
305 310 315 320

Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala Asn
325 330 335

Phe Tyr Lys Leu Ile Gln Ser Gly Phe Lys Met Glu Gln Pro Phe Tyr
340 345 350

Ala Thr Glu Gly Ile Tyr Phe Val Met Gln Ser Cys Trp Ala Phe Asp
355 360 365

Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly Cys
370 375 380

Gln Leu Ala Glu Ala Glu Glu Ala Met Tyr Gln Asn Met Gly Gly Asn
385 390 395 400

Val Pro Glu His Pro Ser Ile Tyr Gln Asn Arg Arg Pro Leu Ser Arg
405 410 415

Glu Ala Gly Ser Glu Pro Pro Ser Pro Gln Ala Gln Val Lys Ile His
420 425 430

eolf-seql

Gly Glu Arg Ser
435

<210> 88
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of hinge domain derived from TLR4

<400> 88

Gln Leu Tyr Ser Leu Ser Thr Leu Asp Cys Ser Phe Asn Arg Ile Glu
1 5 10 15

Thr Ser Lys Gly Ile Leu Gln His Phe Pro Lys Ser Leu Ala Phe Phe
20 25 30

Asn Leu Thr Asn Asn Ser Val Ala Cys Ile Cys Glu His Gln Lys Phe
35 40 45

Leu Gln Trp Val Lys Glu Gln Lys Gln Phe Leu Val Asn Val Glu Gln
50 55 60

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

Phe Asn Asn Ser Thr Cys Tyr Met Tyr Lys Thr Ile Ile Ser Val Ser
85 90 95

Val Val Ser

<210> 89
<211> 21
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> Amino acid sequence of a transmembrane domain derived from TLR4

<400> 89

Val Ile Val Val Ser Thr Val Ala Phe Leu Ile Tyr His Phe Tyr Phe
1 5 10 15

His Leu Ile Leu Ile
20

<210> 90

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an intracellular domain derived from TLR4

<400> 90

Ala Gly Cys Lys Lys Tyr Ser Arg Gly Glu Ser Ile Tyr Asp Ala Phe
1 5 10 15

Val Ile Tyr Ser Ser Gln Asn Glu Asp Trp Val Arg Asn Glu Leu Val
20 25 30

Lys Asn Leu Glu Glu Gly Val Pro Arg Phe His Leu Cys Leu His Tyr
35 40 45

Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile Gln Glu
50 55 60

Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser Arg His Phe
65 70 75 80

Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp
85 90 95

eolf-seq1

Gln Phe Leu Ser Ser Arg Ser Gly Ile Ile Phe Ile Val Leu Glu Lys
100 105 110

Val Glu Lys Ser Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu
115 120 125

Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Asn Pro Leu Gly Arg His
130 135 140

Ile Phe Trp Arg Arg Leu Lys Asn Ala Leu Leu Asp Gly Lys Ala Ser
145 150 155 160

Asn Pro Glu Gln Thr Ala Glu Glu Glu Gln Glu Thr Ala Thr Trp Thr
165 170 175

<210> 91

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of hinge domain derived from CCR2

<400> 91

Met Glu Asp Asn Asn Met Leu Pro Gln Phe Ile His Gly Ile Leu Ser
1 5 10 15

Thr Ser His Ser Leu Phe Thr Arg Ser Ile Gln Glu Leu Asp Glu Gly
20 25 30

Ala Thr Thr Pro Tyr Asp Tyr Asp Asp Gly Glu Pro Cys His Lys Thr
35 40 45

Ser Val Lys Gln Ile Gly Ala
50 55

<210> 92

<211> 118

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of hinge domain derived from ITGB2

<400> 92

Asn Ala Arg Leu Val Glu Cys Ser Gly Arg Gly His Cys Gln Cys Asn
1 5 10 15

Arg Cys Ile Cys Asp Glu Gly Tyr Gln Pro Pro Met Cys Glu Asp Cys
20 25 30

Pro Ser Cys Gly Ser His Cys Arg Asp Asn His Thr Ser Cys Ala Glu
35 40 45

Cys Leu Lys Phe Asp Lys Gly Pro Phe Glu Lys Asn Cys Ser Val Gln
50 55 60

Cys Ala Gly Met Thr Leu Gln Thr Ile Pro Leu Lys Lys Lys Pro Cys
65 70 75 80

Lys Glu Arg Asp Ser Glu Gly Cys Trp Ile Thr Tyr Thr Leu Gln Gln
85 90 95

Lys Asp Gly Arg Asn Ile Tyr Asn Ile His Val Glu Asp Ser Leu Glu
100 105 110

Cys Val Lys Gly Pro Asn
115

<210> 93

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a transmembrane domain derived from ITGB2

eolf-seql

<400> 93

Val Ala Ala Ile Val Gly Gly Thr Val Val Gly Val Val Leu Ile Gly
1 5 10 15

Val Leu Leu Leu Val Ile Trp
20

<210> 94

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an intracellular domain derived from ITGB2

