

eolf-seql
SEQUENCE LISTING

<110> MOLMED SpA

<120> Chimeric Antigen Receptors

<130> P105739PCT

<150> EP 14184838.2

<151> 2014-09-15

<160> 40

<170> PatentIn version 3.5

<210> 1

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Spacer LNGFR wild-type long (NWL)

<400> 1

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

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
50 55 60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
85 90 95

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Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
130 135 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145 150 155 160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
165 170 175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
180 185 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
195 200 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
210 215 220

<210> 2
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> Spacer LNGFR wild-type long (NWL)

<400> 2
aaagaggcct gccccaccgg cctgtacacc cacagcggag agtgctgcaa ggcctgcaac 60
ctgggagagg gcgtggccca gccttgccggc gccaatcaga ccgtgtgcga gccctgcctg 120
gacagcgtga ccttcagcga cgtgggtgtcc gccaccgagc cctgcaagcc ttgcaccgag 180

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tgtgtgggcc tgcagagcat gagcgcccc tgcgtggaag ccgacgacgc cgtgtgtaga 240
 tgcgcctacg gctactacca ggacgagaca accggcagat gcgaggcctg tagagtgtgc 300
 gaggccggca gcggcctggt gttcagttgt caagacaagc agaataccgt gtgtgaagag 360
 tgccccgacg gcacctacag cgacgaggcc aaccacgtgg acccctgcct gccctgcact 420
 gtgtgcgagg acaccgagcg gcagctgcgc gagtgcacaa gatgggccga cgccgagtgc 480
 gaagagatcc ccggcagatg gatcaccaga agcaccccc ctgagggcag cgacagcacc 540
 gcccttagca cccaggaacc tgaggcccct cccgagcagg acctgatcgc ctctacagtg 600
 gccggcgtgg tgacaaccgt gatgggcagc tctcagcccg tggtagacacg gggcaccacc 660
 gacaat 666

<210> 3
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Spacer LNGFR wild-type short (NWS)

<400> 3

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

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
 20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
 35 40 45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
 50 55 60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
 65 70 75 80

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Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
85 90 95

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
130 135 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145 150 155 160

Glu Glu

<210> 4
<211> 486
<212> DNA
<213> Artificial Sequence

<220>
<223> Spacer LNGFR wild-type short (NWS)

<400> 4
aaagaggcct gccccaccgg cctgtacacc cacagcggag agtgctgcaa ggcctgcaac 60
ctgggagagg gcgtggccca gccttgccgc gccaatcaga ccgtgtgcga gccctgcctg 120
gacagcgtga ccttcagcga cgtggtgtcc gccaccgagc cctgcaagcc ttgcaccgag 180
tgtgtgggcc tgcagagcat gagcgcccc tgcgtggaag ccgacgacgc cgtgtgtaga 240
tgcgcctacg gctactacca ggacgagaca accggcagat gcgaggcctg tagagtgtgc 300
gaggccggca gcggcctggt gttcagttgt caggacaagc agaacaccgt gtgtgaagag 360
tgccccgacg gcacctacag cgacgaggcc aaccacgtgg acccctgcct gccctgcact 420

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gtgtgcgagg acaccgagcg gcagctgcgc gaggcgacaa gatgggcccga cgccgagtg 480

gaggaa 486

<210> 5

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Spacer LNGFR mutated long (NML)

<400> 5

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

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
50 55 60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
85 90 95

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Ala Arg Ala Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg

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130

135

140

Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro
145 150 155 160

Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser
165 170 175

Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val
180 185 190

Val Thr Arg Gly Thr Thr Asp Asn
195 200

<210> 6
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> Spacer LNGFR mutated long (NML)

<400> 6
aaagaggcct gccccaccgg cctgtacacc cacagcggag agtgctgcaa ggcctgcaac 60
ctgggagagg gcgtggccca gccttgccggc gccaatcaga ccgtgtgcga gccctgcctg 120
gacagcgtga ccttcagcga cgtgggtgtcc gccaccgagc cctgcaagcc ttgcaccgag 180
tgtgtgggcc tgcagagcat gagcgcccc tgcgtggaag ccgacgacgc cgtgtgtaga 240
tgcgcctacg gctactacca ggacgagaca accggcagat gcgaggcctg tagagtgtgc 300
gaggccggca gcggcctggt gttcagttgt caagacaagc agaataccgt gtgtgaagag 360
tgccccgacg gcacctacag cgacgaagcc gccagagccg ccgacgccga gtgcgaagag 420
atccccggca gatggatcac cagaagcacc ccccttgagg gcagcgacag caccgcccct 480
agcaccagg aacctgaggc ccctcccag caggacctga tcgcctctac agtggccggc 540
gtggtgacaa ccgtgatggg cagctctcag cccgtgggtga cacggggcac caccgacaat 600

