

SEQUENCE LISTING

<110> Tessa Therapeutics Pte. Ltd.
Clegg, Richard I

<120> Chimeric Antigen Receptor

<130> RIC/FP7291040

<150> US62/366729

<151> 2016-07-26

<150> US62/366731

<151> 2016-07-26

<160> 126

<170> PatentIn version 3.5

<210> 1

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> GC33 heavy chain variable region sequence

<400> 1

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

Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr
			20					25					30		

Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Lys	Trp	Ile
		35					40					45			

Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser	Gln	Lys	Phe
	50					55					60				

Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
65					70				75					80	

Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
			100					105					110		

Val	Ser	Ala
		115

<210> 2

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> GC33 HC-CDR1

<400> 2

Asp Tyr Glu Met His
1 5

<210> 3

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> GC33 HC-CDR2

<400> 3

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

Gly

<210> 4

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> GC33 HC-CDR3

<400> 4

Phe Tyr Ser Tyr Thr Tyr
1 5

<210> 5

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> GC33 light chain variable region sequence

<400> 5

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Asn
85 90 95

Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 6
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> GC33 LC-CDR1

<400> 6

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> GC33 LC-CDR2

<400> 7

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> GC33 LC-CDR3

<400> 8

Ser Gln Asn Thr His Val Pro Pro Thr
1 5

<210> 9
<211> 242
<212> PRT
<213> Artificial Sequence

<220>

<223> GC33 scFv

<400> 9

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 10
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain

<400> 10

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile
20

<210> 11
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8alpha transmembrane domain

<400> 11

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

Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
20 25

<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM motif

<220>
<221> misc_feature
<222> (2)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Leu or Ile

<400> 12

Tyr Xaa Xaa Xaa
1

<210> 13
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM motif

<220>
<221> misc_feature
<222> (2)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Leu or Ile

<220>
<221> misc_feature
<222> (5)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa = Leu or Ile

<400> 13

Tyr Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10

<210> 14
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3-zeta intracellular domain

<400> 14

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

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

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 15

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Human CD226; UniProt Q15762 (CD226_HUMAN)

<400> 15

Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala
1 5 10 15

Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn
20 25 30

Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val
35 40 45

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

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

Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
85 90 95

Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
100 105 110

Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp
115 120 125

Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro
130 135 140

Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val
145 150 155 160

Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu
165 170 175

Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro
180 185 190

Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val
195 200 205

Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu
210 215 220

Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val
225 230 235 240

Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly
245 250 255

Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val
260 265 270

Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
275 280 285

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
290 295 300

Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
305 310 315 320

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
325 330 335

<210> 16

<211> 66

<212> PRT

<213> Artificial Sequence

<220>

<223> CD226 intracellular domain (amino acid positions 271 to 336 of
UniProt Q15762)

<400> 16

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

Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser
20 25 30

Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg
35 40 45

Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr
50 55 60

Arg Val
65

<210> 17
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 intracellular domain

<400> 17

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
1 5 10 15

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
20 25 30

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 18
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular domain

<400> 18

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 19
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 hinge region

<400> 19

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 20

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> F36V-FKBP dimerization sequence

<400> 20

Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
1 5 10 15

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
20 25 30

Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

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

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
85 90 95

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
100 105

<210> 21

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ig heavy chain signal sequence

<400> 21

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 22

<211> 466
<212> PRT
<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/CD226/CD3zeta

<400> 22

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

[illegible]

<210> 23
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/F36V-FKBP/CD226/CD3zeta

<400> 23

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser

210

215

220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
260 265 270

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
275 280 285

Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
290 295 300

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
305 310 315 320

Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
325 330 335

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
340 345 350

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

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
370 375 380

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ile Val Ile Phe Leu
385 390 395 400

Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp
405 410 415

Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser
420 425 430

Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val
435 440 445

Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val Arg Val Lys
450 455 460

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln

465 470 475 480
 Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 485 490 495
 Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 500 505 510
 Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 515 520 525
 Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 530 535 540
 Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 545 550 555 560
 Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 565 570

 <210> 24
 <211> 510
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> scFV GC33/hIgG1 hinge/CD8alpha TMD/CD226/CD28/CD3zeta

 <400> 24

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

 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

 Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
 35 40 45

 Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
 50 55 60

 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

 Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly		
		115					120					125					
Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser		
		130				135					140						
Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val		
145					150					155					160		
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly		
				165					170					175			
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly		
			180					185					190				
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu		
		195					200					205					
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser		
	210					215					220						
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu		
225					230					235					240		
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys		
				245					250					255			
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly		
			260					265					270				
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn		
		275					280					285					
Ile	Val	Ile	Phe	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu		
	290					295					300						
Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser		
305					310					315					320		
Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg		
				325					330					335			
Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr		
			340					345					350				
Arg	Val	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp		
		355					360					365					

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
370 375 380

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
385 390 395 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
405 410 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
420 425 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
435 440 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
450 455 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465 470 475 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
485 490 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 25

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/F36V-FKBP/CD226/CD28/CD3zeta

<400> 25

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
260 265 270

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
275 280 285

Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
290 295 300

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
305 310 315 320

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

325

330

335

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
 340 345 350

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

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
 370 375 380

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ile Val Ile Phe Leu
 385 390 395 400

Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp
 405 410 415

Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser
 420 425 430

Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val
 435 440 445

Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val Phe Trp Val
 450 455 460

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 465 470 475 480

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 485 490 495

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
 500 505 510

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 515 520 525

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 530 535 540

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 545 550 555 560

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 565 570 575

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp

580

585

590

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 595 600 605

Leu His Met Gln Ala Leu Pro Pro Arg
 610 615

<210> 26

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/CD226/4-1BB/CD3zeta

<400> 26

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
 35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
 165 170 175

Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	
			180					185					190			
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	
		195					200					205				
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	
	210					215					220					
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	
225					230					235					240	
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
				245					250						255	
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	
			260					265						270		
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	
		275					280					285				
Ile	Val	Ile	Phe	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	
	290					295					300					
Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	
305					310					315					320	
Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	
				325					330					335		
Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	
			340					345					350			
Arg	Val	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	
		355					360					365				
Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	
	370					375					380					
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	
385					390					395					400	
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	
				405					410					415		
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	
			420					425					430			

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
435 440 445

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
450 455 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465 470 475 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
485 490 495

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 27

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/F36V-FKBP/CD226/41BB/CD3zeta

<400> 27

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

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

130

135

140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
 165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
 180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
 210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 260 265 270

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
 275 280 285

Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro
 290 295 300

Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp
 305 310 315 320

Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
 325 330 335

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
 340 345 350

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

Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
 370 375 380

Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ile Val Ile Phe Leu

385		390		395		400
Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp						
	405			410		415
Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser						
	420			425		430
Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val						
	435			440		445
Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val Lys Arg Gly						
	450			455		460
Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val						
	465			470		475
Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu						
	485			490		495
Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp						
	500			505		510
Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn						
	515			520		525
Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg						
	530			535		540
Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly						
	545			550		555
Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu						
	565			570		575
Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu						
	580			585		590
Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His						
	595			600		605
Met Gln Ala Leu Pro Pro Arg						
	610			615		

<210> 28
 <211> 552
 <212> PRT
 <213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/CD226/CD28/4-1BB/CD3zeta

<400> 28

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
225 230 235 240

Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	260	265	270
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	275	280	285
Ile	Val	Ile	Phe	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	290	295	300
Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	305	310	315
Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	325	330	335
Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	340	345	350
Arg	Val	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	355	360	365
Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	370	375	380
Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	385	390	395
Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	405	410	415
Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	420	425	430
Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	435	440	445
Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	450	455	460
Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	465	470	475
Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	485	490	495

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 500 505 510

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 515 520 525

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 530 535 540

His Met Gln Ala Leu Pro Pro Arg
 545 550

<210> 29
 <211> 659
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFV GC33/hIgG1 hinge/CD8alpha
 TMD/F36V-FKBP/CD226/CD28/41BB/CD3zeta

<400> 29

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
 35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 130 135 140

Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155	160
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175	
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205	
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220	
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	260	265	270	
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	275	280	285	
Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro	290	295	300	
Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	Asp	305	310	315	320
Gly	Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe	325	330	335	
Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala	340	345	350	
Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	355	360	365	
Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	370	375	380	
Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Ile	Val	Ile	Phe	Leu	385	390	395	400

Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	
				405					410					415		
Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	
			420					425					430			
Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	
		435					440					445				
Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	Val	
	450					455					460					
Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	
465					470					475					480	
Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	
				485					490					495		
Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu	
			500					505					510			
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	
		515					520					525				
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	
	530					535					540					
Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	
545					550					555					560	
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	
				565					570					575		
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	
			580					585					590			
Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	
		595					600					605				
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	
	610					615					620					
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	
625					630					635					640	
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	
				645					650					655		

Pro Pro Arg

<210> 30

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> hlgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/CD226/CD3zeta

<400> 30

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg

195

200

205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
 290 295 300

His Arg Asn Ile Val Ile Phe Leu Asn Arg Arg Arg Arg Glu Arg
 305 310 315 320

Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn
 325 330 335

Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp
 340 345 350

Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg
 355 360 365

Pro Lys Thr Arg Val Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370 375 380

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

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln

450

455

460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
 485

<210> 31

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
 TMD/F36V-FKBP/CD226/CD3zeta

<400> 31

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
 50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
 115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 165 170 175

Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	180	185	190	
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	195	200	205	
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	210	215	220	
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	225	230	235	240
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	245	250	255	
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	260	265	270	
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	275	280	285	
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	290	295	300	
His	Arg	Asn	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	305	310	315	320
Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	325	330	335	
Leu	Glu	Asp	Gly	Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	340	345	350	
Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	355	360	365	
Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	370	375	380	
Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	385	390	395	400
His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Ile	Val	405	410	415	
Ile	Phe	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	420	425	430	