<400> 94

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

Lys Glu Lys Leu Lys Ser Gln Trp Asn Asn Asp Asn Pro Leu Phe Lys
20 25 30

Ser Ala Thr Thr Thr Val Met Asn Pro Lys Phe Ala Glu Ser
35 40 45

<210> 95

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of hinge domain derived from CSF2RB

<400> 95

Thr Gln Lys Met Ala Tyr Ser Phe Ile Glu His Thr Phe Gln Val Gln
1 5 10 15

Tyr Lys Lys Lys Ser Asp Ser Trp Glu Asp Ser Lys Thr Glu Asn Leu
20 25 30

eolf-seql

Asp Arg Ala His Ser Met Asp Leu Ser Gln Leu Glu Pro Asp Thr Ser
35 40 45

Tyr Cys Ala Arg Val Arg Val Lys Pro Ile Ser Asn Tyr Asp Gly Ile
50 55 60

Trp Ser Lys Trp Ser Glu Glu Tyr Thr Trp Lys Thr Asp Trp
65 70 75

<210> 96

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a transmembrane domain derived from CSF2RB

<400> 96

Val Met Pro Thr Leu Trp Ile Val Leu Ile Leu Val Phe Leu Ile Leu
1 5 10 15

Thr Leu Leu Leu Ile Leu
20

<210> 97

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an intracellular domain derived from CSF2RB

<400> 97

Arg Phe Gly Cys Val Ser Val Tyr Arg Thr Tyr Arg Lys Trp Lys Glu
1 5 10 15

Lys Ile Pro Asn Pro Ser Lys Ser Leu Leu Phe Gln Asp Gly Gly Lys

eolf-seql

20

25

30

Gly Leu Trp Pro Pro Gly Ser Met Ala Ala Phe Ala Thr Lys Asn Pro
35 40 45

Ala Leu Gln Gly Pro Gln Ser Arg Leu Leu Ala Glu Gln Gln Gly Glu
50 55 60

Ser Tyr Ala His Leu Glu Asp Asn Asn Val Ser Pro Leu Thr Ile Glu
65 70 75 80

Asp Pro Asn Ile Ile Arg Val Pro Pro Ser Gly Pro Asp Thr Thr Pro
85 90 95

Ala Ala Ser Ser Glu Ser Thr Glu Gln Leu Pro Asn Val Gln Val Glu
100 105 110

Gly Pro Thr Pro Asn Arg Pro Arg Lys Gln Leu Pro Ser Phe Asp Phe
115 120 125

Asn Gly Pro Tyr Leu Gly Pro Pro Gln Ser His Ser Leu Pro Asp Leu
130 135 140

Pro Asp Gln Leu Gly Ser Pro Gln Val Gly Gly Ser Leu Lys Pro Ala
145 150 155 160

Leu Pro Gly Ser Leu Glu Tyr Met Cys Leu Pro Pro Gly Gly Gln Ala
165 170 175

Gln Leu Val Pro Leu Ser Gln Val Met Gly Gln Gly Gln Ala Met Asp
180 185 190

Val Gln Cys Gly Ser Ser Leu Glu Thr Ser Gly Ser Pro Ser Val Glu
195 200 205

Pro Lys Glu Asn Pro Pro Val Glu Leu Ser Met Glu Glu Gln Glu Ala

eolf-seql

210

215

220

Arg Asp Asn Pro Val Thr Leu Pro Ile Ser Ser Gly Gly Pro Glu Gly
225 230 235 240

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

Leu Pro Thr Gly Pro Leu Ser Thr Ser Leu Gly Pro Ser Leu Gly Leu
260 265 270

Pro Ser Ala Gln Ser Pro Arg Leu Cys Leu Lys Leu Pro Arg Val Pro
275 280 285

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

Leu Pro Pro Ser Val Ser Gln Ala Ala Lys Ser Pro Pro Gly His Pro
305 310 315 320

Ala Pro Pro Val Ala Ser Ser Pro Thr Val Ile Pro Gly Glu Pro Arg
325 330 335

Glu Glu Val Gly Pro Ala Ser Pro His Pro Glu Gly Leu Leu Val Leu
340 345 350

Gln Gln Val Gly Asp Tyr Cys Phe Leu Pro Gly Leu Gly Pro Gly Ser
355 360 365

Leu Ser Pro His Ser Lys Pro Pro Ser Pro Ser Leu Cys Ser Glu Thr
370 375 380

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

Met Pro Gln Ala Pro Ala Ile Gln Phe Phe Lys Ser Leu Lys His Gln

eolf-seql
 405 410 415

Asp Tyr Leu Ser Leu Pro Pro Trp Asp Asn Ser Gln Ser Gly Lys Val
 420 425 430

Cys

<210> 98
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of hinge domain derived from CCR1
 <400> 98

