

SEQUENCE LISTING

<110> Invectys

<120> CHIMERIC ANTIGEN RECEPTORS AGAINST HLA-G

<130> PR2348EP00

<160> 86

<170> PatentIn version 3.5

<210> 1

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> LFFT-1 VH

<400> 1

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

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

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

Gly	Trp	Ile	Tyr	Thr	Tyr	Ser	Gly	Val	Pro	Thr	Tyr	Ala	Asp	Asp	Leu
	50					55					60				

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

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

Ala	Arg	Val	Arg	Asp	Gly	Tyr	Tyr	Arg	Tyr	Ala	Met	Asp	Tyr	Trp	Gly
			100					105					110		

Gln Gly Thr Ser Val Thr Val Ser Ser Cys
115 120

<210> 2
<211> 106
<212> PRT
<213> artificial

<220>
<223> LFFT-1 VL

<400> 2

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

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

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

His Phe Thr Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp Leu Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 3
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E57 VH

<400> 3

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

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

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

Gly Thr Ile Tyr Pro Ser Asp Ser Ser Thr His Tyr Asn Gln Glu Phe
50 55 60

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Gly Leu Ala Gly Val Phe Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 4

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> 1E57 VL

<400> 4

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

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

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

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

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

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

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

Lys

<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> LFFT-1 VH CDR1

<400> 5

Gly Tyr Thr Phe Thr Thr Tyr Gly
1 5

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> LFFT-1 VH CDR2

<400> 6

Ile Tyr Thr Tyr Ser Gly Val Pro
1 5

<210> 7
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> LFFT-1 VH CDR3

<400> 7

Ala Arg Val Arg Asp Gly Tyr Tyr Arg Tyr Ala Met Asp Tyr
1 5 10

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> LFFT-1 VL CDR1

<400> 8

Gln Asp Ile Asn Arg Tyr
1 5

<210> 9
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> LFFT-1 VL CDR2

<400> 9

Phe Thr Ser
1

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> LFFT-1 VL CDR3

<400> 10

Leu Gln Tyr Asp Asp Leu Arg Thr
1 5

<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 1E57 VH CDR1

<400> 11

Gly Tyr Thr Phe Thr Asp Tyr Trp
1 5

<210> 12

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 1E57 VH CDR2

<400> 12

Ile Tyr Pro Ser Asp Ser Ser Thr
1 5

<210> 13

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 1E57 VH CDR3

<400> 13

Ala Arg Glu Gly Leu Ala Gly Val Phe Tyr Phe Asp Tyr
1 5 10

<210> 14
<211> 11
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<220>
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<400> 14

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

<210> 15
<211> 3
<212> PRT
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<220>
<223> 1E57 VL CDR2

<400> 15

Lys Val Ser
1

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E57 VL CDR3

<400> 16

Phe Gln Gly Ser His Leu Pro Pro Thr
1 5

<210> 17
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Signal Peptide CD8a

<400> 17

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala

<210> 18

<211> 90

<212> PRT

<213> Artificial Sequence

<220>

<223> CD8a Hinge

<400> 18

Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe
1 5 10 15

Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
20 25 30

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
35 40 45

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

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

Ser Leu Leu Val Thr Val Ala Phe Ile Ile
85 90

<210> 19

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 Hinge

<400> 19

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
1 5 10 15

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
20 25 30

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
35 40 45

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
50 55 60

<210> 20

<211> 68

<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 human

<400> 20

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 Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
50 55 60

Ala Tyr Arg Ser
65

<210> 21
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB human

<400> 21

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 Glu Gly Gly Cys Glu Leu
35 40

<210> 22
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3z human endodomain

<400> 22

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> 23
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag Tag

<400> 23

Gly Ala Cys Thr Ala Cys Ala Ala Ala Gly Ala Cys Gly Ala Cys Gly
1 5 10 15

Ala Thr Gly Ala Cys Ala Ala Gly
20

<210> 24
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse IgKappa Signal Peptide

<400> 24

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser

<210> 25
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge hIgG4

<400> 25

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 26
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated CH2 human IgG4

<400> 26

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1 5 10 15

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

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35 40 45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60

Phe Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65 70 75 80

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85 90 95

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 27
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3 human IgG4