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<210> 7
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Spacer LNGFR mutated short (NMS)

<400> 7

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

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
 20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
 35 40 45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
 50 55 60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
 65 70 75 80

Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
 85 90 95

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
 100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
 115 120 125

Glu Ala Ala Arg Ala Ala Asp Ala Glu Cys Glu Glu
 130 135 140

<210> 8

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<211> 420
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Spacer LNGFR mutated short (NMS)

<400> 8
 aaagaggcct gccccaccgg cctgtacacc cacagcggag agtgctgcaa ggcctgcaac 60
 ctgggagagg gcgtggccca gccttgcggc gccaatcaga ccgtgtgcga gccctgcctg 120
 gacagcgtga ccttcagcga cgtggtgtcc gccaccgagc cctgcaagcc ttgcaccgag 180
 tgtgtgggcc tgcagagcat gagcgcccc tgcgtggaag ccgacgacgc cgtgtgtaga 240
 tgcgcctacg gctactacca ggacgagaca accggcagat gcgaggcctg tagagtgtgc 300
 gaggccggca gcggcctggt gttcagttgt caggacaagc agaacaccgt gtgtgaagag 360
 tgccccgacg gcacctacag cgacgaggcc gcccgggccc ccgacgccga gtgcgaggaa 420

<210> 9
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 9

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

Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
 20 25 30

Val Cys

<210> 10
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 10

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Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu
1 5 10 15

Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala
20 25 30

Pro Cys Val Glu Ala Asp Asp Ala Val Cys
35 40

<210> 11
<211> 39
<212> PRT
<213> Homo sapiens

<400> 11

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys
35

<210> 12
<211> 41
<212> PRT
<213> Homo sapiens

<400> 12

Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro
1 5 10 15

Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu
20 25 30

Cys Thr Arg Trp Ala Asp Ala Glu Cys

eolf-seql

35

40

<210> 13
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 13

Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu
 1 5 10 15

Arg Gln Leu Arg Glu Cys Thr Arg Trp
 20 25

<210> 14
 <211> 427
 <212> PRT
 <213> Homo sapiens

<400> 14

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
 1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
 20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
 35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
 50 55 60

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

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
 85 90 95

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Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115 120 125

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

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
225 230 235 240

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
245 250 255

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
260 265 270

Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg
275 280 285

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Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
290 295 300

Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Pro His
305 310 315 320

Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Gly Leu Tyr
325 330 335

Ser Ser Leu Pro Pro Ala Lys Arg Glu Glu Val Glu Lys Leu Leu Asn
340 345 350

Gly Ser Ala Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr
355 360 365

Gln Pro Glu His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg
370 375 380

