

<110> HK INNO.N CORPORATION
Y-BIOLOGICS INC.

<120> Anti-OX40L antibody, anti-OX40L and anti-TNFa bispecific
antibody, and uses thereof

<130> P20-099-HKI

<160> 94

<170> KoPatentIn 3.0

<210> 1

<211> 183

<212> PRT

<213> Unknown

<220>

<223> OX40L seq

<400> 1

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

Pro Arg Phe Glu Arg Asn Lys Leu Leu Leu Val Ala Ser Val Ile Gln
20 25 30

Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser
35 40 45

Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val
50 55 60

Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln
65 70 75 80

Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn
85 90 95

Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu
100 105 110

Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln
115 120 125

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

Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu
 145 150 155 160
 Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn
 165 170 175
 Pro Gly Glu Phe Cys Val Leu
 180

<210> 2
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OX40L-his

<400> 2
 His His His His His Gln Val Ser His Arg Tyr Pro Arg Ile Gln
 1 5 10 15
 Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile
 20 25 30
 Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser
 35 40 45
 Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr
 50 55 60
 Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu
 65 70 75 80
 Pro Leu Phe Gln Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val
 85 90 95
 Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp
 100 105 110
 Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu
 115 120 125
 Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu
 130 135

<210> 3

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

<220>
 <223> epitope 93-100

<400> 3
 Val Ile Ile Asn Cys Asp Gly Phe
 1 5

<210> 4
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> epitope 141-151

<400> 4
 Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu
 1 5 10

<210> 5
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1 HC

<400> 5
 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	Asp	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	Asn	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> 6
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1 HC N297A

<400> 6
 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 Asp 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

6

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> 7
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG4 HC

<400> 7
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Glu Ser 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 65	Ser	Ser	Val	Val	Thr 70	Val	Pro	Ser	Ser	Ser 75	Leu	Gly	Thr	Lys	Thr 80
Tyr	Thr	Cys	Asn	Val 85	Asp	His	Lys	Pro	Ser 90	Asn	Thr	Lys	Val	Asp 95	Lys
Arg	Val	Glu	Ser 100	Lys	Tyr	Gly	Pro	Pro 105	Cys	Pro	Ser	Cys	Pro	Ala 110	Pro
Glu	Phe	Leu	Gly 115	Gly	Pro	Ser	Val	Phe 120	Leu	Phe	Pro	Pro 125	Lys	Pro	Lys
Asp 130	Thr	Leu	Met	Ile	Ser	Arg 135	Thr	Pro	Glu	Val	Thr 140	Cys	Val	Val	Val
Asp 145	Val	Ser	Gln	Glu	Asp 150	Pro	Glu	Val	Gln	Phe 155	Asn	Trp	Tyr	Val	Asp 160
Gly	Val	Glu	Val	His 165	Asn	Ala	Lys	Thr	Lys 170	Pro	Arg	Glu	Glu	Gln 175	Phe
Asn	Ser	Thr	Tyr 180	Arg	Val	Val	Ser	Val 185	Leu	Thr	Val	Leu	His 190	Gln	Asp
Trp	Leu	Asn 195	Gly	Lys	Glu	Tyr	Lys 200	Cys	Lys	Val	Ser	Asn 205	Lys	Gly	Leu
Pro 210	Ser	Ser	Ile	Glu	Lys	Thr 215	Ile	Ser	Lys	Ala	Lys 220	Gly	Gln	Pro	Arg
Glu 225	Pro	Gln	Val	Tyr	Thr 230	Leu	Pro	Pro	Ser	Gln 235	Glu	Glu	Met	Thr	Lys 240
Asn	Gln	Val	Ser	Leu 245	Thr	Cys	Leu	Val	Lys 250	Gly	Phe	Tyr	Pro	Ser 255	Asp
Ile	Ala	Val	Glu 260	Trp	Glu	Ser	Asn	Gly 265	Gln	Pro	Glu	Asn 270	Asn	Tyr	Lys
Thr	Thr	Pro 275	Pro	Val	Leu	Asp	Ser 280	Asp	Gly	Ser	Phe	Phe 285	Leu	Tyr	Ser
Arg 290	Leu	Thr	Val	Asp	Lys	Ser 295	Arg	Trp	Gln	Glu	Gly 300	Asn	Val	Phe	Ser
Cys 305	Ser	Val	Met	His 310	Glu	Ala	Leu	His	Asn 315	His	Tyr	Thr	Gln	Lys	Ser 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 8
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4 HC S228P

<400> 8
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15
Ser Thr Ser Glu Ser 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 Lys Thr
65 70 75 80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

<210> 9
 <211> 981
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG4 HC S228P

<400> 9
 gcttccacca agggcccatc cgtcttcccc ctggcgcctt gctccaggag cacctccgag 60
 agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 240
 tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 300

10

aaatatggtc ccccatgccc accatgcccc gcacctgagt tcctgggggg accatcagtc 360
 ttctgtttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 420
 tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 480
 ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 540
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 600
 tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 660
 gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 720
 aaccagggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 780
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 840
 gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg 900
 aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc 960
 ctctccctgt ctctgggtaa a 981

<210> 10
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG LC

<400> 10
 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

11

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> 11
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG LC

<400> 11
cgtacggtgg cggcgccatc tgtcttcac tccccgcat ctgatgagca gttgaaatct 60
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300
agcttcaaca ggggagagtg t 321

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-0X40L antibody VH CDR1

<400> 12
Tyr Ala Trp Met Ser
1 5

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VH CDR1

<400> 13
 Asp Tyr Trp Met His
 1 5

<210> 14
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VH CDR1

<400> 14
 Asn Tyr Trp Met Gln
 1 5

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

<220>
 <223> Anti-OX40L antibody VH CDR2

<400> 15
 Arg Ile Lys Gly Glu Pro Asp Gly Gly Thr Thr Glu Tyr Ala Asp Ser
 1 5 10 15

Val Lys Gly

<210> 16
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VH CDR2

<400> 16
 Glu Ile Asp Pro Pro Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe Lys
 1 5 10 15

Ser

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

<220>
 <223> Anti-OX40L antibody VH CDR2

<400> 17
 Glu Ile Asp Pro Gly Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe Lys
 1 5 10 15

Asn

<210> 18
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VH CDR2

<400> 18
 Glu Ile Asp Pro Ser Asp Gly Arg Thr Asn Tyr Asn Glu Lys Phe Lys
 1 5 10 15

Asn

<210> 19
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Anti-OX40L antibody VH CDR3

<400> 19
Arg Arg Gly Leu Asp Val
1 5

<210> 20
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-OX40L antibody VH CDR3

<400> 20
Gly Ile Tyr Tyr Val Asp Tyr
1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-OX40L antibody VH CDR3

<400> 21
Glu Gly Ala Gly Arg Gly Phe Pro Tyr
1 5

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-OX40L antibody VH CDR3

<400> 22
Glu Val Ser Leu Arg Ser Met Asp Tyr
1 5

<210> 23
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR1

<400> 23
 Arg Ala Ser Gln Ser Ile Gly Arg Trp Leu Ala
 1 5 10

<210> 24
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR1

<400> 24
 Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 1 5 10 15

<210> 25
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR2

<400> 25
 Lys Ala Thr Ile Leu Glu Ser
 1 5

<210> 26
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR2

<400> 26
 Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 27
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR3

<400> 27
 Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
 1 5

<210> 28
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR3

<400> 28
 Ser Gln Ser Thr His Val Pro Pro Thr
 1 5

<210> 29
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-OX40L antibody VL CDR3

<400> 29
 Ser Gln Ser Thr His Val Pro Trp Thr
 1 5

<210> 30
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-0X40L antibody VL CDR3

<400> 30
 Ser Gln Ser Thr His Val Pro Phe Thr
 1 5

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

<220>
 <223> linker 1

<400> 31
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 32
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker 2

<400> 32
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser
 20

<210> 33
 <211> 120

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Oxelumab VH

<400> 33
 Glu Val Gln Leu Leu 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 Thr Phe Asn Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ile Ile Ser Gly Ser Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Arg Leu Val Ala Pro Gly Thr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Ala Leu Val Thr Val Ser Ser
 115 120

<210> 34
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Oxelumab VL

<400> 34
 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 Gly Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
 35 40 45 19
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 35
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humira VH

<400> 35
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60
 Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 36
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humira VL

<400> 36
 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 Gly Ile Arg Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 37
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 02C09 VH

<400> 37
 Gln Met Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Tyr Ala
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Gly Arg Ile Lys Gly Glu Pro Asp Gly Gly Thr Thr Glu Tyr Ala Asp
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Val Ser Arg Arg Gly Leu Asp Val Trp Gly Gln Gly Thr Thr
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 38
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 02C09 VL

<400> 38
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Arg Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Thr Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ser Ala Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 39
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 02C09 VH

<400> 39
 caaatgcagc ttgttcaatc cggcggaggc ctggttaagc ctggcggatc tctgagagtg 60
 tcttgtgccg ccagcggctt caccttcaat tacgcctgga tgagctgggt ccgacaggcc 120
 cctggaaaag gactggaatg ggtcggaaga atcaagggcg agcctgatgg cggaaccaca 180
 gagtacgccg atagcgtgaa gggcagattc accatcagcc gggacaacag caagaacacc 240
 ctgtacctgc agatgaactc cctgagagcc gaggacacag ccgtgtacta ctgtgtgtct 300
 agaagaggcc tggatgtgtg gggccaggga acaacagtga cagtttcttc t 351