<400> 27

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
100 105

<210> 28
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A Cleavage peptide

<400> 28

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 29
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated human CD19 Reporter

<400> 29

Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
1 5 10 15

Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
20 25 30

Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
35 40 45

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
50 55 60

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
65 70 75 80

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
85 90 95

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
100 105 110

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
115 120 125

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
130 135 140

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
145 150 155 160

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
165 170 175

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
180 185 190

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
195 200 205

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
210 215 220

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
225 230 235 240

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
245 250 255

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
260 265 270

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
275 280 285

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

Cys Ser Leu Val Gly Ile Leu His Leu
305 310

<210> 30

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> ScFV 15E7

<400> 30

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

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

Ser Gly Asn Thr Tyr Leu Glu 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 Tyr Cys Phe Gln Gly
85 90 95

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125

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

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp
145 150 155 160

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

Thr Ile Tyr Pro Ser Asp Ser Ser Thr His Tyr Asn Gln Glu Phe Lys
180 185 190

Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
195 200 205

His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
210 215 220

Arg Glu Gly Leu Ala Gly Val Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Thr Leu Thr Val Ser Ser
245

<210> 31
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> ScFV LFTT1

<400> 31

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

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

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

His Phe Thr Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp Leu Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu Val Gln Ser
115 120 125

Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys
130 135 140

Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Gly Met Ser Trp Val Lys Gln
145 150 155 160

Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile Tyr Thr Tyr Ser
165 170 175

Gly Val Pro Thr Tyr Ala Asp Asp Leu Glu Gly Arg Phe Ala Phe Ser
180 185 190

Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys
195 200 205

Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Arg Asp Gly Tyr
210 215 220

Tyr Arg Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser

<210> 32

<211> 1046

<212> PRT

<213> Artificial Sequence

<220>

<223> LFTT1 HingeCH2CH3 hIgG4

<400> 32

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser Asp Ile His Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

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

Asn Arg Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn
85 90 95

Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp
100 105 110

Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu
130 135 140

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

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Gly Met Ser Trp
165 170 175

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile Tyr
180 185 190

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

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Asn
210 215 220

Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Arg
225 230 235 240

Asp Gly Tyr Tyr Arg Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
245 250 255

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
260 265 270

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
275 280 285

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
290 295 300

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
305 310 315 320

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
325 330 335

Gln Phe Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
340 345 350

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
355 360 365

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
370 375 380

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
405 410 415

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
420 425 430

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
435 440 445

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465 470 475 480

Lys Ser Leu Ser Leu Ser Leu Gly Lys Phe Trp Val Leu Val Val Val
485 490 495

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
500 505 510

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
515 520 525

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
530 535 540

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly
545 550 555 560

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
565 570 575

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
580 585 590

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
595 600 605

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
610 615 620

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
625 630 635 640

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
645 650 655

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
660 665 670

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
675 680 685

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
690 695 700

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
705 710 715 720

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro Pro
725 730 735

Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met Glu Val Arg
740 745 750

Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val
755 760 765

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
770 775 780

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
785 790 795 800

Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
805 810 815

Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
820 825 830

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
835 840 845

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
850 855 860

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
865 870 875 880

Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
885 890 895

Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
900 905 910

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
915 920 925

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
930 935 940

Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
945 950 955 960

Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
965 970 975

Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr
980 985 990

Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
995 1000 1005

Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp
1010 1015 1020

Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu Cys
1025 1030 1035

Ser Leu Val Gly Ile Leu His Leu
1040 1045

<210> 33
<211> 937
<212> PRT
<213> Artificial Sequence

<220>
<223> LFTT1 CH3 hIgG4

<400> 33

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser Asp Ile His Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

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

Asn Arg Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn
85 90 95

Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp
100 105 110

Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu
130 135 140

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

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Gly Met Ser Trp
165 170 175

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile Tyr
180 185 190

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

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Asn
210 215 220

Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Arg
225 230 235 240

Asp Gly Tyr Tyr Arg Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
245 250 255