Thr Pro Cys Gln Lys Thr Ala Val Arg Ala Phe Gly Ala
 1 5 10

<210> 99
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of hinge domain derived from CCR5
 <400> 99

Met Ser Ala Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala
 1 5 10 15

<210> 100
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of hinge domain derived from CXCR4
 <400> 100

eolf-seql

Phe Arg Asp Glu Asn Val His Phe Asn Arg
1 5 10

<210> 101
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of hinge domain derived from SELPLG

<400> 101

Ile Ala Thr Thr Asp Pro Thr Ala Pro Gly Thr Gly Gly Thr Ala Val
1 5 10 15

Gly Met Leu Ser Thr Asp Ser Ala Thr Gln Trp Ser Leu Thr Ser Val
20 25 30

Glu Thr Val Gln Pro Ala Ser Thr Glu Val Glu Thr Ser Gln Pro Ala
35 40 45

Pro Met Glu Ala Glu Thr Ser Gln Pro Ala Pro Met Glu Ala Glu Thr
50 55 60

Ser Gln Pro Ala Pro Met Glu Ala Asp Thr Ser Lys Pro Ala Pro Thr
65 70 75 80

Glu Ala Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala Glu Thr Ser Gln
85 90 95

Pro Ala Pro Asn Glu Ala Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala
100 105 110

Glu Thr Ser Lys Pro Ala Pro Thr Glu Ala Glu Thr Thr Gln Leu Pro
115 120 125

Arg Ile Gln Ala Val Lys Thr Leu Phe Thr Thr Ser Ala Ala Thr Glu

eolf-seql

130

135

140

Val Pro Ser Thr Glu Pro Thr Thr Met Glu Thr Ala Ser Thr Glu Ser
145 150 155 160

Asn Glu Ser Thr Ile Phe Leu Gly Pro Ser Val Thr His Leu Pro Asp
165 170 175

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

Pro Thr Leu Pro Gly Ser Ser Asp Leu Ile Pro Val Lys Gln Cys
195 200 205

<210> 102

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a transmembrane domain derived from SELPLG

<400> 102

Leu Leu Ile Ile Leu Ile Leu Ala Ser Leu Ala Thr Ile Phe Leu Val
1 5 10 15

Cys Thr Val Val Leu
20

<210> 103

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an intracellular domain derived from SELPLG

<400> 103

eolf-seql

Ala Val Arg Leu Ser Arg Lys Thr His Met Tyr Pro Val Arg Asn Tyr
1 5 10 15

Ser Pro Thr Glu Met Ile Cys Ile Ser Ser Leu Leu Pro Glu Gly Gly
20 25 30

Asp Gly Ala Pro Val Thr Ala Asn Gly Gly Leu Pro Lys Val Gln Asp
35 40 45

Leu Lys Thr Glu Pro Ser Gly Asp Arg Asp Gly Asp Asp Leu Thr Leu
50 55 60

His Ser Phe Leu Pro
65

<210> 104
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of peptide that facilitates DNA engineering

<400> 104

Thr Gly
1

<210> 105
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of IgK domain (for FRP5 and trastuzumab)

<400> 105
atggattttc aggtgcagat tttctctttc ctcctcatth cgcctcagt gattatgtca 60

agggggg 66

eolf-seql

<210> 106
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IgK domain (for pertuzumab)

<400> 106
 atgggattttc aggtgcagat tttctccttt ctcttcattt cagccagcgt gattatgtct 60

cggggg 66

<210> 107
 <211> 6
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of a peptide that facilitates DNA engineering

<400> 107
 accggt 6

<210> 108
 <211> 6
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of a peptide that facilitates DNA engineering

<400> 108
 accggg 6

<210> 109
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IgK domain (for EVIR-N1)

eolf-seql

<400> 109
 atggacttcc aggtgcagat cttcagcttc ctgctgatct ccgccagcgt gatcatgagc 60
 agaggc 66

<210> 110
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IgK domain (for EVIR-N2)

<400> 110
 atggattttc aggtgcagat cttcagcttc ctgctgatct ccgccagcgt gatcatgagc 60
 agaggc 66

<210> 111
 <211> 744
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of anti-TYRP1 scFv TA99

