

SEQUENCE LISTING

<110> XYPHOS BIOSCIENCES INC.

<120> NON-NATURAL NKG2D RECEPTORS THAT DO NOT DIRECTLY SIGNAL THE CELLS
TO WHICH THEY ARE ATTACHED

<130> A251193

<150> US 62/755,776

<151> 2018-11-05

<160> 202

<170> PatentIn version 3.5

<210> 1

<211> 183

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide MICA alpha1-alpha2 domain

<400> 1

Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu Thr Val Leu Ser Trp
1 5 10 15

Asp Gly Ser Val Gln Ser Gly Phe Leu Thr Glu Val His Leu Asp Gly
20 25 30

Gln Pro Phe Leu Arg Cys Asp Arg Gln Lys Cys Arg Ala Lys Pro Gln
35 40 45

Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp Asp Arg Glu
50 55 60

Thr Arg Asp Leu Thr Gly Asn Gly Lys Asp Leu Arg Met Thr Leu Ala
65 70 75 80

His Ile Lys Asp Gln Lys Glu Gly Leu His Ser Leu Gln Glu Ile Arg
85 90 95

Val Cys Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser Gln His Phe
100 105 110

Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Lys Glu
115 120 125

Trp Thr Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val
130 135 140

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

Ala Met His Ala Asp Cys Leu Gln Glu Leu Arg Arg Tyr Leu Lys Ser
165 170 175

Gly Val Val Leu Arg Arg Thr
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<210> 2
<211> 182
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide MICB alpha1-alpha2 domain

<400> 2

Ala Glu Pro His Ser Leu Arg Tyr Asn Leu Met Val Leu Ser Gln Asp
1 5 10 15

Glu Ser Val Gln Ser Gly Phe Leu Ala Glu Gly His Leu Asp Gly Gln
20 25 30

Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg Arg Ala Lys Pro Gln Gly
35 40 45

Gln Trp Ala Glu Asp Val Leu Gly Ala Lys Thr Trp Asp Thr Glu Thr
50 55 60

Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu Arg Arg Thr Leu Thr His
65 70 75 80

Ile Lys Asp Gln Lys Gly Gly Leu His Ser Leu Gln Glu Ile Arg Val
85 90 95

Cys Glu Ile His Glu Asp Ser Ser Thr Arg Gly Ser Arg His Phe Tyr
100 105 110

Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Gln Glu Ser
115 120 125

Thr Val Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Thr
130 135 140

Asn Phe Trp Lys Glu Asp Ala Met Lys Thr Lys Thr His Tyr Arg Ala
145 150 155 160

Met Gln Ala Asp Cys Leu Gln Lys Leu Gln Arg Tyr Leu Lys Ser Gly
165 170 175

Val Ala Ile Arg Arg Thr
180

<210> 3
<211> 187
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide ULBP1 alpha1-alpha2 domain

<400> 3

Ala Ala Glu Pro His Cys Leu Cys Tyr Asp Phe Ile Ile Thr Pro Lys
1 5 10 15

Ser Arg Pro Glu Pro Gln Trp Cys Glu Val Gln Gly Leu Val Asp Glu
20 25 30

Arg Pro Phe Leu His Tyr Asp Cys Val Asn His Lys Ala Lys Ala Phe
35 40 45

Ala Ser Leu Gly Lys Lys Val Asn Val Thr Lys Thr Trp Glu Glu Gln
50 55 60

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

Asp Ile Gln Val Glu Asn Leu Ile Pro Ile Glu Pro Leu Thr Leu Gln
85 90 95

Ala Arg Met Ser Cys Glu His Glu Ala His Gly His Gly Arg Gly Ser
100 105 110

Trp Gln Phe Leu Phe Asn Gly Gln Lys Phe Leu Leu Phe Asp Ser Asn
115 120 125

Asn Arg Lys Trp Thr Ala Leu His Pro Gly Ala Lys Lys Met Thr Glu
130 135 140

Lys Trp Glu Lys Asn Arg Asp Val Thr Met Phe Phe Gln Lys Ile Ser
145 150 155 160

Leu Gly Asp Cys Lys Met Trp Leu Glu Glu Phe Leu Met Tyr Trp Glu
165 170 175

Gln Met Leu Asp Pro Thr Lys Pro Pro Met Val
180 185

<210> 4

<211> 189

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide ULBP2 alpha1-alpha2 domain

<400> 4

Ala Ala Glu Pro His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys
1 5 10 15

Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu
20 25 30

Lys Thr Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val
35 40 45

Ser Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
50 55 60

Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Arg
65 70 75 80

Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln
85 90 95

Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser
100 105 110

Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu
115 120 125

Lys Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu
130 135 140

Lys Trp Glu Asn Asp Lys Val Val Ala Met Ser Phe His Tyr Phe Ser
145 150 155 160

Met Gly Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp
165 170 175

Ser Thr Leu Glu Pro Ser Ala Gly Ala Pro Pro Met Val
180 185

<210> 5

<211> 187

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide ULBP3 alpha1-alpha2 domain

<400> 5

Ala Ala Glu Pro His Ser Leu Trp Tyr Asn Phe Thr Ile Ile His Leu
1 5 10 15

Pro Arg His Gly Gln Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln
20 25 30

Lys Asn Phe Leu Ser Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met
35 40 45

Gly His Leu Glu Glu Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln
50 55 60

Leu Glu Met Leu Arg Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala
65 70 75 80

Asp Thr Glu Leu Glu Asp Phe Thr Pro Ser Gly Pro Leu Thr Leu Gln
85 90 95

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

Trp Gln Phe Ser Phe Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn
115 120 125

Asn Arg Lys Trp Thr Val Val His Ala Gly Ala Arg Arg Met Lys Glu
130 135 140

Lys Trp Glu Lys Asp Ser Gly Leu Thr Thr Phe Phe Lys Met Val Ser
145 150 155 160

Met Arg Asp Cys Lys Ser Trp Leu Arg Asp Phe Leu Met His Arg Lys
165 170 175

Lys Arg Leu Glu Pro Thr Ala Pro Pro Met Val
180 185

<210> 6
<211> 187
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide ULBP4 alpha1-alpha2 domain

<400> 6

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

Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala Gln Val Phe Leu Asn Lys
20 25 30

Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn Asn Met Val Lys Pro Leu
35 40 45

Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu
50 55 60

Thr Gln Thr Leu Gly Glu Val Gly Arg Asp Leu Arg Met Leu Leu Cys
65 70 75 80

Asp Ile Lys Pro Gln Ile Lys Thr Ser Asp Pro Ser Thr Leu Gln Val
85 90 95

Glu Met Phe Cys Gln Arg Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp
100 105 110

Gln Phe Ala Thr Asn Gly Glu Lys Ser Leu Leu Phe Asp Ala Met Asn
115 120 125

Met Thr Trp Thr Val Ile Asn His Glu Ala Ser Lys Ile Lys Glu Thr
130 135 140

Trp Lys Lys Asp Arg Gly Leu Glu Lys Tyr Phe Arg Lys Leu Ser Lys
145 150 155 160

Gly Asp Cys Asp His Trp Leu Arg Glu Phe Leu Gly His Trp Glu Ala
165 170 175

Met Pro Glu Pro Thr Val Ser Pro Pro Met Val
180 185

<210> 7

<211> 198

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide ULBP5 alpha1-alpha2 domain

<400> 7

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

Lys Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp
20 25 30

Glu Lys Thr Phe Leu His Tyr Asp Cys Gly Ser Lys Thr Val Thr Pro
35 40 45

Val Ser Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala
50 55 60

Gln Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
65 70 75 80

Leu Asp Ile Gln Leu Glu Asn Tyr Ile Pro Lys Glu Pro Leu Thr Leu
85 90 95

Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Gly Ser Gly
100 105 110

Ser Trp Gln Leu Ser Phe Asp Gly Gln Ile Phe Leu Leu Phe Asp Ser
115 120 125

Glu Asn Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys
130 135 140

Glu Lys Trp Glu Asn Asp Lys Asp Met Thr Met Ser Phe His Tyr Ile
145 150 155 160

Ser Met Gly Asp Cys Thr Gly Trp Leu Glu Asp Phe Leu Met Gly Met
165 170 175

Asp Ser Thr Leu Glu Pro Ser Ala Gly Ala Pro Pro Thr Met Ser Ser
180 185 190

Gly Thr Ala Gln Pro Arg
195

<210> 8

<211> 189

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide ULBP6 alpha1-alpha2 domain

<400> 8

Ala Ala Glu Pro His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys
1 5 10 15

Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu
20 25 30

Lys Thr Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val
35 40 45

Ser Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
50 55 60

Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Leu
65 70 75 80

Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln
85 90 95

Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser
100 105 110

Trp Gln Phe Ser Ile Asp Gly Gln Thr Phe Leu Leu Phe Asp Ser Glu
115 120 125

Lys Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu
130 135 140

Lys Trp Glu Asn Asp Lys Asp Val Ala Met Ser Phe His Tyr Ile Ser
145 150 155 160

Met Gly Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp
165 170 175

Ser Thr Leu Glu Pro Ser Ala Gly Ala Pro Pro Met Val
180 185

<210> 9

<211> 161

<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide OMCP alpha1-alpha2 domain

<400> 9

Ala Ala Ala Glu Pro His Lys Leu Ala Phe Asn Phe Asn Leu Glu Ile
1 5 10 15

Asn Gly Ser Asp Thr His Ser Thr Val Asp Val Tyr Leu Asp Asp Ser
20 25 30

Gln Ile Ile Thr Phe Asp Gly Lys Asp Ile Arg Pro Thr Ile Pro Phe
35 40 45

Met Ile Gly Asp Glu Ile Phe Leu Pro Phe Tyr Lys Asn Val Phe Ser
50 55 60

Glu Phe Phe Ser Leu Phe Arg Arg Val Pro Thr Ser Thr Pro Tyr Glu
65 70 75 80

Asp Leu Thr Tyr Phe Tyr Glu Cys Asp Tyr Thr Asp Asn Lys Ser Thr
85 90 95

Phe Asp Gln Phe Tyr Leu Tyr Asn Gly Glu Glu Tyr Thr Val Lys Thr
100 105 110

Gln Glu Ala Thr Asn Lys Asn Met Trp Leu Thr Thr Ser Glu Phe Arg
115 120 125

Leu Lys Lys Trp Phe Asp Gly Glu Asp Cys Ile Met His Leu Arg Ser
130 135 140

Leu Val Arg Lys Met Glu Asp Ser Lys Arg Arg Thr Val Pro Pro Met
145 150 155 160

Val

<210> 10

<211> 543

<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding MICA alpha1-alpha2 domain

<400> 10

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gggttttctca ctgaggtaca tctggatggg cagcccttcc tgcgctgtga caggcagaaa     120
tgcagggcaa agccccaggg acagtgggca gaagatgtcc tgggaaataa gacatgggac      180
agagagacca gagacttgac agggaacgga aaggacctca ggatgaccct ggctcatatc      240
aaggaccaga aagaaggctt gcattccctc caggagatta gggctctgtga gatccatgaa      300
gacaacagca ccaggagctc ccagcatttc tactacgatg gggagctctt cctctcccaa      360
aacctggaga ctaaggaatg gacaatgccc cagtcctcca gagctcagac cttggccatg      420
aacgtcagga atttcttgaa ggaagatgcc atgaagacca agacacacta tcacgctatg      480
catgcagact gcctgcagga actacggcga tatctaaaat ccggcgtagt cctgaggaga      540
aca                                                                    543
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<210> 11

<211> 561

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding ULBP1 alpha1-alpha2 domain

<400> 11

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cctcagtggg gcgaagtaca aggtttgggt gacgaaaggc ctttccttca ctacgattgt      120
gtgaaccata aggcaaaggc tttcgccagc ctgggtaaga aggtaaacgt tactaagacg      180
tgggaggagc agacggaaac cctccgtgat gtggttgact ttcttaaggg tcagctcctc      240
gatatccaag tggagaattt aatccctatc gaaccgctca ctctgcaggc cagaatgtca      300
tgcgaacatg aagcacacgg tcatggaaga ggtagttggc aatttttatt taacgggtcaa      360
aaattcctgc tgttcgactc aaacaaccgc aaatggactg cgctgcaccc tggagctaag      420
aagatgactg aaaaatggga gaagaacaga gacgttacca tgttcttcca gaagatttcc      480
ctgggagatt gtaagatgtg gttagaggag ttcttaatgt actgggaaca gatgctggac      540
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cccacaaaac ccccatggt g 561

<210> 12
<211> 567
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP2 alpha1-alpha2 domain

<400> 12
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ccgcgctggt gtgccgtgca aggacaagtc gacgaaaaaa cttttcttca ttacgattgc 120
ggaaataaga ctgtaacgcc agtctctcct ttaggtaaga agttaaacgt cactacggcg 180
tggaaggcac aaaaccccg tctgcgcgag gtcgtcgaca tcctgactga acaattgcgc 240
gacatccagc tcgagaatta cactccaaag gagcctctta ccctgcaggc tagaatgtct 300
tgcgagcaaa aggagagagg ccactcctcc ggcagctggc agttcagttt cgacggacaa 360
atctttctgt tattcgattc agagaagaga atgtggacta cagttcaccc cggtgcccgt 420
aaaatgaagg agaagtggga aaacgacaaa gtggtggcga tgtcattcca ctatttctcg 480
atgggagact gcatcggttg gctggaagat ttctcatgg gtatggactc cactttggag 540
ccatcggctg gtgccccccc catggtg 567

<210> 13
<211> 561
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP3 alpha1-alpha2 domain

<400> 13
gctgctgagc cccacagctt gtggtacaac ttcaccatta tccacttgcc gagacatggc 60
cagcagtggg gcgaagtgca atcgcaagtc gacaaaaaaa acttcttatc atacgactgc 120
ggcagcgata aggtcttatc tatgggtcat ttggagggaac agctctacgc gaccgacgcc 180
tggggtaaac agctcgagat gctccgtgag gttggacaga ggctgagact ggaactggct 240
gacactgagc tggaagattt cacacctagt ggtccactca cattgcaagt acgcatgagc 300
tgcgagtgtg aggccgatgg atacattagg ggcagctggc agtttagctt cgacggaagg 360

aaattcctgc tcttcgacag taacaatagg aagtggactg ttgtgcatgc tgggtgcgcgc	420
agaatgaagg aaaagtggga gaaagatagc ggcctgacga ctttcttcaa gatggtgtct	480
atgcgtgact gtaagagctg gctcagagat ttcctcatgc atcgcaagaa gaggttagaa	540
cctaccgctc ccccatggt g	561

<210> 14
 <211> 561
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding ULBP4 alpha1-alpha2 domain

<400> 14	
gctgctgagc cccactctct ttgcttcaac ttcaccatta aatccctgag caggcctgggt	60
cagccgtgggt gtgaggcgca ggtctttctt aacaagaatc tcttcctcca atacaactct	120
gataacaaca tggtaaagcc actgggtctc ctgggtaaaa aagtctatgc tacgagcact	180
tggggagaac tcaccagac tcttggcgag gtaggaagag acctgcgcat gtcctctgc	240
gatataaagc cccaaattaa gaccagtgat ccgtccactt tacaagtcga aatgttctgc	300
caaagggagg ctgaacgctg caccggagcc tcttggcagt tcgcgaccaa tggcgaaaag	360
tccctcttgt tcgatgcat gaatatgacc tggaccgtga tcaatcatga ggcctctaag	420
atcaaggaga cgtggaaaaa ggaccgcggc cttgaaaagt actttaggaa gttgtctaaa	480
ggagactgcg accattgggtt acgcgagttc ctcggccatt gggaagcgat gcccgagcca	540
acggttagcc ccccatggt g	561

<210> 15
 <211> 567
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding ULBP6 alpha1-alpha2 domain

<400> 15	
gctgctgagc cccactcctt atgctatgat atcaccgtga ttccaaagtt ccgaccagga	60
ccccgatgggt gcgccgtaca gggacaggtc gacgaaaaga cttttttaca ttacgactgc	120
ggtaacaaga cagtcacacc ggtaagtcct ttgggaaaaa agttaaacgt aaccactgct	180

tggaaggccc agaaccccg t ctttcgagaa gtagtggata ttttgactga acagctgctt	240
gacatccagc tggaaaacta cacacccaaa gagcccctga ctcttcaagc gcgtatgtcg	300
tgtgagcaaa aggccgaagg acacagctcc ggatcctggc agttcagtat cgacggtcag	360
accttcctcc tcttcgattc agaaaagcgc atgtggacta ctgtgcaccc cggcgctcgt	420
aagatgaagg aaaagtggga gaatgataag gacgttgcca tgagttttca ttacattagt	480
atggggagatt gcatcggttg gctggaagac ttcctgatgg gtatggatag tacccttgaa	540
cctagtgccg gagctcccc catggtg	567

<210> 16
 <211> 483
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding OMCP alpha1-alpha2 domain

<400> 16	
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accattcaa ccgtggacgt ttatttagac gattcgcaga taatcacctt tgacggcaag	120
gacatccgcc caactatccc gttcatgata ggtgacgaaa tcttccttcc tttttataag	180
aatgtgttct ctgagttctt cagtttgttc cgccgcgtcc ctacctcaac cccctacgaa	240
gacttgactt atttctatga atgcgactac accgacaaca aatctacatt cgatcaattc	300
tacctgtaca acggtgaaga gtacaccgtg aagactcaag aggctactaa caagaacatg	360
tggctgacca cttccgagtt cagactgaag aagtggttcg acggcgagga ctgtatcatg	420
caccttagaa gtttagtgag gaaaatggaa gatagcaaga gaagaacagt gcccccatg	480
gtg	483

<210> 17
 <211> 139
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide natural NKG2D ectodomain

<400> 17

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 18
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152A ectodomain

<400> 18

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 19

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y199A ectodomain

<400> 19

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Ala Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 20
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152A/Y199A ectodomain

<400> 20

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Ala Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 21

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y199F eNKG2D1 ectodomain

<400> 21

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 22
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<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152S eNKG2D2 ectodomain

<400> 22

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ser His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 23
<211> 139
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y152T eNKG2D3 ectodomain

<400> 23

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Thr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 24

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y152V eNKG2D4 ectodomain

<400> 24

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Val His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 25
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152A/Y199F eNKG2D5
ectodomain

<400> 25

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala

35

40

45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
 50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly Leu
 65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
 85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
 100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
 115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
 130 135

<210> 26

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y152L/Y199F eNKG2D6
 ectodomain

<400> 26

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
 1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
 20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
 35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
 50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Leu His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 27
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152S/Y199F eNKG2D7
ectodomain

<400> 27

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ser His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 28
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152T/Y199F eNKG2D8
ectodomain

<400> 28

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Thr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 29
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152V/Y199F eNKG2D9
ectodomain

<400> 29

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Val His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 30

<211> 139
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y199D eNKG2D10 ectodomain

<400> 30

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Asp Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 31
<211> 139
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y199E eNKG2D11 ectodomain

<400> 31

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Glu Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 32
<211> 139
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide non-natural NKG2D Y152D/Y199D eNKG2D12
ectodomain

<400> 32

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Asp His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Asp Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 33

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y152E/Y199E eNKG2D13
ectodomain

<400> 33

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu

50

55

60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Glu His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Glu Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 34

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y152L eNKG2D14 ectodomain

<400> 34

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Leu His Trp Met Gly Leu
65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile

85

90

95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
 100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr
 115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
 130 135

<210> 35

<211> 139

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide non-natural NKG2D Y152F/Y199F eNKG2D15
 ectodomain

<400> 35

Phe Leu Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu
 1 5 10 15

Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn
 20 25 30

Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala
 35 40 45

Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu
 50 55 60

Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Phe His Trp Met Gly Leu
 65 70 75 80

Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile
 85 90 95

Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys
 100 105 110

Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr
115 120 125

Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
130 135

<210> 36
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide MHCI signal sequence

<400> 36

Met Gly Leu Gly Pro Val Phe Leu Leu Leu Ala Gly Ile Phe Pro Phe
1 5 10 15

Ala Pro Pro Gly Ala Ala Ala
20

<210> 37
<211> 69
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding MHCI signal sequence

<400> 37
atgggccttg gccagtggtt tctgctgttg gcaggcattt tcccttttgc tccgcccggc 60
gccgcagcc 69

<210> 38
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide human IgG1 Fc with IEGR linker

<400> 38

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys Ile Glu Gly Arg
225 230 235

<210> 39
<211> 711
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding human IgG1 Fc with IEGR linker

<400> 39
atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaaactg 60
ctgggtggcc cctccgtggt cctgttcccg cctaagccta aggacaccct tatgatcagc 120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag 180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa 240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg 300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag 360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc 420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct 480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc 540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag 600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac 660
cactacacc cagaagtcact gagcctctcc cccggaaaga tcgaaggacg c 711

<210> 40
<211> 376
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide human IgG1 Fc-NKG2D fusion

<400> 40

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 41

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152A fusion

<400> 41

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 42

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y199A ectodomain

<400> 42

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Ala Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 43

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152A/Y199A ectodomain

<400> 43

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Ala Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 44

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y199F eNKG2D1 fusion

<400> 44

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 45

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152S eNKG2D2 fusion

<400> 45

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 46

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152T eNKG2D3 fusion

<400> 46

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Thr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 47

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152V eNKG2D4 fusion

<400> 47

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Val His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 48

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152A/Y199F eNKG2D5 fusion

<400> 48

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 49

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152L/Y199F eNKG2D6 fusion

<400> 49

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Leu His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 50

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152S/Y199F eNKG2D7 fusion

<400> 50

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Ser His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 51

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152T/Y199F eNKG2D8 fusion

<400> 51

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Thr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 52

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152V/Y199F eNKG2D9 fusion

<400> 52

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Val His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 53

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y199D eNKG2D10 fusion

<400> 53

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Asp Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 54

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y199E eNKG2D11 fusion

<400> 54

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Glu Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 55
<211> 376
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide human IgG1 Fc-NKG2D Y152D/Y199D eNKG2D12 fusion

<400> 55

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Asp His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Asp Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 56

<211> 376

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152E/Y199E eNKG2D13 fusion

<400> 56

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Glu His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Glu Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 57
 <211> 376
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic peptide human IgG1 Fc-NKG2D Y152L eNKG2D14 fusion

 <400> 57

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Leu His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 58
<211> 376
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 Fc-NKG2D Y152F/Y199F eNKG2D15 fusion

<400> 58

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

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

Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
245 250 255

Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
260 265 270

Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
275 280 285

Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
290 295 300

Leu Leu Lys Leu Val Lys Ser Phe His Trp Met Gly Leu Val His Ile
305 310 315 320

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
325 330 335

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
340 345 350

Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser Thr Pro Asn Thr
355 360 365

Tyr Ile Cys Met Gln Arg Thr Val
370 375

<210> 59
<211> 1128

<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D fusion

<400> 59

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccc cctaagccta aggacaccct tatgatcagc	120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggagggtcaag	180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgttataa aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcatatcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 60
<211> 1128
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y152A fusion

<400> 60
atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg 60
ctgggtggcc cctccgtggt cctgttcccg cctaagccta aggacaccct tatgatcagc 120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag 180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa 240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg 300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag 360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc 420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct 480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc 540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag 600
tcgagatggc agcagggaag tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac 660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac 720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct 780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg 840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa 900
gaggaccagg atttacttaa actggtgaag tcagctcatt ggatgggact agtacacatt 960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca 1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata 1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg 1128

<210> 61

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y199A ectodomain

<400> 61

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg 60
ctgggtggcc cctccgtggt cctgttcccg cctaagccta aggacaccct tatgatcagc 120

cgcacccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgttacia aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcataccatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcaccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcgctata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 62
 <211> 1128
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
 Y152A/Y199A ectodomain

<400> 62	
atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcacccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240

cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgttacia aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcagctcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcgctata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 63

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y199F eNKG2D1 fusion

<400> 63

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420

cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcataccatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 64

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y152S eNKG2D2 fusion

<400> 64

atggaccga aaagctgcga caagactcac acttgtccgc cgtgccccgc cccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540

ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacaccc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcataccatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 65

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y152T eNKG2D3 fusion

<400> 65

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggc acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacaccc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720

tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgttctca aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcaactcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata	1080
gaaaactgtt caactccaaa tacatacatc tgcattgcaaa ggactgtg	1128

<210> 66

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y152V eNKG2D4 fusion

<400> 66

atggaccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggacct ggaggtcaag	180
ttcaatttgt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcattgagg gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840

tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcagctgatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata	1080
gaaaactgtt caactccaaa tacatacatc tgcattgcaa ggactgtg	1128

<210> 67
 <211> 1128
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
 Y152A/Y199F eNKG2D5 fusion

<400> 67	
atggaccga aaagctgcga caagactcac acttgtccgc cgtgccccgc cccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgacaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcattgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgttataa aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcagctcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020

ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata	1080
gaaaactgtt caactccaaa tacatacatc tgcatacaaa ggactgtg	1128

<210> 68
 <211> 1128
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
 Y152L/Y199F eNKG2D6 fusion

<400> 68	
atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaag tgtgttcagc tgctccgtga tgcatagagg gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgttacia aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcaactgcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata	1080
gaaaactgtt caactccaaa tacatacatc tgcatacaaa ggactgtg	1128

<210> 69
<211> 1128
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
Y152S/Y199F eNKG2D7 fusion

<400> 69
atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaaactg 60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc 120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag 180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa 240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg 300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag 360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc 420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct 480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc 540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag 600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac 660
cactacacc cagaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac 720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct 780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg 840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa 900
gaggaccagg atttacttaa actggtgaag tcaagtcatt ggatgggact agtacacatt 960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca 1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata 1080
gaaaactgtt caactccaaa tacatacatc tgcattgcaaa ggactgtg 1128

<210> 70
<211> 1128
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
Y152T/Y199F eNKG2D8 fusion

<400> 70

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccc cctaagccta aggacaccct tatgatcagc	120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcaactcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 71

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
Y152V/Y199F eNKG2D9 fusion

<400> 71
atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg 60
ctgggtggcc cctccgtggt cctgttcccg cctaagccta aggacaccct tatgatcagc 120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag 180
ttcaattggt acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa 240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg 300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag 360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc 420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct 480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc 540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag 600
tcgagatggc agcagggaag tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac 660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac 720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct 780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg 840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa 900
gaggaccagg atttacttaa actggtgaag tcagtgcatt ggatgggact agtacacatt 960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca 1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata 1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg 1128

<210> 72

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y199D eNKG2D10 fusion

<400> 72

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg 60
ctgggtggcc cctccgtggt cctgttcccg cctaagccta aggacaccct tatgatcagc 120

cgcacccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacaccc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgttacia aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcatatcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcgatata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 73

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y199E eNKG2D11 fusion

<400> 73

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcacccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtgggtgtca gtcctgactg tgctgcacca ggactggctg	300

aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcataccatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcgagata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 74

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
Y152D/Y199D eNKG2D12 fusion

<400> 74

atggaccgga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcacccttg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggc acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420

cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacaccc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcagatcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcgatata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 75

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
Y152E/Y199E eNKG2D13 fusion

<400> 75

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc cccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggc acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttcctgtact ccaagctgac cgtggacaag	600

tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacaccc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaa	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttaca aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tcagagcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcgagata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 76

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D Y152L eNKG2D14 fusion

<400> 76

atggacccga aaagctgcga caagactcac acttgtccgc cgtgccccgc ccccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggaccc ggaggtcaag	180
ttcaattggg acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcatgaggc gctgcacaac	660
cactacaccc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaa	720

tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttacaa aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900
gaggaccagg atttacttaa actggtgaag tctactgcatt ggatgggact agtacacatt	960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca	1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata	1080
gaaaactgtt caactccaaa tacatacatc tgcatgcaaa ggactgtg	1128

<210> 77

<211> 1128

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding human IgG1 Fc-NKG2D
Y152F/Y199F eNKG2D15 fusion

<400> 77

atggaccga aaagctgcga caagactcac acttgtccgc cgtgccccgc cccgaactg	60
ctgggtggcc cctccgtgtt cctgttcccg cctaagccta aggacaccct tatgatcagc	120
cgcaccctg aagtgacctg tgtcgtcgtg gatgtgtcac acgaggacct ggaggtcaag	180
ttcaattggc acgtggacgg cgtggaagtg cataacgcaa agaccaagcc tcgggaggaa	240
cagtacaact cgacctaccg cgtggtgtca gtcctgactg tgctgcacca ggactggctg	300
aacgggaagg agtacaagtg caaagtgtcg aacaaggccc tgccggctcc aattgaaaag	360
accatcagca aggccaaggg ccagccaagg gaaccacagg tgtacaccct ccctccttcc	420
cgggacgagc tgaccaaaaa ccaagtgtcc ctgacttgcc ttgtgaaggg gttctaccct	480
tctgacattg ccgtcgaatg ggaatcgaac ggacagcctg aaaacaacta taagactacc	540
ccgcccgtgc tggattccga cggaagcttc ttctgtact ccaagctgac cgtggacaag	600
tcgagatggc agcagggaaa tgtgttcagc tgctccgtga tgcattgaggc gctgcacaac	660
cactacacc agaagtcact gagcctctcc cccggaaaga tcgaaggacg cttcttaaac	720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct	780
aaaaactgga tatgtttacaa aaataactgc taccaatttt ttgatgagag taaaaactgg	840
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa	900

gaggaccagg atttacttaa actggtgaag tcattccatt ggatgggact agtacacatt 960
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca 1020
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggcttcata 1080
gaaaactgtt caactccaaa tacatacatc tgcatacaaa ggactgtg 1128

<210> 78
<211> 181
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide MICwed alpha1-alpha2

<400> 78

Glu Pro His Ser Leu Arg Tyr Asn Leu Thr Val Leu Ser Trp Asp Gly
1 5 10 15

Ser Val Gln Ser Gly Phe Leu Thr Glu Val His Leu Asp Gly Gln Pro
20 25 30

Phe Leu Arg Cys Asp Arg Gln Lys Cys Arg Ala Lys Pro Gln Gly Gln
35 40 45

Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp Asp Arg Glu Thr Arg
50 55 60

Asp Leu Thr Gly Trp Gly Lys Asp Leu Arg Met Thr Leu Ala His Ile
65 70 75 80

Lys Asp Gln Lys Glu Gly Leu His Ser Leu Gln Glu Ile Arg Val Cys
85 90 95

Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser Gln His Phe Tyr Tyr
100 105 110

Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Lys Glu Trp Thr
115 120 125

Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Arg Asn
130 135 140

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

His	Ala	Asp	Cys	Leu	Gln	Glu	Leu	Arg	Arg	Tyr	Leu	Lys	Ser	Gly	Val
				165					170					175	

Val	Leu	Arg	Arg	Thr
				180

<210> 79
 <211> 543
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding MICwed alpha1-alpha2

<400> 79	
gagcctcaca gcctccggtg taatttgact gtactctctt gggatggctc cgtgcagtcc	60
ggctttctga ctgaagttca tctcgacggt caacctttcc tgcgctgcga ccgacaaaaa	120
tgccgcgcca agccccaagg gcagtgggcc gaagatgtac tgggaaacaa gacctgggac	180
cgggagacac gagacctgac aggctggggc aaggacttgc gcatgacact cgcccatatc	240
aaggaccaga aggaaggatt gcactctttg caagagattc gcgtgtgtga aatccacgag	300
gacaattcaa cgaggagctc ccagcacttc tattacgatg gagaactctt cttgtcacag	360
aacttggaac ccaaggaatg gactatgcct cagagctctc gggcacagac tctcgctatg	420
aacgttagaa acttccttaa ggaggatgct atggagaccg atactcacta ccacgccatg	480
cacgccgact gcctccagga actgcggaga tatctgaagt ccggcgtggt ttgagaaga	540
acc	543

<210> 80
 <211> 181
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide MIC25 alpha1-alpha2

<400> 80

Glu Pro His Ser Leu Arg Tyr Asn Leu Thr Val Leu Ser Trp Asp Gly
1 5 10 15

Ser Val Gln Ser Gly Phe Leu Thr Glu Val His Leu Asp Gly Gln Pro
20 25 30

Phe Leu Arg Cys Asp Arg Gln Lys Cys Arg Ala Lys Pro Gln Gly Gln
35 40 45

Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp Asp Arg Glu Thr Arg
50 55 60

Asp Leu Thr Gly Trp Gly Lys Asp Leu Arg Met Thr Leu Ala His Ile
65 70 75 80

Lys Asp Gln Lys Glu Gly Leu His Ser Leu Gln Glu Ile Arg Val Cys
85 90 95

Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser Gln His Phe Tyr Tyr
100 105 110

Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Leu Glu Trp Thr
115 120 125

Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Arg Asn
130 135 140

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

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

Val Leu Arg Arg Thr
180

<210> 81

<211> 543

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding MIC25 alpha1-alpha2

<400> 81

```
gagcctcaca gcctccggta taatttgact gtactctctt gggatggctc cgtgcagtcc      60
ggctttctga ctgaagttca tctcgacggt caacctttcc tgcgctgcga ccgacaaaaa    120
tgccgcgcca agccccaagg gcagtgggcc gaagatgtac tgggaaacaa gacctgggac     180
cgggagacac gagacctgac aggctggggc aaggacttgc gcatgacact cgcccatatc    240
aaggaccaga aggaaggatt gcactctttg caagagattc gcgtgtgtga aatccacgag     300
gacaattcaa cgaggagctc ccagcacttc tattacgatg gagaactctt cttgtcacag    360
aacttgaaa ccctcgaatg gactatgcct cagagctctc gggcacagac tctcgctatg     420
aacgttagaa acttccttaa ggaggatgct atggagaccg atactcacta ccacgccatg     480
cgcgccgact gcctctctga actgcggaga tatctgaagt ccggcgtggt tttgagaaga    540
acc                                                                    543
```

<210> 82

<211> 330

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide human IgG1 heavy chain CH1-CH2-CH3 D265A/N297A

<400> 82

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

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

```
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
          35          40          45
```

```
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
          50          55          60
```

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
          65          70          75          80
```

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
305					310					315					320

Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
				325					330

<210> 83
 <211> 990
 <212> DNA
 <213> Artificial sequence

<220>
 <223> human IgG1 heavy chain CH1-CH2-CH3 D265A/N297A

<400> 83	
gcgtcgacca agggcccgtc agtgttcccg ctggccccgt catccaagtc cacgtctggg	60
ggcacagcag ccctgggatg cttggtcaag gactacttcc ccgagcccgt gactgtgtcc	120
tggaactccg gagcactgac ctccggagtg cacacctttc ccgcggtgct gcagtcctcc	180
ggactgtact ccctgtcgtc ggtcgtgacc gtgccgagct cctcgctcgg aaccagacc	240
tacatctgca acgtgaacca caagccctcg aacaccaaag tggacaagaa ggtcgagccc	300
aaaagctgcg acaagactca cacttgtccg ccgtgccccg ccccggaact gctgggtggc	360
ccctccgtgt tcctgttccc gcctaagcct aaggacaccc ttatgatcag ccgcacccct	420
gaagtgacct gtgtcgtcgt ggcagtgtca cacgaggacc cggagggtcaa gttcaattgg	480
tacgtggacg gcgtggaagt gcataacgca aagaccaagc ctcgggagga acagtacgcc	540
tcgacctacc gcgtggtgtc agtcctgact gtgctgcacc aggactggct gaacgggaag	600
gagtacaagt gcaaagtgtc gaacaaggcc ctgccggctc caattgaaaa gaccatcagc	660
aaggccaagg gccagccaag ggaaccacag gtgtacaccc tccctccttc ccgggacgag	720
ctgacaaaaa accaagtgtc cctgacttgc cttgtgaagg ggttctaccc ttctgacatt	780
gccgtcgaat gggaatcgaa cggacagcct gaaaacaact ataagactac cccgcccgtg	840
ctggattccg acggaagctt cttcctgtac tccaagctga ccgtggacaa gtcgagatgg	900
cagcagggaa atgtgttcag ctgctccgtg atgcatgagg cgctgcacaa ccactacacc	960
cagaagtcac tgagcctctc ccccggaag	990

<210> 84
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide human kappa light chain

<400> 84

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

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 85
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding human kappa light chain

<400> 85

agaaccgtgg	ccgccccgag	cgtgttcatt	ttccctccct	ccgacgagca	gttgaaatcg	60
ggcaccgcta	gcgtggtctg	ccttctcaac	aatttctatc	cacgggaagc	caaagtgcag	120
tggaaggctg	acaacgcgct	ccaatccggg	aactcacagg	aatccgtgac	tgagcaggat	180
tccaaggact	cgacctactc	cctgtcatcc	acgctgaccc	tgagcaaggc	agactacgag	240

aagcacaagg tctacgcctg cgaagtgaca caccagggac tgtccagccc cgtgaccaag 300
agcttcaaca gaggagaatg c 321

<210> 86
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide trastuzumab VH

<400> 86

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 87
<211> 360
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding trastuzumab VH

<400> 87

```
gaagtc caat tggtcgaatc aggcgggtgga ctctgtgcaac ctggagggttc gttacgctta      60
tcattgtgctg caagtggtgatt taatattaaa gataacctaca tccactgggt acgtcaagct      120
cccggaagg gtctcgagtg ggtcgcacgc atttaccacca ccaacggata cacgcgtac      180
gccgattcag tgaagggacg tttcacaatc tctgtgtgata ctagcaaaaa taccgcatac      240
ctccagatga actctcttag ggccgaggac acagctgtgt actactgtag ccgttgggga      300
ggagacggtt tttacgcaat ggattactgg ggccaaggaa ccctgggtcac agtttcatcg      360
```

<210> 88

<211> 107

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide trastuzumab VL

<400> 88

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

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

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

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

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

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

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          100              105
```

<210> 89
<211> 321
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding trastuzumab VL

<400> 89
gatatccaaa tgactcaatc accatcttca ctctccgcga gcgtgggtga tcgggtcacc 60
atcacatgta gggcgagcca agatgtgaat accgccgtcg cgtgggtatca acaaaagccg 120
ggaaaagcac caaaactgct tatatactct gcataccttc tgtactctgg ggtgccaagc 180
cggttctccg gtagtagatc tggtagtgac ttacactca ctatcagcag tctgcaacct 240
gaggactttg cgacatacta ttgccagcag cactacacaa cccacctac atttggtcag 300
gggacaaagg tggagatcaa g 321

<210> 90
<211> 121
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide rituximab VH

<400> 90

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

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

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

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn 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 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
100 105 110

Ala Gly Thr Thr Val Thr Val Ser Ala
115 120

<210> 91
<211> 363
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab VH

<400> 91
caagttcagc ttcagcagcc gggggctgag ttggtgaaac ccggggccag tgtgaagatg 60
agctgtaaag cgagcggcta caccttcact tcttataata tgcattgggt taagcaaacg 120
ccaggaaggg ggctggagtg gatcggcgct atttaccag gtaacggtga cacatcatat 180
aaccaaaagt ttaagggaaa ggcaaccctc acagcggaca agagtagctc aaccgcatac 240
atgcaactgt caagccttac ctccgaagac agcgcagtgt actactgcgc cagaagcacc 300
tactatgggg gtgattggta cttcaacgtc tggggggctg gcaccacagt gactgtaagc 360
gca 363