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
435 440 445

Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
450 455 460

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
465 470 475 480

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
485 490 495

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
500 505 510

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
515 520 525

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
530 535 540

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
545 550 555 560

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
565 570 575

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
580 585 590

<210> 32

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/CD226/CD28/CD3zeta

<400> 32

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr	Asp	Tyr	Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu
50						55					60				
Lys	Trp	Ile	Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser
65					70					75					80
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105						110	
Tyr	Tyr	Cys	Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr
		115					120					125			
Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				
Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu
145					150					155					160
Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
				165					170						175
Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln
			180					185					190		
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg
		195					200						205		
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
	210					215					220				
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr
225					230					235					240
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr
				245					250					255	
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys
			260					265					270		
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly
		275					280						285		
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn
	290					295					300				

His Arg Asn Ile Val Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg
305 310 315 320

Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn
325 330 335

Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp
340 345 350

Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg
355 360 365

Pro Lys Thr Arg Val Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
370 375 380

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
385 390 395 400

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
405 410 415

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
420 425 430

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
435 440 445

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
450 455 460

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
465 470 475 480

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
485 490 495

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
500 505 510

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
515 520 525

Arg

<210> 33
<211> 636
<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/F36V-FKBP/CD226/CD28/CD3zeta

<400> 33

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
290 295 300

His Arg Asn Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
305 310 315 320

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
325 330 335

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
340 345 350

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
355 360 365

Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
370 375 380

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
385 390 395 400

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ile Val
405 410 415

Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
420 425 430

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
435 440 445

Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
450 455 460

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
465 470 475 480

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
485 490 495

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
500 505 510

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
515 520 525

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
530 535 540

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
545 550 555 560

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
565 570 575

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
580 585 590

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
595 600 605

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
610 615 620

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
625 630 635

<210> 34

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/CD226/4-1BB/CD3zeta

<400> 34

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu

50

55

60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
290 295 300

His Arg Asn Ile Val Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg

305		310		315		320
Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn	325		330		335	
Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp	340		345		350	
Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg	355		360		365	
Pro Lys Thr Arg Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe	370		375		380	
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly	385		390		395	400
Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg	405		410		415	
Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln	420		425		430	
Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp	435		440		445	
Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro	450		455		460	
Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp	465		470		475	480
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg	485		490		495	
Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr	500		505		510	
Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg	515		520		525	

<210> 35
 <211> 634
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
 TMD/F36V-FKBP/CD226/41BB/CD3zeta

<400> 35

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys		
			260					265					270				
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly		
		275					280					285					
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn		
	290					295					300						
His	Arg	Asn	Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg		
305					310					315					320		
Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met		
				325					330					335			
Leu	Glu	Asp	Gly	Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro		
			340					345					350				
Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu		
		355					360					365					
Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser		
	370					375					380						
Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro		
385					390					395					400		
His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Ile	Val		
				405					410					415			
Ile	Phe	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr		
			420					425					430				
Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile		
		435					440					445					
Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp		
	450					455					460						
Ile	Tyr	Val	Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val		
465					470					475					480		
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met		
				485					490					495			
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe		
			500					505					510				

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
515 520 525

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
530 535 540

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
545 550 555 560

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
565 570 575

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
580 585 590

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
595 600 605

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
610 615 620

Ala Leu His Met Gln Ala Leu Pro Pro Arg
625 630

<210> 36

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/CD226/CD28/4-1BB/CD3zeta

<400> 36

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
 115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
 180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
 290 295 300

His Arg Asn Ile Val Ile Phe Leu Asn Arg Arg Arg Arg Glu Arg
 305 310 315 320

Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn
 325 330 335

Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp
 340 345 350

Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg
 355 360 365

Pro Lys Thr Arg Val Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
 370 375 380

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
 385 390 395 400

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
 405 410 415

Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
 420 425 430

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
 435 440 445

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
 450 455 460

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
 465 470 475 480

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 485 490 495

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
 500 505 510

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
 515 520 525

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 530 535 540

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 545 550 555 560

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 565 570

<210> 37
 <211> 678
 <212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/F36V-FKBP/CD226/CD28/41BB/CD3zeta

<400> 37

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
290 295 300

His Arg Asn Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
305 310 315 320

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
325 330 335

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
340 345 350

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
355 360 365

Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
370 375 380

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
385 390 395 400

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ile Val
405 410 415

Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
420 425 430

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
435 440 445

Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
450 455 460

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
465 470 475 480

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
485 490 495

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
500 505 510

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg
515 520 525

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
530 535 540

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
545 550 555 560

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
565 570 575

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
580 585 590

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
595 600 605

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
610 615 620

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
625 630 635 640

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
645 650 655

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
660 665 670

Gln Ala Leu Pro Pro Arg
675

<210> 38
<211> 545
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/F36V-FKBP/41BB/CD3zeta
<400> 38

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

Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	20	25	30
Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Lys	Trp	Ile	35	40	45
Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser	Gln	Lys	Phe	50	55	60
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	65	70	75
Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	85	90	95
Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	100	105	110
Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	115	120	125
Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	130	135	140
Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270

Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Gly	Val	Gln	Val	275	280	285
Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro	Lys	Arg	Gly	Gln	290	295	300
Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	Asp	Gly	Lys	Lys	Val	305	310	315
Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe	Met	Leu	Gly	Lys	325	330	335
Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala	Gln	Met	Ser	Val	340	345	350
Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	355	360	365
Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	Leu	Val	Phe	Asp	370	375	380
Val	Glu	Leu	Leu	Lys	Leu	Glu	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	385	390	395
Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	405	410	415
Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	420	425	430
Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	435	440	445
Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	450	455	460
Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	465	470	475
Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	485	490	495
Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	500	505	510
Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	515	520	525

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
530 535 540

Arg
545

<210> 39
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/41BB/CD3zeta

<400> 39

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205	
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220	
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	260	265	270	
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	275	280	285	
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	290	295	300	
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	305	310	315	320
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	325	330	335	
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	340	345	350	
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	355	360	365	
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	370	375	380	
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	385	390	395	400
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	405	410	415	
Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	420	425	430	

Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440

<210> 40

<211> 549

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/F36V-FKBP/41BB/CD3zeta

<400> 40

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

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

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
465 470 475 480

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
485 490 495

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
500 505 510

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
515 520 525

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
530 535 540

Ala Leu Pro Pro Arg
545

<210> 41
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/CD28/CD3zeta

<400> 41

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		115					120					125			
Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser
		130				135					140				
Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val
145					150					155					160
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly
				165					170					175	
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly
			180					185					190		
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu
		195					200					205			
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser
		210				215					220				
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu
225					230					235					240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
				245					250					255	
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly
			260					265					270		
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn
		275					280					285			
Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met
		290				295					300				
Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro
305					310					315					320
Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe
				325					330					335	
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
			340					345					350		
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
		355					360					365			

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
370 375 380

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

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
405 410 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440

<210> 42

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD8alpha TMD/F36V-FKBP/CD28/CD3zeta

<400> 42

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155	160
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175	
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205	
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220	
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	260	265	270	
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	275	280	285	
Gly	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro	290	295	300	
Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	Asp	305	310	315	320
Gly	Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe	325	330	335	
Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala	340	345	350	
Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	355	360	365	
Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	370	375	380	
Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Phe	Trp	Val	Arg	Ser	385	390	395	400

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
405 410 415

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
420 425 430

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
435 440 445

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
450 455 460

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
465 470 475 480

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
485 490 495

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
500 505 510

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
515 520 525

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
530 535 540

Met Gln Ala Leu Pro Pro Arg
545 550

<210> 43

<211> 564

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28
TMD/F36V-FKBP/41BB/CD3zeta

<400> 43

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr	Asp	Tyr	Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	50	55	60
Lys	Trp	Ile	Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser	65	70	75
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	85	90	95
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	100	105	110
Tyr	Tyr	Cys	Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	115	120	125
Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	130	135	140
Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	145	150	155
Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	165	170	175
Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	180	185	190
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	195	200	205
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	210	215	220
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	225	230	235
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	245	250	255
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	260	265	270
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	275	280	285
Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Gly	290	295	300

Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	Pro	Lys	305	310	315	320
Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	Asp	Gly	325	330	335	
Lys	Lys	Val	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys	Phe	Met	340	345	350	
Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	Ala	Gln	355	360	365	
Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	Tyr	Ala	370	375	380	
Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	Thr	Leu	385	390	395	400
Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu	Lys	Arg	Gly	Arg	Lys	Lys	405	410	415	
Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	420	425	430	
Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	435	440	445	
Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	450	455	460	
Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	465	470	475	480
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	485	490	495	
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	500	505	510	
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	515	520	525	
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	530	535	540	
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	545	550	555	560

Leu Pro Pro Arg

<210> 44

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/41BB/CD3zeta

<400> 44

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
 290 295 300

His Arg Asn Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
 305 310 315 320

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 325 330 335

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
 340 345 350

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
 355 360 365

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 370 375 380

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 385 390 395 400

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 405 410 415

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 420 425 430

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 435 440 445

Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
450						455					460	

<210> 45

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/F36V-FKBP/41BB/CD3zeta

<400> 45

Met	Asp	Trp	Ile	Trp	Arg	Ile	Leu	Phe	Leu	Val	Gly	Ala	Ala	Thr	Gly
1				5					10					15	

Ala	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg
			20				25						30		

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

Thr	Asp	Tyr	Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu
	50					55					60				