<400> 111
 gacatccaga tgagccagag ccctgccagc ctgtctgcct ctgtgggcga gacagtgacc 60
 atcacctgta gagccagcgg caacatctac aactacctgg cctggatatca gcagaagcag 120
 ggcaagagcc cccatctgct ggtgtacgac gccaagacac tggccgacgg cgtgccctct 180
 agattctctg gcagcggctc cggcaccagc tacagcctga agatcagctc cctgcagacc 240
 gaggactccg gcaactacta ctgccagcac ttctgggtccc tgcccttcac cttcggcagc 300
 ggaccaagc tggaaatcaa gagaggcggc ggaggctctg gcggaggcgg atctgggggc 360
 ggaggaagtg gcgggggagg atctgaagtg cagctgcagc agtctggcgc tgagctcgtg 420
 cgacctggcg ctctcgtgaa gctgagctgc aagaccagcg gcttcaatat caaggactac 480
 ttcttgcaact gggtgcgaca gaggcctgac cagggcctgg aatggatcgg ctggatcaac 540
 cccgacaacg gcaacaccgt gtacgaccct aagttccagg gcaccgccag cctgacagcc 600

eolf-seql

gacacaagct ccaacacagt gtacctgcag ctgagcggcc tgacctccga ggataccgcc 660
gtgtacttct gcaccagaag agactacacc tacgagaagg ccgccctgga ctactggggc 720
caggaacaa ccgtgaccgt gtcc 744

<210> 112
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of anti-GD2 scFv 14G2a

<400> 112
gaagttcagc tgctgcagag cggacccgaa ctggaaaaac ctggcgcctc cgtgatgatc 60
agctgcaagg cctctggcag ctccctcacc ggctacaaca tgaactgggt ccgacagaac 120
atcggcaaga gcctggaatg gatcggcgcc atcgatcctt actacggcgg caccagctac 180
aaccagaagt tcaagggcag agccacactg accgtggaca agagcagcag cacagcctac 240
atgcatctga agtccctgac cagcaggagc agcggcgtgt actactgtgt gtccggcatg 300
gaatactggg gccagggcac aagcgtgaca gtctcttctg gcggcgggtg atctggcgga 360
ggcggaagtg gtggcggcgg atctgatgtg gtcattgacac agaccctct gagcctgcct 420
gtgtctctgg gagatcaggc cagcatcagc tgtagaagca gccagagcct ggtgcacaga 480
aacggcaaca cctacctgca ctggtatctg cagaagcccg gccagtctcc taagctgctg 540
atccacaagg tgtccaacag attcagcggc gtgcccagca gattctctgg ctctggaagc 600
ggcaccgact tcaccctgaa gattagcaga gtggaagccg aggacctggg cgtgtacttc 660
tgtagccaga gcacacacgt gccacctctg acatttggcg ctggcaccaa gctggaactg 720

<210> 113
<211> 248
<212> PRT
<213> Artificial Sequence

<220>

eolf-seql

<223> Amino acid sequence of TA99-based anti-TYRP1 scFv

<400> 113

Asp Ile Gln Met Ser Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile Tyr Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro His Leu Leu Val
35 40 45

Tyr Asp Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Ser Ser Leu Gln Thr
65 70 75 80

Glu Asp Ser Gly Asn Tyr Tyr Cys Gln His Phe Trp Ser Leu Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
130 135 140

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

Phe Leu His Trp Val Arg Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
165 170 175

eolf-seq1

Gly Trp Ile Asn Pro Asp Asn Gly Asn Thr Val Tyr Asp Pro Lys Phe
180 185 190

Gln Gly Thr Ala Ser Leu Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
195 200 205

Leu Gln Leu Ser Gly Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys
210 215 220

Thr Arg Arg Asp Tyr Thr Tyr Glu Lys Ala Ala Leu Asp Tyr Trp Gly
225 230 235 240

Gln Gly Thr Thr Val Thr Val Ser
245

<210> 114
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of 14G2a-based anti-GD2 scFv

<400> 114

Glu Val Gln Leu Leu Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1 5 10 15

Ser Val Met Ile Ser Cys Lys Ala Ser Gly Ser Ser Phe Thr Gly Tyr
20 25 30

Asn Met Asn Trp Val Arg Gln Asn Ile Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

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

eolf-seql

Met His Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Val Ser Gly Met Glu Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
130 135 140