<210> 92
<211> 106
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide rituximab VL

<400> 92

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
 50 55 60

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
 85 90 95

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

<210> 93
 <211> 318
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding rituximab VL

<400> 93
 cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
 atgacttgcc gcgcttcaag ttccgtatcc tacattcact ggttccagca gaagcccgga 120
 agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgttaga 180
 ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
 gatgcggcta cttattattg ccaacagtgg acctctaacc cacccacatt cggcggcggc 300
 actaagttgg aaattaag 318

<210> 94
 <211> 450
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide trastuzumab heavy chain

<400> 94

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 95
<211> 1350
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding trastuzumab heavy chain

<400> 95
gaagtccaat tggtcgaatc aggcggtgga ctcgtgcaac ctggagggtc gttacgctta 60
tcatgtgctg caagtggatt taatattaaa gataacctaca tccactgggt acgtcaagct 120
cccggcaagg gtctcgagtg ggtcgcacgc atttacccca ccaacggata cacgcgctac 180
gccgattcag tgaagggacg tttcacaatc tctgctgata ctagcaaaaa taccgcatac 240
ctccagatga actctcttag ggccgaggac acagctgtgt actactgtag ccgttgggga 300
ggagacggtt tttacgcaat ggattactgg ggccaaggaa ccctgggtcac agtttcatcg 360
gcgtcgacca agggcccgtc agtgttcccg ctggccccgt catccaagtc cacgtctggg 420
ggcacagcag ccctgggatg cttgggtcaag gactacttcc ccgagcccgt gactgtgtcc 480
tggaactccg gagcactgac ctccggagtg cacacctttc ccgcggtgct gcagtcctcc 540
ggactgtact ccctgtcgtc ggtcgtgacc gtgccgagct cctcgtcgcg aaccagacc 600
tacatctgca acgtgaacca caagccctcg aacaccaaag tggacaagaa ggtcgagccc 660
aaaagctgcg acaagactca cacttgtccg ccgtgccccg ccccggaact gctgggtggc 720
ccctccgtgt tcctgttccc gcctaagcct aaggacaccc ttatgatcag ccgcaccct 780
gaagtgacct gtgtcgtcgt ggatgtgtca cacgaggacc cggagggtcaa gttcaattgg 840
tacgtggacg gcgtggaagt gcataacgca aagaccaagc ctcgggagga acagtacaac 900
tcgacctacc gcgtgggtgtc agtcctgact gtgctgcacc aggactggct gaacgggaag 960
gagtacaagt gcaaagtgtc gaacaaggcc ctgccggctc caattgaaaa gaccatcagc 1020
aaggccaagg gccagccaag ggaaccacag gtgtacaccc tccctccttc ccgggacgag 1080
ctgacaaaaa accaagtgtc cctgacttgc cttgtgaagg gggttctaccc ttctgacatt 1140
gccgtcgaat gggaatcgaa cggacagcct gaaaacaact ataagactac cccgcccgtg 1200
ctggattccg acggaagctt cttcctgtac tccaagctga ccgtggacaa gtcgagatgg 1260

cagcagggaa atgtgttcag ctgctccgtg atgcatgagg cgctgcacaa ccactacacc 1320
 cagaagtcac tgagcctctc ccccggaag 1350

<210> 96
 <211> 213
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide trastuzumab light chain

<400> 96

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 97
<211> 642
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding trastuzumab light chain

<400> 97
gatatcaaaa tgactcaatc accatcttca ctctccgcga gcgtgggtga tcgggtcacc 60
atcacatgta gggcgagcca agatgtgaat accgccgtcg cgtggtatca aaaaaagccg 120
ggaaaagcac caaaactgct tatatactct gcataccttc tgtactctgg ggtgccaagc 180
cggttctccg gtagtagatc tggtagtgac tttaactca ctatcagcag tctgcaacct 240
gaggactttg cgacatacta ttgccagcag cactacacaa cccacctac atttggtcag 300
gggacaaaagg tggagatcaa gaccgtggcc gcccgcagcg tgttcatttt ccctccctcc 360
gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaacaa tttctatcca 420
cggaagcca aagtgcagtg gaaggctgac aacgcgctcc aatccgggaa ctacagga 480
tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg 540
agcaaggcag actacagaaa gcacaaggctc tacgcctgcg aagtgacaca ccagggactg 600
tccagccccg tgaccaagag cttcaacaga ggagaatgct ag 642

<210> 98
<211> 451
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide rituximab heavy chain

<400> 98

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

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

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

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn 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 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
100 105 110

Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 99
<211> 1353
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab heavy chain

<400> 99
caagttcagc ttcagcagcc gggggctgag ttggtgaaac ccggggccag tgtgaagatg 60
agctgtaaag cgagcggcta caccttcact tcttataata tgcattgggt taagcaaacg 120
ccaggaaggg ggctggagtg gatcggcgct atttaccag gtaacgggtga cacatcatat 180
aaccaaaagt ttaagggaag ggcaaccctc acagcggaca agagtagctc aaccgcatac 240
atgcaactgt caagccttac ctccgaagac agcgcagtgt actactgcgc cagaagcacc 300
tactatgggg gtgattggta cttcaacgtc tggggggctg gcaccacagt gactgtaagc 360
gcagcgtcga ccaagggccc gtcagtgttc ccgctggccc cgtcatcaa gtccacgtct 420
gggggcacag cagccctggg atgcttggtc aaggactact tccccgagcc cgtgactgtg 480
tcctggaact ccggagcact gacctccgga gtgcacacct ttcccgcggt gctgcagtcc 540
tccggactgt actccctgtc gtcggctgtg accgtgccga gtcctcgtc cggaaccag 600
acctacatct gcaacgtgaa ccacaagccc tcgaacacca aagtggacaa gaaggtcgag 660
cccaaaagct gcgacaagac tcacacttgt ccgccgtgcc ccgccccga actgctgggt 720
ggcccctccg tgttcctgtt cccgcctaag cctaaggaca cccttatgat cagccgcacc 780
cctgaagtga cctgtgtcgt cgtggatgtg tcacacgagg acccgagggt caagttcaat 840
tggtacgtgg acggcgtgga agtgcataac gcaaagacca agcctcggga ggaacagtac 900
aactcgacct accgcgtggt gtcagtcctg actgtgtctg accaggactg gctgaacggg 960

aaggagtaca agtgcaaagt gtcgaacaag gccctgccgg ctccaattga aaagaccatc 1020
agcaaggcca agggccagcc aagggaacca caggtgtaca ccctccctcc ttcccgggac 1080
gagctgacca aaaaccaagt gtccttgact tgccttgtga aggggttcta cccttctgac 1140
attgccgtcg aatgggaatc gaacggacag cctgaaaaca actataagac taccgcccc 1200
gtgctggatt ccgacggaag cttcttctg tactccaagc tgaccgtgga caagtcgaga 1260
tggcagcagg gaaatgtgtt cagctgctcc gtgatgcatg aggcgctgca caaccactac 1320
accagaagt cactgagcct ctccccgga aag 1353

<210> 100
<211> 212
<212> PRT
<213> Artificial sequence
<220>
<223> Synthetic peptide rituximab light chain
<400> 100

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Ang Phe Ser Gly Ser
50 55 60

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
85 90 95

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

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
115 120 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
130 135 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145 150 155 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
165 170 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
180 185 190

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

Arg Gly Glu Cys
210

<210> 101
<211> 639
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab light chain

<400> 101
cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact gggtccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgttaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagac cgtggccgcc ccgagcgtgt tcattttccc tccctccgac 360
gagcagttga aatcgggcac cgctagcgtg gtctgccttc tcaacaattt ctatccacgg 420
gaagccaaag tgcagtggaa ggtcgacaac gcgctccaat ccgggaactc acaggaatcc 480
gtgactgagc aggattccaa ggactcgacc tactccctgt catccacgct gaccctgagc 540

aaggcagact acgagaagca caaggtctac gcctgcgaag tgacacacca gggactgtcc 600
agccccgtga ccaagagctt caacagagga gaatgctag 639

<210> 102
<211> 634
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide trastuzumab HC_MICwed

<400> 102

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ala Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Gly Gly Gly Ser Glu Pro His Ser Leu Arg Tyr Asn Leu Thr Val
450 455 460

Leu Ser Trp Asp Gly Ser Val Gln Ser Gly Phe Leu Thr Glu Val His
465 470 475 480

Leu Asp Gly Gln Pro Phe Leu Arg Cys Asp Arg Gln Lys Cys Arg Ala
485 490 495

Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp
500 505 510

Asp Arg Glu Thr Arg Asp Leu Thr Gly Trp Gly Lys Asp Leu Arg Met
515 520 525

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

Glu Ile Arg Val Cys Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser
545 550 555 560

Gln His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu
565 570 575

Thr Lys Glu Trp Thr Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala
580 585 590

Met Asn Val Arg Asn Phe Leu Lys Glu Asp Ala Met Glu Thr Asp Thr
595 600 605

His Tyr His Ala Met His Ala Asp Cys Leu Gln Glu Leu Arg Arg Tyr
610 615 620

Leu Lys Ser Gly Val Val Leu Arg Arg Thr
625 630

<210> 103
<211> 1902
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding trastuzumab HC_MICwed

<400> 103
gaagtccaat tggtcgaatc aggcggtgga ctcgtgcaac ctggagggtc gttacgctta 60
tcatgtgctg caagtggatt taatattaaa gatactaca tccactgggt acgtcaagct 120
cccggcaagg gtctcgagtg ggtcgcacgc atttacccca ccaacggata cacgcgctac 180
gccgattcag tgaagggacg tttcacaatc tctgctgata ctagcaaaaa taccgcatac 240
ctccagatga actctcttag ggccgaggac acagctgtgt actactgtag ccgttgggga 300
ggagacgggtt tttacgcaat ggattactgg ggccaaggaa ccctgggtcac agtttcatcg 360
gcgtcgacca agggcccgtc agtggtcccg ctggccccgt catccaagtc cacgtctggg 420
ggcacagcag ccctgggatg cttgggtcaag gactacttcc ccgagcccgt gactgtgtcc 480
tggaactccg gagcactgac ctccggagtg cacacctttc ccgcggtgct gcagtcctcc 540
ggactgtact ccctgtcgtc ggctcgtgacc gtgccgagct cctcgctcgg aaccagacc 600
tacatctgca acgtgaacca caagccctcg aacaccaaag tggacaagaa ggtcgagccc 660
aaaagctgcg acaagactca cacttgtccg ccgtgccccg ccccggaact gctgggtggc 720
ccctccgtgt tcctgttccc gcctaagcct aaggacaccc ttatgatcag ccgcaccct 780
gaagtgacct gtgtcgtcgt ggcatgttca cacgaggacc cggagggtcaa gttcaattgg 840
tacgtggacg gcgtggaagt gcataacgca aagaccaagc ctcgggagga acagtacgcc 900
tcgacctacc gcgtgggtgtc agtcctgact gtgctgcacc aggactggct gaacgggaag 960

gagtacaagt	gcaaagtgtc	gaacaaggcc	ctgccggctc	caattgaaaa	gaccatcagc	1020
aaggccaagg	gccagccaag	ggaaccacag	gtgtacaccc	tccctccttc	ccgggacgag	1080
ctgacaaaa	accaagtgtc	cctgacttgc	cttgtgaagg	ggttctaccc	ttctgacatt	1140
gccgtcgaat	gggaatcgaa	cggacagcct	gaaaacaact	ataagactac	cccgcccgtg	1200
ctggattccg	acggaagctt	cttcctgtac	tccaagctga	ccgtggacaa	gtcgagatgg	1260
cagcagggaa	atgtgttcag	ctgctccgtg	atgcatgagg	cgctgcacaa	ccactacacc	1320
cagaagtcac	tgagcctctc	ccccggagga	ggtggcagcg	agcctcacag	cctccggtat	1380
aatttgactg	tactctcttg	ggatggctcc	gtgcagtccg	gctttctgac	tgaagttcat	1440
ctcgacggtc	aacctttcct	gcgctgcgac	cgacaaaaat	gccgcgccaa	gccccaaagg	1500
cagtgggccg	aagatgtact	gggaaacaag	acctgggacc	gggagacacg	agacctgaca	1560
ggctggggca	aggacttgcg	catgacactc	gcccataatc	aggaccagaa	ggaaggattg	1620
cactctttgc	aagagattcg	cgtgtgtgaa	atccacgagg	acaattcaac	gaggagctcc	1680
cagcacttct	attacgatgg	agaactcttc	ttgtcacaga	acttggaaac	caaggaatgg	1740
actatgcctc	agagctctcg	ggcacagact	ctcgctatga	acgttagaaa	cttccttaag	1800
gaggatgcta	tggagaccga	tactcactac	cacgccatgc	acgccgactg	cctccaggaa	1860
ctgcgagat	atctgaagtc	cggcgtgggt	ttgagaagaa	cc		1902

$\langle 210 \rangle$ 104

 $\langle 220 \rangle$

$\langle 400 \rangle$ 104

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ala Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Gly Gly Gly Ser Glu Pro His Ser Leu Arg Tyr Asn Leu Thr Val
450 455 460

Leu Ser Trp Asp Gly Ser Val Gln Ser Gly Phe Leu Thr Glu Val His
465 470 475 480

Leu Asp Gly Gln Pro Phe Leu Arg Cys Asp Arg Gln Lys Cys Arg Ala
485 490 495

Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp
500 505 510

Asp Arg Glu Thr Arg Asp Leu Thr Gly Trp Gly Lys Asp Leu Arg Met
515 520 525

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

Glu Ile Arg Val Cys Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser
545 550 555 560

Gln His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu
565 570 575

Thr Leu Glu Trp Thr Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala
580 585 590

Met Asn Val Arg Asn Phe Leu Lys Glu Asp Ala Met Glu Thr Asp Thr
595 600 605

His Tyr His Ala Met Arg Ala Asp Cys Leu Ser Glu Leu Arg Arg Tyr
610 615 620

Leu Lys Ser Gly Val Val Leu Arg Arg Thr
625 630

<210> 105
<211> 1902
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding trastuzumab HC_MIC25

<400> 105
gaagtc caat tggtc gaatc aggcggtgga ctcgtgcaac ctggagggttc gttacgctta 60
tcattgtgctg caagtg gatt taatattaaa gataacctaca tccactgggt acgtcaagct 120

cccggcaagg gtctcgagtg ggtcgcacgc atttacccca ccaacggata cacgcgctac	180
gccgattcag tgaagggacg tttcacaatc tctgctgata ctagcaaaaa taccgcatac	240
ctccagatga actctcttag ggccgaggac acagctgtgt actactgtag ccgttgggga	300
ggagacggtt tttacgcaat ggattactgg ggccaaggaa ccctgggtcac agtttcatcg	360
gcgtcgacca agggcccgtc agtgttcccg ctggccccgt catccaagtc cacgtctggg	420
ggcacagcag ccctgggatg cttgggtcaag gactacttcc ccgagcccgt gactgtgtcc	480
tggaactccg gagcactgac ctccggagtg cacacctttc ccgcggtgct gcagtcctcc	540
ggactgtact ccctgtcgtc ggtcgtgacc gtgccgagct cctcgctcgg aaccagacc	600
tacatctgca acgtgaacca caagccctcg aacaccaaag tggacaagaa ggtcgagccc	660
aaaagctgcg acaagactca cacttgtccg ccgtgccccg ccccggaact gctgggtggc	720
ccctccgtgt tcctgttccc gcctaagcct aaggacaccc ttatgatcag ccgcaccct	780
gaagtgacct gtgtcgtcgt ggacgtgtca cacgaggacc cggagggtcaa gttcaattgg	840
tacgtggacg gcgtggaagt gcataacgca aagaccaagc ctcgggagga acagtacgcc	900
tcgacctacc gcgtgggtgtc agtcctgact gtgctgcacc aggactggct gaacgggaag	960
gagtacaagt gcaaagtgtc gaacaaggcc ctgccggctc caattgaaaa gaccatcagc	1020
aaggccaagg gccagccaag ggaaccacag gtgtacaccc tccctccttc ccgggacgag	1080
ctgacaaaaa accaagtgtc cctgacttgc cttgtgaagg gggttctaccc ttctgacatt	1140
gccgtcgaat gggaatcgaa cggacagcct gaaaacaact ataagactac cccgcccgtg	1200
ctggattccg acggaagctt cttcctgtac tccaagctga ccgtggacaa gtcgagatgg	1260
cagcagggaa atgtgttcag ctgctccgtg atgcatgagg cgctgcacaa ccactacacc	1320
cagaagtcac tgagcctctc ccccgaggga ggtggcagcg agcctcacag cctccggtat	1380
aatttgactg tactctcttg ggatggctcc gtgcagtccg gctttctgac tgaagttcat	1440
ctcgacggtc aacctttcct gcgctgcgac cgacaaaaat gccgcgcaa gcccgaagg	1500
cagtggggccg aagatgtact gggaaacaag acctgggacc gggagacacg agacctgaca	1560
ggctgggggca aggacttgcg catgacactc gccatatca aggaccagaa ggaaggattg	1620
cactctttgc aagagattcg cgtgtgtgaa atccacgagg acaattcaac gaggagctcc	1680
cagcacttct attacgatgg agaactcttc ttgtcacaga acttggaac cctcgaatgg	1740

actatgcctc agagctctcg ggcacagact ctcgctatga acgtagaaa cttccttaag 1800
gaggatgcta tggagaccga tactcactac cagccatgc gcgccgactg cctctctgaa 1860
ctgcggagat atctgaagtc cggcgtggtt ttgagaagaa cc 1902

<210> 106
<211> 404
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide rituximab LC_ULBP2.wt

<400> 106

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys Ala Pro Thr Ser Ser Ser Gly Gly Gly Gly Ser
210 215 220

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
225 230 235 240

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
245 250 255

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
260 265 270

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
275 280 285

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Arg Asp Ile
290 295 300

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
305 310 315 320

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
325 330 335

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
355 360 365

Glu Asn Asp Lys Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly
370 375 380

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
385 390 395 400

Leu Glu Pro Ser

<210> 107
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab LC_ULBP2.wt

<400> 107
cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact gggtccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgttaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagcg gaccgtggcc gcccgcagcg tggtcatctt ccctccctcc 360
gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaacaa tttctatcca 420
cgggaagcca aagtgcagtg gaaggtcgac aacgcgtcc aatccgggaa ctcacaggaa 480
tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg 540
agcaaggcag actacgagaa gcacaaggtc tacgcctgcg aagtgcacac ccagggactg 600
tccagccccg tgaccaagag cttcaacaga ggagaatgcg cacctacctc aagctctgga 660
ggaggtggca gcgagcccca tagtctgagc tacgacatca cagttattcc caagttcagg 720
cccggaccgc gctggtgtgc cgtgcaagga caagtcgacg aaaaaacctt tcttcattac 780
gattgcggaa ataagactgt aacgccagtc tctcctttag gtaagaagtt aaacgtcact 840
acggcgtgga aggcacaaaa ccccgctcctg cgcgaggctg tcgacatcct gactgaacaa 900
ttgcgcgaca tccagctcga gaattacact ccaaaggagc ctcttacctt gcaggctaga 960

atgtcttgcg agcaaaaggc agagggccac tcctccggca gctggcagtt cagtttcgac 1020
ggacaaatct ttctgttatt cgattcagag aagagaatgt ggactacagt tcaccccggt 1080
gcccgtaaaa tgaaggagaa gtgggaaaac gacaaagtgg tggcgatgtc attccactat 1140
ttctcgatgg gagactgcat cggttggctg gaagatttcc tcatgggtat ggactccact 1200
ttggagccat cg 1212