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
260 265 270

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

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
290 295 300

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
305 310 315 320

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
325 330 335

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
355 360 365

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Phe Trp Val Leu
370 375 380

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

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
405 410 415

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
420 425 430

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
435 440 445

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
450 455 460

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
465 470 475 480

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
485 490 495

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
500 505 510

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
515 520 525

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
530 535 540

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
545 550 555 560

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
565 570 575

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
580 585 590

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn
595 600 605

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
610 615 620

Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
625 630 635 640

Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
645 650 655

Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
660 665 670

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
675 680 685

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
690 695 700

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
705 710 715 720

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
725 730 735

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
740 745 750

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
755 760 765

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
770 775 780

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
785 790 795 800

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
805 810 815

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
820 825 830

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
835 840 845

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
850 855 860

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
865 870 875 880

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
885 890 895

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
900 905 910

Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu
915 920 925

Cys Ser Leu Val Gly Ile Leu His Leu
930 935

<210> 34
<211> 830
<212> PRT
<213> Artificial Sequence

<220>
<223> LFTT1 hIgG4

<400> 34

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser Asp Ile His Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

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

Asn Arg Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn
85 90 95

Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp
100 105 110

Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu
130 135 140

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

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Gly Met Ser Trp
165 170 175

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile Tyr
180 185 190

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

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Asn
210 215 220

Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Arg
225 230 235 240

Asp Gly Tyr Tyr Arg Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
245 250 255

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
260 265 270

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
275 280 285

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
290 295 300

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
305 310 315 320

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
325 330 335

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
340 345 350

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
355 360 365

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
370 375 380

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

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

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
420 425 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
435 440 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
450 455 460

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

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

Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu
500 505 510

Glu Asn Pro Gly Pro Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu
515 520 525

Phe Leu Thr Pro Met Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys
530 535 540

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

Asp Gly Pro Thr Gln Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys
565 570 575

Pro Phe Leu Lys Leu Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met
580 585 590

Arg Pro Leu Ala Ile Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met
595 600 605

Gly Gly Phe Tyr Leu Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp
610 615 620

Gln Pro Gly Trp Thr Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg
625 630 635 640

Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg
645 650 655

Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys
660 665 670

Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro
675 680 685

Pro Cys Leu Pro Pro Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp
690 695 700

Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro
705 710 715 720

Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp Thr His Val His Pro
725 730 735

Lys Gly Pro Lys Ser Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro
740 745 750

Ala Arg Asp Met Trp Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala
755 760 765

Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr
770 775 780

Met Ser Phe His Leu Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp
785 790 795 800

Leu Leu Arg Thr Gly Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr
805 810 815

Leu Ile Phe Cys Leu Cys Ser Leu Val Gly Ile Leu His Leu
820 825 830

<210> 35
<211> 1051
<212> PRT
<213> Artificial Sequence

<220>
<223> 15E7 CH2CH3 hIgG4

<400> 35

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

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

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
35 40 45

Val His Arg Ser Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

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

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
100 105 110

Phe Gln Gly Ser His Leu Pro Pro Thr Phe Gly Gly Gly Thr Thr Leu
115 120 125

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

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

Gly Ser Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
165 170 175

Asp Tyr Trp Met Asp Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
180 185 190

Trp Ile Gly Thr Ile Tyr Pro Ser Asp Ser Ser Thr His Tyr Asn Gln
195 200 205

Glu Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr
210 215 220

Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
225 230 235 240

Tyr Cys Ala Arg Glu Gly Leu Ala Gly Val Phe Tyr Phe Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro
260 265 270

Pro Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
275 280 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
290 295 300

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
305 310 315 320

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
325 330 335

Lys Pro Arg Glu Glu Gln Phe Gln Ser Thr Tyr Arg Val Val Ser Val
340 345 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
355 360 365

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
370 375 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385 390 395 400

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
405 410 415

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
420 425 430

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

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
450 455 460

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465 470 475 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Phe Trp
485 490 495