<210> 40
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 02C09 VL

<400> 40
 gatatccaga tgacacagag ccctagcagc ctgtctgcct ctctgggcga tagagtgacc 60
 atcacatgtc gggccagcca gtctattgga cggctggctgg cctggtatca gcaaaagcct 120
 ggaaacgccc ctaagctgct gatctacaag gccaccatcc tggaaagcgg agtgccttct 180
 agattttctg gcagcggctc tggcaccgag ttgcccctga caattagctc cctgcagcct 240
 gacgacttca ggcctacta ctgccagcag tacaacagct acccctacac cttcggccag 300
 ggcacaaaagc tggaaatcaa g 321

<210> 41
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu3F07 VH

<400> 41
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Pro Asp Tyr
 20 25 30
 Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Ile Asp Pro Pro Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Ile Tyr Tyr Val Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 42
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu3F07 VL

<400> 42
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser

			20					25		24			30		
Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75					80
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Ser	Gln	Ser
				85					90					95	
Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

[illegible]

<223> hu3F07 VL

<400> 44

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gatatcgtga tgacacagag ccctctgagc ctgcctgtga cactgggaga acctgccagc      60
atcagctgta gaagcagcca gagcctggtg cacagcaacg gcaataccta cctgcactgg      120
tatctgcaga agcccggaca gtctccccag ctgctgatct acaagggtgtc caacagattc      180
agcggcgtgc ccgatagatt ttctggcagc ggctctggca ccgacttcac cctgaagatt      240
agcagagtgg aagccgagga cgtgggcgtg tactactgta gccagtctac ccacgtgcca      300
cctacctttg gcggcggaac aaagctggaa atcaag                                336

```

<210> 45

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> 10H07 VH

<400> 45

```

Gln Val Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1             5             10             15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
      20             25             30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
      35             40             45
Gly Glu Ile Asp Pro Gly Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
      50             55             60
Lys Asn Lys Ala Thr Leu Ser Val Asp Lys Ser Ser Asn Thr Ala Tyr
      65             70             75             80
Met Gln Phe Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Phe Tyr Cys
      85             90             95
Ala Ser Glu Gly Ala Gly Arg Gly Phe Pro Tyr Trp Gly Gln Gly Thr
      100             105             110
Leu Val Thr Val Ser Ala

```

115

<210> 46
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10H07 VL

<400> 46
 Asp Val Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 47
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 10H07 VH

<400> 47
 caggtttatc tacagcagtc tggggctgaa ctggtgaagc ctggggcttc agtgaagctg

60

27

tcctgcaagg cttctggcta caccttcacc gactactgga tgcactgggt gaagcagagg	120
cctggacaag gccttgagtg gattggagag attgacctg gcaacggtcg tactaactac	180
aatgagaagt tcaagaacaa ggccacactg agtgtagaca aatcctccaa tacagcctac	240
atgcaattca gcagcctgac atctgaggac tctgcggtct tttactgtgc aagcgaggga	300
gctggacgtg gatttcctta ctggggccaa gggactctgg tcactgtctc cgca	354

<210> 48
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 10H07 VL

<400> 48	
gatgttgtgc tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc	60
atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg	120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt	180
tctgggggtcc cagacagggtt cagtggcagt ggatcaggga cagatttcac actcaagatc	240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg	300
tggacgttcg gtggaggcac caagctggaa atcaaa	336

<210> 49
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 21G07 VH

<400> 49	
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala	
1 5 10 15	
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	

Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asp Pro Ser Asp Gly Arg Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Asn Lys Ala Thr Leu Thr Val Asp Arg Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Ile Lys Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Val Ser Leu Arg Ser Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Ser Val Thr Val Ser Ser
 115

<210> 50
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 21G07 VL

<400> 50
 Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys

100

105

110

<210> 51
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 21G07 VH

<400> 51
 caggtccaac tgcagcagtc tggggctgaa ctggtgaagc ctggggcttc agtgaagctg 60
 tcctgcaagg cttctggcta caccttcacc aactactgga tgcaatgggt gaaacagagg 120
 cccggacaag gccttgagtg gattggagag attgatacta gcgacggctg tactaactac 180
 aatgagaagt tcaagaacaa ggccacactg actgtagaca gatcctccag cacagcctac 240
 ataaaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aagagaggtt 300
 tcactacggt caatggacta ctggggccaa gggacctcag tcaccgtctc ctca 354

<210> 52
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 21G07 VL

<400> 52
 gacattgttc tcacccagtc tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
 atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
 tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
 tctgggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttcca 300
 ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 53
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> I3F07 VH

<400> 53
 Gln Ile Gln Leu Ala Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Thr Phe Pro Asp Tyr
 20 25 30
 Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asp Pro Pro Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Ser Lys Ala Thr Leu Thr Val Asp Ser Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Ile Tyr Tyr Val Asp Tyr Trp Gly Gln Gly Thr Thr Leu
 100 105 110
 Thr Val Ser Ser
 115

<210> 54
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> I3F07 VL

<400> 54
 Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Pro Thr Phe Gly Gly Gly Ser Lys Leu Glu Ile Lys
 100 105 110

<210> 55
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> I3F07 VH

<400> 55
 cagattcagc tggctcagtc tggcgccgaa cttgtgaaac ctggcgcctc tgtgaagctg 60
 agctgcaagg ccagcggctt cacctttcct gactactgga tgcactgggt caagcagagg 120
 cctggacagg gactcgaatg gatcggcgag atcgatcctc ctaacggccg gaccaactac 180
 aacgagaagt tcaagagcaa ggccacactg accgtggaca gcagcagcaa taccgcctac 240
 atgcagctga gcagactgac ctctgaggac agcgccgtgt actactgtgc cagaggcatc 300
 tactacgtgg actactgggg ccagggcaca accctgacag tttcttct 348

<210> 56
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>

<223> I3F07 VL

<400> 56

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gatatcgtgc tgacacagag ccctctgagc ctgcctgttt ctctgggaga tcaggccagc      60
atcagctgca gataccttca gagcctggtg cacagcaacg gcaataccta cctgcactgg      120
tatctgcaga agcccggcca gtctcctaag ctgctgatct acaagggtgtc caacaggttc      180
agcggcgtgc ccgatagatt ttctggctct ggagcgggca ccgacttcac cctgaagatt      240
tctagagtgg aagccgagga cctgggctgt tacttctgtt ctacgtctac ccacgtgcca      300
cctacctttg gcggcggaag caagctggaa atcaag                                336

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<210> 57

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> 02C09-TNFai HC heavy chain

<400> 57