Ala Leu Leu Ala Ser Trp Ala Thr Gln Asp Ser Ala Thr Leu Asp Ala
385 390 395 400

Leu Leu Ala Ala Leu Arg Arg Ile Gln Arg Ala Asp Leu Val Glu Ser
405 410 415

Leu Cys Ser Glu Ser Thr Ala Thr Ser Pro Val
420 425

<210> 15

<211> 2046

<212> DNA

<213> Artificial Sequence

<220>

<223> CD44v6-specific second-generation CAR construct sequence,
CD44v6-CAR.28z

<400> 15

atggaagccc ctgcccagct gctgttcctg ctgctgctgt ggctgcccga caccaccggc

60

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gagatcgtgc tgacacagag ccccgccacc ctgtctctga gccctggcga gagagccacc	120
ctgagctgta gcgccagcag cagcatcaac tacatctact ggctgcagca gaagcccggc	180
caggccccca gaatcctgat ctacctgacc agcaacctgg ccagcggcgt gcccgccaga	240
ttttctggca gcggcagcgg caccgacttc accctgacca tcagcagcct ggaacccgag	300
gacttcgccg tgtactactg cctgcagtgg tccagcaacc ccctgacctt cggcggaggc	360
accaaggtgg aaatcaagcg ggggtggtgg gtgtctggtg gtggtgggtt tggcggcggc	420
ggctccggtg gtggtggatc tgagggtgcag ctggtggaaa gcggcggagg cctggtcaag	480
cctggcggca gcctgagact gagctgtgcc gccagcggct tcaccttcag cagctacgac	540
atgagctggg tccgacaggc tccaggcaag ggactggaat ggggtgtccac catcagcagc	600
ggcggcagct acacctacta cctggacagc atcaagggcc gggttcacat cagccgggac	660
aacgccaaga acagcctgta cctgcagatg aacagcctgc gggccgagga caccgccgtc	720
tactactgtg cccggcaggg cctcgactac tggggcagag gcaccctggc caccgtgtcc	780
agcggggatc ccgccgagcc caaatctcct gacaaaactc acacatgccc accgtgcccc	840
gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc	900
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac	960
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag	1020
ccgcgggagg agcagtacaa cagcacgtac cgtgtgggtc gcgtcctcac cgtcctgcac	1080
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc	1140
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc	1200
ctgcccccat cccgggatga gctgaccaag aaccagggtc gcctgacctg cctggtcaaa	1260
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcaacc ggagaacaac	1320
tacaagacca cgctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc	1380
accgtggaca agagcagggt gcagcagggg aacgtcttct catgctccgt gatgcatgag	1440
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa aaaagatccc	1500

eolf-seql

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aaatttttggg tgctggtggt ggttgggtgga gtcctggctt gctatagctt gctagtaaca      1560
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atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgccccca      1680
ccacgcgact tcgcagccta tcgctccaga gtgaagttca gcaggagcgc agacgcccccc      1740
gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag      1800
tacgatgttt tggacaagag acgtggccgg gaccctgaga tgggggggaaa gccgagaagg      1860
aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac      1920
agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cttttaccag      1980
ggtctcagta cagccacca gacacacctac gacgcccttc acatgcaggc cctgccccct      2040
cgctaa                                                                    2046

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<210> 16
 <211> 681
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD44v6-CAR.28z protein

<400> 16

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 1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
 20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
 35 40 45

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

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Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

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Val Thr Val Ser Ser Gly Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys
260 265 270

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
275 280 285

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
325 330 335

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

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
370 375 380

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
405 410 415

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

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

eolf-seq1

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480

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

Lys Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu
500 505 510

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
515 520 525

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

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
545 550 555 560

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
565 570 575

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

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

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

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

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Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
645 650 655

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

Leu His Met Gln Ala Leu Pro Pro Arg
675 680

<210> 17
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-specific single-chain fragment

<400> 17

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

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Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

Val Thr Val Ser Ser
260

<210> 18
<211> 68
<212> PRT
<213> Homo sapiens

<400> 18

eolf-seql

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

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

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

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

Ala Tyr Arg Ser
65

<210> 19
<211> 222
<212> PRT
<213> Homo sapiens

<400> 19

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

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
50 55 60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

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Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
85 90 95

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
130 135 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145 150 155 160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
165 170 175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
180 185 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
195 200 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
210 215 220

<210> 20
<211> 113
<212> PRT
<213> Homo sapiens

<400> 20

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

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr

eolf-seql

20

25

30

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

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

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

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

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

Arg

<210> 21
<211> 669
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-CAR28z with spacer LNGFR wild-type long (NWL)

<400> 21

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

eolf-seql

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

eolf-seql

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
275 280 285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
385 390 395 400

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
405 410 415

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile
420 425 430

eolf-seql

Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr
435 440 445

Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val
450 455 460

Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr
465 470 475 480

Arg Gly Thr Thr Asp Asn Pro Lys Phe Trp Val Leu Val Val Val Gly
485 490 495

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

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

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

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

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
565 570 575

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
580 585 590

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg
595 600 605

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
610 615 620

eolf-seql

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
625 630 635 640

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
645 650 655

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
660 665

<210> 22
<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-CAR28z with spacer LNGFR wild-type short (NWS)

<400> 22

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser

eolf-seql

100

105

110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
275 280 285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu

eolf-seql

290

295

300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
385 390 395 400

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
405 410 415

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Pro Lys Phe Trp Val Leu
420 425 430

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
435 440 445

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
450 455 460

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
465 470 475 480

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser

eolf-seql

485

490

495

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

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

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

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

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

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

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

Arg

<210> 23

<211> 647

<212> PRT

<213> Artificial Sequence

<220>

<223> CD44v6-CAR28z with spacer LNGFR mutated long (NML)