<210> 108
<211> 187
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide ULPB2 alpha1-alpha2 variant R80W

<400> 108

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
1 5 10 15

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
20 25 30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35 40 45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser Ala Gly Ala Pro Pro Met Val
180 185

<210> 109
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULPB2 alpha1-alpha2 variant
R80W

<400> 109
gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60
tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120
aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180
gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc 240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaattctt 360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg 420
aaggagaagt gggaaaacga caaagtgggtg gcgatgtcat tccactatct ctcgatggga 480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg 540

<210> 110
<211> 513
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULPB2 alpha1-alpha2 variant
R80W NNK library

<220>
<221> misc_feature
<222> (457)..(458)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (460)..(461)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (463)..(464)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (466)..(467)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (469)..(470)
<223> n is a, c, g, or t

<400> 110
gagccccata gcctcagcta tgacattacg gtgattccca aatttcgccc aggaccacgt 60
tggtgcgccg tccagggtca ggtagatgaa aagactttcc tgcattatga ttgcggcaat 120
aaaaccgtga cgccggtatc gccgttaggc aaaaaattga atgtcacgac agcgtggaaa 180
gcacagaacc cggtgttgcg cgaggtagtc gatattttga cggaacaact ctgggacatt 240
cagctcgaga attacacccc aaaagaaccg ctgacgctgc aagcgcgtat gtcgtgcgaa 300
caaaaagcag aaggtcactc tagcgggagt tggcagtttt ctttcgatgg gcagattttt 360
ctgctgtttg attcggagaa acgcatgtgg actacagtcc acccgggtgc ccggaaaatg 420
aaagagaagt gggagaatga taaagtgggt gccactnnkn nknnknnknn ktccatgggc 480
gattgcattg gctggttaga ggattttctc atg 513

<210> 111
<211> 180
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide, ULBP2 alpha1-alpha2 variant ULBP2.C

<400> 111

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
1 5 10 15

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
20 25 30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35 40 45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Ile Leu Trp Gln Thr Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser
180

<210> 112

<211> 540

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding ULBP2 alpha1-alpha2 variant
ULBP2.C

<400> 112

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gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc      60
tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat      120
aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcttggaag      180
gcacaaaacc ccgtcctgcg cgaggctcgtc gacatcctga ctgaacaatt gtgggacatc      240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag      300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt      360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccgggtgc ccgtaaaatg      420
aaggagaagt gggaaaacga caaagtgggtg gcgactattc tgtggcagac ttcgatggga      480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg      540
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<210> 113

<211> 180

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide, ULBP2 alpha1-alpha2 variant ULBP2.R

<400> 113

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Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
1              5              10             15

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
                20             25             30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35              40              45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50              55              60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65              70              75             80
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Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Leu Leu Trp Gly Trp Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser
180

<210> 114
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP2 alpha1-alpha2 variant
ULBP2.R

<400> 114
gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60
tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120
aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180
gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc 240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt 360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg 420
aaggagaagt gggaaaacga caaagtgggtg gcgactttgt tgtgggggtg gtcgatggga 480

gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg

540

<210> 115

<211> 180

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide, ULBP2 alpha1-alpha2 variant ULBP2.AA

<400> 115

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
1 5 10 15

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
20 25 30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35 40 45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Met Phe Trp Ser Trp Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser
180

<210> 116
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP2 alpha1-alpha2 variant
ULBP2.AA

<400> 116
gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60
tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120
aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180
gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc 240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaactttt 360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccgggtgc ccgtaaaatg 420
aaggagaagt gggaaaacga caaagtgttg gcgactatgt tttggagttg gtcgatggga 480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg 540

<210> 117
<211> 180
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide, ULBP2 alpha1-alpha2 variant ULBP2.AB

<400> 117

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
1 5 10 15

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
20 25 30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35 40 45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Leu Met Trp Gln Trp Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser
180

<210> 118
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP2 alpha1-alpha2 variant
ULBP2.AB

<400> 118
gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60
tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120

aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag	180
gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc	240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag	300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt	360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg	420
aaggagaagt gggaaaacga caaagtgggtg gcgactctta tgtggcagtg gtcgatggga	480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg	540

<210> 119
 <211> 404
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic peptide rituximab LC_ULBP2.C

 <400> 119

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

Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile
			20					25					30		

His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser
	50					55					60				

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

Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Thr	Ser	Asn	Pro	Pro	Thr
				85					90					95	

Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro
			100					105						110	

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys Ala Pro Thr Ser Ser Ser Gly Gly Gly Gly Ser
210 215 220

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
225 230 235 240

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
245 250 255

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
260 265 270

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
275 280 285

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
290 295 300

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
305 310 315 320

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
325 330 335

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
355 360 365

Glu Asn Asp Lys Val Val Ala Thr Ile Leu Trp Gln Thr Ser Met Gly
370 375 380

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
385 390 395 400

Leu Glu Pro Ser

<210> 120
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab LC_ULBP2.C

<400> 120
cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact gggtccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgttaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagcg gaccgtggcc gccccgagcg tggttcatttt ccctccctcc 360
gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaaca tttctatcca 420
cgggaagcca aagtgcagtg gaaggtcgac aacgcgctcc aatccgggaa ctacaggaa 480
tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg 540
agcaaggcag actacagaa gcacaaggtc tacgcctgcg aagtgcaca ccagggactg 600
tccagccccg tgaccaagag cttcaacaga ggagaatgcg cacctacctc aagctctgga 660
ggaggtggca gcgagcccca tagtctgagc tacgacatca cagttattcc caagttcagg 720

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cccgaccgc gctggtgtgc cgtgcaagga caagtcgacg aaaaaacctt tcttcattac      780
gattgcggaa ataagactgt aacgccagtc tctccttttag gtaagaagtt aaacgtcact      840
acggcgtgga aggcacaaaa ccccgctcctg cgcgagggtcg tcgacatcct gactgaacaa      900
ttgtgggaca tccagctcga gaattacact ccaaaggagc ctcttaccct gcaggctaga      960
atgtcttgcg agcaaaaggc agagggccac tcctccggca gctggcagtt cagtttcgac     1020
ggacaaatct ttctgttatt cgattcagag aagagaatgt ggactacagt tcaccccggt     1080
gcccgtaaaa tgaaggagaa gtgggaaaac gacaaagtgg tggcgactat tctgtggcag     1140
acttcgatgg gagactgcat cggttggctg gaagatttcc tcatgggtat ggactccact     1200
ttggagccat cg                                                                1212

```

```

<210> 121
<211> 404
<212> PRT
<213> Artificial sequence

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```

<220>
<223> Synthetic peptide rituximab LC_ULBP2.R

```

```

<400> 121

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

```

```

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
          20           25           30

```

```

His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
          35           40           45

```

```

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
          50           55           60

```