Lys	Trp	Ile	Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser
65					70					75				80	

Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
			85						90					95	

Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105					110		

Tyr	Tyr	Cys	Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr
		115					120					125			

Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				

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

Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
				165					170					175	

Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln
			180					185					190		

Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195

200

205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 275 280 285

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
 290 295 300

His Arg Asn Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
 305 310 315 320

Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
 325 330 335

Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
 340 345 350

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
 355 360 365

Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
 370 375 380

Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
 385 390 395 400

His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Lys Arg
 405 410 415

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
 420 425 430

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
 435 440 445

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala

450

455

460

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 465 470 475 480

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 485 490 495

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 500 505 510

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 515 520 525

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 530 535 540

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 545 550 555 560

His Met Gln Ala Leu Pro Pro Arg
 565

<210> 46

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
 TMD/CD28/CD3zeta

<400> 46

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
 50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

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

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
355 360 365

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
370 375 380

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
385 390 395 400

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
405 410 415

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
420 425 430

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
435 440 445

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
450 455 460

<210> 47

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD8alpha
TMD/F36V-FKBP/CD28/CD3zeta

<400> 47

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

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

Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
 355 360 365
 Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
 370 375 380
 Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
 385 390 395 400
 His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Phe Trp
 405 410 415
 Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 420 425 430
 Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 435 440 445
 Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
 450 455 460
 Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 465 470 475 480
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 485 490 495
 Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 500 505 510
 Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 515 520 525
 Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 530 535 540
 Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 545 550 555 560
 Ala Leu His Met Gln Ala Leu Pro Pro Arg
 565 570

<210> 48

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> 3-17I heavy chain variable region sequence

<400> 48

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val

<210> 49

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 3-17I HC-CDR1

<400> 49

Ser Tyr Ala Ile Ser
1 5

<210> 50

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 3-17I HC-CDR2

<400> 50

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

Gly

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-17I HC-CDR3

<400> 51

Gly Leu Leu Trp Asn Tyr
1 5

<210> 52
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-17I light chain variable region sequence

<400> 52

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

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

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

Tyr Gly Ala Ser Thr Thr Ala Ser Gly Ile Pro Ala Arg Phe Ser Ala
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
85 90 95

Ala Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 53
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-17I LC-CDR1

<400> 53

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 54
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-17I LC-CDR2

<400> 54

Gly Ala Ser Thr Thr Ala Ser
1 5

<210> 55
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-17I LC-CDR3

<400> 55

Gln Gln Tyr Asn Asn Trp Pro Pro Ala Tyr Thr
1 5 10

<210> 56
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-17I scFv

<400> 56

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

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

Gly Glu Phe Ser Glu Ala Arg Val Glu Ile Val Met Thr Gln Ser Pro
 130 135 140

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

Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

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

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

Gln Gln Tyr Asn Asn Trp Pro Pro Ala Tyr Thr Phe Gly Gln Gly Thr
 225 230 235 240

Lys Leu Glu Ile Lys
 245

<210> 57

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> CD226 TMD

<400> 57

Gly Gly Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile
 1 5 10 15

Ile Val Ile Phe Leu
 20

<210> 58

<211> 61

<212> PRT

<213> Artificial Sequence

<220>

<223> CD226 ICD v1

<400> 58

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

Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser
20 25 30

Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val
35 40 45

Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
50 55 60

<210> 59

<211> 63

<212> PRT

<213> Artificial Sequence

<220>

<223> CD226 ICD v2

<400> 59

Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu
1 5 10 15

Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser
20 25 30

Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile
35 40 45

Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
50 55 60

<210> 60

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> CD226 TMD

<400> 60

Gly Gly Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile
1 5 10 15

Ile Val Ile Phe Leu

<210> 61
 <211> 415
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28
 TMD/CD3zeta

<400> 61

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
 50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
 115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
 180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
275 280 285

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

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
305 310 315 320

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
325 330 335

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
340 345 350

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
355 360 365

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
370 375 380

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
385 390 395 400

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
405 410 415

<210> 62

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28
TMD/CD226 ICD v2

<400> 62

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

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
275 280 285

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

Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser
305 310 315 320

Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr
325 330 335

Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr
340 345 350

Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
355 360 365

<210> 63

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28
TMD/41BB/CD3zeta

<400> 63

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

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

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
355 360 365

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
370 375 380

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
385 390 395 400

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
405 410 415

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
420 425 430

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
435 440 445

Leu His Met Gln Ala Leu Pro Pro Arg
450 455

<210> 64

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD226 ICD v1/41BB/CD3zeta

<400> 64

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val

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

355

360

365

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
 370 375 380

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
 385 390 395 400

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

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 420 425 430

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 435 440 445

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 450 455 460

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
 465 470 475 480

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
 485 490 495

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
 500 505 510

Gln Ala Leu Pro Pro Arg
 515

<210> 65

<211> 520

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
 CD226 ICD v2/41BB/CD3zeta

<400> 65

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 20 25 30

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

Thr	Asp	Tyr	Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	50	55	60
Lys	Trp	Ile	Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser	65	70	75
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	85	90	95
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	100	105	110
Tyr	Tyr	Cys	Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	115	120	125
Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	130	135	140
Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	145	150	155
Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	165	170	175
Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	180	185	190
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	195	200	205
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	210	215	220
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	225	230	235
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	245	250	255
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	260	265	270
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	275	280	285
Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	290	295	300

Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser
305 310 315 320

Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr
325 330 335

Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr
340 345 350

Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val Lys Arg
355 360 365

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
370 375 380

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
385 390 395 400

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
405 410 415

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
420 425 430

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
435 440 445

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
450 455 460

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
465 470 475 480

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
485 490 495

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
500 505 510

His Met Gln Ala Leu Pro Pro Arg
515 520

<210> 66

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD226 ICD v1/CD3zeta

<400> 66

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

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

<210> 67
 <211> 478
 <212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD226 ICD v2/CD3zeta

<400> 67

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val Gly Gly
275 280 285

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

Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser
305 310 315 320

Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr
325 330 335

Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr
340 345 350

Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val Arg Val
355 360 365

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
370 375 380

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 68
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD28 ICD/CD3zeta

<400> 68

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

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

210

215

220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
 275 280 285

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

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
 305 310 315 320

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
 325 330 335

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
 340 345 350

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
 355 360 365

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 370 375 380

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
 385 390 395 400

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
 405 410 415

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 420 425 430

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 435 440 445

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 450 455

<210> 69

<211> 520
<212> PRT
<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD226 ICD v1/ CD28 ICD/CD3zeta

<400> 69

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	225	230	235	240
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	245	250	255	
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	260	265	270	
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	275	280	285	
Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Asn	290	295	300	
Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	305	310	315	320
Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	325	330	335	
Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	340	345	350	
Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	Val	Arg	355	360	365	
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	370	375	380	
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	385	390	395	400
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	405	410	415	
Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	420	425	430	
Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	435	440	445	
Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	450	455	460	
Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	465	470	475	480

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
485 490 495

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
500 505 510

His Met Gln Ala Leu Pro Pro Arg
515 520

<210> 70

<211> 522

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD226 ICD v2/ CD28 ICD/CD3zeta

<400> 70

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

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

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
420 425 430

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
435 440 445

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
450 455 460

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
465 470 475 480

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
485 490 495

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
500 505 510

Ala Leu His Met Gln Ala Leu Pro Pro Arg
515 520

<210> 71
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD28 ICD/CD226 ICD v1/CD3zeta

<400> 71

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

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

Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala
355 360 365

Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln
370 375 380

Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe
385 390 395 400

Ser Arg Arg Pro Lys Thr Arg Val Arg Val Lys Phe Ser Arg Ser Ala
405 410 415

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
420 425 430

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
435 440 445

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
450 455 460

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
465 470 475 480

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
485 490 495

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
500 505 510

His Met Gln Ala Leu Pro Pro Arg
515 520

<210> 72
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD28 ICD/41BB/CD3zeta

<400> 72

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35

40

45

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
275 280 285

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe

290

295

300

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
 305 310 315 320

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
 325 330 335

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys
 340 345 350

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
 355 360 365

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
 370 375 380

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

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
 405 410 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 420 425 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 435 440 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 450 455 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 465 470 475 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 485 490 495

Ala Leu Pro Pro Arg
 500

<210> 73

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
 CD226 ICD v1/ CD28 ICD/41BB/CD3zeta

<400> 73

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

Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	
			260					265					270			
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	
		275					280					285				
Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Asn	
	290					295					300					
Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	
305					310					315					320	
Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	
				325					330					335		
Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	
			340					345					350			
Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	Val	Arg	
		355					360					365				
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	
	370					375					380					
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	
385					390					395					400	
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	
				405					410					415		
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	
			420					425					430			
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	
		435					440					445				
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	
	450					455					460					
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	
465					470					475					480	
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	
				485					490					495		
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	
			500					505					510			

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
515 520 525

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
530 535 540

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
545 550 555 560

Pro Arg

<210> 74

<211> 564

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD226 ICD v2/ CD28 ICD/41BB/CD3zeta

<400> 74

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	145	150	155	160
Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	165	170	175	
Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	180	185	190	
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	195	200	205	
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	210	215	220	
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	225	230	235	240
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	245	250	255	
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	260	265	270	
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	275	280	285	
Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	290	295	300	
Leu	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	305	310	315	320
Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	325	330	335	
Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	340	345	350	
Val	Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	355	360	365	
Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	370	375	380	
Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	385	390	395	400