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

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
165 170 175

Pro Lys Leu Leu Ile His Lys Val Ser Asn Arg Phe Ser Gly Val Pro
180 185 190

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
195 200 205

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
210 215 220

Thr His Val Pro Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

<210> 115

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

eolf-seq1

<223> Nucleic acid sequence of Cxcl9_Fw_XmaI

<400> 115

aaaaacccgg gtcactccaa cacagtgact c

31

<210> 116

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of Cxcl9_Rv_SalI/NheI

<400> 116

aaaaagtcga cgctagccag ggtgcttggt ggtaaagt

38

<210> 117

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of Cxcl9

<400> 117

tcactccaac acagtgactc aatagaactc agctctgcca tgaagtccgc tggtcttttc 60

ctcttgggca tcattcttct ggagcagtgt ggagttcgag gaaccctagt gataaggaat 120

gcacgatgct cctgcatcag caccagccga ggcacgatcc actacaaatc cctcaaagac 180

ctcaaacagt ttgccccaaag cccaattgc aaaaaactg aaatcattgc tacactgaag 240

aacggagatc aaacctgcct agatccggac tcggcaaattg tgaagaagct gatgaaagaa 300

tgggaaaaaga agatcagcca aaagaaaaaag caaaagaggg ggaaaaaaca tcaaaagaac 360

atgaaaaaca gaaaacccaa aacaccccaa agtcgtcgtc gttcaaggaa gactacataa 420

gagaccatta ctttaccac aagcaccctg 450

<210> 118

<211> 32

<212> DNA

<213> Artificial Sequence

eolf-seql

<220>

<223> Nucleic acid sequence of GM-CSF_Fw_XmaI

<400> 118

aaaaacccgg gcagagagaa aggctaaggt cc

32

<210> 119

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of GM-CSF_Rv_SalI/NheI

<400> 119

aaaaagtcga cgctagcagt ctgagaagct ggatt

35

<210> 120

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of GM-CSF

<400> 120

cagagagaaa ggctaaggct ctgaggagga tgtggctgca gaatttactt ttcctgggca

60

ttgtgggtcta cagcctctca gcacccaccc gctcacccat cactgtcacc cggccttgga

120

agcatgtaga ggccatcaaa gaagccctga acctcctgga tgacatgcct gtcacgttga

180

atgaagaggt agaagtcgtc tctaacgagt tctccttcaa gaagctaaca tgtgtgcaga

240

cccgcttgaa gatattcgag cagggtctac ggggcaattt caccaaactc aagggcgcct

300

tgaacatgac agccagctac taccagacat actgcccccc aactccggaa acggactgtg

360

aaacacaagt taccacctat gcggatttca tagacagcct taaaaccttt ctgactgata

420

tcccctttga atgcaaaaaa ccaggccaaa aatgaggaag cccaggccag ctctgaatcc

480

agcttctcag act

493

eolf-seql

<210> 121
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IFNg _Fw_XmaI

<400> 121
 aaaaacccgg gagttctggg cttctcctcc t 31

<210> 122
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IFNg _Rv_SalI/NheI

<400> 122
 aaaaagtcga cgctagcgac aatctcttcc ccacccc 37

<210> 123
 <211> 530
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IFNg

<400> 123
 agttctgggc ttctcctcct gcggcctagc tctgagacaa tgaacgctac aactgcatc 60
 ttggctttgc agctcttcct catggctggt tctggctggt actgccacgg cacagtcatt 120
 gaaagcctag aaagtctgaa taactatctt aactcaagtg gcatagatgt ggaagaaaag 180
 agtctcttct tggatatctg gaggaactgg caaaaggatg gtgacatgaa aatcctgcag 240
 agccagatta tctcttttcta cctcagactc tttgaagtct tgaaagacaa tcaggccatc 300
 agcaacaaca taagcgatcat tgaatcacac ctgattacta ctttcttcag caacagcaag 360
 gcgaaaaagg atgcattcat gattattgcc aagtttgagg tcaacaaccc acaggtccag 420
 cgccaagcat tcaatgagct catccgagtg gtccaccagc tggtgccgga atccagcctc 480

eolf-seql

aggaagcgga aaaggagtcg ctgctgattc ggggtgggga agagattgtc 530

<210> 124
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of LIN28_Fw_BamHI

<400> 124
aaaaaggatc cctttgcctc cggacttctc tgg 33

<210> 125
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of LIN28_Rv_SalI

<400> 125
aaaaagtcga caaagacagg gtgacactgg ga 32

<210> 126
<211> 857
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of LIN28 (PstI and SmaI- mouse trophoblast cells)

<400> 126
ctttgcctcc ggacttctct ggggccagca gccgcccgc ctggggcccg gggccacggg 60
ctcagcagac gaccatgggc tcggtgtcca accagcagtt tgcaggtggc tgcgccaagg 120
cagcggagaa ggcgccagag gaggcgccgc ctgacgcggc ccgagcggca gacgagccgc 180
agctgctgca cggggccggc atctgtaagt ggttcaacgt gcgcatgggg ttcggcttcc 240
tgtctatgac cgcccgcgct ggggtcgcg tcgaccccc ggtggacgtc tttgtgcacc 300