```

Gln Met Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1             5             10             15
Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Tyr Ala
      20             25             30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35             40             45
Gly Arg Ile Lys Gly Glu Pro Asp Gly Gly Thr Thr Glu Tyr Ala Asp
      50             55             60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
      65             70             75             80
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
      85             90             95
Tyr Cys Val Ser Arg Arg Gly Leu Asp Val Trp Gly Gln Gly Thr Thr
      100            105            110

```

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

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
 405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly
 435 440 445

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
 450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
 465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val
 485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp
 500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr
 515 520 525

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
 530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr
 545 550 555 560

Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
 565 570 575

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 580 585 590

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
 595 600 605

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 610 615 620

Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

625										35							
					630					635						640	
Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Thr	Leu	Gln	Ser		
				645					650					655			
Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
			660					665					670				
Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys		
		675					680					685					
Gln	Arg	Tyr	Asn	Arg	Ala	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val		
	690					695					700						
Glu	Ile	Lys															
705																	

<210> 58
 <211> 2121
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 02C09-TNFai HC heavy chain

<400> 58	
caaatgcagc ttgttcaatc cggcggaggc ctggttaagc ctggcggatc tctgagagtg	60
tcttgtgccg ccagcggctt caccttcaat tacgcctgga tgagctgggt ccgacaggcc	120
cctggaaaag gactggaatg ggtcgggaaga atcaagggcg agcctgatgg cggaaccaca	180
gagtacgccg atagcgtgaa gggcagattc accatcagcc gggacaacag caagaacacc	240
ctgtacctgc agatgaactc cctgagagcc gaggacacag ccgtgtacta ctgtgtgtct	300
agaagaggcc tggatgtgtg gggccaggga acaacagtga cagtttcttc tgcttcacc	360
aaggggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc	420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc	600
aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt	660

cccccatgcc caccatgccc agcacctgag ttcttggggg gaccatcagt cttcctgttc	720
cccccaaac ccaaggacac tctcatgac tcccggaccc ctgaggtcac gtgcgtggtg	780
gtggacgtga gccaggaaga ccccgaggtc cagttcaact ggtacgtgga tggcgtggag	840
gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc	900
agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc	960
tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc	1020
cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc	1080
agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc	1140
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc	1200
ttcttctctt acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc	1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg	1320
tctctgggta aaggtggtgg cggatctggc ggcgaggagaa gcggaggcgg aggctccgaa	1380
gtgcaactgg ttgaatctgg cggaggactg gtgcagcctg gaagaagcct gagactgtct	1440
tgtgccgcca gcggcttcac cttcgatgat tatgccatgc actgggtccg acaggcccct	1500
ggaaaaggac ttgaatgggt gtccgccatc acctggaaca gcggccacat cgattacgcc	1560
gatagcgtgg aaggccggtt caccatcagc agagacaacg ccaagaacag cctgtacctg	1620
cagatgaact ccctgagagc cgaggacacc gccgtgtact actgtgccaa agtgtcttac	1680
ctgagcaccg cctccagcct ggattattgg ggacagggca cactggtcac agtgtcctct	1740
ggtggcggag gttctggcgg aggtggtagt ggtggcggtg gaagtgggtg cggcggatct	1800
gatatccaga tgacacagag ccctagcagc ctgtctgcct ctgtgggcga tagagtgacc	1860
atcacctgta gagccagcca gggcatcaga aactacctgg cctggtatca gcagaagccc	1920
ggaaaggccc ctaagctgct gatctatgcc gcctctacac tgcagagcgg cgtgccatct	1980
agatcttctg gcagcggctc tggcaccgac ttaccctga caatttctag cctgcagcct	2040
gaggacgtgg ccacctacta ctgccagaga tacaacagag ccccttacac cttcggccag	2100

ggcaccaagg tggaatcaa g

2121

<210> 59
 <211> 477
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 02C09-TNFai LC light chain

<400> 59
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Arg Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Thr Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ser Ala Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu 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
 145 150 155 160
 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 210 215 220

Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 225 230 235 240

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 245 250 255

Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
 260 265 270

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

Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 290 295 300

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 305 310 315 320

Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser
 325 330 335

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 340 345 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 370 375 380

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg
 385 390 395 400

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 405 410 415

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

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
 435 440 445

Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala

450

455

460

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 465 470 475

<210> 60
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 02C09-TNFai LC light chain

<400> 60
 gatatccaga tgacacagag ccctagcagc ctgtctgcct ctctgggcga tagagtgacc 60
 atcacatgtc gggccagcca gtctattgga cgggtggctgg cctgggtatca gcaaaagcct 120
 ggaaacgccc ctaagctgct gatctacaag gccaccatcc tggaaagcgg agtgccttct 180
 agattttctg gcagcggctc tggcaccgag tttgccctga caattagctc cctgcagcct 240
 gacgacttca ggcctacta ctgccagcag tacaacagct acccctacac cttcggccag 300
 ggcacaaagc tggaaatcaa gcgtacggtg gcggcgccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtggtggtgg cggatctggc 660
 ggcggaggaa gcggaggcgg aggctccgaa gtgcaactgg ttgaatctgg cggaggactg 720
 gtgcagcctg gaagaagcct gagactgtct tgtgccgcca gcggcttcac cttcgatgat 780
 tatgccatgc actgggtccg acaggcccct ggaaaaggac ttgaatgggt gtccgccatc 840
 acctggaaca gcggccacat cgattacgcc gatagcgtgg aaggccggtt caccatcagc 900
 agagacaacg ccaagaacag cctgtacctg cagatgaact ccctgagagc cgaggacacc 960
 gccgtgtact actgtgccaa agtgtcttac ctgagcaccg cctccagcct ggattattgg 1020

ggacagggca cactgggtcac agtgtcctct ggtggcggag gttctggcgg aggtggtagt 1080
 ggtggcgggtg gaagtgggtg cggcggatct gatatccaga tgacacagag ccctagcagc 1140
 ctgtctgcct ctgtgggcga tagagtgacc atcacctgta gagccagcca gggcatcaga 1200
 aactacctgg cctggtatca gcagaagccc ggaaaggccc ctaagctgct gatctatgcc 1260
 gcctctacac tgcagagcgg cgtgccatct agattttctg gcagcggctc tggcaccgac 1320
 ttcaccctga caatttctag cctgcagcct gaggacgtgg ccacctacta ctgccagaga 1380
 tacaacagag ccccttacac cttcggccag ggcaccaagg tggaaatcaa g 1431

<210> 61
 <211> 706
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu3F07-TNFai HC heavy chain

<400> 61
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Pro Asp Tyr
 20 25 30
 Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Ile Asp Pro Pro Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Ile Tyr Tyr Val Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125

Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu
	130					135					140				
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
145					150					155					160
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
				165					170					175	
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
			180					185					190		
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr
		195					200					205			
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro
	210					215					220				
Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
225					230					235					240
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				245					250					255	
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn
			260					265					270		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
		275				280						285			
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
	290					295					300				
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
305					310					315					320
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
				325					330					335	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
			340					345					350		
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
		355					360					365			
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	370					375					380				

42

Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	385		390		395		400
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly		405		410		415	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr		420		425		430	
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gly	Gly	Gly	Gly	Ser		435		440		445	
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu		450		455		460	
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	465		470		475		480
Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala	Met	His	Trp	Val	Arg		485		490		495	
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ala	Ile	Thr	Trp	Asn		500		505		510	
Ser	Gly	His	Ile	Asp	Tyr	Ala	Asp	Ser	Val	Glu	Gly	Arg	Phe	Thr	Ile		515		520		525	
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	530		535		540		
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Val	Ser	Tyr	Leu	545		550		555		560
Ser	Thr	Ala	Ser	Ser	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr		565		570		575	
Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly		580		585		590	
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser		595		600		605	
Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	610		615		620		
Ser	Gln	Gly	Ile	Arg	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	625		630		635		640
Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Thr	Leu	Gln	Ser	Gly							