```

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

```

```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
          85           90           95

```

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys Ala Pro Thr Ser Ser Ser Gly Gly Gly Gly Ser
210 215 220

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
225 230 235 240

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
245 250 255

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
260 265 270

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
275 280 285

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
290 295 300

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
305 310 315 320

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
325 330 335

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
355 360 365

Glu Asn Asp Lys Val Val Ala Thr Leu Leu Trp Gly Trp Ser Met Gly
370 375 380

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
385 390 395 400

Leu Glu Pro Ser

<210> 122
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab LC_ULBP2.R

<400> 122
cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact gggtccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtg tcccgttaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagcg gaccgtggcc gccccgagcg tggtcatttt ccctccctcc 360
gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaacaa tttctatcca 420
cgggaagcca aagtgcagtg gaaggtcgac aacgcgtcc aatccgggaa ctacaggaa 480
tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg 540
agcaaggcag actacagaa gcacaaggtc tacgcctgcg aagtgcacac ccagggactg 600

tccagccccg tgaccaagag cttcaacaga ggagaatgcg cacctacctc aagctctgga	660
ggaggtggca gcgagcccca tagtctgagc tacgacatca cagttattcc caagttcagg	720
cccggaccgc gctggtgtgc cgtgcaagga caagtcgacg aaaaaacctt tcttcattac	780
gattgcggaa ataagactgt aacgccagtc tctccttttag gtaagaagtt aaacgtcact	840
acggcgtgga aggcacaaaa ccccgctcctg cgcgaggctg tcgacatcct gactgaacaa	900
ttgtgggaca tccagctcga gaattacact ccaaaggagc ctcttaccct gcaggctaga	960
atgtcttgcg agcaaaaggc agagggccac tcctccggca gctggcagtt cagtttcgac	1020
ggacaaatct ttctgttatt cgattcagag aagagaatgt ggactacagt tcaccccggt	1080
gcccgtaaaa tgaaggagaa gtgggaaaac gacaaagtgg tggcgacttt gttgtggggg	1140
tggtcgatgg gagactgcat cggttggctg gaagatttcc tcatgggtat ggactccact	1200
ttggagccat cg	1212

<210> 123
 <211> 404
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide rituximab LC_ULBP2.AA

<400> 123

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

Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile
			20					25					30		

His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser
	50					55					60				

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys Ala Pro Thr Ser Ser Ser Gly Gly Gly Gly Ser
210 215 220

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
225 230 235 240

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
245 250 255

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
260 265 270

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
275 280 285

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
290 295 300

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
305 310 315 320

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
325 330 335

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
355 360 365

Glu Asn Asp Lys Val Val Ala Thr Met Phe Trp Ser Trp Ser Met Gly
370 375 380

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
385 390 395 400

Leu Glu Pro Ser

<210> 124
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab LC_ULBP2.AA

<400> 124
cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact ggttccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgtaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagcg gaccgtggcc gcccgcagcg tgttcatttt ccctccctcc 360
gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaacaa tttctatcca 420
cgggaagcca aagtgcagtg gaaggctgac aacgcgtcc aatccgggaa ctcacaggaa 480

tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg	540
agcaaggcag actacgagaa gcacaaggtc tacgcctgcg aagtgcacac ccagggactg	600
tccagccccg tgaccaagag cttcaacaga ggagaatgcg cacctacctc aagctctgga	660
ggaggtggca gcgagcccca tagtctgagc tacgacatca cagttattcc caagttcagg	720
cccggaccgc gctggtgtgc cgtgcaagga caagtcgacg aaaaaacctt tcttcattac	780
gattgcggaa ataagactgt aacgccagtc tctccttttag gtaagaagtt aaacgtcact	840
acggcgtgga aggcacaaaa ccccgctcctg cgcgaggctc tcgacatcct gactgaacaa	900
ttgtgggaca tccagctcga gaattacact ccaaaggagc ctcttaccct gcaggctaga	960
atgtcttgcg agcaaaaggc agagggccac tcctccggca gctggcagtt cagtttcgac	1020
ggacaaatct ttctgttatt cgattcagag aagagaatgt ggactacagt tcaccccggt	1080
gcccgtaaaa tgaaggagaa gtgggaaaac gacaaagtgg tggcgactat gttttggagt	1140
tggtcgatgg gagactgcat cggttggctg gaagatttcc tcatgggtat ggactccact	1200
ttggagccat cg	1212

<210> 125
 <211> 404
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide rituximab LC_ULBP2.AB

<400> 125

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

Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile
			20					25					30		

His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser
	50					55					60				

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys Ala Pro Thr Ser Ser Ser Gly Gly Gly Gly Ser
210 215 220

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
225 230 235 240

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
245 250 255

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
260 265 270

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
275 280 285

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
290 295 300

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
305 310 315 320

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
325 330 335

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
355 360 365

Glu Asn Asp Lys Val Val Ala Thr Leu Met Trp Gln Trp Ser Met Gly
370 375 380

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
385 390 395 400

Leu Glu Pro Ser

<210> 126
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab LC_ULBP2.AB

<400> 126
cagatcgtgt tgtccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact gggtccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgttaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagcg gaccgtggcc gcccagagcg tgttcatttt ccctccctcc 360

gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaacaa tttctatcca	420
cgggaagcca aagtgcagtg gaaggctgac aacgcgctcc aatccgggaa ctcacaggaa	480
tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg	540
agcaaggcag actacgagaa gcacaaggtc tacgcctgcg aagtgcaca ccagggactg	600
tccagccccg tgaccaagag cttcaacaga ggagaatgcg cacctacctc aagctctgga	660
ggaggtggca gcgagcccca tagtctgagc tacgacatca cagttattcc caagttcagg	720
cccggaccgc gctggtgtgc cgtgcaagga caagtcgacg aaaaaacctt tcttcattac	780
gattgcggaa ataagactgt aacgccagtc tctccttttag gtaagaagtt aaacgtcact	840
acggcgtgga aggcacaaaa ccccgctcctg cgcgaggctg tcgacatcct gactgaacaa	900
ttgtgggaca tccagctcga gaattacact ccaaaggagc ctcttaccct gcaggctaga	960
atgtcttgcg agcaaaaggc agagggccac tcctccggca gctggcagtt cagtttcgac	1020
ggacaaatct ttctgttatt cgattcagag aagagaatgt ggactacagt tcaccccggt	1080
gcccgtaaaa tgaaggagaa gtgggaaaac gacaaagtgg tggcgactct tatgtggcag	1140
tggtcgatgg gagactgcat cggttggctg gaagatttcc tcatgggtat ggactccact	1200
ttggagccat cg	1212

<210> 127
 <211> 180
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide, ULBP2 alpha1-alpha2 variant ULBP2.S3

<400> 127

Glu	Pro	His	Ser	Leu	Ser	Tyr	Asp	Ile	Thr	Val	Ile	Pro	Lys	Phe	Arg
1				5					10					15	

Pro	Gly	Pro	Arg	Trp	Cys	Ala	Val	Gln	Gly	Gln	Val	Asp	Glu	Lys	Thr
			20					25					30		

Phe	Leu	His	Tyr	Asp	Cys	Gly	Asn	Lys	Thr	Val	Thr	Pro	Val	Ser	Pro
		35					40					45			

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Lys Leu Tyr Leu Trp Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser
180

<210> 128
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP2 alpha1-alpha2 variant
ULBP2.S3

<400> 128
gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60
tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120
aagactgtaa cgccagtctc tcctttaggt aagaagttaa acgtcactac ggcgtggaag 180
gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc 240

cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag	300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt	360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccgggtgc ccgtaaaatg	420
aaggagaagt gggaaaacga caaagtgggtg gcgactaagc tttatctttg gtcgatggga	480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg	540

<210> 129
 <211> 404
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide rituximab LC_ULBP2.S3

<400> 129

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

Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile
			20					25					30		

His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser
	50					55					60				

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

Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Thr	Ser	Asn	Pro	Pro	Thr
				85					90					95	

Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro
			100					105					110		

Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr
		115					120					125			

Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130

135

140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys Ala Pro Thr Ser Ser Ser Gly Gly Gly Gly Ser
 210 215 220

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
 225 230 235 240

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
 245 250 255

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
 260 265 270

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
 275 280 285

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
 290 295 300

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
 305 310 315 320

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
 325 330 335

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
355 360 365

Glu Asn Asp Lys Val Val Ala Thr Lys Leu Tyr Leu Trp Ser Met Gly
370 375 380

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
385 390 395 400

Leu Glu Pro Ser

<210> 130
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab LC_ULBP2.S3

<400> 130
cagatcgtgt tgtcccaatc acccgcaatt ctctctgcga gcccagggga gaaggtgacc 60
atgacttgcc gcgcttcaag ttccgtatcc tacattcact ggttccagca gaagcccgga 120
agttccccta agccctggat ctatgctaca tccaatctgg caagcgggtgt tcccgttaga 180
ttttccggaa gcgggtctgg aaccagttac agtctgacta tttccagggt cgaggccgaa 240
gatgcggcta cttattattg ccaacagtgg acctctaacc caccacatt cggcggcggc 300
actaagttgg aaattaagcg gaccgtggcc gcccgcagcg tgttcatttt ccctccctcc 360
gacgagcagt tgaaatcggg caccgctagc gtggtctgcc ttctcaacaa tttctatcca 420
cgggaagcca aagtgcagtg gaaggtcgac aacgcgctcc aatccgggaa ctcacaggaa 480
tccgtgactg agcaggattc caaggactcg acctactccc tgtcatccac gctgaccctg 540
agcaaggcag actacgagaa gcacaaggtc tacgcctgcg aagtgcaca ccagggactg 600
tccagccccg tgaccaagag cttcaacaga ggagaatgcg cacctacctc aagctctgga 660
ggaggtggca gcgagcccca tagtctgagc tacgacatca cagttattcc caagttcagg 720
cccgaccgc gctggtgtgc cgtgcaagga caagtcgacg aaaaaacctt tcttcattac 780
gattgcggaa ataagactgt aacgccagtc tctcctttag gtaagaagtt aaacgtcact 840

acggcgtgga aggcacaaaa ccccgctcctg cgcgaggtcg tcgacatcct gactgaacaa 900
ttgtggggaca tccagctcga gaattacact ccaaaggagc ctcttaccct gcaggctaga 960
atgtcttgcg agcaaaaggc agagggccac tcctccggca gctggcagtt cagtttcgac 1020
ggacaaatct ttctgttatt cgattcagag aagagaatgt ggactacagt tcaccccggt 1080
gcccgtaaaa tgaaggagaa gtgggaaaac gacaaagtgg tggcgactaa gctttatctt 1140
tggtcgatgg gagactgcat cggttggctg gaagatttcc tcatgggtat ggactccact 1200
ttggagccat cg 1212

<210> 131
<211> 634
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide rituximab HC_ULBP2.R80W

<400> 131

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

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

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

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn 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 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
100 105 110

Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser

115

120

125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ala Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Ser Glu Pro His Ser Leu Ser Tyr Asp Ile Thr
450 455 460

Val Ile Pro Lys Phe Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly
465 470 475 480

Gln Val Asp Glu Lys Thr Phe Leu His Tyr Asp Cys Gly Asn Lys Thr
485 490 495

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

Trp Lys Ala Gln Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr
515 520 525

Glu Gln Leu Trp Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro
530 535 540

Leu Thr Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His

545 550 555 560

Ser Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
565 570 575

Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala Arg
580 585 590

Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met Ser Phe
595 600 605

His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu
610 615 620

Met Gly Met Asp Ser Thr Leu Glu Pro Ser
625 630

<210> 132
<211> 1902
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding rituximab HC_ULBP2.R80W

<400> 132
caagttcagc ttcagcagcc gggggctgag ttgggtgaaac ccggggccag tgtgaagatg 60
agctgtaaag cgagcggcta caccttcact tcttataata tgcattgggt taagcaaacg 120
ccaggaaggg ggctggagtg gatcggcgct atttaccag gtaacggtga cacatcatat 180
aaccaaaagt ttaagggaaa ggcaaccctc acagcggaca agagtagctc aaccgcatac 240
atgcaactgt caagccttac ctccgaagac agcgcagtgt actactgcgc cagaagcacc 300
tactatgggg gtgattggta cttcaacgtc tggggggctg gcaccacagt gactgtaagc 360
gcagcgtcga ccaagggccc gtcagtgttc ccgctggccc cgtcatcaa gtccacgtct 420
ggggggcacag cagccctggg atgcttggtc aaggactact tccccgagcc cgtgactgtg 480
tcctggaact ccggagcact gacctccgga gtgcacacct ttcccgcggt gctgcagtcc 540
tccggactgt actccctgtc gtcggtcgtg accgtgccga gtcctctgct cggaaccag 600
acctacatct gcaacgtgaa ccacaagccc tcgaacacca aagtggacaa gaaggtcgag 660

cccaaaagct gcgacaagac tcacacttgt ccgccgtgcc ccgccccga actgctgggt	720
ggccccctccg tgttcctggt cccgcctaag cctaaggaca cccttatgat cagccgcacc	780
cctgaagtga cctgtgtcgt cgtggcagtg tcacacgagg acccggaggt caagttcaat	840
tggtagctgg acggcgtgga agtgcataac gcaaagacca agcctcggga ggaacagtac	900
gcctcgacct accgcgtggt gtcagtcctg actgtgctgc accaggactg gctgaacggg	960
aaggagtaca agtgcaaagt gtcgaacaag gccctgccgg ctccaattga aaagaccatc	1020
agcaaggcca agggccagcc aagggaacca cagggtgtaca ccctccctcc ttcccgggac	1080
gagctgacca aaaaccaagt gtccctgact tgccttgtga aggggttcta cccttctgac	1140
attgccgtcg aatgggaatc gaacggacag cctgaaaaca actataagac taccgccccc	1200
gtgctggatt ccgacggaag cttcttcctg tactccaagc tgaccgtgga caagtcgaga	1260
tggcagcagg gaaatgtggt cagctgctcc gtgatgcatg aggcgctgca caaccactac	1320
accagaagt cactgagcct ctccccgga ggaggtggca gcgagcccca tagtctgagc	1380
tacgacatca cagttattcc caagttcagg cccggaccgc gctgggtgtgc cgtgcaagga	1440
caagtcgacg aaaaaacctt tcttcattac gattgcggaa ataagactgt aacgccagtc	1500
tctcctttag gtaagaagtt aaacgtcact acggcgtgga aggcacaaaa cccgctcctg	1560
cgcgaggtcg tcgacatcct gactgaacaa ttgtgggaca tccagctcga gaattacact	1620
ccaaaggagc ctcttaccct gcaggctaga atgtcttgcg agcaaaaggc agagggccac	1680
tcctccggca gctggcagtt cagtttcgac ggacaaatct ttctgttatt cgattcagag	1740
aagagaatgt ggactacagt tcaccccggt gcccgtaaaa tgaaggagaa gtgggaaaac	1800
gacaaagtgg tggcgatgtc attccactat ttctcgatgg gagactgcat cggttggctg	1860
gaagatttcc tcatgggtat ggactccact ttggagccat cg	1902

<210> 133
 <211> 405
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide trastuzumab LC_ULBP2.R

<400> 133

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

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

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

Arg Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys
245 250 255

Thr Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
260 265 270

Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn
275 280 285

Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp
290 295 300

Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala
305 310 315 320

Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp
325 330 335

Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Lys
340 345 350

Arg Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys
355 360 365

Trp Glu Asn Asp Lys Val Val Ala Thr Leu Leu Trp Gly Trp Ser Met
370 375 380

Gly Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser
385 390 395 400

Thr Leu Glu Pro Ser
405

<210> 134
<211> 1215
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding trastuzumab LC_ULBP2.R

<400> 134

gatatccaaa tgactcaatc accatcttca ctctccgcga gcgtgggtga tcgggtcacc	60
atcacatgta gggcgagcca agatgtgaat accgccgtcg cgtgggtatca acaaaagccg	120
ggaaaagcac caaaactgct tatatactct gcctccttcc tgtactctgg ggtgccaaagc	180
cggttctccg gtagtagatc tgggtactgac tttaactca ctatcagcag tctgcaacct	240
gaggactttg cgacatacta ttgccagcag cactacacaa cccacacctac atttgggtcag	300
gggacaaaagg tggagatcaa gcggaccgtg gccgccccga gcgtgttcat tttccctccc	360
tccgacgagc agttgaaatc gggcaccgct agcgtggtct gccttctcaa caatttctat	420
ccacgggaag ccaaagtga gtggaaggtc gacaacgcgc tccaatccgg gaactcacag	480
gaatccgtga ctgagcagga ttccaaggac tcgacctact ccctgtcatc cacgtgacc	540
ctgagcaagg cagactacga gaagcacaag gtctacgcct gcgaagtga acaccaggga	600
ctgtccagcc ccgtgaccaa gagcttcaac agaggagaat gcgcacctac ctcaagctct	660
ggaggagggtg gcagcgagcc ccatagtctg agctacgaca tcacagttat tccaagttc	720
aggcccggac cgcgctgggtg tgccgtgcaa ggacaagtcg acgaaaaaac ctttcttcat	780
tacgattgcg gaaataagac tgtaacgcca gtctctcctt taggtaagaa gttaaactgc	840
actacggcgt ggaaggcaca aaaccccgct ctgcgcgagg tcgtcgacat cctgactgaa	900
caattgtggg acatccagct cgagaattac actccaaagg agcctcttac cctgcaggct	960
agaatgtctt gcgagcaaaa ggcagagggc cactcctccg gcagctggca gttcagtttc	1020
gacggacaaa tctttctgtt attcgattca gagaagagaa tgtggactac agttcacccc	1080
ggtgcccgtg aaatgaagga gaagtgggaa aacgacaaag tgggtggcgac tttgttgtgg	1140
gggtgggtcga tgggagactg catcggttgg ctggaagatt tcctcatggg tatggactcc	1200
actttggagc catcg	1215

<210> 135

<211> 156

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide NKG2D.wt ectodomain

<400> 135

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

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
145 150 155

<210> 136

<211> 468

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding NKG2D.wt ectodomain

<400> 136

atggcattgc ctgttacagc tctgctgctg cccttggtc tgcttctgca tgctgccaga

60

cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct	120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg	180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa	240
gaggaccagg atctgctgaa gctgggtcaag agctaccact ggatgggact cgtgcacatc	300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc	360
atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc	420
gagaactgca gcacccctaa cacctacatc tgtatgcagc ggaccgtg	468

<210> 137
 <211> 156
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic peptide NKG2D.YA ectodomain

 <400> 137

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

His	Ala	Ala	Arg	Pro	Leu	Phe	Asn	Gln	Glu	Val	Gln	Ile	Pro	Leu	Thr
			20					25					30		

Glu	Ser	Tyr	Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn
		35					40					45			

Asn	Cys	Tyr	Gln	Phe	Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln
	50					55					60				

Ala	Ser	Cys	Met	Ser	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys
65					70					75					80

Glu	Asp	Gln	Asp	Leu	Leu	Lys	Leu	Val	Lys	Ser	Ala	His	Trp	Met	Gly
				85					90					95	

Leu	Val	His	Ile	Pro	Thr	Asn	Gly	Ser	Trp	Gln	Trp	Glu	Asp	Gly	Ser
			100					105					110		

Ile	Leu	Ser	Pro	Asn	Leu	Leu	Thr	Ile	Ile	Glu	Met	Gln	Lys	Gly	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
 130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
 145 150 155

<210> 138
 <211> 468
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding NKG2D.YA ectodomain

<400> 138
 atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
 cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120
 aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
 tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
 gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc 300
 cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc 360
 atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc 420
 gagaactgca gcaccctaa cacctacatc tgtatgcagc ggaccgtg 468

<210> 139
 <211> 156
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide NKG2D.AF ectodomain

<400> 139

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

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
 20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val
145 150 155

<210> 140
<211> 468
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding NKG2D.AF ectodomain

<400> 140
atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc 300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc 360

atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggcttcac	420
gagaactgca gcacccta cactacatc tgtatgcagc ggaccgtg	468

<210> 141
 <211> 69
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide CD8alpha hinge and transmembrane domain

<400> 141

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala	
1 5 10 15	

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly	
20 25 30	

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile	
35 40 45	

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val	
50 55 60	

Ile Thr Leu Tyr Cys	
65	

<210> 142
 <211> 207
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding CD8alpha hinge and transmembrane domain

<400> 142	
accaccacac cagctcctag acctccaact cctgctccta caatcgccag ccagcctctg	60
tctctgaggc cagaagcttg tagacctgct gcaggcggag ccgtgcatac aagaggactg	120
gatttcgcct gcgacatcta catctgggcc cctctggctg gaacatgtgg cgtgctgctg	180
ctgagcctgg tcatcacct gtactgc	207

<210> 143
<211> 42
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide 4-1BB

<400> 143

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> 144
<211> 126
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding 4-1BB

<400> 144
aagcggggca gaaagaagct gctgtacatc tttaagcagc cttcatgcg gcccgtgcag 60
accacacaag aggaagatgg ctgctcctgc agattccccc aggaagaaga aggcggctgc 120
gagctg 126

<210> 145
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide CD3zeta

<400> 145

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys 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> 146
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding CD3zeta

<400> 146
agagtgaagt tcagccgttc tgccgacgct cccgcctata agcagggaca gaaccagctg 60
tacaacgagc tgaacctggg gagaagagaa gagtacgacg tgctggacaa gcggagaggg 120
agagatcctg agatgggcgg caagcccaga cggaagaatc ctcaagaggg cctgtataat 180
gagctgcaga aagacaagat ggccgaggcc tacagcgaga tcggaatgaa gggcgagcgc 240
agaagaggca agggacacga tggactgtac cagggcctga gcaccgccac caaggatacc 300
tatgatgccc tgcacatgca ggccctgcct ccaaga 336

<210> 147
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide EGFP

<400> 147

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 148
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding EGFP

<400> 148
atggtgtcta aaggcgagga actgttcacc ggcgtggtgc ccattctggt ggaactggac 60
ggggatgtga acggccacaa gtttagcggt agcggcgaag gcgaagggga tgccacatac 120
ggaaagctga ccctgaagtt catctgcacc accggcaagc tgcctgtgcc ttggcctaca 180
ctggtcacca cactgacata cggcgtgcag tgcttttagca gataccccga ccatatgaag 240
cagcacgact tcttcaagtc cgccatgcct gagggctacg tgcaagagcg gaccatcttc 300
ttaaaggacg acggcaacta caagaccagg gccgaagtga agtttgaggg cgacaccctg 360
gtcaaccgga tcgagctgaa gggcatcgac ttcaaagagg atggcaacat cctggggccac 420
aagctcgagt acaactacaa cagccacaac gtgtacatca tggccgacaa gcagaagaac 480
ggcatcaagg ccaacttcaa gatccggcac aacatcgagg acggcagcgt tcagctggcc 540
gatcactacc agcagaacac ccctatcgga gatggccctg tgctgctccc cgacaatcac 600
tacctgagca cacagagcgc cctgagcaag gaccccaacg agaagaggga tcacatggtg 660
ctgctggaat ttgtgaccgc cgcaggcatc accctcggca tggacgaact gtacaaa 717

<210> 149
<211> 473
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide CD8hingeTM_4-1BB_CD3zeta_EGFP

<400> 149

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
35 40 45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
50 55 60

Ile Thr Leu Tyr Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr
65 70 75 80

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
85 90 95

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
100 105 110

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
115 120 125

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
130 135 140

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
145 150 155 160

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
165 170 175

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
180 185 190

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
195 200 205

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
210 215 220

Arg Ser Gly Ser Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu
225 230 235 240

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
245 250 255

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
260 265 270

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
275 280 285

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
290 295 300

Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
305 310 315 320

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
325 330 335

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
340 345 350

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
355 360 365

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
370 375 380

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
385 390 395 400

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
405 410 415

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
420 425 430

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

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
450 455 460

Thr Leu Gly Met Asp Glu Leu Tyr Lys
465 470

<210> 150
<211> 1419
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding CD8hingeTM_4-1BB_CD3zeta_EGFP

<400> 150
accaccacac cagctcctag acctccaact cctgctccta caatcgccag ccagcctctg 60
tctctgaggc cagaagcttg tagacctgct gcaggcggag ccgtgcatac aagaggactg 120
gatttcgcct gcgacatcta catctgggcc cctctggctg gaacatgtgg cgtgctgctg 180
ctgagcctgg tcatcaccct gtactgcagc ctgaagcggg gcagaaagaa gctgctgtac 240
atctttaagc agcccttcat gcggcccgtg cagaccacac aagaggaaga tggctgctcc 300
tgcagattcc ccgaggaaga agaaggcggc tgcgagctga gagtgaagtt cagccgttct 360
gccgacgctc ccgcctataa gcagggacag aaccagctgt acaacgagct gaacctgggg 420
agaagagaag agtacgacgt gctggacaag cggagaggca gagatcctga gatgggcggc 480
aagcccagac ggaagaatcc tcaagagggc ctgtataatg agctgcagaa agacaagatg 540
gccgaggcct acagcgagat cggaatgaag ggcgagcgca gaagaggcaa gggacacgat 600
ggactgtacc agggcctgag caccgccacc aaggatacct atgatgccct gcacatgcag 660
gccctgcctc caagatcagg ctctggttct ggcagcggca gcatgggtgc taaaggcgag 720
gaactgttca ccggcgtggg gccatttctg gtggaactgg acggggatgt gaacggccac 780
aagtttagcg ttagcggcga aggcgaaggg gatgccacat acggaaagct gaccctgaag 840
ttcatctgca ccaccggcaa gctgcctgtg ctttggccta cactgggtcac cacactgaca 900
tacggcgtgc agtgctttag cagatacccc gaccatatga agcagcacga cttcttcaag 960
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aacagccaca acgtgtacat catggccgac aagcagaaga acggcatcaa ggccaacttc	1200
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accctatcgc gagatggccc tgtgctgctc cccgacaatc actacctgag cacacagagc	1320
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<210> 151
 <211> 629
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic peptide NKG2D.wt_CD8hingeTM_4-1BB_CD3zeta_EGFP complete
 chimeric antigen receptor

 <400> 151

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