eolf-seql

agagcaagct gcacatggaa gggttccgaa gcctcaagga gggtagggcg gtggagttca 360
 cctttaagaa gtctgccaaag ggtctggaat ccatccgtgt cactggccct ggtggtgtgt 420
 tctgtattgg aagtgagcgg cggccaaagg ggaagaacat gcagaagcga agatccaaag 480
 gagacaggtg ctacaactgc ggtgggctag accatcatgc caaggaatgc aagctgccac 540
 cccagcccaa gaagtgccac ttttgccaaa gcatcaacca tatggtggcc tcgtgtccac 600
 tgaaggccca gcagggcccc agttctcagg gaaagcctgc ctacttccgg gaggaagagg 660
 aagagatcca cagccctgcc ctgctcccag aagcccagaa ttgaggccca ggagtcaggg 720
 ttattctttg gctaattgggg agtttaagga aagaggcatc aatctgcaga gtggagaaag 780
 tgggggtaag ggtgggttgc gtgggtagct tgactgccc tgtctcaggc cgggggttccc 840
 agtgtcacc tgtcttt 857

<210> 127

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of CD40 (GeneArt CD40 Blunt sites (SmaI - AgeI-blunted) in AfeI/NheI-blunted bidirectional)

<400> 127

gccacatgg tctctctccc tcggctgtgt gctctgtggg gttgtctgct caccgctgtg 60
 catctcggcc agtgtgtgac ttgttctgat aaacagtacc tgcattgacgg gcagtgtgt 120
 gatctgtgcc agcccgggtc taggctcacc agtcattgta cagccctgga gaagactcag 180
 tgccaccctt gtgactcagg ggagttcagc gctcagtgga accgagaaat taggtgccac 240
 cagcatagac actgtgagcc taatcagggg ctgcgggtga agaaagaggg taccgcagaa 300
 agtgacactg tctgcacctg taaggagggc cagcattgca cctcaaaaga ttgcgaagct 360
 tgtgcacagc acacaccttg tatcccaggc ttcggagtga tggagatggc tactgaaacc 420
 acagacaccg tgtgccaccc atgtcccgtc ggattctttt ctaaccagag ctccctcttt 480
 gagaagtgt atccatggac aagctgtgag gataagaacc tggaagtgt ccagaaaggc 540

eolf-seq1

acatcccaga ctaatgtcat ttgcggactg aaatctcgga tgcgcgccct gctcgtgatc	600
ccagtgggtca tgggcatcct cattactatc ttcggagtgt ttctgtacat taagaaagtg	660
gtcaagaaac ccaaggacaa cgagatcctc ccacctgcag ctaggagaca ggacccccag	720
gagatggaag attatcctgg acataatata gcagccccag tgcaggaaac tctgcacggg	780
tgtcagccccg tcaccagga ggatggcaag gaaagcagaa tctccgtcca ggaaaggcag	840
gtcactgata gcatcgact ccgcccactc gtctga	876

<210> 128

<211> 762

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of anti-HER2 scFv CHA21 (1)

<400> 128

gatattgtcc tcacacagac tcccagctcc ctgcctgtgt ccgtcggaga gaaagtgacc	60
atgacatgca agtctagtca gacactgctc tactctaaca atcagaagaa ctacctcgca	120
tggtatcagc agaaaccagg acagagcccc aagctgctca tctcctgggc tttcaccggg	180
aaatccgggg tgcctgaccg cttcacaggt agcggctccg gaactgattt tactctgacc	240
attggatctg tgaaggcaga ggacctcgcc gtctactatt gccagcagta cagtaattat	300
ccatggactt ttggcggagg gaccaggctg gaaatcaaga gaggtggagg aggggtccggt	360
ggaggagggt ctggtggagg agggagtggg ggaggagggt cagagggtgca gctgcagcag	420
tctggccccg aagtgggtcaa aactggagct tcagtcaaaa tcagctgtaa ggcatctggg	480
tacagcttca ccggctactt catcaactgg gtgaagaaaa attcaggga gagccctgag	540
tggatcggcc acatttcaag ctctacgcc acaagcactt acaaccagaa gttcaaaaat	600
aaggccgctt ttaccgtgga cacatctagt tcaaccgct tcatgcagct gaactccctc	660
acatctgaag atagtgtgt gtactattgt gtcaggagcg gcaactacga agaatatgct	720
atggattact gggggcaggg gacctccgtg actgtctcaa gc	762

eolf-seql

<210> 129
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of IgK domain (1)

<400> 129
 atggattttc aggtccagat tttctccttc ctctcattt cagccagcgt cattatgtct 60
 cggggg 66

<210> 130
 <211> 1602
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of EVIR-N1