43 645 650 655															
Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu
			660				665				670				
Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln
			675				680				685				
Arg	Tyr	Asn	Arg	Ala	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu
		690				695				700					
Ile	Lys														
705															

ccaaaaccca	aggacactct	catgatctcc	cggacccttg	aggtcacgtg	cgtggtggtg	780
gacgtgagcc	aggaagaccc	cgaggtccag	ttcaactggt	acgtggatgg	cgtggaggtg	840
cataatgcca	agacaaagcc	gcgggaggag	cagttcaaca	gcacgtaccg	tgtggtcagc	900
gtcctcaccg	tcctgcacca	ggactggctg	aacggcaagg	agtacaagtg	caaggtctcc	960
aacaaaggcc	tcccgtcctc	catcgagaaa	accatctcca	aagccaaagg	gcagccccga	1020
gagccacagg	tgtacaccct	gccccatcc	caggaggaga	tgaccaagaa	ccaggtcagc	1080
ctgacctgcc	tgggtcaaagg	cttctacccc	agcgacatcg	ccgtggagtg	ggagagcaat	1140
gggcagccgg	agaacaacta	caagaccacg	cctcccgtgc	tggactccga	cggctccttc	1200
ttcctctaca	gcaggctaac	cgtggacaag	agcaggtggc	aggaggggaa	tgtcttctca	1260
tgctccgtga	tgcatgaggc	tctgcacaac	cactacacac	agaagagcct	ctccctgtct	1320
ctgggtaaag	gtggtggcgg	atctggcggc	ggaggaagcg	gaggcggagg	ctccgaagtg	1380
caactggttg	aatctggcgg	aggactggtg	cagcctggaa	gaagcctgag	actgtcttgt	1440
gccgccagcg	gcttcacctt	cgatgattat	gccatgcact	gggtccgaca	ggccccctgga	1500
aaaggacttg	aatgggtgtc	cgccatcacc	tggaacagcg	gccacatcga	ttacgccgat	1560
agcgtggaag	gccggttcac	catcagcaga	gacaacgcca	agaacagcct	gtacctgcag	1620
atgaactccc	tgagagccga	ggacaccgcc	gtgtactact	gtgccaaagt	gtcttacctg	1680
agcaccgcct	ccagcctgga	ttattgggga	cagggcacac	tggtcacagt	gtcctctggt	1740
ggcggagggtt	ctggcggagg	tggtagtggg	ggcgggtggaa	gtggtggcgg	cggatctgat	1800
atccagatga	cacagagccc	tagcagcctg	tctgcctctg	tgggcgatag	agtgaccatc	1860
acctgtagag	ccagccaggg	catcagaaac	tacctggcct	ggtatcagca	gaagcccgga	1920
aaggccccta	agctgctgat	ctatgccgcc	tctacactgc	agagcggcgt	gccatctaga	1980
ttttctggca	gcggctctgg	caccgacttc	accctgacaa	tttctagcct	gcagcctgag	2040
gacgtggcca	cctactactg	ccagagatac	aacagagccc	cttacacctt	cggccagggc	2100
accaaggtgg	aaatcaag					2118

<210> 63
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hu3F07-TNFai LC light chain

<400> 63
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205

46

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

465		47	
	470	475	480

Ile Lys

<210> 64
 <211> 1446
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hu3F07-TNFai LC light chain

<400> 64
 gatatcgtga tgacacagag ccctctgagc ctgcctgtga cactgggaga acctgccagc 60
 atcagctgta gaagcagcca gagcctggtg cacagcaacg gcaataccta cctgcactgg 120
 tatctgcaga agcccggaca gtctccccag ctgctgatct acaaggtgtc caacagattc 180
 agcggcggtgc ccgatagatt ttctggcagc ggctctggca ccgacttcac cctgaagatt 240
 agcagagtgg aagccgagga cgtgggcgtg tactactgta gccagtctac ccacgtgcca 300
 cctacctttg gcggcggaac aaagctggaa atcaagcgta cgggtggcggc gccatctgtc 360
 ttcattcttc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480
 tcgggtaact ccagggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540
 agcagcacc ctgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
 gtcacccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgtggt 660
 ggtggcggat ctggcggcgg aggaagcgga ggcgaggct ccgaagtgca actggttgaa 720
 tctggcggag gactggtgca gcctggaaga agcctgagac tgtcttgtgc cgccagcggc 780
 ttcaccttcg atgattatgc catgcactgg gtccgacagg cccctggaaa aggacttgaa 840
 tgggtgtccg ccatcacctg gaacagcggc cacatcgatt acgccgatag cgtggaaggc 900
 cggttcacca tcagcagaga caacgccaaag aacagcctgt acctgcagat gaactccctg 960
 agagccgagg acaccgccgt gtactactgt gccaaagtgt cttacctgag caccgcctcc 1020

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agcctggatt attggggaca gggcacactg gtcacagtgt cctctggtgg cggaggttct      1080
ggcggagggtg gtagtggtgg cggtggaagt ggtggcggcg gatctgatat ccagatgaca      1140
cagagcccta gcagcctgtc tgcctctgtg ggcgatagag tgaccatcac ctgtagagcc      1200
agccagggca tcagaaacta cctggcctgg tatcagcaga agcccggaaa ggcccctaag      1260
ctgctgatct atgccgcctc tacactgcag agcggcgtgc catctagatt ttctggcagc      1320
ggctctggca ccgacttcac cctgacaatt tctagcctgc agcctgagga cgtggccacc      1380
tactactgcc agagatacaa cagagcccct tacaccttcg gccagggcac caaggtggaa      1440
atcaag                                                                1446

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<210>      65
<211>      707
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      TNFai-02C09 HC heavy chain

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<400>      65
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1              5              10              15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20              25              30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35              40              45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
          50              55              60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
          65              70              75              80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85              90              95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
          100             105             110

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Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

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

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser

370					375					50		380				
Asn 385	Gly	Gln	Pro	Glu	Asn 390	Asn	Tyr	Lys	Thr	Thr 395	Pro	Pro	Val	Leu	Asp 400	
Ser	Asp	Gly	Ser	Phe 405	Phe	Leu	Tyr	Ser	Arg 410	Leu	Thr	Val	Asp	Lys 415	Ser	
Arg	Trp	Gln	Glu 420	Gly	Asn	Val	Phe	Ser 425	Cys	Ser	Val	Met	His 430	Glu	Ala	
Leu	His	Asn 435	His	Tyr	Thr	Gln	Lys 440	Ser	Leu	Ser	Leu	Ser 445	Leu	Gly	Lys	
Gly	Gly 450	Gly	Gly	Ser	Gly	Gly 455	Gly	Gly	Ser	Gly	Gly 460	Gly	Gly	Ser	Gln	
Met 465	Gln	Leu	Val	Gln 470	Ser	Gly	Gly	Gly	Leu	Val 475	Lys	Pro	Gly	Gly	Ser 480	
Leu	Arg	Val	Ser	Cys 485	Ala	Ala	Ser	Gly	Phe 490	Thr	Phe	Asn	Tyr	Ala 495	Trp	
Met	Ser	Trp	Val 500	Arg	Gln	Ala	Pro	Gly 505	Lys	Gly	Leu	Glu	Trp 510	Val	Gly	
Arg	Ile	Lys 515	Gly	Glu	Pro	Asp	Gly 520	Gly	Thr	Thr	Glu	Tyr 525	Ala	Asp	Ser	
Val	Lys 530	Gly	Arg	Phe	Thr	Ile 535	Ser	Arg	Asp	Asn	Ser 540	Lys	Asn	Thr	Leu	
Tyr 545	Leu	Gln	Met	Asn 550	Ser	Leu	Arg	Ala	Glu	Asp 555	Thr	Ala	Val	Tyr	Tyr 560	
Cys	Val	Ser	Arg	Arg 565	Gly	Leu	Asp	Val	Trp 570	Gly	Gln	Gly	Thr	Thr 575	Val	
Thr	Val	Ser	Ser 580	Gly	Gly	Gly	Gly	Ser 585	Gly	Gly	Gly	Gly	Ser 590	Gly	Gly	
Gly	Gly	Ser 595	Gly	Gly	Gly	Gly	Ser 600	Asp	Ile	Gln	Met	Thr 605	Gln	Ser	Pro	
Ser	Ser 610	Leu	Ser	Ala	Ser	Leu 615	Gly	Asp	Arg	Val	Thr 620	Ile	Thr	Cys	Arg	
Ala 625	Ser	Gln	Ser	Ile	Gly 630	Arg	Trp	Leu	Ala	Trp 635	Tyr	Gln	Gln	Lys	Pro 640	

Gly Asn Ala Pro Lys Leu Leu Ile Tyr Lys Ala Thr Ile Leu Glu Ser
 645 650 655

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Ala
 660 665 670

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ser Ala Tyr Tyr Cys
 675 680 685

Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu
 690 695 700

Glu Ile Lys
 705

<210> 66
 <211> 2121
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TNFai-02C09 HC heavy chain

<400> 66
 gaagtgaac tggttgaatc tggcggagga ctggtgcagc ctggaagaag cctgagactg 60
 tcttgtgccg ccagcggctt caccttcgat gattatgcc a tgcactgggt ccgacaggcc 120
 cctggaaaag gacttgaatg ggtgtccgcc atcacctgga acagcggcca catcgattac 180
 gccgatagcg tggaaggccg gttcaccatc agcagagaca acgccaagaa cagcctgtac 240
 ctgcagatga actccctgag agccgaggac accgccgtgt actactgtgc caaagtgtct 300
 tacctgagca ccgcctccag cctggattat tggggacagg gcacactgggt cacagtgtcc 360
 tctgcttcca ccaagggccc atccgtcttc cccctggcgc cctgctccag gagcacctcc 420
 gagagcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacgaag 600
 acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gagagttgag 660

tccaaatatg gtcccccatg cccaccatgc ccagcacctg agttcctggg gggaccatca	720
gtcttcctgt tcccccaaa acccaaggac acttcatga tctcccgac ccctgaggtc	780
acgtgcgtgg tgggtggacgt gagccaggaa gaccccgagg tccagttcaa ctggtacgtg	840
gatggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagtt caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaacgg caaggagtac	960
aagtgcaagg tctccaacaa aggcctcccg tcctccatcg agaaaacat ctccaaagcc	1020
aaagggcagc cccgagagcc acaggtgtac accctgcccc catcccagga ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttcct ctacagcagg ctaaccgtgg acaagagcag gtggcaggag	1260
gggaatgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag	1320
agcctctccc tgtctctggg taaaggtggt ggcgatctg gcggcggagg aagcggaggc	1380
ggaggatccc aaatgcagct tgttcaatcc ggcgagggcc tggttaagcc tggcgatct	1440
ctgagagtgt cttgtgccgc cagcggcttc accttcaatt acgcctggat gagctgggtc	1500
cgacaggccc ctggaaaagg actggaatgg gtcggaagaa tcaagggcga gcctgatggc	1560
ggaaccacag agtacgccga tagcgtgaag ggcagattca ccatcagccg ggacaacagc	1620
aagaacaccc tgtacctgca gatgaactcc ctgagagccg aggacacagc cgtgtactac	1680
tgtgtgtcta gaagaggcct ggatgtgtgg ggccaggga caacagtac agtttcttct	1740
ggtggcggag gttctggcgg aggtggtagt ggtggcggtg gaagtgggtg cggcgatct	1800
gatatccaga tgacacagag ccctagcagc ctgtctgcct ctctgggcga tagagtgacc	1860
atcacatgtc gggccagcca gtctattgga cgggtggctgg cctggtatca gcaaaagcct	1920
ggaaacgccc ctaagctgct gatctacaag gccaccatcc tggaaagcgg agtgccttct	1980
agattttctg gcagcggctc tggcaccgag tttgccctga caattagctc cctgcagcct	2040
gacgacttca ggcctacta ctgccagcag tacaacagct acccctacac cttcggccag	2100
ggcacaaaagc tggaaatcaa g	2121

<210> 67
 <211> 473
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TNFai-02C09 LC light chain

<400> 67
 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 Gly Ile Arg Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro 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
 145 150 155 160
 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	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
210						215					220				
Gly	Gly	Gly	Gly	Ser	Gln	Met	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu
225					230					235					240
Val	Lys	Pro	Gly	Gly	Ser	Leu	Arg	Val	Ser	Cys	Ala	Ala	Ser	Gly	Phe
				245					250					255	
Thr	Phe	Asn	Tyr	Ala	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys
			260					265					270		
Gly	Leu	Glu	Trp	Val	Gly	Arg	Ile	Lys	Gly	Glu	Pro	Asp	Gly	Gly	Thr
		275					280					285			
Thr	Glu	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp
	290					295					300				
Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu
305					310					315					320
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val	Ser	Arg	Arg	Gly	Leu	Asp	Val	Trp
				325					330					335	
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly
			340					345					350		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile
		355					360					365			
Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg
	370					375					380				
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Arg	Trp	Leu	Ala
385					390					395					400
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Asn	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Lys
				405					410					415	
Ala	Thr	Ile	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly
			420					425					430		
Ser	Gly	Thr	Glu	Phe	Ala	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp	Asp
		435					440					445			
Phe	Ser	Ala	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Tyr	Thr	Phe
	450					455					460				

Gly Gln Gly Thr Lys Leu Glu Ile Lys
465 470

<210> 68
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> TNFai-02C09 LC light chain

<400> 68
gatatccaga tgacacagag ccctagcagc ctgtctgcct ctgtgggcga tagagtgacc 60
atcacctgta gagccagcca gggcatcaga aactacctgg cctggtatca gcagaagccc 120
ggaaaggccc ctaagctgct gatctatgcc gcctctacac tgcagagcgg cgtgccatct 180
agatcttctg gcagcggctc tggcaccgac ttcaccctga caatttctag cctgcagcct 240
gaggacgtgg ccacctacta ctgccagaga tacaacagag ccccttacac cttcggccag 300
ggcaccaagg tggaatcaa gcgtacggtg gcggcgccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtggtggtgg cggatctggc 660
ggcggaggaa gcggaggcgg aggatcccaa atgcagcttg ttcaatccgg cggaggcctg 720
gttaagcctg gcggatctct gagagtgtct tgtgccgcca gcggcttcac cttcaattac 780
gcctggatga gctgggtccg acaggcccct ggaaaaggac tggaatgggt cggaagaatc 840
aagggcgagc ctgatggcgg aaccacagag tacgccgata gcgtgaaggg cagattcacc 900
atcagccggg acaacagcaa gaacaccctg tacctgcaga tgaactccct gagagccgag 960
gacacagccg tgtactactg tgtgtctaga agaggcctgg atgtgtgggg ccagggaaca 1020

acagtgcacag tttcttctgg tggcggaggt tctggcggag gtggtagtgg tggcgggtgga 1080
 agtgggtggcg gcggatctga tatccagatg acacagagcc ctagcagcct gtctgcctct 1140
 ctgggcgata gagtgaccat cacatgtcgg gccagccagt ctattggacg gtggctggcc 1200
 tgggtatcagc aaaagcctgg aaacgccctt aagctgctga tctacaaggc caccatcctg 1260
 gaaagcggag tgccttctag attttctggc agcggctctg gcaccgagtt tgccttgaca 1320
 attagctccc tgcagcctga cgacttcagc gcctactact gccagcagta caacagctac 1380
 ccctacacct tcggccaggg cacaaagctg gaaatcaag 1419

<210> 69
 <211> 711
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> TNFai-hu3F07 HC heavy chain

<400> 69
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60
 Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140 57
 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220
 Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270
 Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp

385																390																58 395																400															
Ser	Asp	Gly	Ser	Phe 405		Phe	Leu	Tyr	Ser	Arg 410	Leu	Thr	Val	Asp	Lys 415	Ser																																															
Arg	Trp	Gln	Glu 420	Gly	Asn	Val	Phe	Ser 425	Cys	Ser	Val	Met	His 430	Glu	Ala																																																
Leu	His	Asn 435	His	Tyr	Thr	Gln	Lys 440	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys																																																
Gly	Gly 450	Gly	Gly	Ser	Gly	Gly 455	Gly	Gly	Ser	Gly	Gly 460	Gly	Gly	Ser	Gln																																																
Val 465	Gln	Leu	Val	Gln	Ser 470	Gly	Ala	Glu	Val	Lys 475	Lys	Pro	Gly	Ala	Ser																																																
Val	Lys	Val	Ser	Cys 485	Lys	Ala	Ser	Gly	Phe 490	Thr	Phe	Pro	Asp	Tyr 495	Trp																																																
Met	His	Trp	Val 500	Arg	Gln	Ala	Pro	Gly 505	Gln	Gly	Leu	Glu	Trp 510	Met	Gly																																																
Glu	Ile	Asp 515	Pro	Pro	Asn	Gly	Arg 520	Thr	Asn	Tyr	Asn	Glu 525	Lys	Phe	Lys																																																
Ser	Arg 530	Val	Thr	Met	Thr	Arg 535	Asp	Thr	Ser	Ile	Ser 540	Thr	Ala	Tyr	Met																																																
Glu 545	Leu	Ser	Arg	Leu	Arg 550	Ser	Asp	Asp	Thr	Ala 555	Val	Tyr	Tyr	Cys	Ala 560																																																
Arg	Gly	Ile	Tyr	Tyr 565	Val	Asp	Tyr	Trp	Gly 570	Gln	Gly	Thr	Thr	Val 575	Thr																																																
Val	Ser	Ser	Gly 580	Gly	Gly	Gly	Ser	Gly 585	Gly	Gly	Gly	Ser	Gly 590	Gly	Gly																																																
Gly	Ser	Gly 595	Gly	Gly	Gly	Ser	Asp 600	Ile	Val	Met	Thr	Gln 605	Ser	Pro	Leu																																																
Ser	Leu 610	Pro	Val	Thr	Leu	Gly 615	Glu	Pro	Ala	Ser	Ile 620	Ser	Cys	Arg	Ser																																																
Ser 625	Gln	Ser	Leu	Val	His 630	Ser	Asn	Gly	Asn	Thr 635	Tyr	Leu	His	Trp	Tyr 640																																																
Leu	Gln	Lys	Pro	Gly 645	Gln	Ser	Pro	Gln	Leu 650	Leu	Ile	Tyr	Lys	Val 655	Ser																																																

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
 660 665 670

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
 675 680 685

Val Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Pro Thr Phe Gly Gly
 690 695 700

Gly Thr Lys Leu Glu Ile Lys
 705 710

<210> 70
 <211> 2133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TNFai-hu3F07 HC heavy chain

<400> 70
 gaagtgaac tggttgaatc tggcggagga ctggtgcagc ctggaagaag cctgagactg 60
 tcttgtgccg ccagcggcctt caccttcgat gattatgcc a tgcaactgggt ccgacaggcc 120
 cctggaaaag gacttgaatg ggtgtccgcc atcacctgga acagcggcca catcgattac 180
 gccgatagcg tggaaggccg gttcaccatc agcagagaca acgccaagaa cagcctgtac 240
 ctgcagatga actccctgag agccgaggac accgccgtgt actactgtgc caaagtgtct 300
 tacctgagca ccgcctccag cctggattat tggggacagg gcacactgggt cacagtgtcc 360
 tctgcttcca ccaagggccc atccgtcttc cccctggcgc cctgctccag gagcacctcc 420
 gagagcacag ccgccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacgaag 600
 acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gagagttgag 660
 tccaaatatg gtcccccatg cccaccatgc ccagcacctg agttcctggg gggaccatca 720
 gtcttcctgt tcccccaaaa acccaaggac acttctcatga tctcccgga c cctgaggtc 780

acgtgcgtgg	tggtggacgt	gagccaggaa	gaccccagg	tccagttcaa	ctggtacgtg	840
gatggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg	aggagcagtt	caacagcacg	900
taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaacgg	caaggagtac	960
aagtgcaagg	tctccaacaa	aggcctcccg	tcctccatcg	agaaaacat	ctccaaagcc	1020
aaagggcagc	cccgagagcc	acaggtgtac	accctgcccc	catcccagga	ggagatgacc	1080
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	accccagcga	catcgccgtg	1140
gagtgggaga	gcaatgggca	gccggagaa	aactacaaga	ccacgcctcc	cgtgctggac	1200
tccgacggct	ccttcttcct	ctacagcagg	ctaaccgtgg	acaagagcag	gtggcaggag	1260
gggaatgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacacagaag	1320
agcctctccc	tgtctctggg	taaaggtggt	ggcggatctg	gcggcggagg	aagcggaggc	1380
ggaggatccc	aagttcaact	ggttcagtct	ggcgccgaag	tgaagaaacc	aggcgccagc	1440
gtgaaggtgt	cctgcaaggc	ctctggcttc	acattccccg	actactggat	gcactgggtt	1500
cgacaggctc	caggacaggg	actcgaatgg	atgggcgaga	tcgatcctcc	taacggccgg	1560
accaactaca	acgagaagtt	caagagcaga	gtgaccatga	ccagagacac	cagcatcagc	1620
accgcctaca	tggaactgag	cagactgaga	agcgacgaca	ccgccgtgta	ctactgtgcc	1680
agaggcatct	actacgtgga	ctactggggc	cagggcacca	cagtgcagct	tagctctggt	1740
ggcggagggtt	ctggcggagg	tggtagtgg	ggcgggtgaa	gtggtggcgg	cggatctgat	1800
atcgtgatga	cacagagccc	tctgagcctg	cctgtgacac	tgggagaacc	tgccagcatc	1860
agctgtagaa	gcagccagag	cctggtgcac	agcaacggca	atacctacct	gcactggtat	1920
ctgcagaagc	ccggacagtc	tccccagctg	ctgatctaca	aggtgtccaa	cagattcagc	1980
ggcgtgcccc	atagattttc	tggcagcggc	tctggcaccg	acttcaccct	gaagattagc	2040
agagtggaag	ccgaggacgt	gggcgtgtac	tactgtagcc	agtctaccca	cgtgccacct	2100
acctttggcg	gcggaacaaa	gctggaaatc	aag			2133

<211> 477
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TNFai- hu3F07 LC light chain

<400> 71
 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 Gly Ile Arg Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro 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
 145 150 155 160
 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

										62					
	210					215				220					
Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val
225					230					235					240
Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe
				245					250					255	
Thr	Phe	Pro	Asp	Tyr	Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln
			260					265					270		
Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Pro	Asn	Gly	Arg	Thr	Asn
		275					280					285			
Tyr	Asn	Glu	Lys	Phe	Lys	Ser	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser
	290					295					300				
Ile	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr
305					310					315					320
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Ile	Tyr	Tyr	Val	Asp	Tyr	Trp	Gly
				325					330					335	
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			340					345					350		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val
		355					360					365			
Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly	Glu	Pro	Ala
	370					375					380				
Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn
385					390					395					400
Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu
				405				410						415	
Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe
			420					425					430		
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val
		435					440					445			
Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	His	Val
	450					455					460				
Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys			
465					470					475					

<210> 72
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TNFai- hu3F07 LC light chain

<400> 72
 gatatccaga tgacacagag ccctagcagc ctgtctgcct ctgtgggcga tagagtgacc 60
 atcacctgta gagccagcca gggcatcaga aactacctgg cctgggtatca gcagaagccc 120
 ggaaaggccc ctaagctgct gatctatgcc gcctctacac tgcagagcgg cgtgccatct 180
 agatcttctg gcagcggctc tggcaccgac ttcaccctga caatttctag cctgcagcct 240
 gaggacgtgg ccacctacta ctgccagaga tacaacagag ccccttacac cttcggccag 300
 ggcaccaagg tggaatcaa gcgtacggtg gcggcgccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtggtggtgg cggatctggc 660
 ggcggaggaa gcggaggcgg aggatcccaa gttcaactgg ttcagtctgg cgccgaagtg 720
 aagaaaccag gcgccagcgt gaaggtgtcc tgcaaggcct ctggcttcac attccccgac 780
 tactggatgc actgggttcg acaggctcca ggacagggac tcgaatggat gggcgagatc 840
 gatcctccta acggccggac caactacaac gagaagttca agagcagagt gaccatgacc 900
 agagacacca gcatcagcac cgcctacatg gaactgagca gactgagaag cgacgacacc 960
 gccgtgtact actgtgccag aggcatctac tacgtggact actggggcca gggcaccaca 1020
 gtgacagtta gctctggtgg cggaggttct ggcggagggtg gtagtggtgg cgggtggaagt 1080
 ggtggcggcg gatctgatat cgtgatgaca cagagccctc tgagcctgcc tgtgacactg 1140