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys
405 410 415

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
420 425 430

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
435 440 445

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
450 455 460

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
465 470 475 480

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
485 490 495

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
500 505 510

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
515 520 525

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
530 535 540

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
545 550 555 560

Leu Pro Pro Arg

<210> 75

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/
CD28 ICD/CD226 ICD v1/41BB/CD3zeta

<400> 75

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe		
	35						40					45					
Thr	Asp	Tyr	Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu		
	50					55					60						
Lys	Trp	Ile	Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser		
65					70					75					80		
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser		
				85					90					95			
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val		
			100					105						110			
Tyr	Tyr	Cys	Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr		
		115					120					125					
Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
	130					135					140						
Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu		
145					150					155					160		
Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln		
				165					170					175			
Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln		
			180					185					190				
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg		
		195					200					205					
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp		
		210				215					220						
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr		
225					230					235					240		
Phe	Cys	Ser	Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr		
				245					250					255			
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys		
			260					265					270				
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly		
		275					280					285					

Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe
290						295					300				
Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn
305					310					315					320
Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr
				325					330					335	
Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Asn	Arg	Arg	Arg	Arg
			340					345					350		
Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala
		355					360						365		
Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln
	370					375					380				
Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	Phe
385					390					395					400
Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu
				405					410					415	
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu
			420					425						430	
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys
		435					440						445		
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln
	450					455					460				
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu
465					470					475					480
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly
				485					490					495	
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu
			500					505						510	
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly
		515					520					525			
Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser
	530					535					540				

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
545 550 555 560

Pro Arg

<210> 76

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD226
TMD/CD226 ICD v1/41BB/CD3zeta

<400> 76

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln

180

185

190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 195 200 205

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Gly Gly Thr Val Leu Leu Leu Leu Phe
 275 280 285

Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg Arg
 290 295 300

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

Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn
 325 330 335

Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr
 340 345 350

Phe Ser Arg Arg Pro Lys Thr Arg Val Lys Arg Gly Arg Lys Lys Leu
 355 360 365

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 370 375 380

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly
 385 390 395 400

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 405 410 415

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 420 425 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met

435

440

445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 450 455 460

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 465 470 475 480

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 485 490 495

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 500 505 510

Pro Pro Arg
 515

<210> 77
 <211> 364
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hIgG heavy chain signal sequence/scFV 3-17I/hIgG1 hinge/CD226
 TMD/CD226 ICD v1

<400> 77

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
 35 40 45

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

Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
 65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr
 115 120 125

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

Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Glu Ile Val Met Thr
 145 150 155 160

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
 165 170 175

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ala Pro Arg Leu Ile Ile Tyr Gly Ala Ser Thr
 195 200 205

Thr Ala Ser Gly Ile Pro Ala Arg Phe Ser Ala Ser Gly Ser Gly Thr
 210 215 220

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

Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro Ala Tyr Thr Phe Gly
 245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr
 260 265 270

His Thr Cys Pro Pro Cys Pro Asp Pro Lys Gly Gly Thr Val Leu Leu
 275 280 285

Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn
 290 295 300

Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp
 305 310 315 320

Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln
 325 330 335

Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn
 340 345 350

Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 355 360

<210> 78
 <211> 415

<212> PRT
 <213> Artificial Sequence
 <220>
 <223> hIgG heavy chain signal sequence/scFV 3-17I/hIgG1 hinge/CD226
 TMD/ CD3zeta
 <400> 78

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
 35 40 45

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

Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
 65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr
 115 120 125

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

Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Glu Ile Val Met Thr
 145 150 155 160

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
 165 170 175

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ala Pro Arg Leu Ile Ile Tyr Gly Ala Ser Thr
 195 200 205

Thr Ala Ser Gly Ile Pro Ala Arg Phe Ser Ala Ser Gly Ser Gly Thr
 210 215 220

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

Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro Ala Tyr Thr Phe Gly
245 250 255

Gln Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr
260 265 270

His Thr Cys Pro Pro Cys Pro Asp Pro Lys Gly Gly Thr Val Leu Leu
275 280 285

Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Arg
290 295 300

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
305 310 315 320

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
325 330 335

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
340 345 350

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
355 360 365

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
370 375 380

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
385 390 395 400

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
405 410 415

<210> 79

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV 3-17I/hIgG1 hinge/CD226
TMD/CD226 ICD v1/CD3zeta

<400> 79

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	20	25	30
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	35	40	45
Ser	Ser	Tyr	Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	50	55	60
Glu	Trp	Met	Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	65	70	75
Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	85	90	95
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	100	105	110
Tyr	Tyr	Cys	Ala	Arg	Gly	Leu	Leu	Trp	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	115	120	125
Leu	Val	Thr	Val	Ser	Ser	Lys	Leu	Ser	Gly	Ser	Ala	Ser	Ala	Pro	Lys	130	135	140
Leu	Glu	Glu	Gly	Glu	Phe	Ser	Glu	Ala	Arg	Val	Glu	Ile	Val	Met	Thr	145	150	155
Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	165	170	175
Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asn	Leu	Ala	Trp	Tyr	Gln	180	185	190
Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Ile	Ile	Tyr	Gly	Ala	Ser	Thr	195	200	205
Thr	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Ala	Ser	Gly	Ser	Gly	Thr	210	215	220
Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	225	230	235
Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Asn	Trp	Pro	Pro	Ala	Tyr	Thr	Phe	Gly	245	250	255
Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	260	265	270

His Thr Cys Pro Pro Cys Pro Asp Pro Lys Gly Gly Thr Val Leu Leu
275 280 285

Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn
290 295 300

Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp
305 310 315 320

Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln
325 330 335

Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn
340 345 350

Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val Arg Val Lys Phe
355 360 365

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
370 375 380

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
385 390 395 400

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
405 410 415

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
420 425 430

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
435 440 445

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
450 455 460

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 80
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/CD3zeta
<400> 80

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

Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	20	25	30
Glu	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Lys	Trp	Ile	35	40	45
Gly	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Asp	Thr	Ala	Tyr	Ser	Gln	Lys	Phe	50	55	60
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	65	70	75
Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	85	90	95
Thr	Arg	Phe	Tyr	Ser	Tyr	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	100	105	110
Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	115	120	125
Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	130	135	140
Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Arg Val Lys Phe
275 280 285

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
290 295 300

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
305 310 315 320

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
325 330 335

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
340 345 350

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
355 360 365

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
370 375 380

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
385 390 395

<210> 81

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/CD226 ICD v2

<400> 81

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
 165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
 180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
 210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Asp Pro Lys Phe Trp Val Leu Val Val Gly Gly Val Leu Ala
 260 265 270

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Leu Asn Arg
 275 280 285

Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr
 290 295 300

Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro
 305 310 315 320

Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr
 325 330 335

Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
340 345

<210> 82
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/41BB/CD3zeta

<400> 82

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

$\langle 210 \rangle$	83
$\langle 211 \rangle$	499

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/41BB/CD3zeta

<400> 83

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270	
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Asn	Arg	Arg	Arg	275	280	285	
Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	290	295	300	
Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	305	310	315	320
Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	325	330	335	
Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Lys	Arg	Gly	Arg	Lys	Lys	Leu	340	345	350	
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	355	360	365	
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	370	375	380	
Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	385	390	395	400
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	405	410	415	
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	420	425	430	
Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	435	440	445	
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	450	455	460	
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	465	470	475	480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
485 490 495

Pro Pro Arg

<210> 84
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/41BB/CD3zeta
<400> 84

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu
		195					200					205			
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser
	210					215					220				
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu
225					230					235					240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
				245					250					255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala
			260					265					270		
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Leu	Asn	Arg
		275					280					285			
Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr
	290					295					300				
Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro
305					310					315					320
Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr
				325					330					335	
Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Lys	Arg	Gly	Arg	Lys
			340					345					350		
Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr
		355					360					365			
Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu
	370					375					380				
Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro
385					390					395					400
Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly
				405					410					415	
Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro
			420					425					430		
Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr
		435					440					445			

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
450 455 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465 470 475 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
485 490 495

Ala Leu Pro Pro Arg
500

<210> 85

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/CD3zeta

<400> 85

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155	160
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175	
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205	
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220	
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270	
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Asn	Arg	Arg	Arg	275	280	285	
Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	290	295	300	
Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	305	310	315	320
Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	325	330	335	
Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Arg	Val	Lys	Phe	Ser	Arg	Ser	340	345	350	
Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	355	360	365	
Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	370	375	380	
Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	385	390	395	400

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
405 410 415

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
420 425 430

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
435 440 445

Leu His Met Gln Ala Leu Pro Pro Arg
450 455

<210> 86
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/CD3zeta

<400> 86

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

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

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
420 425 430

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
435 440 445

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
450 455

<210> 87

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/CD3zeta

<400> 87

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
 165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
 180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
 210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
 260 265 270

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
 275 280 285

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 290 295 300

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 305 310 315 320

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
 325 330 335

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 340 345 350

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 355 360 365

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 370 375 380

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

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 405 410 415

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
420 425 430

His Met Gln Ala Leu Pro Pro Arg
435 440

<210> 88

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/ CD28 ICD/CD3zeta

<400> 88

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu
		195					200					205			
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser
	210					215					220				
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu
225					230					235					240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
				245					250					255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala
			260					265					270		
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Asn	Arg	Arg	Arg
		275					280					285			
Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys
	290					295					300				
Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn
305					310					315					320
Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr
				325					330					335	
Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	Val	Arg	Ser	Lys	Arg
			340					345					350		
Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro
		355					360					365			
Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe
	370					375					380				
Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro
385					390					395					400
Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly
				405					410					415	
Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro
			420					425					430		
Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr
		435					440					445			

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
450 455 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465 470 475 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
485 490 495