<400> 130
 atggacttcc aggtgcagat cttcagcttc ctgctgatct ccgccagcgt gatcatgagc 60
 agaggcgaca tccagatgag ccagagccct gccagcctgt ctgcctctgt gggcgagaca 120
 gtgaccatca cctgtagagc cagcggcaac atctacaact acctggcctg gtatcagcag 180
 aagcagggca agagcccca tctgctgggtg tacgacgcca agacactggc cgacggcgtg 240
 ccctctagat tctctggcag cggctccggc acccagtaca gcctgaagat cagctccctg 300
 cagaccgagg actccggcaa ctactactgc cagcacttct ggtccctgcc cttcaccttc 360
 ggcagcggca ccaagctgga aatcaagaga ggcggcggag gctctggcgg aggcggatct 420
 gggggcggag gaagtggcgg gggaggatct gaagtgcagc tgcagcagtc tggcgctgag 480
 ctcgtgcgac ctggcgctct cgtgaagctg agctgcaaga ccagcggctt caatatcaag 540
 gactacttcc tgactgggt gcgacagagg cctgaccagg gcctggaatg gatcggctgg 600
 atcaaccccg acaacggcaa caccgtgtac gaccctaagt tccagggcac cgccagcctg 660
 acagccgaca caagctcaa cacagtgtac ctgcagctga gcggcctgac ctccgaggat 720

eolf-seql

accgccgtgt acttctgcac cagaagagac tacacctacg agaaggccgc cctggactac	780
tggggccagg gaacaaccgt gaccgtgtcc accggtcttc tgggggtgtc ccttgagggt	840
gccaaggagg catgccccac aggctgtac acacacagcg gtgagtgtg caaagcctgc	900
aacctgggcg aggggtgtggc ccagccttgt ggagccaacc agaccgtgtg tgagccctgc	960
ctggacagcg tgacgttctc cgacgtgggtg agcgcgaccg agccgtgcaa gccgtgcacc	1020
gagtgcgtgg ggctccagag catgtcggcg ccgtgcgtgg aggccgacga cgccgtgtgc	1080
cgctgcgcct acggctacta ccaggatgag acgactgggc gctgcgaggc gtgccgcgtg	1140
tgcgaggcgg gctcgggcct cgtgttctcc tgccaggaca agcagaacac cgtgtgcgag	1200
gagtgccccg acggcacgta ttccgacgag gccaaccacg tggacccgtg cctgccctgc	1260
accgtgtgcg aggacaccga gcgccagctc cgcgagtgc cagctgggc cgacgccgag	1320
tgcgaggaga tccctggccg ttggattaca cgggtccacac cccagaggg ctcggacagc	1380
acagccccca gcaccagga gcctgaggca cctccagaac aagacctcat agccagcacg	1440
gtggcagggtg tggtgaccac agtgatgggc agctcccagc ccgtgggtgac ccgaggcacc	1500
accgacaacc tcatccctgt ctattgctcc atcctggctg ctgtggttgt gggccttgtg	1560
gcctacatag ccttcaagag gtggaacagg gggatcctct ag	1602

<210> 131

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of EVIR-N2

<400> 131

atggattttc aggtgcagat cttcagcttc ctgctgatct ccgccagcgt gatcatgagc	60
agaggcgaag ttcagctgct gcagagcgga cccgaactgg aaaaacctgg cgcctccgtg	120
atgatcagct gcaaggcctc tggcagctcc ttaccggct acaacatgaa ctgggtccga	180
cagaacatcg gcaagagcct ggaatggatc ggcgccatcg atccttacta cggcggcacc	240

eolf-seq1

agctacaacc agaagttcaa gggcagagcc acactgaccg tggacaagag cagcagcaca	300
gcctacatgc atctgaagtc cctgaccagc gaggacagcg ccgtgtacta ctgtgtgtcc	360
ggcatggaat actggggcca gggcacaagc gtgacagtct cttctggcgg cgggtgatct	420
ggcggaggcg gaagtgggtg cggcggatct gatgtggtca tgacacagac ccctctgagc	480
ctgcctgtgt ctctgggaga tcaggccagc atcagctgta gaagcagcca gagcctgggtg	540
cacagaaacg gcaacaccta cctgcactgg tatctgcaga agcccggcca gtctcctaag	600
ctgctgatcc acaagggtgc caacagattc agcggcgtgc ccgacagatt ctctggctct	660
ggaagcggca ccgacttcac cctgaagatt agcagagtgg aagccgagga cctgggcgtg	720
tacttctgta gccagagcac acacgtgcca cctctgacat ttggcgctgg caccaagctg	780
gaactgaccg gtcttctggg ggtgtccctt ggaggtgcca aggaggcatg cccacaggc	840
ctgtacacac acagcgggtga gtgctgcaaa gcctgcaacc tgggcgaggg tgtggcccag	900
ccttgtggag ccaaccagac cgtgtgtgag ccctgcctgg acagcgtgac gttctccgac	960
gtggtgagcg cgaccgagcc gtgcaagccg tgcaccgagt gcgtggggct ccagagcatg	1020
tcggcgccgt gcgtggaggc cgacgacgcc gtgtgccgct gcgcctacgg ctactaccag	1080
gatgagacga ctgggcgctg cgaggcgtgc cgcgtgtgcg aggcgggctc gggcctcgtg	1140
ttctcctgcc aggacaagca gaacaccgtg tgcgaggagt gccccgacgg cacgtattcc	1200
gacgaggcca accacgtgga cccgtgcctg ccctgcaccg tgtgagagga caccgagcgc	1260
cagctccgcg agtgacacg ctgggccgac gccgagtgcg aggagatccc tggccgttgg	1320
attacacggg ccacaccccc agagggtctg gacagcacag cccccagcac ccaggagcct	1380
gaggcacctc cagaacaaga cctcatagcc agcacgggtg caggtgtggt gaccacagtg	1440
atgggcagct cccagcccgt ggtgaccgga ggcaccaccg acaacctcat ccctgtctat	1500
tgctccatcc tggctgctgt ggttgtgggc cttgtggcct acatagcctt caagagggtg	1560
aacaggggga tcctctag	1578