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His	Ala	Ala	Arg	Pro	Leu	Phe	Asn	Gln	Glu	Val	Gln	Ile	Pro	Leu	Thr
			20					25					30		

Glu	Ser	Tyr	Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn
		35					40					45			

Asn	Cys	Tyr	Gln	Phe	Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln
	50					55					60				

Ala	Ser	Cys	Met	Ser	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys
65					70					75					80

Glu	Asp	Gln	Asp	Leu	Leu	Lys	Leu	Val	Lys	Ser	Tyr	His	Trp	Met	Gly
				85					90					95	

Leu	Val	His	Ile	Pro	Thr	Asn	Gly	Ser	Trp	Gln	Trp	Glu	Asp	Gly	Ser
			100					105						110	

Ile	Leu	Ser	Pro	Asn	Leu	Leu	Thr	Ile	Ile	Glu	Met	Gln	Lys	Gly	Asp
		115					120					125			

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
260 265 270

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
275 280 285

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
290 295 300

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
305 310 315 320

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
325 330 335

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly

340

345

350

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 355 360 365

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
 370 375 380

Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr
 385 390 395 400

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 405 410 415

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 420 425 430

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 435 440 445

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
 450 455 460

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
 465 470 475 480

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 485 490 495

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 500 505 510

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 515 520 525

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 530 535 540

Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His
 545 550 555 560

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
565 570 575

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
580 585 590

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
595 600 605

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
610 615 620

Asp Glu Leu Tyr Lys
625

<210> 152
<211> 1887
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding
NKG2D.wt_CD8hingeTM_4-1BB_CD3zeta_EGFP complete chimeric antigen
receptor

<400> 152
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aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
gaggaccagg atctgctgaa gctgggtcaag agctaccact ggatgggact cgtgcacatc 300
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gtgtacatca tggccgacaa gcagaagaac ggcacatcaagg ccaacttcaa gatccggcac	1680
aacatcgagg acggcagcgt tcagctggcc gatcactacc agcagaacac ccctatcgga	1740
gatggccctg tgctgctccc cgacaatcac tacctgagca cacagagcgc cctgagcaag	1800
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accctcggca tggacgaact gtacaaa	1887

<210> 153
 <211> 629
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide NKG2D.YA_CD8hingeTM_4-1BB_CD3zeta_EGFP complete
 chimeric antigen receptor

<400> 153

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
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Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
260 265 270

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
275 280 285

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
290 295 300

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
305 310 315 320

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
325 330 335

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
340 345 350

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
355 360 365

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
370 375 380

Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr
385 390 395 400

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
405 410 415

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
420 425 430

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
435 440 445

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
450 455 460

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
465 470 475 480

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
485 490 495

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
500 505 510

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
515 520 525

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
530 535 540

Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His
545 550 555 560

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
565 570 575

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
580 585 590

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
595 600 605

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
610 615 620

Asp Glu Leu Tyr Lys
625

<210> 154
<211> 1887

<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding
NKG2D.YA_CD8hingeTM_4-1BB_CD3zeta_EGFP complete chimeric antigen
receptor

<400> 154

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aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg	180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa	240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc	300
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accctcggca tggacgaact gtacaaa	1887

<210> 155
 <211> 629
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide NKG2D.AF_CD8hingeTM_4-1BB_CD3zeta_EGFP complete chimeric antigen receptor

<400> 155

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
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His	Ala	Ala	Arg	Pro	Leu	Phe	Asn	Gln	Glu	Val	Gln	Ile	Pro	Leu	Thr
			20					25					30		
Glu	Ser	Tyr	Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn
		35					40					45			
Asn	Cys	Tyr	Gln	Phe	Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln
	50					55					60				
Ala	Ser	Cys	Met	Ser	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys
65					70					75					80
Glu	Asp	Gln	Asp	Leu	Leu	Lys	Leu	Val	Lys	Ser	Ala	His	Trp	Met	Gly
				85					90					95	

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Phe Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
260 265 270

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
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Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
290 295 300

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg

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Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His
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Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp
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Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro
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Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn
				485					490					495	
Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn
			500					505					510		
Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu
		515					520					525			

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
530 535 540

Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His
545 550 555 560

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
565 570 575

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
580 585 590

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
595 600 605

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
610 615 620

Asp Glu Leu Tyr Lys
625

<210> 156
<211> 1887
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding
NKG2D.AF_CD8hingeTM_4-1BB_CD3zeta_EGFP complete chimeric antigen
receptor

<400> 156
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gccgaagtga agtttgaggg cgacaccctg gtcaaccgga tcgagctgaa gggcatcgac	1560
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gtgtacatca tggccgacaa gcagaagaac ggcacatcaagg ccaacttcaa gatccggcac	1680
aacatcgagg acggcagcgt tcagctggcc gatcactacc agcagaacac ccctatcgga	1740
gatggccctg tgctgctccc cgacaatcac tacctgagca cacagagcgc cctgagcaag	1800
gaccccaacg agaagaggga tcacatggtg ctgctggaat ttgtgaccgc cgcaggcatc	1860
accctcggca tggacgaact gtacaaa	1887

<210> 157

<211> 473

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide NKG2D.YA_CD8hingeTM_EGFP silent chimeric antigen receptor

<400> 157

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

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Gly Ser Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu
225 230 235 240

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
245 250 255

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
260 265 270

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
275 280 285

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
290 295 300

Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
305 310 315 320

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
325 330 335

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
340 345 350

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
355 360 365

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
370 375 380

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
385 390 395 400

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
405 410 415

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
420 425 430

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

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
450 455 460

Thr Leu Gly Met Asp Glu Leu Tyr Lys
465 470

<210> 158
<211> 1419
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding NKG2D.YA_CD8hingeTM_EGFP
silent chimeric antigen receptor

<400> 158
atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc 300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc 360
atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc 420
gagaactgca gcacccctaa cacctacatc tgtatgcagc ggaccgtgac caccacacca 480
gtcctagac ctccaactcc tgctcctaca atgccagcc agcctctgtc tctgaggcca 540
gaagcttgta gacctgctgc aggcggagcc gtgcatacaa gaggactgga tttcgctgctg 600
gacatctaca tctgggcccc tctggctgga acatgtggcg tgctgctgct gagcctggtc 660
atcacctgt actgctcagg ctctggttct ggcagcggca gcatgggtgtc taaaggcgag 720

gaactgttca ccggcgtggt gcccattctg gtggaactgg acggggatgt gaacggccac	780
aagtttagcg ttagcggcga aggcgaaggg gatgccacat acggaaagct gaccctgaag	840
ttcatctgca ccaccggcaa gctgcctgtg ccttggccta cactggtcac cacactgaca	900
tacggcgtgc agtgctttag cagatacccc gaccatatga agcagcacga cttcttcaag	960
tccgccatgc ctgagggcta cgtgcaagag cggaccatct tctttaagga cgacggcaac	1020
tacaagacca gggccgaagt gaagtttgag ggcgacaccc tgggtcaaccg gatcgagctg	1080
aaggggcatcg acttcaaaga ggatggcaac atcctggggc acaagctcga gtacaactac	1140
aacagccaca acgtgtacat catggccgac aagcagaaga acggcatcaa ggccaacttc	1200
aagatccggc acaacatcga ggacggcagc gttcagctgg ccgatcacta ccagcagaac	1260
accctatcg gagatggccc tgtgctgctc cccgacaatc actacctgag cacacagagc	1320
gccctgagca aggaccccaa cgagaagagg gatcacatgg tgctgctgga atttgtgacc	1380
gccgcaggca tcaccctcgg catggacgaa ctgtacaaa	1419

<210> 159

<211> 225

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide NKG2D.YA_CD8hingeTM silent chimeric antigen receptor

<400> 159

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

His	Ala	Ala	Arg	Pro	Leu	Phe	Asn	Gln	Glu	Val	Gln	Ile	Pro	Leu	Thr
			20				25						30		

Glu	Ser	Tyr	Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn
		35				40						45			

Asn	Cys	Tyr	Gln	Phe	Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln
	50					55					60				

Ala	Ser	Cys	Met	Ser	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys
65					70					75					80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys
225

<210> 160
<211> 675
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding NKG2D.YA_CD8hingeTM silent
chimeric antigen receptor

<400> 160
atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60

cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct	120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg	180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa	240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc	300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc	360
atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc	420
gagaactgca gcaccctaa cacctacatc tgtatgcagc ggaccgtgac caccacacca	480
gctcctagac ctccaactcc tgctcctaca atgccagcc agcctctgtc tctgaggcca	540
gaagcttgta gacctgtgc aggcggagcc gtgcatacaa gaggactgga tttgcctgc	600
gacatctaca tctgggcccc tctggctgga acatgtggcg tgctgctgct gagcctggtc	660
atcacctgt actgc	675

<210> 161
 <211> 629
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide NKG2D.YA_CD8hingeTM_4-1BBtraf2_CD3zeta_EGFP
 complete chimeric antigen receptor

<400> 161

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

His	Ala	Ala	Arg	Pro	Leu	Phe	Asn	Gln	Glu	Val	Gln	Ile	Pro	Leu	Thr
			20					25					30		

Glu	Ser	Tyr	Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn
		35					40					45			

Asn	Cys	Tyr	Gln	Phe	Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln
	50					55					60				

Ala	Ser	Cys	Met	Ser	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys
65					70					75					80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Ala Ala Ala Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Ala Ala Ala Gly Gly Cys Glu Leu Arg Val Lys
260 265 270

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
275 280 285

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
290 295 300

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
305 310 315 320

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
325 330 335

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
340 345 350

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
355 360 365

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
370 375 380

Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr
385 390 395 400

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
405 410 415

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
420 425 430

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
435 440 445

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
450 455 460

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
465 470 475 480

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
485 490 495

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
500 505 510

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
515 520 525

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
530 535 540

Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His
545 550 555 560

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
565 570 575

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
580 585 590

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
595 600 605

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
610 615 620

Asp Glu Leu Tyr Lys
625

<210> 162
<211> 1887
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding
NKG2D.YA_CD8hingeTM_4-1BBtraf2_CD3zeta_EGFP complete chimeric
antigen receptor

<400> 162
atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc 300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc 360

atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc	420
gagaactgca gcaccctaa cacctacatc tgtatgcagc ggaccgtgac caccacacca	480
gctcctagac ctccaactcc tgctcctaca atcgccagcc agcctctgtc tctgaggcca	540
gaagcttgta gacctgctgc aggcggagcc gtgcatacaa gaggactgga tttgcctgc	600
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cccttcatgc ggcccgtgca gaccacaaa gccgctgcag gctgctcctg cagattcccc	780
gaggctgccg caggcggctg cgagctgaga gtgaagttca gccgttctgc cgacgctccc	840
gcctataagc agggacagaa ccagctgtac aacgagctga acctggggag aagagaagag	900
tacgacgtgc tggacaagcg gagaggcaga gatcctgaga tgggcggcaa gccagacgg	960
aagaatcctc aagagggcct gtataatgag ctgcagaaag acaagatggc cgaggcctac	1020
agcgagatcg gaatgaaggg cgagcgcaga agaggcaagg gacacgatgg actgtaccag	1080
ggcctgagca ccgccaccaa ggatacctat gatgccctgc acatgcaggc cctgcctcca	1140
agatcaggct ctggttctgg cagcggcagc atggtgtcta aaggcgagga actgttcacc	1200
ggcgtggtgc ccattctggt ggaactggac ggggatgtga acggccacaa gtttagcggt	1260
agcggcgaag gcgaagggga tgccacatac ggaaagctga ccctgaagtt catctgcacc	1320
accggcaagc tgcctgtgcc ttggcctaca ctggtcacca cactgacata cggcgtgcag	1380
tgctttagca gataccccga ccatatgaag cagcacgact tcttcaagtc cgccatgcct	1440
gagggtacg tgcaagagcg gaccatcttc tttaaggacg acggcaacta caagaccagg	1500
gccgaagtga agtttgaggg cgacaccctg gtcaaccgga tcgagctgaa gggcatcgac	1560
ttcaaagagg atggcaacat cctgggccac aagctcgagt acaactacaa cagccacaac	1620
gtgtacatca tggccgacaa gcagaagaac ggcacatcaagg ccaacttcaa gatccggcac	1680
aacatcgagg acggcagcgt tcagctggcc gatcactacc agcagaacac ccctatcgga	1740
gatggccctg tgctgctccc cgacaatcac tacctgagca cacagagcgc cctgagcaag	1800
gacccaacg agaagaggga tcacatggtg ctgctggaat ttgtgaccgc cgaggcatc	1860
accctcgga tggacgaact gtacaaa	1887

<210> 163
<211> 629
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide NKG2D.YA_CD8hingeTM_4-1BB_CD3itam_EGFP complete
chimeric antigen receptor

<400> 163

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

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
260 265 270

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
275 280 285

Leu Phe Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Phe Asp Val Leu
290 295 300

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
305 310 315 320

Lys Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met
325 330 335

Ala Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
340 345 350

Lys Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp
355 360 365

Thr Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
370 375 380

Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr

385		390		395		400
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His						
		405		410		415
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys						
		420		425		430
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp						
		435		440		445
Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg						
		450		455		460
Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro						
465		470		475		480
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn						
		485		490		495
Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn						
		500		505		510
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu						
		515		520		525
Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met						
		530		535		540
Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His						
545		550		555		560
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn						
		565		570		575
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu						
		580		585		590
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His						
		595		600		605

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
610 615 620

Asp Glu Leu Tyr Lys
625

<210> 164
<211> 1887
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding
NKG2D.YA_CD8hingeTM_4-1BB_CD3itam_EGFP complete chimeric antigen
receptor

<400> 164
atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc 300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc 360
atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc 420
gagaactgca gcacccctaa cacctacatc tgtatgcagc ggaccgtgac caccacacca 480
gctcctagac ctccaactcc tgctcctaca atcgccagcc agcctctgtc tctgaggcca 540
gaagcttgta gacctgctgc aggcggagcc gtgcatacaa gaggactgga tttcgctgctg 600
gacatctaca tctgggcccc tctggctgga acatgtggcg tgctgctgct gagcctggctc 660
atcacctgt actgcagcct gaagcggggc agaaagaagc tgctgtacat cttaagcag 720
cccttcatgc ggcccgtgca gaccacacaa gaggaagatg gctgctcctg cagattcccc 780
gaggaagaag aaggcggctg cgagctgaga gtgaagttca gccgttctgc cgacgctccc 840
gcctataagc agggacagaa ccagctgttc aacgagctga acctggggag aagagaagag 900
ttcgacgtgc tggacaagcg gagaggcaga gatcctgaga tgggcggcaa gccagacgg 960
aagaatcctc aagagggcct gtttaatgag ctgcagaaag acaagatggc cgaggccttc 1020

agcgagatcg gaatgaaggg cgagcgcaga agaggcaagg gacacgatgg actgttccag	1080
ggcctgagca ccgccaccaa ggataccttt gatgccctgc acatgcaggc cctgcctcca	1140
agatcaggct ctggttctgg cagcggcagc atggtgtcta aaggcgagga actgttcacc	1200
ggcgtggtgc ccattctggt ggaactggac ggggatgtga acggccacaa gtttagcggt	1260
agcggcgaag gcgaagggga tgccacatac ggaaagctga ccctgaagtt catctgcacc	1320
accggcaagc tgcctgtgcc ttggcctaca ctggtcacca cactgacata cggcgtgcag	1380
tgcttttagca gataccccga ccatatgaag cagcacgact tcttcaagtc cgccatgcct	1440
gagggctacg tgcaagagcg gaccatcttc ttttaaggacg acggcaacta caagaccagg	1500
gccgaagtga agtttgaggg cgacaccctg gtcaaccgga tcgagctgaa gggcatcgac	1560
ttcaaagagg atggcaacat cctggggccac aagctcgagt acaactacaa cagccacaac	1620
gtgtacatca tggccgacaa gcagaagaac ggcatcaagg ccaacttcaa gatccggcac	1680
aacatcgagg acggcagcgt tcagctggcc gatcactacc agcagaacac ccctatcgga	1740
gatggccctg tgctgctccc cgacaatcac tacctgagca cacagagcgc cctgagcaag	1800
gaccccaacg agaagaggga tcacatggtg ctgctggaat ttgtgaccgc cgcaggcatc	1860
accctcgga tggacgaact gtacaaa	1887

<210> 165
 <211> 629
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide NKG2D.YA_CD8hingeTM_4-1BBtraf2_CD3itam_EGFP
 complete chimeric antigen receptor

<400> 165

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

His	Ala	Ala	Arg	Pro	Leu	Phe	Asn	Gln	Glu	Val	Gln	Ile	Pro	Leu	Thr
			20				25					30			

Glu	Ser	Tyr	Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn
		35				40						45			

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Ala Ala Ala Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Ala Ala Ala Gly Gly Cys Glu Leu Arg Val Lys
260 265 270

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
275 280 285

Leu Phe Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Phe Asp Val Leu
290 295 300

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
305 310 315 320

Lys Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met
325 330 335

Ala Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
340 345 350

Lys Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp
355 360 365

Thr Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
370 375 380

Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr
385 390 395 400

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
405 410 415

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
420 425 430

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
435 440 445

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
450 455 460

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
465 470 475 480

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
485 490 495

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
500 505 510

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
515 520 525

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
530 535 540

Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His
545 550 555 560

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
565 570 575

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
580 585 590

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
595 600 605

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
610 615 620

Asp Glu Leu Tyr Lys
625

<210> 166
<211> 1887
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding
NKG2D.YA_CD8hingeTM_4-1BBtraf2_CD3itam_EGFP complete chimeric
antigen receptor

<400> 166
atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120

aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg	180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa	240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc	300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc	360
atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc	420
gagaactgca gcaccctaa cacctacatc tgtatgcagc ggaccgtgac caccacacca	480
gctcctagac ctccaactcc tgctcctaca atgccagcc agcctctgtc tctgaggcca	540
gaagcttgta gacctgtgc aggcggagcc gtgcatacaa gaggactgga tttcgctgc	600
gacatctaca tctgggcccc tctggctgga acatgtggcg tgctgtgct gagcctggtc	660
atcacctgt actgcagcct gaagcggggc agaaagaagc tgctgtacat ctttaagcag	720
cccttcatgc ggcccgtgca gaccacacaa gccgctgcag gctgctcctg cagattcccc	780
gaggctgccg caggcggctg cgagctgaga gtgaagttca gccgttctgc cgacgctccc	840
gcctataagc agggacagaa ccagctgttc aacgagctga acctggggag aagagaagag	900
ttcgacgtgc tggacaagcg gagaggcaga gatcctgaga tgggcggcaa gccagacgg	960
aagaatcctc aagagggcct gtttaatgag ctgcagaaag acaagatggc cgaggccttc	1020
agcgagatcg gaatgaaggg cgagcgcaga agaggcaagg gacacgatgg actgttccag	1080
ggcctgagca ccgccaccaa ggataccttt gatgccctgc acatgcaggc cctgcctcca	1140
agatcaggct ctggttctgg cagcggcagc atggtgtcta aaggcgagga actgttcacc	1200
ggcgtggtgc ccattctggt ggaactggac ggggatgtga acggccacaa gtttagcgtt	1260
agcggcgaag gcgaagggga tgccacatac ggaaagctga ccctgaagtt catctgcacc	1320
accggcaagc tgcctgtgcc ttggcctaca ctggtcacca cactgacata cggcgtgcag	1380
tgcttttagca gataccccga ccatatgaag cagcacgact tcttcaagtc cgccatgcct	1440
gagggtacg tgcaagagcg gaccatcttc ttttaaggacg acggcaacta caagaccagg	1500
gccgaagtga agtttgaggg cgacaccctg gtcaaccgga tcgagctgaa gggcatcgac	1560
ttcaaagagg atggcaacat cctgggccac aagctcgagt acaactacaa cagccacaac	1620
gtgtacatca tggccgacaa gcagaagaac ggcacatcaagg ccaacttcaa gatccggcac	1680
aacatcgagg acggcagcgt tcagctggcc gatcactacc agcagaacac ccctatcgga	1740

gatggccctg tgctgctccc cgacaatcac tacctgagca cacagagcgc cctgagcaag 1800
gaccccaacg agaagaggga tcacatggtg ctgctggaat ttgtgaccgc cgcaggcatc 1860
accctcggca tggacgaact gtacaaa 1887

<210> 167
<211> 517
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide NKG2D.YA_CD8hingeTM_4-1BB_EGFP complete
chimeric antigen receptor

<400> 167

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

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
180 185 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
245 250 255

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Ser Gly Ser
260 265 270

Gly Ser Gly Ser Gly Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr
275 280 285

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
290 295 300

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
305 310 315 320

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
325 330 335

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
340 345 350

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro

355

360

365

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 370 375 380

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 385 390 395 400

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 405 410 415

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 420 425 430

Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His
 435 440 445

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 450 455 460

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 465 470 475 480

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 485 490 495

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
 500 505 510

Asp Glu Leu Tyr Lys
 515

<210> 168
 <211> 1551
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding NKG2D.YA_CD8hingeTM_4-1BB_EGFP
 complete chimeric antigen receptor

<400> 168
 atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60

cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct	120
aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg	180
tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa	240
gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc	300
cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc	360
atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc	420
gagaactgca gcaccctaata cacctacatc tgtatgcagc ggaccgtgac caccacacca	480
gctcctagac ctccaactcc tgctcctaca atgccagcc agcctctgtc tctgaggcca	540
gaagcttgta gacctgctgc aggcggagcc gtgcatacaa gaggactgga tttcgctgc	600
gacatctaca tctgggcccc tctggctgga acatgtggcg tgctgctgct gagcctggtc	660
atcacctgt actgcagcct gaagcggggc agaaagaagc tgctgtacat cttaagcag	720
cccttcatgc ggcccgtgca gaccacacaa gaggaagatg gctgctcctg cagattcccc	780