```

ggagaacctg ccagcatcag ctgtagaagc agccagagcc tgggtgcacag caacggcaat      1200
acctacctgc actggtatct gcagaagccc ggacagtctc cccagctgct gatctacaag      1260
gtgtccaaca gattcagcgg cgtgcccgat agattttctg gcagcggctc tggcaccgac      1320
ttcacctga agattagcag agtgggaagcc gaggacgtgg gcgtgtacta ctgtagccag      1380
tctaccacg tgccacctac ctttggcggc ggaacaaagc tggaaatcaa g                  1431

```

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<210>      73
<211>      706
<212>      PRT
<213>      Artificial Sequence

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<220>
<223>      I3F07-TNFai HC heavy chain

```

```

<400>      73
Gln Ile Gln Leu Ala Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1              5              10              15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Thr Phe Pro Asp Tyr
      20              25              30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
      35              40              45
Gly Glu Ile Asp Pro Pro Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
      50              55              60
Lys Ser Lys Ala Thr Leu Thr Val Asp Ser Ser Ser Asn Thr Ala Tyr
      65              70              75              80
Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
      85              90              95
Ala Arg Gly Ile Tyr Tyr Val Asp Tyr Trp Gly Gln Gly Thr Thr Leu
      100             105             110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
      115             120             125
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
      130             135             140

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										65									
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly				
145					150					155					160				
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser				
				165					170					175					
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu				
			180					185					190						
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr				
		195					200					205							
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro				
	210					215					220								
Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro				
225					230					235					240				
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr				
				245					250					255					
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn				
			260					265					270						
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg				
		275					280					285							
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val				
	290					295					300								
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser				
305					310					315					320				
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys				
				325					330					335					
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu				
			340					345					350						
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe				
		355					360					365							
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu				
	370					375					380								
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe				
385					390					395					400				
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly				

66

405	410	415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
420	425	430
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser		
435	440	445
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu		
450	455	460
Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys		
465	470	475
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg		
485	490	495
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn		
500	505	510
Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile		
515	520	525
Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu		
530	535	540
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu		
545	550	555
Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr		
565	570	575
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly		
580	585	590
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser		
595	600	605
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala		
610	615	620
Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly		
625	630	635
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly		
645	650	655
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu		
660	665	670

Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln
 675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
 690 695 700

Ile Lys
 705

<210> 74
 <211> 2118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> I3F07-TNFai HC heavy chain

<400> 74
 cagattcagc tggctcagtc tggcgccgaa cttgtgaaac ctggcgcctc tgtgaagctg 60
 agctgcaagg ccagcggctt cacctttcct gactactgga tgcactgggt caagcagagg 120
 cctggacagg gactcgaatg gatcggcgag atcgatcctc ctaacggccg gaccaactac 180
 aacgagaagt tcaagagcaa ggccacactg accgtggaca gcagcagcaa taccgcctac 240
 atgcagctga gcagactgac ctctgaggac agcgccgtgt actactgtgc cagaggcatc 300
 tactacgtgg actactgggg ccagggcaca accctgacag tttcttctgc ttccaccaag 360
 ggcccatccg tcttccccct ggcgccctgc tccaggagca cctccgagag cacagccgcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac 600
 gtagatcaca agcccagcaa caccaagggtg gacaagagag ttgagtccaa atatggtccc 660
 ccatgcccac catgcccagc acctgagttc ctgggggggac catcagtcctt cctgttcccc 720
 ccaaaccaca aggacactct catgatctcc cggaccctg aggtcacgtg cgtgggtggtg 780
 gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcc	agacaaagcc	gcgggaggag	cagttcaaca	gcacgtaccg	tgtggtcagc	900
gtcctcaccg	tcctgcacca	ggactggctg	aacggcaagg	agtacaagt	caaggtctcc	960
aacaaaggcc	tcccgtcctc	catcgagaaa	accatctcca	aagccaaagg	gcagccccga	1020
gagccacagg	tgtacaccct	gccccatcc	caggaggaga	tgaccaagaa	ccaggtcagc	1080
ctgacctgcc	tgggtcaaagg	cttctacccc	agcgacatcg	ccgtggagtg	ggagagcaat	1140
gggcagccgg	agaacaacta	caagaccacg	cctcccgtgc	tggactccga	cggctccttc	1200
ttcctctaca	gcaggctaac	cgtggacaag	agcagggtggc	aggaggggaa	tgtctttctca	1260
tgctccgtga	tgcatgaggc	tctgcacaac	cactacacac	agaagagcct	ctccctgtct	1320
ctgggtaaag	gtgggtggcgg	atctggcggc	ggaggaagcg	gaggcggagg	atccgaagtg	1380
caactggttg	aatctggcgg	aggactggtg	cagcctggaa	gaagcctgag	actgtcttgt	1440
gccgccagcg	gcttcacctt	cgatgattat	gccatgcact	gggtccgaca	ggccccctgga	1500
aaaggacttg	aatgggtgtc	cgccatcacc	tggaacagcg	gccacatcga	ttacgccgat	1560
agcgtggaag	gccggttcac	catcagcaga	gacaacgcca	agaacagcct	gtacctgcag	1620
atgaactccc	tgagagccga	ggacaccgcc	gtgtactact	gtgccaaagt	gtcttacctg	1680
agcaccgcct	ccagcctgga	ttattgggga	cagggcacac	tggtcacagt	gtcctctggt	1740
ggcggagggt	ctggcggagg	tggtagtgg	ggcgggtgaa	gtgggtggcgg	cggatctgat	1800
atccagatga	cacagagccc	tagcagcctg	tctgcctctg	tgggcgatag	agtgaccatc	1860
acctgtagag	ccagccaggg	catcagaaac	tacctggcct	ggtatcagca	gaagcccgga	1920
aaggccccta	agctgctgat	ctatgccgcc	tctacactgc	agagcggcgt	gccatctaga	1980
ttttctggca	gcggctctgg	caccgacttc	accctgacaa	tttctagcct	gcagcctgag	2040
gacgtggcca	cctactactg	ccagagatac	aacagagccc	cttacacctt	cggccagggc	2100
accaaggtgg	aatcaag					2118

<210> 75
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>

<223> I3F07-TNFai LC light chain

<400> 75

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

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

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

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

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

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

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

Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
		115					120					125			

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
	130					135					140				

Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150					155					160

Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165					170					175	

Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180					185					190		

Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
		195					200					205			

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

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

[illegible]

<210> 76
 <211> 1446
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> I3F07-TNFai LC light chain

<400> 76
 gatatacgtgc tgacacagag ccctctgagc ctgcctgttt ctctgggaga tcaggccagc 60
 atcagctgca gataccttca gagcctggtg cacagcaacg gcaataccta cctgcactgg 120
 tatctgcaga agcccggcca gtctcctaag ctgctgatct acaaggtgtc caacaggttc 180
 agcggcgtgc ccgatagatt ttctggctct ggacgcggca ccgacttcac cctgaagatt 240
 tctagagtgg aagccgagga cctgggcgtg tacttctgtt ctacgtctac ccacgtgcca 300
 cctacctttg gcggcggaag caagctggaa atcaagcgta cggcggcggc gccatctgtc 360
 ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtggga aggtggataa cgccctccaa 480
 tcgggtaact ccaggagag tgacacagag caggacagca aggacagcac ctacagcctc 540
 agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
 gtcacccatc agggcctgag ctgcgccgtc acaaagagct tcaacagggg agagtgtggt 660
 ggtggcggat ctggcggcgg aggaagcgga ggcggaggat ccgaagtgca actggttgaa 720
 tctggcggag gactggtgca gcctggaaga agcctgagac tgtcttgtgc cgccagcggc 780
 ttcaccttcg atgattatgc catgcactgg gtccgacagg cccctggaaa aggacttgaa 840
 tgggtgtccg ccatcacctg gaacagcggc cacatcgatt acgccgatag cgtggaaggc 900