<400> 23

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

eolf-seql

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
195 200 205

eolf-seql

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
275 280 285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Ala Arg Ala Ala Asp Ala
385 390 395 400

eolf-seql

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
405 410 415

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
420 425 430

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
435 440 445

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
450 455 460

Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
465 470 475 480

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
485 490 495

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
500 505 510

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
515 520 525

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
530 535 540

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
545 550 555 560

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
565 570 575

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
580 585 590

eolf-seql

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
595 600 605

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
610 615 620

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
625 630 635 640

Met Gln Ala Leu Pro Pro Arg
645

<210> 24
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-CAR28z with spacer LNGFR mutated short (NMS)

<400> 24

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

eolf-seql

85

90

95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
 100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
 195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
 245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
 260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly

eolf-seql

275

280

285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
 290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
 305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
 325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
 340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
 355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
 370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Ala Arg Ala Ala Asp Ala
 385 390 395 400

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

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
 420 425 430

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 435 440 445

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 450 455 460

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg

eolf-seql

465	470	475	480
Ser Ala Asp Ala	Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn		
	485	490	495
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg			
	500	505	510
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn			
	515	520	525
Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu			
	530	535	540
Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly			
545	550	555	560
His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr			
	565	570	575
Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg			
	580	585	

<210> 25
 <211> 668
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD44v6-CAR28z with spacer LNGFR wild-type long (NWL)

<400> 25

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro			
1	5	10	15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser			
20	25	30	

eolf-seql

Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Ser	Ala	Ser	Ser	Ser	35	40	45	
Ile	Asn	Tyr	Ile	Tyr	Trp	Leu	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	50	55	60	
Ile	Leu	Ile	Tyr	Leu	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	65	70	75	80
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	85	90	95	
Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Leu	Gln	Trp	Ser	Ser	100	105	110	
Asn	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Gly	115	120	125	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	130	135	140	
Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	145	150	155	160
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	165	170	175	
Ser	Ser	Tyr	Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	180	185	190	
Glu	Trp	Val	Ser	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Tyr	Tyr	Leu	195	200	205	
Asp	Ser	Ile	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	210	215	220	

eolf-seql

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
275 280 285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
385 390 395 400

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
405 410 415

eolf-seql

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile
420 425 430

Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr
435 440 445

Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val
450 455 460

Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr
465 470 475 480

Arg Gly Thr Thr Asp Asn Pro Lys Phe Trp Val Leu Val Val Val Gly
485 490 495

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

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

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

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

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
565 570 575

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
580 585 590

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
595 600 605

eolf-seql

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
610 615 620

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
625 630 635 640

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
645 650 655

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
660 665

<210> 26
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-CAR28z with spacer LNGFR wild-type short (NWS)

<400> 26

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

eolf-seql

85

90

95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
 100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
 195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
 245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
 260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly

eolf-seql

275

280

285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
 290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
 305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
 325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
 340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
 355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
 370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys
 385 390 395 400

Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
 405 410 415

Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Pro Lys Phe Trp Val Leu
 420 425 430

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
 435 440 445

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
 450 455 460

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys

eolf-seql

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
195 200 205

eolf-seql

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly
275 280 285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Ala Arg Ala Ala Asp Ala
385 390 395 400

eolf-seql

Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro
405 410 415

Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro
420 425 430

Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr
435 440 445

Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
450 455 460

Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
465 470 475 480

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
485 490 495

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
500 505 510

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
515 520 525

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
530 535 540

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
545 550 555 560

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
565 570 575

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
580 585 590

eolf-seql

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
595 600 605

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
610 615 620

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
625 630 635 640

Gln Ala Leu Pro Pro Arg
645

<210> 28
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-CAR28z with spacer LNGFR mutated short (NWL)

<400> 28

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

eolf-seql

85

90

95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
 100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 165 170 175

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

Glu Trp Val Ser Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Leu
 195 200 205

Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 225 230 235 240

Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr Trp Gly Arg Gly Thr Leu
 245 250 255

Val Thr Val Ser Ser Gly Asp Pro Lys Glu Ala Cys Pro Thr Gly Leu
 260 265 270

Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn Leu Gly Glu Gly

eolf-seql

275

280

285

Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys Glu Pro Cys Leu
 290 295 300

Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu Pro Cys Lys
 305 310 315 320

Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala Pro Cys Val
 325 330 335

Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp
 340 345 350

Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser
 355 360 365

Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu
 370 375 380

Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Ala Arg Ala Ala Asp Ala
 385 390 395 400