gaggaagaag aaggcggctg cgagctgtca ggctctggtt ctggcagcgg cagcatggtg	840
tctaaaggcg aggaactgtt caccggcgtg gtgcccattc tgggtggaact ggacggggat	900
gtgaacggcc acaagtttag cgtttagcggc gaaggcgaag gggatgccac atacggaaag	960
ctgaccctga agttcatctg caccaccggc aagctgcctg tgccctggcc tacactggtc	1020
accacactga catacggcgt gcagtgcctt agcagatacc ccgaccatat gaagcagcac	1080
gacttcttca agtccgcat gcctgagggc tacgtgcaag agcggaccat cttctttaag	1140
gacgacggca actacaagac cagggccgaa gtgaagtttg agggcgacac cctggtcaac	1200
cggatcgagc tgaaggcat cgacttcaaa gaggatggca acatcctggg ccacaagctc	1260
gagtacaact acaacagcca caacgtgtac atcatggccg acaagcagaa gaacggcatc	1320
aaggccaact tcaagatccg gcacaacatc gaggacggca gcgttcagct ggccgatcac	1380
taccagcaga acacccctat cggagatggc cctgtgctgc tccccgacaa tcactacctg	1440
agcacacaga gcgccctgag caaggacccc aacgagaaga gggatcacat ggtgctgctg	1500
gaatttgtga ccgccgcagg catcacctc ggcatggacg aactgtacaa a	1551

<210> 169

<211> 269

<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide NKG2D.YA_CD8hingeTM_4-1BB complete chimeric antigen receptor

<400> 169

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

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Ala His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His

180

185

190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
 195 200 205

Ala Gly Thr Cys Gly Val Leu Leu Ser Leu Val Ile Thr Leu Tyr
 210 215 220

Cys Ser Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
 225 230 235 240

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 245 250 255

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
 260 265

<210> 170
 <211> 807
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding NKG2D.YA_CD8hingeTM_4-1BB
 complete chimeric antigen receptor

<400> 170
 atggcattgc ctgttacagc tctgctgctg cccctggctc tgcttctgca tgctgccaga 60
 cctctgttca atcaagaggt gcagatccct ctgaccgaga gctactgtgg cccctgtcct 120
 aagaactgga tctgctacaa gaacaactgc taccagttct tcgacgagag caagaattgg 180
 tacgagagcc aggccagctg catgagccag aatgccagcc tgctgaaggt gtacagcaaa 240
 gaggaccagg atctgctgaa gctgggtcaag agcgcccact ggatgggact cgtgcacatc 300
 cctacaaacg gcagctggca gtgggaggac ggctctatcc tgtctcctaa cctgctgacc 360
 atcatcgaga tgcagaaggg cgactgcgcc ctgtacgcca gcagctttaa gggctacatc 420
 gagaactgca gcacccctaa cacctacatc tgtatgcagc ggaccgtgac caccacacca 480
 gctcctagac ctccaactcc tgctcctaca atcgccagcc agcctctgtc tctgaggcca 540
 gaagcttgta gacctgtgc aggcggagcc gtgcatacaa gaggactgga tttgcctgctg 600
 gacatctaca tctgggcccc tctggctgga acatgtggcg tgctgctgct gagcctggctc 660

atcacccctgt actgcagcct gaagcggggc agaaagaagc tgctgtacat cttaaagcag 720
 cccttcatgc ggcccgtgca gaccacacaa gaggaagatg gctgctcctg cagattcccc 780
 gaggaagaag aaggcggctg cgagctg 807

<210> 171
 <211> 736
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide CD19scFv_CD8hingeTM_4-1BB_CD3zeta_EGFP complete
 chimeric antigen receptor

<400> 171

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

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

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

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
 50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
 65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
 100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 130 135 140

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

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Ser Leu Lys Arg
325 330 335

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

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu

355

360

365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
 370 375 380

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

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

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 420 425 430

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

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 450 455 460

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

His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser Gly Ser Gly Ser Gly
 485 490 495

Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 500 505 510

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 515 520 525

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 530 535 540

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 545 550 555 560

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 565 570 575

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
580 585 590

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
595 600 605

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
610 615 620

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
625 630 635 640

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
645 650 655

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
660 665 670

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
675 680 685

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
690 695 700

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

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
725 730 735

<210> 172

<211> 2208

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding
CD19scFv_CD8hingeTM_4-1BB_CD3zeta_EGFP complete chimeric antigen
receptor

<400> 172

atggcattgc ctgttacagc tctgctgctg cccttggtc tgcttctgca tgctgccaga

60

cctgacatcc agatgaccca gacaaccagc agcctgtctg ccagcctggg cgatagagtg	120
accatcagct gtagagccag ccaggacatc agcaagtacc tgaactggta tcagcagaaa	180
cccgacggca ccgtgaagct gctgatctac cacaccagca gactgcacag cggcgtgccca	240
agcagatfff ctggcagcgg ctctggcacc gactacagcc tgacaatcag caacctggaa	300
caagaggata tcgctaccta cttctgccag caaggcaaca ccctgcctta cacctttggc	360
ggaggcacca agctggaaat cacaggcggc ggaggaagcg gaggcggagg atctggtggt	420
ggtggatctg aagtgaact gcaagagtct ggccctggcc tgggtggccc atctcaatct	480
ctgagcgtga cctgtaccgt cagcggagtg tccctgcctg attatggcgt gtcctggatc	540
cggcagcctc ctagaaaagg cctggaatgg ctgggcgtga tctggggcag cgagacaacc	600
tactacaaca gcgccctgaa gtcccggctg accatcatca aggacaactc caagagccag	660
gtgttcctga agatgaacag cctgcagacc gacgacaccg ccatctacta ttgcgccaag	720
cactactact acggcggcag ctacgccatg gattattggg gccagggcac cagcgtgacc	780
gtttcttcta ccaccacacc agctcctaga cctccaactc ctgctcctac aatcgccagc	840
cagcctctgt ctctgaggcc agaagcttgt agacctgctg caggcggagc cgtgcataca	900
agaggactgg atttcgcctg cgacatctac atctgggccc ctctggctgg aacatgtggc	960
gtgctgctgc tgagcctggt catcacctg tactgcagcc tgaagcgggg cagaaagaag	1020
ctgctgtaca tctttaagca gcccttcatg cggcccgtgc agaccacaca agaggaagat	1080
ggctgctcct gcagattccc cgaggaagaa gaaggcggct gcgagctgag agtgaagttc	1140
agccgttctg ccgacgtccc cgcctataag caggacaga accagctgta caacgagctg	1200
aacctgggga gaagagaaga gtacgacgtg ctggacaagc ggagaggcag agatcctgag	1260
atgggcggca agcccagacg gaagaatcct caagagggcc tgtataatga gctgcagaaa	1320
gacaagatgg ccgaggccta cagcgagatc ggaatgaagg gcgagcgag aagaggcaag	1380
ggacacgatg gactgtacca gggcctgagc accgccacca aggataccta tgatgccctg	1440
cacatgcagg ccctgcctcc aagatcaggc tctggttctg gcagcggcag catggtgtct	1500
aaaggcgagg aactgttcac cggcgtggtg ccatttctgg tggaactgga cggggatgtg	1560
aacggccaca agtttagcgt tagcggcgaa ggcgaagggg atgccacata cggaaagctg	1620
accctgaagt tcatctgcac caccggcaag ctgcctgtgc cttggcctac actggtcacc	1680

aactgacat acggcgtgca gtgcttttagc agataccccc accatatgaa gcagcacgac 1740
 ttcttcaagt ccgccatgcc tgagggtctac gtgcaagagc ggaccatctt cttaaggac 1800
 gacggcaact acaagaccag ggccgaagtg aagtttgagg gcgacaccct ggtcaaccgg 1860
 atcgagctga agggcatcga cttcaaagag gatggcaaca tcctgggcca caagctcgag 1920
 tacaactaca acagccacaa cgtgtacatc atggccgaca agcagaagaa cggcatcaag 1980
 gccaacttca agatccggca caacatcgag gacggcagcg ttcagctggc cgatcactac 2040
 cagcagaaca cccctatcgg agatggccct gtgctgctcc ccgacaatca ctacctgagc 2100
 acacagagcg ccctgagcaa ggaccccaac gagaagaggg atcacatggt gctgctggaa 2160
 tttgtgaccg ccgcaggcat caccctcggc atggacgaac tgtacaaa 2208

<210> 173
 <211> 1115
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide
 CD19scFv_CD8hingeTM_4-1BB_CD3zeta_EGFP-T2A-NKG2D.YA_CD8hingeTM

<400> 173

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

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

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

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
 50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
 65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

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

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Ser Leu Lys Arg
325 330 335

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

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

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

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

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

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

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

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

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

His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser Gly Ser Gly Ser Gly
485 490 495

Ser Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
500 505 510

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
515 520 525

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
530 535 540

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
545 550 555 560

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
565 570 575

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
580 585 590

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
595 600 605

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
610 615 620

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
625 630 635 640

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
645 650 655

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
660 665 670

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
675 680 685

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
690 695 700

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

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
725 730 735

Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
740 745 750

Val Glu Glu Asn Pro Gly Pro Arg Met Leu Leu Leu Val Thr Ser Leu
755 760 765

Leu Leu Cys Glu Leu Pro His Pro Ala Phe Leu Leu Ile Pro Leu Phe
770 775 780

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

Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln Phe Phe Asp
805 810 815

Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met Ser Gln Asn
820 825 830

Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp Leu Leu Lys
835 840 845

Leu Val Lys Ser Ala His Trp Met Gly Leu Val His Ile Pro Thr Asn
850 855 860

Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro Asn Leu Leu
865 870 875 880

Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr Ala Ser Ser
885 890 895

Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr Tyr Ile Cys
900 905 910

Met Gln Arg Thr Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys Gly Pro
915 920 925

Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln Phe Phe
930 935 940

Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met Ser Gln
945 950 955 960

Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp Leu Leu
965 970 975

Lys Leu Val Lys Ser Ala His Trp Met Gly Leu Val His Ile Pro Thr
980 985 990

Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro Asn Leu
995 1000 1005

Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr Ala
1010 1015 1020

Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
1025 1030 1035

Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro Ala Pro Arg
1040 1045 1050

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
1055 1060 1065

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
1070 1075 1080

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
1085 1090 1095

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
1100 1105 1110

Tyr Cys
1115

<210> 174
<211> 3345
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding
CD19scFv_CD8hingeTM_4-1BB_CD3zeta_EGFP-T2A-NKG2D.YA_CD8hingeTM

<400> 174

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cctgacatcc agatgaccca gacaaccagc agcctgtctg ccagcctggg cgatagagtg	120
accatcagct gtagagccag ccaggacatc agcaagtacc tgaactggta tcagcagaaa	180
cccgacggca ccgtgaagct gctgatctac cacaccagca gactgcacag cggcgtgcc	240
agcagatttt ctggcagcgg ctctggcacc gactacagcc tgacaatcag caacctggaa	300
caagaggata tcgctaccta cttctgccag caaggcaaca ccctgcctta cacctttggc	360
ggaggcacca agctggaaat cacaggcggc ggaggaagcg gaggcggagg atctggtggt	420
ggtggatctg aagtgaact gcaagagtct ggccctggcc tgggtggccc atctcaatct	480
ctgagcgtga cctgtaccgt cagcggagtg tccctgcctg attatggcgt gtcctggatc	540
cggcagcctc ctagaaaagg cctggaatgg ctgggcgtga tctggggcag cgagacaacc	600
tactacaaca gcgccctgaa gtcccggctg accatcatca aggacaactc caagagccag	660
gtgttcctga agatgaacag cctgcagacc gacgacaccg ccatctacta ttgcgccaag	720
cactactact acggcggcag ctacgccatg gattattggg gccagggcac cagcgtgacc	780
gtttcttcta ccaccacacc agctcctaga cctccaactc ctgctcctac aatcgccagc	840
cagcctctgt ctctgaggcc agaagcttgt agacctgctg caggcggagc cgtgcataca	900
agaggactgg atttcgcctg cgacatctac atctggggcc ctctggctgg aacatgtggc	960
tgctgtctgc tgagcctggt catcaccctg tactgcagcc tgaagcgggg cagaaagaag	1020
ctgctgtaca tctttaagca gcccttcatg cggcccgtgc agaccacaca agaggaagat	1080
ggctgctcct gcagattccc cgaggaagaa gaaggcggct gcgagctgag agtgaagttc	1140
agccgttctg ccgacgtcc cgcctataag caggacaga accagctgta caacgagctg	1200
aacctgggga gaagagaaga gtacgacgtg ctggacaagc ggagaggcag agatcctgag	1260
atgggcggca agcccagacg gaagaatcct caagagggcc tgtataatga gctgcagaaa	1320
gacaagatgg ccgaggccta cagcgagatc ggaatgaagg gcgagcgag aagaggcaag	1380
ggacacgatg gactgtacca gggcctgagc accgccacca aggataccta tgatgccctg	1440
cacatgcagg ccctgcctcc aagatcaggc tctggttctg gcagcggcag catggtgtct	1500
aaaggcgagg aactgttcac cggcgtggtg ccatttctgg tggaactgga cggggatgtg	1560
aacggccaca agtttagcgt tagcggcgaa ggcgaagggg atgccacata cggaaagctg	1620

accctgaagt	tcattctgcac	caccggcaag	ctgcctgtgc	cttggcctac	actggtcacc	1680
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ttcttcaagt	ccgccatgcc	tgagggtctac	gtgcaagagc	ggaccatctt	ctttaaggac	1800
gacggcaact	acaagaccag	ggccgaagtg	aagtttgagg	gcgacaccct	ggtcaaccgg	1860
atcgagctga	agggcacgca	cttcaaagag	gatggcaaca	tcctggggcca	caagctcgag	1920
tacaactaca	acagccacaa	cgtgtacatc	atggccgaca	agcagaagaa	cggcatcaag	1980
gccaacttca	agatccggca	caacatcgag	gacggcagcg	ttcagctggc	cgatcactac	2040
cagcagaaca	cccctatcgg	agatggccct	gtgctgctcc	ccgacaatca	ctacctgagc	2100
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atcccactgt	tcaaccagga	ggttcagatt	ccgctgaccg	aaagctactg	tggacatgt	2400
cccaagaact	ggatctgcta	caaaaacaat	tgttatcaat	ttttcgacga	aagcaagaat	2460
tggtacgaaa	gccaggcttc	atgcatgagc	caaaatgcat	ccctgctgaa	ggtgtacagc	2520
aaggaggacc	aggacctgct	gaaacttgct	aaatccgctc	actggatggg	actggtccat	2580
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actatcatag	agatgcagaa	gggagattgt	gcattgtatg	ctagttcatt	caagggatac	2700
attgaaaact	gctcaacacc	taatacctac	atatgtatgc	agcgcacagt	gcagatccct	2760
ctgaccgaga	gctactgtgg	cccctgtcct	aagaactgga	tctgctacaa	gaacaactgc	2820
taccagttct	tcgacgagag	caagaattgg	tacgagagcc	aggccagctg	catgagccag	2880
aatgccagcc	tgctgaaggt	gtacagcaaa	gaggaccagg	atctgctgaa	gctggtcaag	2940
agcgcccact	ggatgggact	cgtgcacatc	cctacaaacg	gcagctggca	gtgggaggac	3000
ggctctatcc	tgtctcctaa	cctgctgacc	atcatcgaga	tgcagaaggg	cgactgcgcc	3060
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tgtatgcagc	ggaccgtgac	cacgacgcca	gcgccgcgac	caccaacacc	ggcgcccacc	3180
atcgcgctgc	agcccctgtc	cctgcgcccc	gaggcggtgc	ggccagcggc	ggggggcgca	3240

gtgcacacga gggggctgga cttcgcctgt gatatctaca tctgggcgcc cttggccggg 3300
 acttgtgggg tccttctcct gtcactgggtt atcacccttt actgc 3345

<210> 175
 <211> 161
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide FLAG_6xHis_mutIL2

<400> 175

Gly Ser Ser Gly Ser Ser Asp Tyr Lys Asp Asp Asp Asp Lys His His
 1 5 10 15

His His His His His His Gly Ser Ser Gly Ser Ser Ala Pro Thr Ser
 20 25 30

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 35 40 45

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 50 55 60

Thr Ala Met Leu Thr Lys Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 65 70 75 80

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 85 90 95

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 100 105 110

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 115 120 125

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 130 135 140

Phe Leu Asn Arg Trp Ile Thr Phe Ser Gln Ser Ile Ile Ser Thr Leu
 145 150 155 160

Thr

<210> 176
<211> 483
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding FLAG_6xHis_mutIL2

<400> 176
ggaagtagcg gtagtagtga ttacaaggac gatgacgaca agcaccacca tcatcatcat 60
caccacggta gcagcggcag cagtgtcccc acctctagca gcacaaagaa gaccagctg 120
caactggaac acctcctgct ggacctgcag atgatcctga acggcatcaa caactacaag 180
aaccccaagc tgaccgccat gctgaccaa aagttttaca tgcccaagaa ggccaccgag 240
cttaaacacc tgcaatgcct tgaggaggag ctgaagcccc tggaggaggt actgaacctg 300
gcccagagca agaactttca tctgaggccc agggacctga ttagcaacat caacgtgatc 360
gtgttggagt tgaagggcag cgagaccacg ttcattgtgcg agtacgccga cgagacggcc 420
accatagtgg agtttcttaa caggtggatc accttctcac agtctatcat cagcacctg 480
acc 483

<210> 177
<211> 343
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide ULBP2.R80W_FLAG_6xHis_mutIL2

<400> 177

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
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Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
20 25 30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35 40 45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser Gly Thr Gly Ser Ser Gly Ser Ser Asp Tyr Lys Asp
180 185 190

Asp Asp Asp Lys His His His His His His His Gly Ser Ser Gly
195 200 205

Ser Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
210 215 220

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

Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Lys Lys Phe Tyr Met
245 250 255

Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu

260

265

270

Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
 275 280 285

His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
 290 295 300

Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
 305 310 315 320

Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ser Gln
 325 330 335

Ser Ile Ile Ser Thr Leu Thr
 340

<210> 178

<211> 1029

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding ULBP2.R80W_FLAG_6xHis_mutIL2

<400> 178

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tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat	120
aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag	180
gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc	240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag	300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaactttt	360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg	420
aaggagaagt gggaaaacga caaagtgggtg gcgatgtcat tccactatth ctcgatggga	480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg	540
ggtaccggta gtagcggtag tagtgattac aaggacgatg acgacaagca ccaccatcat	600
catcatcacc acggtagcag cggcagcagt gccccacct ctagcagcac aaagaagacc	660

cagctgcaac tggaacacct cctgctggac ctgcagatga tcctgaacgg catcaacaac	720
tacaagaacc ccaagctgac cgccatgctg accaaaaagt ttacatgcc caagaaggcc	780
accgagctta aacacctgca atgccttgag gaggagctga agcccctgga ggaggtactg	840
aacctggccc agagcaagaa ctttcatctg aggcccaggg acctgattag caacatcaac	900
gtgatcgtgt tggagttgaa gggcagcgag accacgttca tgtgcgagta cgccgacgag	960
acggccacca tagtggagtt tcttaacagg tggatcacct tctcacagtc tatcatcagc	1020
acctgacc	1029

<210> 179
 <211> 343
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide ULBP2.S2_FLAG_6xHis_mutIL2

<400> 179

Glu	Pro	His	Ser	Leu	Ser	Tyr	Asp	Ile	Thr	Val	Ile	Pro	Lys	Phe	Arg
1				5					10					15	

Pro	Gly	Pro	Arg	Trp	Cys	Ala	Val	Gln	Gly	Gln	Val	Asp	Glu	Lys	Thr
			20					25					30		

Phe	Leu	His	Tyr	Asp	Cys	Gly	Asn	Lys	Thr	Val	Thr	Pro	Val	Ser	Pro
		35					40					45			

Leu	Gly	Lys	Lys	Leu	Asn	Val	Thr	Thr	Ala	Trp	Lys	Ala	Gln	Asn	Pro
	50					55					60				

Val	Leu	Arg	Glu	Val	Val	Asp	Ile	Leu	Thr	Glu	Gln	Leu	Trp	Asp	Ile
65					70					75					80

Gln	Leu	Glu	Asn	Tyr	Thr	Pro	Lys	Glu	Pro	Leu	Thr	Leu	Gln	Ala	Arg
			85						90					95	

Met	Ser	Cys	Glu	Gln	Lys	Ala	Glu	Gly	His	Ser	Ser	Gly	Ser	Trp	Gln
			100					105					110		

Phe	Ser	Phe	Asp	Gly	Gln	Ile	Phe	Leu	Leu	Phe	Asp	Ser	Glu	Lys	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
 130 135 140

Glu Asn Asp Lys Val Val Ala Thr Leu Met Arg Ile Trp Ser Met Gly
 145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
 165 170 175

Leu Glu Pro Ser Gly Thr Gly Ser Ser Gly Ser Ser Asp Tyr Lys Asp
 180 185 190

Asp Asp Asp Lys His His His His His His His Gly Ser Ser Gly
 195 200 205

Ser Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
 210 215 220

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

Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Lys Lys Phe Tyr Met
 245 250 255

Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
 260 265 270

Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
 275 280 285

His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
 290 295 300

Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
 305 310 315 320

Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ser Gln
 325 330 335

Ser Ile Ile Ser Thr Leu Thr
340

<210> 180
<211> 1029
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding ULBP2.S2_FLAG_6xHis_mutIL2

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aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180
gcacaaaacc ccgtcctgcg cgaggctgctc gacatcctga ctgaacaatt gtgggacatc 240
cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300
caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt 360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg 420
aaggagaagt gggaaaacga caaagtgggtg gcgactctga tgaggatttg gtcgatggga 480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg 540
ggtaccggta gtagcggtag tagtgattac aaggacgatg acgacaagca ccaccatcat 600
catcatcacc acggtagcag cggcagcagt gccccacct ctagcagcac aaagaagacc 660
cagctgcaac tggaacacct cctgctggac ctgcagatga tcctgaacgg catcaacaac 720
tacaagaacc ccaagctgac cgccatgctg accaaaaagt ttacatgcc caagaaggcc 780
accgagctta aacacctgca atgccttgag gaggagctga agcccctgga ggaggtactg 840
aacctggccc agagcaagaa ctttcatctg aggcccaggg acctgattag caacatcaac 900
gtgatcgtgt tggagttgaa gggcagcgag accacgttca tgtgcgagta cgccgacgag 960
acggccacca tagtggagtt tcttaacagg tggatcacct tctcacagtc tatcatcagc 1020
accctgacc 1029

<210> 181
<211> 412
<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide ULBP2.R80W_Fc1

<400> 181

Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
1 5 10 15

Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
20 25 30

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
35 40 45

Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
50 55 60

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
180 185 190

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
195 200 205

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
210 215 220

Thr Cys Val Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe
225 230 235 240

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
245 250 255

Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr
260 265 270

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
275 280 285

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
290 295 300

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
305 310 315 320

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
325 330 335

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
340 345 350

Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
355 360 365

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
385 390 395 400

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

<210> 182
 <211> 1236
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding ULBP2.R80W_Fc1

<400> 182
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 tgggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120
 aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180
 gcacaaaacc ccgtcctgcg cgaggctcgtc gacatcctga ctgaacaatt gtgggacatc 240
 cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300
 caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaattcttt 360
 ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg 420
 aaggagaagt gggaaaacga caaagtgggtg gcgatgtcat tccactatctt ctcgatggga 480
 gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg 540
 gagccccaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg 600
 ggtggcccct ccgtgttcct gttcccgctt aagcctaagg acacccttat gatcagccgc 660
 acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggaccgga ggtcaagttc 720
 aattggtacg tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag 780
 tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac 840
 gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc 900
 atcagcaagg ccaagggcca gccaaaggga ccacaggtgt acaccctccc tccttcccgg 960
 gacgagctga ccaaaaacca agtgtccctg acttgccttg tgaaggggtt ctacccttct 1020
 gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactatga cactaccccg 1080
 cccgtgctgg attccgacgg aagcttcttc ctgtactccg acctgaccgt ggacaagtcg 1140
 agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac 1200
 tacaccaga agtcactgag cctctcccc ggaaag 1236

<210> 183
<211> 368
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide Fc2_mutIL2

<400> 183

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Leu Thr
130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
225 230 235 240

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
245 250 255

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
260 265 270

Ala Met Leu Thr Lys Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
275 280 285

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
290 295 300

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

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
325 330 335

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
340 345 350

Leu Asn Arg Trp Ile Thr Phe Ser Gln Ser Ile Ile Ser Thr Leu Thr
355 360 365

<210> 184
<211> 1104
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding Fc2_mutIL2

<400> 184

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gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg      60
gggtggcccct ccgtgttcct gttcccgctt aagcctaagg acacccttat gatcagccgc      120
accctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggacccgga ggtcaagttc      180
aattggtagc tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag      240
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac      300
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc      360
atcagcaagg ccaagggcca gccaaggga ccacaggtgt acaccctccc tccttcccgg      420
aaggagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct      480
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactaccccg      540
cccgtgctga agtccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg      600
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac      660
tacaccaga agtcactgag cctctcccc ggaggaggtg gcagcgcccc cacctctagc      720
agcacaaga agaccagct gcaactggaa cacctcctgc tggacctgca gatgatcctg      780
aacggcatca acaactacaa gaacccaag ctgaccgcca tgctgaccaa aaagttttac      840
atgcccaaga aggccaccga gcttaaacac ctgcaatgcc ttgaggagga gctgaagccc      900
ctggaggagg tactgaacct ggcccagagc aagaactttc atctgaggcc cagggacctg      960
attagcaaca tcaacgtgat cgtgttgag ttgaagggca gcgagaccac gttcatgtgc     1020
gagtacgccg acgagacggc caccatagtg gagtttctta acaggtggat caccttctca     1080
cagtctatca tcagcacct gacc                                     1104
```