Ala Leu Pro Pro Arg
500

<210> 89

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/ CD28 ICD/CD3zeta

<400> 89

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155	160
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175	
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205	
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220	
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270	
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Leu	Asn	Arg	275	280	285	
Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	290	295	300	
Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	305	310	315	320
Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	325	330	335	
Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	Val	Arg	Ser	340	345	350	
Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	355	360	365	
Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	370	375	380	
Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	385	390	395	400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
405 410 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
420 425 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
435 440 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
450 455 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465 470 475 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
485 490 495

Met Gln Ala Leu Pro Pro Arg
500

<210> 90

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/CD226 ICD v1/CD3zeta

<400> 90

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	115	120	125	
Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	130	135	140	
Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155	160
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175	
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205	
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220	
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270	
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	275	280	285	
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	290	295	300	
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	305	310	315	320
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	325	330	335	
Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	340	345	350	
Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	355	360	365	

Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg
370 375 380

Pro Lys Thr Arg Val Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385 390 395 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
405 410 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
420 425 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
435 440 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
450 455 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465 470 475 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
485 490 495

Ala Leu Pro Pro Arg
500

<210> 91
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/41BB/CD3zeta
<400> 91

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

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

Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu
325 330 335

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
340 345 350

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
355 360 365

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
370 375 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385 390 395 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
405 410 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
420 425 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg

<210> 92
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/ CD28
ICD/41BB/CD3zeta

<400> 92

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile

35

40

45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
 165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
 180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
 210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Asp Pro Lys Phe Trp Val Leu Val Val Gly Gly Val Leu Ala
 260 265 270

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Asn Arg Arg Arg
 275 280 285

Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys

290

295

300

Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn
305 310 315 320

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

Phe Ser Arg Arg Pro Lys Thr Arg Val Phe Trp Val Arg Ser Lys Arg
340 345 350

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
355 360 365

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
370 375 380

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
385 390 395 400

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
405 410 415

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
420 425 430

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
435 440 445

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
450 455 460

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
465 470 475 480

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
485 490 495

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
500 505 510

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
515 520 525

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
530 535 540

<210> 93

<211> 545
<212> PRT
<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/ CD28
ICD/41BB/CD3zeta

<400> 93

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235	240
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255	
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270	
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Leu	Asn	Arg	275	280	285	
Arg	Arg	Arg	Arg	Glu	Arg	Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	290	295	300	
Gln	Lys	Ala	Pro	Asn	Asn	Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	305	310	315	320
Thr	Asn	Gln	Ser	Met	Asp	Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	325	330	335	
Pro	Thr	Phe	Ser	Arg	Arg	Pro	Lys	Thr	Arg	Val	Phe	Trp	Val	Arg	Ser	340	345	350	
Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	355	360	365	
Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	370	375	380	
Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	385	390	395	400
Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	405	410	415	
Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	420	425	430	
Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	435	440	445	
Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	450	455	460	
Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	465	470	475	480

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
485 490 495

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
500 505 510

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
515 520 525

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
530 535 540

Arg
545

<210> 94
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/CD226 ICD
v1/41BB/CD3zeta

<400> 94

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	130	135	140
Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	145	150	155
His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	165	170	175
Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	180	185	190
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	195	200	205
Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	210	215	220
Gln	Asn	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	225	230	235
Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	245	250	255
Pro	Asp	Pro	Lys	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	260	265	270
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	275	280	285
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	290	295	300
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	305	310	315
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Asn	Arg	Arg	Arg	Arg	Arg	Glu	Arg	325	330	335
Arg	Asp	Leu	Phe	Thr	Glu	Ser	Trp	Asp	Thr	Gln	Lys	Ala	Pro	Asn	Asn	340	345	350
Tyr	Arg	Ser	Pro	Ile	Ser	Thr	Ser	Gln	Pro	Thr	Asn	Gln	Ser	Met	Asp	355	360	365
Asp	Thr	Arg	Glu	Asp	Ile	Tyr	Val	Asn	Tyr	Pro	Thr	Phe	Ser	Arg	Arg	370	375	380

Pro Lys Thr Arg Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
385 390 395 400

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
405 410 415

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
420 425 430

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
435 440 445

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
450 455 460

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
465 470 475 480

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
485 490 495

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
500 505 510

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
515 520 525

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
530 535 540

<210> 95

<211> 496

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD226 TMD/CD226 ICD v1/41BB/CD3zeta

<400> 95

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Asp Pro Lys Gly Gly Thr Val Leu Leu Leu Leu Phe Val Ile Ser
260 265 270

Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu
275 280 285

Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn
290 295 300

Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met

305		310		315		320
Asp Asp Thr Arg	Glu Asp Ile Tyr Val	Asn Tyr Pro Thr Phe Ser Arg				
	325	330			335	
Arg Pro Lys Thr Arg Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile						
	340	345			350	
Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp						
	355	360			365	
Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu						
	370	375			380	
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly						
	385	390			395	400
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr						
	405	410			415	
Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys						
	420	425			430	
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys						
	435	440			445	
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg						
	450	455			460	
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala						
	465	470			475	480
Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg						
	485	490			495	

<210> 96

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV 3-17I/hIgG1 hinge/CD226 TMD/CD226 ICD v1

<400> 96

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

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

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	35	40	45	
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	50	55	60	
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr	65	70	75	80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Gly	Leu	Leu	Trp	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	100	105	110	
Val	Ser	Ser	Lys	Leu	Ser	Gly	Ser	Ala	Ser	Ala	Pro	Lys	Leu	Glu	Glu	115	120	125	
Gly	Glu	Phe	Ser	Glu	Ala	Arg	Val	Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	130	135	140	
Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	145	150	155	160
Ala	Ser	Gln	Ser	Val	Ser	Ser	Asn	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	165	170	175	
Gly	Gln	Ala	Pro	Arg	Leu	Ile	Ile	Tyr	Gly	Ala	Ser	Thr	Thr	Ala	Ser	180	185	190	
Gly	Ile	Pro	Ala	Arg	Phe	Ser	Ala	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	195	200	205	
Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	210	215	220	
Gln	Gln	Tyr	Asn	Asn	Trp	Pro	Pro	Ala	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	225	230	235	240
Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	245	250	255	
Pro	Pro	Cys	Pro	Asp	Pro	Lys	Gly	Gly	Thr	Val	Leu	Leu	Leu	Leu	Phe	260	265	270	
Val	Ile	Ser	Ile	Thr	Thr	Ile	Ile	Val	Ile	Phe	Leu	Asn	Arg	Arg	Arg	275	280	285	

Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys
290 295 300

Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn
305 310 315 320

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

Phe Ser Arg Arg Pro Lys Thr Arg Val
340 345

<210> 97

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV 3-17I/hIgG1 hinge/CD226 TMD/ CD3zeta

<400> 97

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

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

Gly Glu Phe Ser Glu Ala Arg Val Glu Ile Val Met Thr Gln Ser Pro
130 135 140

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

145		150		155		160
Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro	165		170		175	
Gly Gln Ala Pro Arg Leu Ile Ile Tyr Gly Ala Ser Thr Thr Ala Ser	180		185		190	
Gly Ile Pro Ala Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr	195		200		205	
Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys	210		215		220	
Gln Gln Tyr Asn Asn Trp Pro Pro Ala Tyr Thr Phe Gly Gln Gly Thr	225		230		235	240
Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys	245		250		255	
Pro Pro Cys Pro Asp Pro Lys Gly Gly Thr Val Leu Leu Leu Leu Phe	260		265		270	
Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Arg Val Lys Phe	275		280		285	
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	290		295		300	
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp	305		310		315	320
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys	325		330		335	
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala	340		345		350	
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys	355		360		365	
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	370		375		380	
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg	385		390		395	

<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> scFV 3-17I/hIgG1 hinge/CD226 TMD/CD226 ICD v1/CD3zeta

<400> 98

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Leu Trp Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

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

Gly Glu Phe Ser Glu Ala Arg Val Glu Ile Val Met Thr Gln Ser Pro
130 135 140

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

Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

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

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

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

<210> 99
 <211> 1254
 <212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/CD3zeta

<400> 99

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atggactgga tctggaggat tttgttcctt gtgggagctg ccaccggtgc acattcgcaa      60
gtgcagttgc agcagtcggg agccgaactg gtccggcctg gagcttccgt gaagcttagc      120
tgcaaggcct ccggctacac ctttaccgac tacgagatgc actgggtcaa gcagaccccc      180
gtgcacggtc tgaagtggat tggggccctg gatcccaaga ccggcgatac tgcgtactca      240
cagaagttca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg      300
gaactcagga gcctgacttc cgaggatagc gcagtgtact actgcacccg cttttactcc      360
tacacttact ggggacaggg caccttggtg actgtgtcag ccggtggagg cggatcaggg      420
ggtggaggat ccggggggagg aggatccgat gtggtcatga ccagacccc actgtccctt      480
cccgtgtccc tgggtgacca agcctcgatc agctgcagat cctcccagtc actggtccac      540
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ctgatctaca aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt      660
tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac      720
ttctgctccc aaaataccca cgtgccgcct acattcggat cgggaactaa gctggagatc      780
aaggagccca aaagctgcga caagaccac acttgcccac cttgcccgga tccgaagttc      840
tgggtgctgg tggtggtcgg gggagtgtc gcctgctact ctctgctggt gaccgtggcc      900
ttcatcatcc gcgtgaagtt cagccggagc gctgatgcc ctgcatacca gcaggggcag      960
aaccagctct acaacgaact gaaccttga cggcgggagg aatacgatgt gctggataag     1020
cgaagaggcc gcgaccaga aatgggcggg aagcccagac gcaagaatcc tcaggaggga     1080
ctgtacaacg agctccagaa agacaagatg gccgaagcgt acagcgagat cggcatgaag     1140
ggggaacgga gaaggggaaa gggccatgac ggattgtacc agggcctgtc gaccgctacc     1200
aaagacacct acgacgccct ccatatgcaa gcactgccgc cacgctgaac gcgt          1254
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<210> 100