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
500 505 510

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
515 520 525

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
530 535 540

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
545 550 555 560

Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
565 570 575

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
580 585 590

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
595 600 605

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
610 615 620

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
625 630 635 640

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
645 650 655

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
660 665 670

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
675 680 685

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
690 695 700

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala
705 710 715 720

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
725 730 735

Gly Pro Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr
740 745 750

Pro Met Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu
755 760 765

Gly Asp Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro
770 775 780

Thr Gln Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu
785 790 795 800

Lys Leu Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu
805 810 815

Ala Ile Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe
820 825 830

Tyr Leu Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly
835 840 845

Trp Thr Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val
850 855 860

Ser Asp Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu
865 870 875 880

Gly Pro Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val
885 890 895

Trp Ala Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu
900 905 910

Pro Pro Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met
915 920 925

Ala Pro Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser
930 935 940

Val Ser Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro
945 950 955 960

Lys Ser Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp
965 970 975

Met Trp Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln
980 985 990

Asp Ala Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe
995 1000 1005

His Leu Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu
1010 1015 1020

Arg Thr Gly Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu
1025 1030 1035

Ile Phe Cys Leu Cys Ser Leu Val Gly Ile Leu His Leu
1040 1045 1050

<210> 36
<211> 942
<212> PRT
<213> Artificial Sequence

<220>
<223> 15E7 CH3 hIgG4

<400> 36

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

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

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
35 40 45

Val His Arg Ser Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

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

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
100 105 110

Phe Gln Gly Ser His Leu Pro Pro Thr Phe Gly Gly Gly Thr Thr Leu
115 120 125

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

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

Gly Ser Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
165 170 175

Asp Tyr Trp Met Asp Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
180 185 190

Trp Ile Gly Thr Ile Tyr Pro Ser Asp Ser Ser Thr His Tyr Asn Gln
195 200 205

Glu Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr
210 215 220

Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
225 230 235 240

Tyr Cys Ala Arg Glu Gly Leu Ala Gly Val Phe Tyr Phe Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro
260 265 270

Pro Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
275 280 285

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
290 295 300

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
305 310 315 320

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
325 330 335

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
340 345 350

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
355 360 365

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
370 375 380

Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
385 390 395 400

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
405 410 415

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
420 425 430

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
435 440 445

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
450 455 460

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
465 470 475 480

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
485 490 495

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

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
515 520 525

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
530 535 540

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

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
565 570 575

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
580 585 590

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
595 600 605

Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu
610 615 620

Glu Asn Pro Gly Pro Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu
625 630 635 640

Phe Leu Thr Pro Met Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys
645 650 655

Val Glu Glu Gly Asp Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser
660 665 670

Asp Gly Pro Thr Gln Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys
675 680 685

Pro Phe Leu Lys Leu Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met
690 695 700

Arg Pro Leu Ala Ile Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met
705 710 715 720

Gly Gly Phe Tyr Leu Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp
725 730 735

Gln Pro Gly Trp Thr Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg
740 745 750

Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg
755 760 765

Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys
770 775 780

Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro
785 790 795 800

Pro Cys Leu Pro Pro Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp
805 810 815

Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro
820 825 830

Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp Thr His Val His Pro
835 840 845

Lys Gly Pro Lys Ser Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro
850 855 860

Ala Arg Asp Met Trp Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala
865 870 875 880

Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr
885 890 895

Met Ser Phe His Leu Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp
900 905 910

Leu Leu Arg Thr Gly Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr
915 920 925

Leu Ile Phe Cys Leu Cys Ser Leu Val Gly Ile Leu His Leu
930 935 940

<210> 37
<211> 835
<212> PRT
<213> Artificial Sequence

<220>
<223> 15E7 hIgG4

<400> 37

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

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

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
35 40 45

Val His Arg Ser Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

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

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
100 105 110

Phe Gln Gly Ser His Leu Pro Pro Thr Phe Gly Gly Gly Thr Thr Leu
115 120 125

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

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

Gly Ser Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
165 170 175

Asp Tyr Trp Met Asp Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
180 185 190

Trp Ile Gly Thr Ile Tyr Pro Ser Asp Ser Ser Thr His Tyr Asn Gln
195 200 205

Glu Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr
210 215 220

Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
225 230 235 240

Tyr Cys Ala Arg Glu Gly Leu Ala Gly Val Phe Tyr Phe Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro
260 265 270

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

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
305 310 315 320

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
325 330 335

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys
340 345 350

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
355 360 365

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
370 375 380

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

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
405 410 415

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
420 425 430

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
435 440 445

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
450 455 460

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
465 470 475 480

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

Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
500 505 510

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Pro Pro Pro Arg Leu
515 520 525

Leu Phe Phe Leu Leu Phe Leu Thr Pro Met Glu Val Arg Pro Glu Glu
530 535 540

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

Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr Trp Ser Arg
565 570 575

Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly Leu Pro Gly
580 585 590

Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe Ile Phe Asn
595 600 605

Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro Gly Pro Pro
610 615 620

Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val Glu Gly Ser
625 630 635 640

Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys
645 650 655

Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys
660 665 670

Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Ile
675 680 685

Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser Leu Asn Gln
690 695 700

Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu
705 710 715 720

Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp
725 730 735

Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser Leu Glu Leu
740 745 750

Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu Thr Gly Leu
755 760 765

Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys His
770 775 780

Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr Ala Arg Pro
785 790 795 800

Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys Val Ser Ala
805 810 815

Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu Cys Ser Leu Val Gly Ile
820 825 830

Leu His Leu
835

<210> 38
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> LFFT-1 VH

<400> 38
cagattcagc ttgtacaatc tgggcctgag ctgaagaaac ccggagaaac cgtcaagatc 60
agctgcaaag caagtgggta tactttcacg acgtatggca tgtcttgggt caagcaagct 120
cctgggaaaag ggctgaaatg gatgggctgg atttacacct attctggagt tcctacatat 180
gccgacgatc tggaagggcg ctttgccttc agcctggaga ctagcgctc aaccgcttat 240
ttgcagatca acaacctcaa gaacgaagat acggcgacct atttctgtgc cagagttcgg 300
gatggctact atagatacgc catggattat tggggccaag gtacatccgt gaccgtttca 360
agctgc 366

<210> 39
<211> 318

<212> DNA
<213> Artificial Sequence

<220>
<223> LFFT-1 VL

<400> 39
gatatccata tgaccagag tccaagctct ctgagcgcta gcctgggcgg caaagtgacc 60
ataacatgca aggctagcca ggacattaac cggtacatag cctggtacca gcataagccc 120
ggaaaaggcc ccagactgct gatccacttc acctccacac tgcagtccgg gattccctca 180
cgattctccg gatcaggttc aggtcgagac tactccttta gcatttccaa cctcgaacct 240
gaggacatcg ccacatacta ctgtctgcag tatgacgacc ttcgcacttt tggcgggtgga 300
actaaactgg agatcaag 318

<210> 40
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> 1E57 VH

<400> 40
caggtgcagt tgcagcaacc cggggccgaa ctggtcagac cgggctcctc tgtgaagctg 60
tcatgcaagg ctagtggcta taccttcacc gactattgga tggattgggt aaagcagcgg 120
ccaggacaag gactggaatg gattgggacc atttacccta gcgacagttc tacgcactac 180
aatcaggagt tcaaaggcaa ggctacaatg acagtggaca agtccagttc tacagcctac 240
atgcaccttt ctagcctcac atcagaggat tccgcagtgt actattgtgc acgtgaaggc 300
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<223> 1E57 VL

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<220>
 <223> LFFT-1 VH CDR1

<400> 42
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<210> 43
 <211> 24
 <212> DNA
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<220>
 <223> LFFT-1 VH CDR2

<400> 43
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<210> 44
 <211> 42
 <212> DNA
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<220>
 <223> LFFT-1 VH CDR3

<400> 44
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<210> 45
<211> 18
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<220>
<223> LFFT-1 VL CDR1

<400> 45
caggacatta accggtac

18

<210> 46
<211> 9
<212> DNA
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<223> LFFT-1 VL CDR2

<400> 46
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<223> LFFT-1 VL CDR3

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24

<210> 49
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<223> 1E57 VH CDR2

<400> 49
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<210> 50
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<223> 1E57 VH CDR3

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<400> 51
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<400> 52
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<210> 53
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 <223> Signal Peptide CD8a

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 <223> CD8a Hinge

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 <220>
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<220>
 <223> CD28 human

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<220>
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 <223> CD3z human endodomain

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 cgggaccccg agatgggagg caagccaagg cgcaagaacc cccaggaggg cctgtacaat 180
 gagctgcaga aggacaagat ggccgaggcc tatagcgaga tcggcatgaa gggagagcgg 240
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<210> 60
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 <212> DNA
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<220>
 <223> Flag Tag

<400> 60
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<210> 61
 <211> 57
 <212> DNA
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<220>
 <223> Mouse IgKappa Signal Peptide