<210> 185

<211> 349

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide Fc2_mutIL15

<400> 185

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

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

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Asn Trp Val Asn Val
225 230 235 240

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
245 250 255

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
260 265 270

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
275 280 285

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
290 295 300

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
305 310 315 320

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
325 330 335

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
340 345

<210> 186
<211> 1047
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding Fc2_mutIL15

<400> 186
gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg 60
ggtagggcccct ccgtgttcct gttcccgccct aagcctaagg acacccttat gatcagccgc 120
acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggaccgga ggtcaagttc 180
aattgggtacg tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag 240
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac 300
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc 360

atcagcaagg ccaagggcca gccaaagggaa ccacaggtgt acaccctccc tccttcccgg	420
aaggagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct	480
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactacccccg	540
cccgtgctga agtccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg	600
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac	660
tacaccaga agtcactgag cctctcccc ggaggaggtg gcagcaattg ggtgaacgtg	720
atttctgact tgaagaaaat cgaggacttg attcaaagta tgcacataga cgcaacgctc	780
tatactgaga gtgatgttca tccctcttgt aaagttaccg ctatgaagtg tttcttgctc	840
gaactccaag ttatcagtct ggagagcggg gatgcctcca tacacgatac agtcgaaaac	900
cttatcattc tcgcaaataa ctcatagagt agcaatggca atgttacaga gtctgggtgt	960
aaggaatgcg aagaacttga agagaaaaac ataaaggagt tcctccaatc attcgtgcat	1020
attgtccaga tgtttatcaa cactagc	1047

<210> 187
 <211> 412
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic peptide ULBP2.S2_Fc1

<400> 187

 Glu Pro His Ser Leu Ser Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg
 1 5 10 15

 Pro Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
 20 25 30

 Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro
 35 40 45

 Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro
 50 55 60

 Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
 65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Leu Met Arg Ile Trp Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
180 185 190

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
195 200 205

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
210 215 220

Thr Cys Val Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe
225 230 235 240

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
245 250 255

Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr
260 265 270

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
275 280 285

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

290

295

300

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 305 310 315 320

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 325 330 335

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 340 345 350

Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 355 360 365

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 385 390 395 400

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 405 410

<210> 188
 <211> 1236
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding ULBP2.S2_Fc1

<400> 188
 gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60
 tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120
 aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180
 gcacaaaacc ccgtcctgcg cgaggctcgtc gacatcctga ctgaacaatt gtgggacatc 240
 cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300
 caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt 360
 ctgttattcg attcagagaa gagaatgtgg actacagttc accccggtgc ccgtaaaatg 420

aaggagaagt gggaaaacga caaagtgggtg gcgactctga tgaggatttg gtcgatggga	480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg	540
gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg	600
ggtggccccct ccgtgttcct gttcccgctt aagcctaagg acacccttat gatcagccgc	660
acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggacccgga ggtcaagttc	720
aattggtagc tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag	780
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac	840
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc	900
atcagcaagg ccaagggcca gccaaaggga ccacagggtg acaccctccc tccttcccgg	960
gacgagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct	1020
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactatga cactaccccg	1080
cccgtagctg attccgacgg aagcttcttc ctgtactccg acctgaccgt ggacaagtcg	1140
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac	1200
tacaccaga agtcactgag cctctcccc ggaag	1236

<210> 189
 <211> 412
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide ULBP2.S3_Fc1

<400> 189

Glu	Pro	His	Ser	Leu	Ser	Tyr	Asp	Ile	Thr	Val	Ile	Pro	Lys	Phe	Arg
1				5					10					15	

Pro	Gly	Pro	Arg	Trp	Cys	Ala	Val	Gln	Gly	Gln	Val	Asp	Glu	Lys	Thr
			20					25					30		

Phe	Leu	His	Tyr	Asp	Cys	Gly	Asn	Lys	Thr	Val	Thr	Pro	Val	Ser	Pro
		35					40					45			

Leu	Gly	Lys	Lys	Leu	Asn	Val	Thr	Thr	Ala	Trp	Lys	Ala	Gln	Asn	Pro
	50					55					60				

Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu Trp Asp Ile
65 70 75 80

Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg
85 90 95

Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln
100 105 110

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

Met Trp Thr Thr Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp
130 135 140

Glu Asn Asp Lys Val Val Ala Thr Lys Leu Tyr Leu Trp Ser Met Gly
145 150 155 160

Asp Cys Ile Gly Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr
165 170 175

Leu Glu Pro Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
180 185 190

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
195 200 205

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
210 215 220

Thr Cys Val Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe
225 230 235 240

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
245 250 255

Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr
260 265 270

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

275

280

285

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 290 295 300

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 305 310 315 320

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 325 330 335

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 340 345 350

Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 355 360 365

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 385 390 395 400

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 405 410

<210> 190

<211> 1236

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide, encoding ULBP2.S3_Fc1

<400> 190

gagccccata gtctgagcta cgacatcaca gttattccca agttcaggcc cggaccgcgc 60

tggtgtgccg tgcaaggaca agtcgacgaa aaaacctttc ttcattacga ttgcggaaat 120

aagactgtaa cgccagtctc tccttttaggt aagaagttaa acgtcactac ggcgtggaag 180

gcacaaaacc ccgtcctgcg cgaggtcgtc gacatcctga ctgaacaatt gtgggacatc 240

cagctcgaga attacactcc aaaggagcct cttaccctgc aggctagaat gtcttgcgag 300

caaaaggcag agggccactc ctccggcagc tggcagttca gtttcgacgg acaaatcttt	360
ctgttattcg attcagagaa gagaatgtgg actacagttc accccgggtgc ccgtaaaatg	420
aaggagaagt gggaaaacga caaagtgggtg gcgactaagc tttatctttg gtcgatggga	480
gactgcatcg gttggctgga agatttcctc atgggtatgg actccacttt ggagccatcg	540
gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg	600
ggtggcccct ccgtgttcct gttcccgct aagcctaagg acacccttat gatcagccgc	660
acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggacccgga ggtcaagttc	720
aattggtagc tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag	780
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac	840
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaagagacc	900
atcagcaagg ccaagggcca gccaaaggga ccacaggtgt acaccctccc tccttcccgg	960
gacgagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct	1020
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactatga cactaccccg	1080
cccgctgctgg attccgacgg aagcttcttc ctgtactccg acctgaccgt ggacaagtcg	1140
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac	1200
tacaccaga agtcactgag cctctcccc ggaaag	1236

<210> 191
 <211> 368
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide Fc2_wtIL2 (wild-type)

<400> 191

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

Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25						30	

Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			

Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Leu Thr
130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
225 230 235 240

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
245 250 255

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr

260

265

270

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
 275 280 285

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
 290 295 300

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

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
 325 330 335

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
 340 345 350

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 355 360 365

<210> 192
 <211> 1104
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding Fc2_wtIL2

<400> 192
 gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg 60
 ggtggcccct ccgtgttcct gttccgcct aagcctaagg acacccttat gatcagccgc 120
 acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggaccgga ggtcaagttc 180
 aattggtacg tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag 240
 tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac 300
 gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc 360
 atcagcaagg ccaagggcca gccaagggaa ccacaggtgt acaccctccc tccttcccgg 420
 aaggagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct 480
 gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactacccccg 540

```

cccggtgctga agtccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg      600
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac      660
tacaccaga agtcactgag cctctcccc ggaggagggtg gcagcgctcc aacctctagc      720
tctacgaaga aaactcaact ccagcttgag catttgcttt tggaccttca aatgatattg      780
aacgggatta acaattacaa gaaccccaaa ctgacgcgaa tgcttacatt caaatTTTtac      840
atgccaaaga aggccaccga gctgaaacac ttgcaatgtc ttgaggaaga gctgaagcca      900
ttggaggagg tcctgaattt ggctcaaagt aagaacttcc acctgcggcc aagggatctc      960
ataagcaaca taaatgtcat tgtattggaa ctgaaaggga gcgaaaccac ctttatgtgc     1020
gagtatgcag atgaaactgc aaccatagtc gagttcctca atcgctggat aactttcgcg     1080
cagtcaatta tatcaacact cacc                                             1104

```

```

<210> 193
<211> 368
<212> PRT
<213> Artificial sequence

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<220>
<223> Synthetic peptide Fc2_IL21.wt (wild-type)

```

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<400> 193

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

```

```

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20           25           30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35           40           45

```

```

Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
          50           55           60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65           70           75           80

```

```

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
          85           90           95

```

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Leu Thr
130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gln Gly Gln Asp Arg
225 230 235 240

His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln Leu Lys
245 250 255

Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp
260 265 270

Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala
275 280 285

Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val
290 295 300

Leu Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg

305		310		315		320									
Arg	Gln	Lys	His	Arg	Leu	Thr	Cys	Pro	Ser	Cys	Asp	Ser	Tyr	Glu	Lys
				325					330					335	
Lys	Pro	Pro	Lys	Glu	Phe	Leu	Glu	Arg	Phe	Lys	Ser	Leu	Leu	Gln	Lys
			340					345					350		
Met	Ile	His	Gln	His	Leu	Ser	Ser	Arg	Thr	His	Gly	Ser	Glu	Asp	Ser
		355					360					365			

<210> 194
 <211> 1104
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding Fc2_IL21.wt (wild-type)

<400> 194	
gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg	60
ggtggcccct ccgtgttcct gttccgcct aagcctaagg acacccttat gatcagccgc	120
accctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggacccgga ggtcaagttc	180
aattggtacg tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag	240
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac	300
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc	360
atcagcaagg ccaagggcca gccaaaggga ccacaggtgt acaccctccc tccttcccgg	420
aaggagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct	480
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactaccccg	540
cccgctgctga agtccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg	600
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac	660
tacaccaga agtcactgag cctctcccc ggaggaggtg gcagccaggg tcaagaccgc	720
catatgatcc gaatgcgaca gctcattgat attgtcgatc aattgaaaaa ttacgtgaat	780
gatcttgtag cggagttcct cccgcacccg gaggacgttg aaacgaattg tgagtgggtca	840
gcattttctt gctttcagaa ggctcaactc aagagtgcaa acacgggtaa caacgagcgc	900

attatcaatg ttctcatcaa aaagctgaaa cgaaaaccgc ctagcaccaa cgcaggcaga	960
cgacagaagc accggctcac gtgccaagt tgcgattctt atgagaaaaa gccaccgaaa	1020
gaattcctgg agcgggttcaa gtccctcttg cagaaaatga ttcattcagca tctctccagc	1080
aggacacacg gctccgagga ctcc	1104

<210> 195
 <211> 368
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide Fc2_IL21.D18A

<400> 195

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

Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25					30		

Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			

Val	Ala	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				

Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75					80

Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				85					90					95	

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

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

Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Lys	Glu	Leu	Thr
	130					135					140				

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gln Gly Gln Asp Arg
225 230 235 240

His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Ala Gln Leu Lys
245 250 255

Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp
260 265 270

Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala
275 280 285

Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val
290 295 300

Leu Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg
305 310 315 320

Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys
325 330 335

Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln Lys
340 345 350

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

355

360

365

<210> 196
 <211> 1104
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide, encoding Fc2_IL21.D18A

<400> 196
 gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg 60
 ggtggcccct ccgtgttcct gttcccgctt aagcctaagg acacccttat gatcagccgc 120
 acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggaccgga ggtcaagttc 180
 aattggtagc tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag 240
 tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac 300
 gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc 360
 atcagcaagg ccaagggcca gccaaaggaa ccacaggtgt acaccctccc tccttcccgg 420
 aaggagctga ccaaaaacca agtgtccctg acttgccttg tgaaggggtt ctacccttct 480
 gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactaccccg 540
 cccgtgctga agtccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg 600
 agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac 660
 tacaccaga agtcactgag cctctcccc ggaggaggtg gcagccaggg tcaagaccgc 720
 catatgatcc gaatgcgaca gtcattgat attgtcgac aattgaaaaa ttacgtgaat 780
 gatcttgtag cggagttcct cccgcaccg gaggacgttg aaacgaattg tgagtgggtca 840
 gcattttctt gctttcagaa ggctcaactc aagagtgcaa acacgggtaa caacgagcgc 900
 attatcaatg ttctcatcaa aaagctgaaa cgaaaaccgc ctagcaccaa cgcaggcaga 960
 cgacagaagc accggctcac gtgccaagt tgcgattctt atgagaaaaa gccaccgaaa 1020
 gaattcctgg agcggttcaa gtccctcttg cagaaaatga ttcacagca tctctccagc 1080
 aggacacacg gctccgagga ctcc 1104

<210> 197
 <211> 368
 <212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide Fc2_IL21.E109R

<400> 197

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Leu Thr
130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gln Gly Gln Asp Arg
225 230 235 240

His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln Leu Lys
245 250 255

Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp
260 265 270

Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala
275 280 285

Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val
290 295 300

Leu Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg
305 310 315 320

Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys
325 330 335

Lys Pro Pro Lys Glu Phe Leu Arg Arg Phe Lys Ser Leu Leu Gln Lys
340 345 350

Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser
355 360 365

<210> 198
<211> 1104
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding Fc2_IL21.E109R

<400> 198

gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg	60
ggtagggcccct ccgtgttcct gttcccgccct aagcctaagg acacccttat gatcagccgc	120
accctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggacccgga ggtcaagttc	180
aattggtacg tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag	240
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac	300
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc	360
atcagcaagg ccaagggcca gccaaaggaa ccacaggtgt acaccctccc tccttcccgg	420
aaggagctga ccaaaaacca agtgtccctg acttgccttg tgaaggggtt ctacccttct	480
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactaccccg	540
cccgtgctga agtccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg	600
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac	660
tacaccaga agtcactgag cctctcccc ggaggaggtg gcagccaggg tcaagaccgc	720
catatgatcc gaatgcgaca gtcattgat attgtcgatc aattgaaaaa ttacgtgaat	780
gatcttgtag cggagttcct ccccgccaccg gaggacgttg aaacgaattg tgagtgggtca	840
gcattttctt gctttcagaa ggctcaactc aagagtgcaa acacgggtaa caacgagcgc	900
attatcaatg ttctcatcaa aaagctgaaa cgaaaaccgc ctagcaccaa cgcaggcaga	960
cgacagaagc accggctcac gtgcccagt tgcgattctt atgagaaaaa gccaccgaaa	1020
gaattcctgc ggcggttcaa gtccctcttg cagaaaatga ttcacagca tctctccagc	1080
aggacacacg gtcgagga ctcc	1104

<210> 199
 <211> 368
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic peptide Fc2_IL21.D18A.E109R

 <400> 199

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

Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gln Gly Gln Asp Arg
 225 230 235 240

His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Ala Gln Leu Lys
245 250 255

Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp
260 265 270

Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala
275 280 285

Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val
290 295 300

Leu Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg
305 310 315 320

Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys
325 330 335

Lys Pro Pro Lys Glu Phe Leu Arg Arg Phe Lys Ser Leu Leu Gln Lys
340 345 350

Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser
355 360 365

<210> 200
<211> 1104
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding Fc2_IL21.D18A.E109R

<400> 200
gagcccaaaa gctgcgacaa gactcacact tgtccgccgt gccccgcccc cgaactgctg 60
ggtagggcccct ccgtgttcct gttcccgccct aagcctaagg acacccttat gatcagccgc 120
acccctgaag tgacctgtgt cgtcgtggca gtgtcacacg aggaccgga ggtcaagttc 180
aattgggtacg tggacggcgt ggaagtgcac aacgcaaaga ccaagcctcg ggaggaacag 240
tacgcctcga cctaccgcgt ggtgtcagtc ctgactgtgc tgcaccagga ctggctgaac 300
gggaaggagt acaagtgcaa agtgtcgaac aaggccctgc cggctccaat tgaaaagacc 360

atcagcaagg ccaagggcca gccaaagggaa ccacaggtgt acaccctccc tccttcccgg	420
gacgagctga ccaaaaacca agtgtccctg acttgccctg tgaaggggtt ctacccttct	480
gacattgccg tcgaatggga atcgaacgga cagcctgaaa acaactataa gactacccccg	540
cccgtgctgg attccgacgg aagcttcttc ctgtactcca agctgaccgt ggacaagtcg	600
agatggcagc agggaaatgt gttcagctgc tccgtgatgc atgaggcgct gcacaaccac	660
tacaccaga agtcactgag cctctcccc ggaggaggtg gcagccaggg tcaagaccgc	720
catatgatcc gaatgcgaca gctcattgat attgtcgcac aattgaaaaa ttacgtgaat	780
gatcttgtag cggagttcct ccccgacccg gaggacgttg aaacgaattg tgagtgggtca	840
gcattttctt gctttcagaa ggctcaactc aagagtgcaa acacgggtaa caacgagcgc	900
attatcaatg ttctcatcaa aaagctgaaa cgaaaaccgc ctagcaccaa cgcaggcaga	960
cgacagaagc accggctcac gtgcccagt tgcgattctt atgagaaaaa gccaccgaaa	1020
gaattcctgc ggcggttcaa gtccctcttg cagaaaatga ttcattcagca tctctccagc	1080
aggacacacg gctccgagga ctcc	1104

<210> 201
 <211> 233
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide Fc2

<400> 201

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

Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
			20					25					30		

Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
		35					40					45			

Val	Val	Ala	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
	50					55					60				

Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65

70

75

80

Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Leu
130 135 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 202
<211> 699
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic polynucleotide, encoding Fc2

<400> 202
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60

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