<211> 1107

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/CD226 ICD v2

<400> 100

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gtgcagttgc agcagtcggg agccgaactg gtccggcctg gagcttccgt gaagcttagc      120
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tgcaaggcct	ccggctacac	ctttaccgac	tacgagatgc	actgggtcaa	gcagaccccc	180
gtgcacggtc	tgaagtggat	tggggccctg	gatcccaaga	ccggcgatac	tgcgtactca	240
cagaagttca	agggaaaggc	cacgctcact	gcggaacaaat	cgtccagcac	cgcgtagatg	300
gaactcagga	gcctgacttc	cgaggatagc	gcagtgtact	actgcacccg	cttttactcc	360
tacacttact	ggggacaggg	caccttgggtg	actgtgtcag	ccggtggagg	cggatcaggg	420
gggtggaggat	ccgggggagg	aggatccgat	gtggatcatga	cccagacccc	actgtccctt	480
cccgtgtccc	tgggtgacca	agcctcgatc	agctgcagat	cctcccagtc	actggtccac	540
agcaacggca	acacctatct	gcattggtac	ctccagaagc	cgggacaatc	ccccaagctc	600
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aaggagccca	aaagctgcga	caagaccac	acttgccac	cttgtccgga	tccgaagttc	840
tgggtgctgg	tgggtggcgg	gggagtgtc	gcctgtact	ctctgctgg	gaccgtggca	900
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tgggacaccc	agaaggcccc	caacaactac	aggtccccta	tctcaacctc	ccaaccaccc	1020
aaccagagca	tggacgatac	tcgcgaggac	atctacgtga	actacccac	tttctcccgg	1080
cggcctaaga	cacgggtgtg	aacgcgt				1107

<210> 101

<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/41BB/CD3zeta

<400> 101

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tgcaaggcct	ccggctacac	ctttaccgac	tacgagatgc	actgggtcaa	gcagaccccc	180
gtgcacggtc	tgaagtggat	tggggccctg	gatcccaaga	ccggcgatac	tgcgtactca	240
cagaagttca	agggaaaggc	cacgctcact	gcggaacaaat	cgtccagcac	cgcgtagatg	300
gaactcagga	gcctgacttc	cgaggatagc	gcagtgtact	actgcacccg	cttttactcc	360
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cccgtgtccc	tgggtgacca	agcctcgatc	agctgcagat	cctcccagtc	actggtccac	540
agcaacggca	acacctatct	gcattggtac	ctccagaagc	cgggacaatc	ccccaagctc	600

ctgatctaca aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt	660
tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac	720
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tgggtgctgg tgggtggtcgg gggagtgtc gcctgtact ctctgctggt gaccgtggcc	900
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gagggactgt acaacgagct ccagaaagac aagatggccg aagcgtacag cgagatcggc	1260
atgaaggggg aacggagaag gggaaagggc catgacggat tgtaccaggg cctgtcgacc	1320
gctaccaaag acacctacga cgccctccat atgcaagcac tgccgccacg ctgaacgcgt	1380

<210> 102

<211> 1563

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/41BB/CD3zeta

<400> 102

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tgcaaggcct ccggctacac ctttaccgac tacgagatgc actgggtcaa gcagaccccc	180
gtgcacggtc tgaagtggat tggggccctg gatcccaaga ccggcgatac tgcgtactca	240
cagaagttca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg	300
gaactcagga gcctgacttc cgaggatagc gcagtgtact actgcacccg cttttactcc	360
tacacttact ggggacaggg caccttgggt actgtgtcag ccggtggagg cggatcaggg	420
ggtggaggat ccgggggagg aggatccgat gtggtcatga ccagacccc actgtccctt	480
cccgtgtccc tgggtgacca agcctcgatc agctgcagat cctcccagtc actggtccac	540
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ctgatctaca aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt	660
tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac	720
ttctgctccc aaaataccca cgtgccgcct acattcggat cgggaactaa gctggagatc	780

aaggagccca aaagctgcga caagaccac acttgcccac cttgtccgga tccgaagttc	840
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ttcattatca acagaaggag gcgccgggag cggcgcgacc tgttctactga atcctgggac	960
acccagaagg cccccaacaa ctacaggtcc cctatctcaa cctcccaacc caccaaccag	1020
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cggcctgtgc agaccacaca ggaagaggat ggctgtcct gccgcttccc ggaggaagag	1200
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ctggataagc gaagaggccg cgaccacaga atgggcggga agcccagacg caagaatcct	1380
caggagggac tgtacaacga gctccagaaa gacaagatgg ccgaagcgta cagcgagatc	1440
ggcatgaagg gggaacggag aaggggaaag ggccatgacg gattgtacca gggcctgtcg	1500
accgctacca aagacaccta cgacgccctc catatgcaag cactgccgcc tagatgaacg	1560
cgt	1563

<210> 103
 <211> 1569
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/41BB/CD3zeta

<400> 103	
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gtgcacggtc tgaagtggat tggggccctg gatcccaaga ccggcgatac tgcgtactca	240
cagaagtcca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg	300
gaactcagga gcctgacttc cgaggatagc gcagtgtact actgcacccg cttttactcc	360
tacacttact ggggacaggg caccttggtg actgtgtcag ccggtggagg cggatcaggg	420
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cccgtgtccc tgggtgacca agcctcgatc agctgcagat cctcccagtc actggtccac	540
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ctgatctaca aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt	660
tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac	720
ttctgctccc aaaataccca cgtgccgcct acattcggat cgggaactaa gctggagatc	780

aaggagccca aaagctgcga caagaccac acttgcccac cttgtccgga tccgaagttc	840
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aatcctcagg agggactgta caacgagctc cagaaagaca agatggccga agcgtacagc	1440
gagatcggca tgaaggggga acggagaagg ggaaagggcc atgacggatt gtaccagggc	1500
ctgtcgaccg ctaccaaaga cacctacgac gccctccata tgcaagcact gccgcctaga	1560
tgaacgcgt	1569

<210> 104
 <211> 1434
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/CD3zeta

<400> 104	
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tgcaaggcct ccggctacac ctttaccgac tacgagatgc actgggtcaa gcagaccccc	180
gtgcacggtc tgaagtggat tggggccctg gatcccaaga ccggcgatac tgcgtactca	240
cagaagttca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg	300
gaactcagga gcctgacttc cgaggatagc gcagtgtact actgcacccg cttttactcc	360
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cccgtgtccc tgggtgacca agcctcgatc agctgcagat cctcccagtc actggtccac	540
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tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac	720

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tgggtcttg	tggtggtggg	aggcgtcctc	gcctgctaca	gcttgctcgt	gaccgttgcc	900
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aagggggaac	ggagaagggg	aaagggccat	gacggattgt	accagggcct	gtcgaccgct	1380
accaaagaca	cctacgacgc	cctccatatg	caagcactgc	cgccacgctg	atag	1434

<210> 105

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/CD3zeta

<400> 105

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gtgcagttgc	agcagtcggg	agccgaactg	gtccggcctg	gagcttccgt	gaagcttagc	120
tgcaaggcct	ccggctacac	ctttaccgac	tacgagatgc	actgggtcaa	gcagaccccc	180
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caggggcaga	accagctcta	caacgaactg	aaccttgac	ggcgggagga	atacgatgtg	1200
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ggcatgaagg	gggaacggag	aaggggaaag	ggccatgacg	gattgtacca	gggcctgtcg	1380
accgtacca	aagacaccta	cgacgccctc	catatgcaag	cactgccgcc	acgtgatag	1440

<210> 106

<211> 1383

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/CD3zeta

<400> 106

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tgcaaggcct	ccggctacac	ctttaccgac	tacgagatgc	actgggtcaa	gcagaccccc	180
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cagaagttca	agggaaaggc	cacgctcact	gcggaacaaat	cgtccagcac	cgcgtagatg	300
gaactcagga	gcctgacttc	cgaggatagc	gcagtgtact	actgcacccg	cttttactcc	360
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ctgatctaca	aggtgtccaa	ccggttcagc	ggagtgccgg	atcgattctc	agggtcgggt	660
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tag						1383

<210> 107
 <211> 1566
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/ CD28 ICD/CD3zeta

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aagaccgcg	tgttctgggt gcgctccaag cgctccagac tgctgcacag cgactacatg 1140
aacatgaccc	caagacgccc aggacctact aggaagcatt atcaacctta tgccccgcgcg 1200

agagacttcg cggcgtaccg gtcccgcgtg aagttcagcc ggagcgtga tgcccctgca	1260
taccagcagg ggcagaacca gctctacaac gaactgaacc ttggacggcg ggaggaatac	1320
gatgtgctgg ataagcgaag aggccgcgac ccagaaatgg gcgggaagcc cagacgcaag	1380
aatcctcagg agggactgta caacgagctc cagaaagaca agatggccga agcgtacagc	1440
gagatcggca tgaaggggga acggagaagg ggaaagggcc atgacggatt gtaccagggc	1500
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tgatag	1566