 cggttcacca tcagcagaga caacgccaaag aacagcctgt acctgcagat gaactccctg 960
 agagccgagg acaccgccgt gtactactgt gccaaagtgt cttacctgag caccgcctcc 1020
 agcctggatt attggggaca gggcacactg gtcacagtgt cctctggtgg cggaggttct 1080
 ggcggaggtg gtagtggtgg cggcgggaagt ggtggcggcg gatctgatat ccagatgaca 1140

cagagcccta gcagcctgtc tgcctctgtg ggcgatagag tgaccatcac ctgtagagcc 1200
 agccagggca tcagaaacta cctggcctgg tatcagcaga agcccggaaa ggcccctaag 1260
 ctgctgatct atgccgcctc tacactgcag agcggcgtgc catctagatt ttctggcagc 1320
 ggctctggca ccgacttcac cctgacaatt tctagcctgc agcctgagga cgtggccacc 1380
 tactactgcc agagatacaa cagagcccct tacaccttcg gccagggcac caaggtggaa 1440
 atcaag 1446

<210> 77
 <211> 711
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TNFai- I3F07 HC heavy chain

<400> 77
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60
 Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala

										73					
	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	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
	210					215					220				
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
			260					265					270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400

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

Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
			660				665	75						670		
Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	
			675				680							685		
Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Gly	
			690				695							700		
Gly	Ser	Lys	Leu	Glu	Ile	Lys										
			705				710									

acgtgcgtgg tgggtggacgt gagccaggaa gaccccgagg tccagttcaa ctggtacgtg 840
 gatggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagtt caacagcacg 900
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaacgg caaggagtac 960
 aagtgaagg tctccaacaa aggcctcccg tcctccatcg agaaaaccat ctccaaagcc 1020
 aaagggcagc cccgagagcc acaggtgtac accctgcccc catcccagga ggagatgacc 1080
 aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1140
 gagtgggaga gcaatgggca gccggagaa aactacaaga ccacgcctcc cgtgctggac 1200
 tccgacggct ctttcttct ctacagcagg ctaaccgtgg acaagagcag gtggcaggag 1260
 gggaatgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1320
 agcctctccc tgtctctggg taaaggtggt ggcggatctg gcggcggagg aagcggaggc 1380
 ggaggatccc agattcagct ggctcagtct ggcgccgaac ttgtgaaacc tggcgcctct 1440
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 accaactaca acgagaagtt caagagcaag gccacactga ccgtggacag cagcagcaat 1620
 accgcctaca tgcagctgag cagactgacc tctgaggaca gcgccgtgta ctactgtgcc 1680
 agaggcatct actacgtgga ctactggggc cagggcacaa ccctgacagt ttcttctggt 1740
 ggcggagggt ctggcggagg tggtagtggt ggcggtggaa gtggtggcgg cggatctgat 1800
 atcgtgctga cacagagccc tctgagcctg cctgtttctc tgggagatca ggccagcatc 1860
 agctgcagat cctctcagag cctggtgcac agcaacggca atacctacct gcactggtat 1920
 ctgcagaagc ccggccagtc tcctaagctg ctgatctaca aggtgtccaa caggttcagc 1980
 ggcgtgccc atagattttc tggctctggc agcggcaccg acttcaccct gaagatttct 2040
 agagtgaag ccgaggacct gggcgtgtac ttctgttctc agtctaccca cgtgccacct 2100
 acctttggcg gcggaagcaa gctggaaatc aag 2133

<210> 79

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> TNFai- I3F07 LC light chain

<400> 79

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 Gly Ile Arg Asn Tyr
 20 25 30

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

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95

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

Pro 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
 145 150 155 160

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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 210 215 220

Gly	Gly	Gly	Gly	Ser	Gln	Ile	Gln	Leu	Ala	Gln	Ser	Gly	Ala	Glu	Leu	225	230	235	240
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Phe	245	250	255	
Thr	Phe	Pro	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	260	265	270	
Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	Asp	Pro	Pro	Asn	Gly	Arg	Thr	Asn	275	280	285	
Tyr	Asn	Glu	Lys	Phe	Lys	Ser	Lys	Ala	Thr	Leu	Thr	Val	Asp	Ser	Ser	290	295	300	
Ser	Asn	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Arg	Leu	Thr	Ser	Glu	Asp	Ser	305	310	315	320
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Ile	Tyr	Tyr	Val	Asp	Tyr	Trp	Gly	325	330	335	
Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	340	345	350	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	355	360	365	
Leu	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	370	375	380	
Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	385	390	395	400
Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	405	410	415	
Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	420	425	430	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	435	440	445	
Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	450	455	460	
Pro	Pro	Thr	Phe	Gly	Gly	Gly	Ser	Lys	Leu	Glu	Ile	Lys				465	470	475	

<210> 80
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TNFai- I3F07 LC light chain

<400> 80
 gatatccaga tgacacagag ccctagcagc ctgtctgcct ctgtgggcga tagagtgacc 60
 atcacctgta gagccagcca gggcatcaga aactacctgg cctgggtatca gcagaagccc 120
 ggaaaggccc ctaagctgct gatctatgcc gcctctacac tgcagagcgg cgtgccatct 180
 agattttctg gcagcggctc tggcaccgac ttcaccctga caatttctag cctgcagcct 240
 gaggacgtgg ccacctacta ctgccagaga tacaacagag ccccttacac cttcggccag 300
 ggcaccaagg tggaatcaa gcgtacggtg gcggcgccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtggtggtgg cggatctggc 660
 ggcggaggaa gcggaggcgg aggatcccag attcagctgg ctcagtctgg cgccgaactt 720
 gtgaaacctg gcgcctctgt gaagctgagc tgcaaggcca gcggcttcac ctttcctgac 780
 tactggatgc actgggtcaa gcagaggcct ggacagggac tcgaatggat cggcgagatc 840
 gatcctccta acggccggac caactacaac gagaagttca agagcaaggc cacactgacc 900
 gtggacagca gcagcaatac cgcctacatg cagctgagca gactgacctc tgaggacagc 960
 gccgtgtact actgtgccag aggcatctac tacgtggact actggggcca gggcacaacc 1020
 ctgacagttt cttctggtgg cggaggttct ggcgagggtg gtagtggtgg cgggtggaagt 1080
 ggtggcggcg gatctgatat cgtgctgaca cagagccctc tgagcctgcc tgtttctctg 1140

80

ggagatcagg ccagcatcag ctgcagatcc tctcagagcc tggatgcacag caacggcaat 1200
 acctacctgc actggtatct gcagaagccc ggccagtctc ctaagctgct gatctacaag 1260
 gtgtccaaca ggttcagcgg cgtgcccgat agattttctg gctctggcag cggcaccgac 1320
 ttcaccctga agattttctag agtgggaagcc gaggacctgg gcgtgtactt ctgtttctcag 1380
 tctacccacg tgccacctac ctttggcggc ggaagcaagc tggaaatcaa g 1431

<210> 81
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ref. Ab heavy chain

<400> 81
 Glu Val Gln Leu Leu 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 Thr Phe Asn Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ile Ile Ser Gly Ser Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Arg Leu Val Ala Pro Gly Thr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Ala Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser

								81							
145				150				155				160			
Trp	Asn	Ser	Gly	Ala 165	Leu	Thr	Ser	Gly	Val 170	His	Thr	Phe	Pro	Ala 175	Val
Leu	Gln	Ser	Ser 180	Gly	Leu	Tyr	Ser	Leu 185	Ser	Ser	Val	Val	Thr 190	Val	Pro
Ser	Ser	Ser 195	Leu	Gly	Thr	Lys	Thr 200	Tyr	Thr	Cys	Asn	Val 205	Asp	His	Lys
Pro	Ser 210	Asn	Thr	Lys	Val	Asp 215	Lys	Arg	Val	Glu	Ser 220	Lys	Tyr	Gly	Pro
Pro 225	Cys	Pro	Pro	Cys	Pro 230	Ala	Pro	Glu	Phe	Leu 235	Gly	Gly	Pro	Ser	Val 240
Phe	Leu	Phe	Pro	Pro 245	Lys	Pro	Lys	Asp	Thr 250	Leu	Met	Ile	Ser	Arg 255	Thr
Pro	Glu	Val	Thr 260	Cys	Val	Val	Val	Asp 265	Val	Ser	Gln	Glu	Asp 270	Pro	Glu
Val	Gln	Phe 275	Asn	Trp	Tyr	Val	Asp 280	Gly	Val	Glu	Val	His 285	Asn	Ala	Lys
Thr	Lys 290	Pro	Arg	Glu	Glu	Gln 295	Phe	Asn	Ser	Thr	Tyr 300	Arg	Val	Val	Ser
Val 305	Leu	Thr	Val	Leu	His 310	Gln	Asp	Trp	Leu	Asn 315	Gly	Lys	Glu	Tyr	Lys 320
Cys	Lys	Val	Ser	Asn 325	Lys	Gly	Leu	Pro	Ser 330	Ser	Ile	Glu	Lys	Thr 335	Ile
Ser	Lys	Ala	Lys 340	Gly	Gln	Pro	Arg	Glu 345	Pro	Gln	Val	Tyr	Thr 350	Leu	Pro
Pro	Ser	Gln 355	Glu	Glu	Met	Thr	Lys 360	Asn	Gln	Val	Ser	Leu 365	Thr	Cys	Leu
Val 370	Lys	Gly	Phe	Tyr	Pro	Ser 375	Asp	Ile	Ala	Val	Glu 380	Trp	Glu	Ser	Asn
Gly 385	Gln	Pro	Glu	Asn	Asn 390	Tyr	Lys	Thr	Thr	Pro 395	Pro	Val	Leu	Asp	Ser 400
Asp	Gly	Ser	Phe	Phe 405	Leu	Tyr	Ser	Arg	Leu 410	Thr	Val	Asp	Lys	Ser 415	Arg

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 82
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ref. Ab light chain

<400> 82
 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 Gly Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
 35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu 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
 145 150 155 160

83

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
210

<210> 83
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Ref. TNFai heavy chain

<400> 83
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala

										84					
	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	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
	210					215					220				
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
			260					265					270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 84

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Ref. TNFai light chain

<400> 84

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 Gly Ile Arg Asn Tyr