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

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
 420 425 430

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 435 440 445

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 450 455 460

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg

eolf-seql

465 470 475 480

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
485 490 495

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
500 505 510

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
515 520 525

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
530 535 540

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

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

Ala Leu His Met Gln Ala Leu Pro Pro Arg
580 585

```
<210> 29
<211> 27
<212> PRT
<213> Homo sapiens
```

<400> 29

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

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

$\langle 210 \rangle$	30
$\langle 211 \rangle$	41

eolf-seql

<212> PRT

<213> Homo sapiens

<400> 30

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 31

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> CD44v6-4GS2, CD44v6-specific single chain fragment

<400> 31

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

eolf-seql

85

90

95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

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

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

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser Trp Val Arg Gln
165 170 175

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

Ser Tyr Thr Tyr Tyr Leu Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr
225 230 235 240

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 32

<211> 658

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> CD44v6-4GS2-CAR28z with spacer LNGFR wild-type long (NWL)

<400> 32

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

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

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

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser Trp Val Arg Gln
165 170 175

eolf-seql

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

Ser Tyr Thr Tyr Tyr Leu Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr
225 230 235 240

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Asp Pro Lys Glu
245 250 255

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

Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
275 280 285

Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser
290 295 300

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
305 310 315 320

Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
325 330 335

Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
340 345 350

Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
355 360 365

eolf-seql

Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
370 375 380

Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu
385 390 395 400

Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu
405 410 415

Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp
420 425 430

Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp
435 440 445

Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser
450 455 460

Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Pro Lys Phe Trp
465 470 475 480

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
485 490 495

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
500 505 510

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
515 520 525

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
530 535 540

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

eolf-seql

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
565 570 575

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
580 585 590

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
595 600 605

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
610 615 620

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
625 630 635 640

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
645 650 655

Pro Arg

<210> 33
<211> 598
<212> PRT
<213> Artificial Sequence

<220>
<223> CD44v6-4GS2-CAR28z with spacer LNGFR wild-type short (NWS)

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser

eolf-seql

35

40

45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
 65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
 85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
 100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
 115 120 125

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

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

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser Trp Val Arg Gln
 165 170 175

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

Ser Tyr Thr Tyr Tyr Leu Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser
 195 200 205

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
 210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr

eolf-seql

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

eolf-seq1

420

425

430

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
 435 440 445

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
 450 455 460

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

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 485 490 495

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 500 505 510

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

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

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

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
 565 570 575

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

Gln Ala Leu Pro Pro Arg
 595

<210> 34

eolf-seql

<211> 636

<212> PRT

<213> Artificial Sequence

<220>

<223> CD44v6-4GS2-CAR28z with spacer LNGFR mutated long (NML)

<400> 34

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

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

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

eolf-seql

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser Trp Val Arg Gln
165 170 175

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

Ser Tyr Thr Tyr Tyr Leu Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr
225 230 235 240

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Asp Pro Lys Glu
245 250 255

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

Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
275 280 285

Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser
290 295 300

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
305 310 315 320

Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
325 330 335

Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
340 345 350

eolf-seql

Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
 355 360 365

Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
 370 375 380

Ala Arg Ala Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile
 385 390 395 400

Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr
 405 410 415

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

Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr
 435 440 445

Arg Gly Thr Thr Asp Asn Pro Lys Phe Trp Val Leu Val Val Val Gly
 450 455 460

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 465 470 475 480

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

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

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

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

eolf-seql

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

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

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

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

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

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

<210> 35

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> CD44v6-4GS2-CAR28z with spacer LNGFR mutated short (NMS)

<400> 35

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
35 40 45

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

eolf-seql

50

55

60

Ile Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110

Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly
115 120 125

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

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

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser Trp Val Arg Gln
165 170 175

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

Ser Tyr Thr Tyr Tyr Leu Asp Ser Ile Lys Gly Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gln Gly Leu Asp Tyr
225 230 235 240

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Asp Pro Lys Glu

eolf-seql

245

250

255

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

Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
275 280 285

Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser
290 295 300

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
305 310 315 320

Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
325 330 335

Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
340 345 350

Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
355 360 365

Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
370 375 380

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

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
405 410 415

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
420 425 430

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys

eolf-seql

435

440

445

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
450 455 460

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
465 470 475 480

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
485 490 495

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
500 505 510

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
515 520 525

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

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
565 570 575

<210> 36

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

eolf-seql

<210> 37
 <211> 8331
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD44v6-4GS2-CAR.28Z NGFR WILD TYPE LONG (V6 NWL)