<210> 108
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/ CD28 ICD/CD3zeta

<400> 108	
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tgcaaggcct ccggctacac ctttaccgac tacgagatgc actgggtcaa gcagaccccc	180
gtgcacggtc tgaagtggat tggggccctg gatcccaaga ccggcgatac tgcgtactca	240
cagaagttca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg	300
gaactcagga gcctgacttc cgaggatagc gcagtgtact actgcacccg cttttactcc	360
tacacttact ggggacaggg caccttgggt actgtgtcag ccggtggagg cggatcaggg	420
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cccgtgtccc tgggtgacca agcctcgatc agctgcagat cctcccagtc actggtccac	540
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ctgatctaca aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt	660
tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac	720
ttctgctccc aaaataccca cgtgccgcct acattcggat cgggaactaa gctggagatc	780
aaggagccca aaagctgcga caagaccac acttgccac cttgcccga tccgaagttc	840
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tgggacaccc agaaggcccc gaacaactac cgctccccga tctccacctc ccaaccgact	1020
aatcaaagca tggacgacac cagggaggac atctacgtga actaccctac tttctccgc	1080
cggcctaaga cccgcgtggt ctgggtgcgc tccaagcgt ccagactgct gcacagcgac	1140

tacatgaaca	tgacccaag	acgcccagga	cctactagga	agcattatca	accttatgcc	1200
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tacagcgaga	tcggcatgaa	gggggaacgg	agaaggggaa	agggccatga	cggattgtac	1500
cagggcctgt	cgaccgctac	caaagacacc	tacgacgccc	tccatatgca	agcactgccg	1560
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<210> 109
 <211> 1566
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/CD226 ICD v1/CD3zeta

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ggtggaggat	ccgggggagg aggatccgat gtggtcatga ccagacccc actgtccctt 480
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agcaacggca	acacctatct gcattggtac ctccagaagc cgggacaatc cccaagctc 600
ctgatctaca	aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt 660
tcgggaaccg	acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac 720
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gacttcgccg	cctaccggtc caaccgcagg cggagaaggg aacggcgcgga cctgttcaact 1080
gagtcatggg	acaccagaa ggccccgaac aactaccgct ccccgatctc cacctcccaa 1140

ccgactaatc aaagcatgga cgacaccagg gaggacatct acgtgaacta ccctactttc	1200
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taccagcagg ggcagaacca gctctacaac gaactgaacc ttggacggcg ggaggaatac	1320
gatgtgctgg ataagcgaag aggccgcgac ccagaaatgg gcgggaagcc cagacgcaag	1380
aatcctcagg agggactgta caacgagctc cagaaagaca agatggccga agcgtacagc	1440
gagatcggca tgaaggggga acggagaagg ggaaagggcc atgacggatt gtaccagggc	1500
ctgtcgaccg ctaccaaaga cacctacgac gccctccata tgcaagcact gccgccacgc	1560
tgatag	1566

<210> 110

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/41BB/CD3zeta

<400> 110

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tgcaaggcct ccggctacac ctttaccgac tacgagatgc actgggtcaa gcagaccccc	180
gtgcacggtc tgaagtggat tggggccctg gatcccaaga ccggcgatac tgcgtactca	240
cagaagttca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg	300
gaactcagga gcctgacttc cgaggatagc gcagtgtact actgcacccg cttttactcc	360
tacacttact ggggacaggg caccttggtg actgtgtcag ccggtggagg cggatcaggg	420
ggtggaggat ccgggggagg aggatccgat gtggtcatga cccagacccc actgtccctt	480
cccgtgtccc tgggtgacca agcctcgatc agctgcagat cctcccagtc actggtccac	540
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ctgatctaca aggtgtccaa ccggttcagc ggagtgccgg atcgattctc agggtcgggt	660
tcgggaaccg acttcaccct taagatttcc cgggtggaag ccgaggatct cggagtgtac	720
ttctgctccc aaaataccca cgtgccgcct acattcggat cgggaactaa gctggagatc	780
aaggagccca aaagctgcga caagaccac acttgccac cttgcccgga tccgaagttc	840
tgggtgctgg tgggtggtcgg gggagtgtc gcctgtact ctctgctggt gaccgtggcc	900
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gatttcgccg cctacagatc caagcgcggt cggaagaagc tgctgtacat cttcaagcag	1080

cccttcatgc	ggcctgtgca	gaccacacag	gaagaggatg	gctgctcctg	ccgcttcccg	1140
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gcataccagc	aggggcagaa	ccagctctac	aacgaactga	accttgagcg	gcgggaggaa	1260
tacgatgtgc	tggataagcg	aagaggccgc	gacccagaaa	tgggcgggaa	gcccagacgc	1320
aagaatcctc	aggagggact	gtacaacgag	ctccagaaaag	acaagatggc	cgaagcgtac	1380
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cgctgatag						1509

<210> 111
 <211> 1692
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v1/ CD28 ICD/41BB/CD3zeta

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cagaagttca	agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg 300
gaactcagga	gcctgacttc cgaggacagc gcagtgtact actgcacccg cttttactcc 360
tacacttact	ggggacaggg caccttggtg actgtgtcag ccggtggagg cggatcaggg 420
ggtggaggat	ccgggggagg aggatccgat gtggtcatga cccagacccc actgtccctt 480
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cgcaagaatc ctcaggaggg actgtacaac gagctccaga aagacaagat ggccgaagcg	1560
tacagcgaga tcggcatgaa gggggaacgg agaaggggaa agggccatga cggattgtac	1620
cagggcctgt cgaccgtac caaagacacc tacgacgcc tccatatgca agcactgccg	1680
ccacgctgat ag	1692

<210> 112

<211> 1698

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD226 ICD v2/ CD28 ICD/41BB/CD3zeta

<400> 112

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tgcaaggcct ccggctacac ctttaccgac tacgagatgc actgggtcaa gcagaccccc	180
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cagaagttca agggaaaggc cacgctcact gcggacaaat cgtccagcac cgcgtacatg	300
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ctgccgccac	gctgatag					1698

<210> 113

<211> 1692

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28 TMD/ CD28 ICD/CD226 ICD v1/41BB/CD3zeta

<400> 113

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cctgcatacc	agcaggggca	gaaccagctc	tacaacgaac	tgaaccttgg	acggcgggag	1440
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cgcaagaatc	ctcaggaggg	actgtacaac	gagctccaga	aagacaagat	ggccgaagcg	1560
tacagcgaga	tcggcatgaa	gggggaacgg	agaaggggaa	agggccatga	cggattgtac	1620
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cctagatgat	ag					1692

<210> 114
 <211> 1554
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD226 TMD/CD226 ICD v1/41BB/CD3zeta

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tgcaaggcct	ccggctacac	ctttaccgac	tacgagatgc	actgggtcaa	gcagaccccc	180
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cccgtgtccc	tgggtgacca	agcctcgatc	agctgcagat	cctcccagtc	actggtccac	540
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gatactcgcg	aggacatcta	cgtgaactac	cccactttct	cccggcggcc	taagaccgc	1080
gtgaagcgcg	gtcggagaag	gctgctgtac	atcttcaagc	agcccttcat	gcggcctgtg	1140
cagaccacac	aggaagagga	tggttgctcc	tgccgcttcc	cggaggaaga	ggagggcgga	1200
tgcgaactgc	gcgtgaagtt	cagccggagc	gctgatgcc	ctgcatacca	gcaggggcag	1260
aaccagctct	acaacgaact	gaaccttga	cggcgggagg	aatacgatgt	gctggataag	1320
cgaagaggcc	gcgaccaga	aatgggcggg	aagcccagac	gcaagaatcc	tcaggaggga	1380
ctgtacaacg	agctccagaa	agacaagatg	gccgaagcgt	acagcgagat	cggcatgaag	1440
ggggaacgga	gaaggggaaa	gggccatgac	ggattgtacc	agggcctgtc	gaccgctacc	1500
aaagacacct	acgacgcct	ccatatgcaa	gcactgccgc	ctagatgaac	gcgt	1554

<210> 115

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<223> (nucleotide) hIgG heavy chain signal sequence/scFV 3-17I/hIgG1 hinge/CD226 TMD/CD226 ICD v1

<400> 115

atggactgga	tctggagaat	tttgttcctt	gtcgggtgctg	ccactggagc	ccactcgcaa	60
gtgcagctcg	tgcaagtctgg	agcagaagtc	aagaagcctg	ggtcctcggg	caaagtgtcc	120
tgcaaagcct	ccggggggcac	tttcagctcg	tacgcaatct	cctgggtccg	ccaagcgccc	180
ggacagggtc	tggaagtggat	gggcgggatt	atccccatct	tcggcaccgc	caactatgct	240
caaaagttcc	agggccgcgt	gactattacc	gcggacgagt	caacctccac	tgcgtagatg	300
gaactgagct	cacttcgggtc	cgaggacacc	gccgtctatt	actgtgcgcg	gggactcctg	360
tggaactact	ggggacaagg	caccctcgtg	accgtgtcct	cgaagctgtc	cgggtcggcc	420
agcgccccca	agttggaaga	gggcgaattc	tccgaggccc	gggtggaaat	cgtgatgacc	480
cagtcgcccg	ccactctctc	cgtgtccccg	ggagaaaggg	cgaccctgtc	atgccggggc	540
tcgcaatccg	tgtcatccaa	cctggcctgg	taccagcaga	agccaggaca	ggcgccccgc	600
ctgattatct	acggcgccag	caccaccgcg	agcgggaattc	cggcccgggt	ttccgcctcc	660
ggttcgggaa	ctgacttcac	gctgactatc	agcagcctgc	aatcggagga	cttcgccgctc	720

tactactgcc agcagtataa caactggccc ccggcttaca cgtttggcca gggaactaag	780
ctggagatca aggagcccaa aagctgcgac aagaccaca cttgccacc ttgtccggac	840
ccgaaggggg gaaccgtgct cctgctgctg ttcgtgatct ccatcaccac aatcatcgtg	900
atcttcctga accgccggcg aagacgcgaa agacgcgatc tgttcaccga gtcatgggac	960
accagaagg cccctaacaa ctacagaagc ccgatcagca ccagccagcc tactaatcag	1020
tcgatggatg ataccgcga ggacatctac gtgaattacc caaccttctc ccggcggccg	1080
aaaaccgcg tgtgaacgcg t	1101