 20 25 30

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

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95

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

Pro 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
 145 150 155 160

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
 210

<210> 85
 <211> 710
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 04L-TNFai HC heavy chain

<400> 85
 Glu Val Gln Leu Leu 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 Thr Phe Asn Ser Tyr
 20 25 30

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

Ser Ile Ile Ser Gly Ser Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Asp Arg Leu Val Ala Pro Gly Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

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

115						120						125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	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	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		210				215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				

Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	385	390	395	400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	405	410	415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	420	425	430	
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gly	435	440	445	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	450	455	460	
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg	Ser	Leu	465	470	475	480
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala	Met	485	490	495	
His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ala	500	505	510	
Ile	Thr	Trp	Asn	Ser	Gly	His	Ile	Asp	Tyr	Ala	Asp	Ser	Val	Glu	Gly	515	520	525	
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	530	535	540	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	545	550	555	560
Val	Ser	Tyr	Leu	Ser	Thr	Ala	Ser	Ser	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	565	570	575	
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	580	585	590	
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	595	600	605	
Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	610	615	620	
Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	625	630	635	640

89

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr
645 650 655

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
660 665 670

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr
675 680 685

Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly
690 695 700

Thr Lys Val Glu Ile Lys
705 710

<210> 86
<211> 2130
<212> DNA
<213> Artificial Sequence

<220>
<223> 04L-TNFai HC heavy chain

<400> 86
gaggtgcagc tgctggaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggcctt caccttcaac agctacgcca tgagctgggt ccgacaggcc 120
cctggcaagg gcctggaatg ggtgtccatc atcagcggca gcggcggcctt tacctactac 180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagccggac caccctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caaggacaga 300
ctggtggccc caggcacctt cgactattgg ggacagggcg ccctcgtgac cgtgtcctct 360
gcttccacca agggcccatc cgtcttcccc ctggcgcctt gctccaggag cacctccgag 420
agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660
aaatatggtc ccccatgccc accatgcccc gcacctgagt tcctgggggg accatcagtc 720

ttcctgttcc ccccaaaacc caaggacact ctcgatgatct cccggacccc tgagggtcacg	780
tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat	840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac	900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag	960
tgaaggtctt ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag	1080
aaccaggtca gcctgacctg cctggtcaaa ggctttctacc ccagcgacat cgccgtggag	1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg	1260
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc	1320
ctctccctgt ctctgggtaa aggtggtggc ggatctggcg gcggaggaag cggaggcgga	1380
ggatccgaag tgcaactggt tgaatctggc ggaggactgg tgcagcctgg aagaagcctg	1440
agactgtctt gtgccgccag cggcttcacc ttcgatgatt atgccatgca ctgggtccga	1500
caggccccctg gaaaaggact tgaatgggtg tccgccatca cctggaacag cggccacatc	1560
gattacgccg atagcgtgga aggccggttc accatcagca gagacaacgc caagaacagc	1620
ctgtacctgc agatgaactc cctgagagcc gaggacaccg ccgtgtacta ctgtgccaaa	1680
gtgtcttacc tgagcaccgc ctccagcctg gattattggg gacagggcac actggtcaca	1740
gtgtcctctg gtggcggagg ttctggcgga ggtggtagtg gtggcggtag aagtggtagc	1800
ggcggatctg atatccagat gacacagagc cctagcagcc tgtctgcctc tgtgggcgat	1860
agagtgacca tcacctgtag agccagccag ggcatcagaa actacctggc ctggtatcag	1920
cagaagcccc gaaaggcccc taagctgctg atctatgccg cctctacact gcagagcggc	1980
gtgccatcta gatcttctgg cagcggctct ggccaccgact tcaccctgac aatttctagc	2040
ctgcagcctg aggacgtggc cacctactac tgccagagat acaacagagc cccttacacc	2100
ttcggccagg gcaccaaggt ggaaatcaag	2130

<210> 87
 <211> 477
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 04L-TNFai LC light chain

<400> 87
 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 Gly Ile Ser Ser Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu 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
 145 150 155 160
 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 210 215 220
 Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 225 230 235 240
 Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 245 250 255
 Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys
 260 265 270
 Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp
 275 280 285
 Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 290 295 300
 Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 305 310 315 320
 Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser
 325 330 335
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 340 345 350
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 355 360 365
 Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 370 375 380
 Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg
 385 390 395 400
 Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 405 410 415
 Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe
 420 425 430
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
 435 440 445
 Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala
 450 455 460

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 465 470 475

<210> 88
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 04L-TNFai LC light chain

<400> 88
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 atcacctgtc gggccagcca gggcatcagc agctggctgg cctggtatca gcagaagccc 120
 gagaaggccc ccaagagcct gatctacgcc gccagctctc tgcagagcgg cgtgcccagc 180
 agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag tacaacagct acccctacac cttcggccag 300
 ggcaccaagc tggaatatca gcgtacggtg gcggcgccat ctgtcttcat cttcccgcga 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtggtggtgg cggatctggc 660
 ggcggaggaa gcggaggcgg aggatccgaa gtgcaactgg ttgaatctgg cggaggactg 720
 gtgcagcctg gaagaagcct gagactgtct tgtgccgcca gcggcttcac cttcgatgat 780
 tatgccatgc actgggtccg acaggcccct ggaaaaggac ttgaatgggt gtccgccatc 840
 acctggaaca gcggccacat cgattacgcc gatagcgtgg aaggccggtt caccatcagc 900
 agagacaacg ccaagaacag cctgtacctg cagatgaact ccctgagagc cgaggacacc 960
 gccgtgtact actgtgccaa agtgtcttac ctgagcaccg cctccagcct ggattattgg 1020
 ggacagggca cactggtcac agtgtcctct ggtggcggag gttctggcgg aggtggtagt 1080

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ggtaggcggtag gaagtggtag cggcggatct gatattcaga tgacacagag ccctagcagc 1140
ctgtctgcct ctgtgggcga tagagtgacc atcacctgta gagccagcca gggcatcaga 1200
aactacctgg cctggtatca gcagaagccc ggaaaggccc ctaagctgct gatctatgcc 1260
gcctctacac tgcagagcgg cgtgccatct agattttctg gcagcggctc tggcaccgac 1320
ttcacctga caatttctag cctgcagcct gaggacgtgg ccacctacta ctgccagaga 1380
tacaacagag ccccttacac cttcggccag ggcaccaagg tggaaatcaa g 1431

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<210>      89
<211>       5
<212>      PRT
<213>      Artificial Sequence

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<220>
<223>      Humira VH CDR 1

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```

<400>      89
Asp Tyr Ala Met His
  1             5

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```

<210>      90
<211>      17
<212>      PRT
<213>      Artificial Sequence

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```

<220>
<223>      Humira VH CDR 2

```

```

<400>      90
Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu
  1             5             10             15

```

Gly

```

<210>      91
<211>      12
<212>      PRT
<213>      Artificial Sequence

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<220>

<223> Humira VH CDR 3

<400> 91

Val	Ser	Tyr	Leu	Ser	Thr	Ala	Ser	Ser	Leu	Asp	Tyr
1				5					10		

<210> 92

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Humira VL CDR 1

<400> 92

Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Tyr	Leu	Ala
1				5					10	

<210> 93

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Humira VL CDR 2

<400> 93

Ala	Ala	Ser	Thr	Leu	Gln	Ser
1				5		

<210> 94

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Humira VL CDR 3

<400> 94

Gln	Arg	Tyr	Asn	Arg	Ala	Pro	Tyr	Thr
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1

5

96