<400> 61
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<210> 62
 <211> 36
 <212> DNA
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<220>
 <223> Hinge hIgG4

<400> 62
 gagagcaagt acggcccacc ctgccctcca tgtcca 36

<210> 63
<211> 327
<212> DNA
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<220>
<223> Mutated CH2 human IgG4

<400> 63
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gaggtgcagt tcaactggta cgtggatggc gtggaggtgc acaatgccaa gaccaagccc 180
cgcgaggagc agtttcagtc cacctaccgg gtgggtgtctg tgctgacagt gctgcaccag 240
gactggctga acggcaagga gtataagtgc aaggtagagca ataagggcct gccttcctct 300
atcgagaaga ccatctccaa ggccaag 327

<210> 64
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> CH3 human IgG4

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<210> 65
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<212> DNA
<213> Artificial Sequence

<220>

<223> P2A Cleavage peptide

<400> 65

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<210> 66

<211> 939

<212> DNA

<213> Artificial Sequence

<220>

<223> Truncated human CD19 Reporter

<400> 66

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<212> DNA
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<223> ScFV 15E7

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accacactga ccgtctcgag c 741

<210> 68
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<212> DNA
<213> Artificial Sequence

<220>
<223> ScFV LFTT1

<400> 68
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 <223> 15E7 CH2CH3 hIgG4

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<213> Artificial Sequence

<220>
<223> 15E7 CH3 hIgG4

<400> 73
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 <223> 15E7 hIgG4

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<211> 21
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<220>
<223> mouse Ig?

<400> 75

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Gly Ser Thr Gly Asp
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Val Thr Asn Ser
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<220>
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<400> 77

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Val His Ser

<210> 78
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<212> PRT
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<220>
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<400> 78

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Ala

<210> 79
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<400> 79
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<220>
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gcttaccgta gc 132

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<220>
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<400> 81
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<220>
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<210> 83
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<212> PRT
<213> artificial

<220>
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<400> 83

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Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

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

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65 70 75 80

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

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

Cys Phe Gln Gly Ser His Leu Pro Pro Thr Phe Gly Gly Gly Thr Thr
115 120 125

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

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

Pro Gly Ser Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
165 170 175

Thr Asp Tyr Trp Met Asp Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190

Glu Trp Ile Gly Thr Ile Tyr Pro Ser Asp Ser Ser Thr His Tyr Asn
195 200 205

Gln Glu Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
210 215 220

Thr Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

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

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Leu Ser Asn Ser
260 265 270

Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro
275 280 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
290 295 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
305 310 315 320

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val
325 330 335

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
340 345 350

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly
355 360 365

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
370 375 380

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
385 390 395 400

Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
405 410 415

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
420 425 430

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
435 440 445

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

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

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

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

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
515 520 525

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
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Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Gly Gly Ser
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Asp Tyr Lys Asp Asp Asp Asp Lys
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<211> 1707
<212> DNA
<213> artificial

<220>
<223> CD8a hinge

<400> 84

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<220>
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<400> 85

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Ser	Leu	Gly	Gly	Lys	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Ile
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Asn	Arg	Tyr	Ile	Ala	Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Gly	Pro	Arg
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Leu	Leu	Ile	His	Phe	Thr	Ser	Thr	Leu	Gln	Ser	Gly	Ile	Pro	Ser	Arg
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Phe	Ser	Gly	Ser	Gly	Ser	Gly	Arg	Asp	Tyr	Ser	Phe	Ser	Ile	Ser	Asn
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Leu	Glu	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Tyr	Asp	Asp
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Leu	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly
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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu
130 135 140

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

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Gly Met Ser Trp
165 170 175

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile Tyr
180 185 190

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

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Asn
210 215 220

Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Val Arg
225 230 235 240

Asp Gly Tyr Tyr Arg Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
245 250 255

Val Thr Val Ser Ser Cys Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr
260 265 270

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

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
290 295 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305 310 315 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
325 330 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
340 345 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
355 360 365

Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
370 375 380

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
385 390 395 400

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
405 410 415

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
420 425 430

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
435 440 445

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg
450 455 460

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

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

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
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Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Asp Tyr Lys
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Asp Asp Asp Asp Lys
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<211> 1602
<212> DNA
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<223> CD28 hinge domain

<400> 86
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