eolf-seql

<210> 132

<211> 533

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of EVIR-N1

<400> 132

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Gln Met Ser Gln Ser Pro Ala Ser
20 25 30

Leu Ser Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Gly Asn Ile Tyr Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys
50 55 60

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys
85 90 95

Ile Ser Ser Leu Gln Thr Glu Asp Ser Gly Asn Tyr Tyr Cys Gln His
100 105 110

Phe Trp Ser Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125

Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu
145 150 155 160

eolf-seql

Leu Val Arg Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Thr Ser Gly
165 170 175

Phe Asn Ile Lys Asp Tyr Phe Leu His Trp Val Arg Gln Arg Pro Asp
180 185 190

Gln Gly Leu Glu Trp Ile Gly Trp Ile Asn Pro Asp Asn Gly Asn Thr
195 200 205

Val Tyr Asp Pro Lys Phe Gln Gly Thr Ala Ser Leu Thr Ala Asp Thr
210 215 220

Ser Ser Asn Thr Val Tyr Leu Gln Leu Ser Gly Leu Thr Ser Glu Asp
225 230 235 240

Thr Ala Val Tyr Phe Cys Thr Arg Arg Asp Tyr Thr Tyr Glu Lys Ala
245 250 255

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Thr Gly
260 265 270

Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys Pro Thr Gly
275 280 285

Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu
290 295 300

Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys
305 310 315 320

Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys
325 330 335

Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys
340 345 350

eolf-seql

Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln
355 360 365

Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly
370 375 380

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

Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro
405 410 415

Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu
420 425 430

Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp
435 440 445

Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser
450 455 460

Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr
465 470 475 480

Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val
485 490 495

Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys Ser Ile Leu
500 505 510

Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe Lys Arg Trp
515 520 525

Asn Arg Gly Ile Leu
530

eolf-seql

<210> 133
 <211> 525
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of EVIR-N2

<400> 133

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Met Ser Arg Gly Glu Val Gln Leu Leu Gln Ser Gly Pro Glu
 20 25 30

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

Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Asn Ile Gly
 50 55 60

Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr Gly Gly Thr
 65 70 75 80

Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
 85 90 95

Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr Ser Glu Asp
 100 105 110

Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu Tyr Trp Gly Gln Gly
 115 120 125

Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

eolf-seql

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

Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
165 170 175

Gln Ser Leu Val His Arg Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile His Lys Val Ser Asn
195 200 205

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
210 215 220

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

Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Leu Thr Phe Gly Ala
245 250 255

Gly Thr Lys Leu Glu Leu Thr Gly Leu Leu Gly Val Ser Leu Gly Gly
260 265 270

Ala Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys
275 280 285

Cys Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala
290 295 300

Asn Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
305 310 315 320

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

eolf-seq1

Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys
340 345 350

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
355 360 365

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
370 375 380

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

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
405 410 415

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
420 425 430

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
435 440 445

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
450 455 460

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
465 470 475 480

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu
485 490 495

Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val
500 505 510

Ala Tyr Ile Ala Phe Lys Arg Trp Asn Arg Gly Ile Leu
515 520 525

eolf-seql

<210> 134
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of TYRP1 Fw

<400> 134
aaaaaaaccg gtgacctgtg ttctgaactc ttgc 34

<210> 135
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of TYRP1 Rv

<400> 135
aaaaaagtcg acactgtcat cactggagag ca 32

<210> 136
<211> 103
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of the anti-B2m gRNA

<400> 136
ggtcgtcagc atggctcgct gttttagagc tagaaatagc aagttaaaat aaggctagtc 60

cgttatcaac ttgaaaaagt ggcaccgagt cggtgctttt ttt 103