<400> 37
 aagcttttgct cttaggagtt tcctaataca tcccaaactc aaatatataa agcatttgac 60
 ttgttctatg ccctaggggg cggggggaag ctaagccagc tttttttaac atttaaaatg 120
 ttaattccat tttaaatgca cagatgtttt tatttcataa gggtttcaat gtgcatgaat 180
 gctgcaatat tcctgttacc aaagctagta taaataaaaa tagataaacg tggaaattac 240
 ttagagtttc tgtcattaac gtttccttcc tcagttgaca acataaatgc gctgctgagc 300
 aagccagttt gcatctgtca ggatcaattt cccattatgc cagtcattat aattactagt 360
 caattagttg atttttattt ttgacatata catgtgaatg aaagacccca cctgtaggtt 420
 tggcaagcta gcttaagtaa cgccattttg caaggcatgg aaaaatacat aactgagaat 480
 agaaaagtgc agatcaaggt caggaacaga tggaacagct gaatatgggc caaacaggat 540
 atctgtggta agcagttcct gccccggctc agggccaaga acagatggaa cagctgaata 600
 tgggccaac aggatattctg tggtaagcag ttcctgcccc ggctcagggc caagaacaga 660
 tgggtccccag atgcgggtcca gccctcagca gtttctagag aaccatcaga tgtttccagg 720
 gtgccccaaag gacctgaaat gacctgtgc cttatttgaa ctaaccaatc agttcgcttc 780
 tcgcttctgt tcgcgcgctt atgctccccg agctcaataa aagagccac aaccctcac 840
 tcggggcgcc agtcctccga ttgactgagt cgccgggta cccgtgtatc caataaaccc 900
 tcttgagtt gcatccgact tgttgtctcg ctgttccttg ggagggtctc ctctgagtga 960
 ttgactaccc gtcagcgggg gtctttcatt tgggggctcg tccgggatcg ggagaccct 1020
 gccagggac caccgacca ccaccgggag gtaagctggc cagcaactta tctgtgtctg 1080
 tccgattgtc tagtgtctat gactgatttt atgcgcctgc gtcggtacta gttagctaac 1140

eolf-seql

tagctctgta tctggcggac ccgtggtgga actgacgagt tcggaacacc cggccgcaac	1200
cctgggagac gtcccaggga cttcgggggc cgtttttgtg gcccgacctg agtcctaaaa	1260
tcccgatcgt ttaggactct ttggtgcacc ccccttagag gagggatatg tggttctggt	1320
aggagacgag aacctaataac agttcccgcc tccgtctgaa tttttgcttt cggtttggga	1380
ccgaagccgc gccgcgcgtc ttgtctgctg cagcatcggt ctgtgttgtc tctgtctgac	1440
tgtgtttctg tattttgtctg aaaatatggg cccgggctag cctgtttacca ctcccttaag	1500
tttgacctta ggtcactgga aagatgtcga gcggatcgct cacaaccagt cggtagatgt	1560
caagaagaga cgttgggtta ctttctgctc tgcagaatgg ccaaccttta acgtcggatg	1620
gccgcgagac ggcaccttta accgagacct catcaccag gttaagatca aggtcttttc	1680
acctggcccc catggacacc cagaccaggt ggggtacatc gtgacctggg aagccttggc	1740
ttttgacccc cctccctggg tcaagccctt tgtacaccct aagcctccgc ctctctttcc	1800
tccatccgcc ccgtctctcc cccttgaacc tcctcgttcg accccgcctc gatcctccct	1860
ttatccagcc ctcaactcct ctctaggcgc ccccatatgg ccatatgaga tcttatatgg	1920
ggcacccccg ccccttgtaa acttccctga ccctgacatg acaagagtta ctaacagccc	1980
ctctctccaa gctcacttac aggctctcta cttagtccag cacgaagtct ggagacctct	2040
ggcggcagcc taccaagaac aactggaccg accggtggta cctcaccctt accgagtcgg	2100
cgacacagtg tgggtccgcc gacaccagac taagaaccta gaacctcgct ggaaaggacc	2160
ttacacagtc ctgctgacca cccccaccgc cctcaaagta gacggcatcg cagcttggat	2220
acacgccgcc cacgtgaagg ctgccgacc cgggggtgga ccatcctcta gactgccatg	2280
gaagcccctg cccagctgct gttcctgctg ctgctgtggc tgcccgacac caccggcgag	2340
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eolf-seql

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