<210> 116
 <211> 1254
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> (nucleotide) hIgG heavy chain signal sequence/scFV 3-17I/hIgG1 hinge/CD226 TMD/ CD3zeta

<400> 116	
atggactgga tctggagaat tttgttcctt gtcggtgctg ccactggagc ccactcgcaa	60
gtgcagctcg tgcagtctgg agcagaagtc aagaagcctg ggtcctcggc caaagtgtcc	120
tgcaaagcct ccggggggcac tttcagctcg tacgcaatct cctgggtccg ccaagcgccc	180
ggacagggtc tggagtggat gggcgggatt atccccatth tccggaccgc caactatgct	240
caaaagttcc agggccgcgt gactattacc gcgagcagat caacctccac tgcgtacatg	300
gaactgagct cacttcggtc cgaggacacc gccgtctatt actgtgcgcg gggactcctg	360
tggaaactact ggggacaagg caccctcgtg accgtgtcct cgaagctgtc cgggtcggcc	420
agcgccccca agttggaaga gggcgaattc tccgaggccc gggtggaat cgtgatgacc	480
cagtcctcgg ccactctctc cgtgtccccg ggagaaaggc cgaccctgtc atgccgggac	540
tcgcaatccg tgtcatccaa cctggcctgg taccagcaga agccaggaca ggcgccccgc	600
ctgattatct acggcgccag caccaccgcg agcggaattc cggcccgggt ttccgcctcc	660
ggttcgggaa ctgacttcac gctgactatc agcagcctgc aatcgaggga cttcgccgtc	720
tactactgcc agcagtataa caactggccc ccggcttaca cgtttggcca gggaactaag	780
ctggagatca aggagcccaa aagctgcgac aagaccaca cttgccacc ttgtccggac	840
ccgaaggggg gaaccgtgct cctgctgctg ttcgtgatct ccatcaccac aatcatcgtg	900
atcttcctgc gcgtgaagtt cagccggagc gctgatgcc ctgcatacca gcaggggcag	960
aaccagctct acaacgaact gaaccttga cggcgggagg aatacgatgt gctggataag	1020
cgaagaggcc gcgaccaga aatgggcggg aagcccagac gcaagaatcc tcaggaggga	1080
ctgtacaacg agctccagaa agacaagatg gccgaagcgt acagcgagat cggcatgaag	1140

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ggggaacgga gaaggggaaa gggccatgac ggattgtacc agggcctgtc gaccgctacc      1200
aaagacacct acgacgccct ccatatgcaa gcactgccgc cacgctgaac gcgt              1254

<210> 117
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> (nucleotide) hIgG heavy chain signal sequence/scFV 3-17I/hIgG1
      hinge/CD226 TMD/CD226 ICD v1/CD3zeta

<400> 117
atggactgga tctggagaat tttgttcctt gtcggtgctg ccactggagc ccactcgcaa      60
gtgcagctcg tgcagtctgg agcagaagtc aagaagcctg ggtcctcggc caaagtgtcc      120
tgcaaagcct ccggggggcac tttcagctcg tacgcaatct cctgggtccg ccaagcgccc      180
ggacaggggtc tggagtggat gggcgggatt atccccatth tggcaccgc caactatgct      240
caaaagtthc agggccgcgt gactattacc gcggacgagt caacctccac tgcgtacatg      300
gaactgagct cacttcgggtc cgaggacacc gccgtctatt actgtgcgcg gggactcctg      360
tggaactact ggggacaagg caccctcgtg accgtgtcct cgaagctgtc cgggtcggcc      420
agcgccccca agttggaaga gggcgaattc tccgaggccc gggtggaat cgtgatgacc      480
cagtccccgg ccactctctc cgtgtccccg ggagaaaggg cgaccctgtc atgccggggc      540
tcgcaatccg tgtcatccaa cctggccttg taccagcaga agccaggaca ggcgccccgc      600
ctgattatct acggcgccag caccaccgcg agcggaattc cggcccgggt ttccgcctcc      660
ggttcgggaa ctgacttcac gctgactatc agcagcctgc aatcgaggga cttcgccgtc      720
tactactgcc agcagtataa caactggccc ccggcttaca cgtttgcca gggaactaag      780
ctggagatca aggagcccaa aagctgcgac aagaccaca cttgccacc ttgtccggac      840
ccgaaggggg gaaccgtgct cctgctgctg ttcgtgatct ccatcaccac aatcatcgtg      900
atcttcctga accgccggcg aagacgcgaa agacgcgata tgttcaccga gtcattggac      960
accagaagg cccctaacaa ctacagaagc ccgatcagca ccagccagcc tactaatcag      1020
tcgatggatg ataccgcga ggacatctac gtgaattacc caaccttctc ccggcggccg      1080
aaaacccgcg tgcgcgtgaa gttcagccgg agcgtgatg cccctgcata ccagcagggg      1140
cagaaccagc tctacaacga actgaacctt ggacggcggg aggaatacga tgtgtcggat      1200
aagcgaagag gccgcgaccc agaaatgggc ggggaagcca gacgcaagaa tcctcaggag      1260
ggactgtaca acgagctcca gaaagacaag atggccgaag cgtacagcga gatcggcatg      1320
aagggggaac ggagaagggg aaagggccat gacggattgt accagggcct gtcgaccgct      1380
accaaagaca cctacgacgc cctccatatg caagcactgc cgccacgctg aacgcgt      1437

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<210> 118
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28
TMD/41BB/CD3zeta /CD226 ICD v1

<400> 118

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
165 170 175

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
180 185 190

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
195 200 205

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

210

215

220

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 225 230 235 240

Phe Cys Ser Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr
 245 250 255

Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly
 275 280 285

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

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
 305 310 315 320

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
 325 330 335

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
 340 345 350

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 355 360 365

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 370 375 380

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 385 390 395 400

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 405 410 415

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
 420 425 430

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 435 440 445

Leu His Met Gln Ala Leu Pro Pro Arg Asn Arg Arg Arg Arg Glu
 450 455 460

Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn

465 470 475 480

Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met
485 490 495

Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg
500 505 510

Arg Pro Lys Thr Arg Val
515

<210> 119

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD28
TMD/41BB/CD226 ICD v1/CD3zeta

<400> 119

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr
115 120 125

Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

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

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
420 425 430

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
435 440 445

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
450 455 460

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
465 470 475 480

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
485 490 495

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
500 505 510

Gln Ala Leu Pro Pro Arg
515

<210> 120

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> hIgG heavy chain signal sequence/scFV GC33/hIgG1 hinge/CD226
TMD/CD226 ICD v1

<400> 120

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

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

Thr Asp Tyr Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu
50 55 60

Lys Trp Ile Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

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

Phe Ser Arg Arg Pro Lys Thr Arg Val
355 360

<210> 121

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/41BB/CD3zeta /CD226 ICD v1

<400> 121

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
180 185 190

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

195

200

205

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
 210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
 260 265 270

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Lys Arg Gly Arg
 275 280 285

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

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
 305 310 315 320

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 325 330 335

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 340 345 350

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 355 360 365

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 370 375 380

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
 385 390 395 400

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
 405 410 415

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
 420 425 430

Gln Ala Leu Pro Pro Arg Asn Arg Arg Arg Arg Glu Arg Arg Asp
 435 440 445

Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg

450

455

460

Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met Asp Asp Thr
 465 470 475 480

Arg Glu Asp Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys
 485 490 495

Thr Arg Val

<210> 122

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> scFV GC33/hIgG1 hinge/CD28 TMD/41BB/CD226 ICD v1/CD3zeta

<400> 122

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
 35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 130 135 140

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

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

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
420 425 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
435 440 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
450 455 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465 470 475 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
485 490 495

Pro Pro Arg

<210> 123
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV GC33/hIgG1 hinge/CD226 TMD/CD226 ICD v1

<400> 123

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Glu Met His Trp Val Lys Gln Thr Pro Val His Gly Leu Lys Trp Ile
35 40 45

Gly Ala Leu Asp Pro Lys Thr Gly Asp Thr Ala Tyr Ser Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Phe Tyr Ser Tyr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 130 135 140

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

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
 165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
 180 185 190

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

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser
 210 215 220

Gln Asn Thr His Val Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu
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Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
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Pro Asp Pro Lys Gly Gly Thr Val Leu Leu Leu Leu Phe Val Ile Ser
 260 265 270

Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu
 275 280 285

Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn
 290 295 300

Asn Tyr Arg Ser Pro Ile Ser Thr Ser Gln Pro Thr Asn Gln Ser Met
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<212> DNA

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<212> DNA

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