

SEQUENCE LISTING

<110> Viela Bio, Inc.

<120> ANTIBODIES TO FELINE MCDONOUGH SARCOMA (FMS)-LIKE TYROSINE KINASE
3 RECEPTOR LIGAND (FLT3L) AND USES THEREOF FOR TREATING
AUTOIMMUNE AND INFLAMMATORY DISEASES

<130> 054493-502001W0

<150> US 62/630,571

<151> 2018-02-14

<160> 72

<170> PatentIn version 3.5

<210> 1

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> "AM40_VH"

<400> 1

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

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

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

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

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

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

Ala Ser Asn Asp Phe Val Tyr Gly Ser Tyr Arg Phe Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala
115 120

<210> 2
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> "AM40_VL"

<400> 2

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

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

Phe Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asp
85 90 95

Tyr Arg Arg Ala Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 3
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> "SC4017_VH"

<400> 3

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

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

<210> 4
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> "SC4017_VL"

<400> 4

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys	1	5	10	15
Thr Val Thr Ile Ser Cys Thr Arg Thr Ser Gly Trp Ile Ala Gly Tyr	20	25	30	
Phe Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val	35	40	45	
Ile Tyr Glu Asp Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser				

50

55

60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asp
85 90 95

Tyr Arg Arg Ala Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 5

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT5D9_VH"

<400> 5

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

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

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

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

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

Ile Glu Leu Ser Ser Leu Lys Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Ser Asn Asn Tyr Val Trp Gly Ser Tyr Arg Phe Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser

115

<210> 6
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT5D9_VL"

<400> 6

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

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

Phe Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Arg Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Pro Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asp
85 90 95

Thr Ser Gln Gly Val Phe Gly Ala Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 7
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_VH"

<400> 7

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 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 Arg Ser Ser Gly Tyr Tyr Gly Ala Asn Phe Asp Phe Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 8
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_VL"

<400> 8

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

Arg Val Ala Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Gly
20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Thr Leu Leu
35 40 45

Ile His Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val
100 105

<210> 9
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT26_VH"

<400> 9

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 Ser Ser Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 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

Val Lys Asp Ala Tyr Gly Ser Ser Trp Tyr Phe Tyr Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 10
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT26_VL"

<400> 10

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn
20 25 30

Pro Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Val Leu
35 40 45

Ile Tyr Ser Asp Lys Tyr Arg Pro Ser Gly Val Ala Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Phe Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Arg Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 11
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> "DYAX3_VH"

<400> 11

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 Ser Met Tyr

20

25

30

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

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

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

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

Arg Tyr Ser Arg Trp Phe Gly Gln Leu Gly Phe Tyr Ser His Tyr Ala
 100 105 110

Met Asp Val Trp Ser Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 12

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> "DYAX3_VL"

<400> 12

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

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

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

Tyr Ala Ala Ser Lys Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Thr Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro

<211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> "DYAX5_VL"

<400> 14

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 Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu 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 Ser Tyr Ser Thr Pro Pro
 85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 15
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "AM40_VH"

<400> 15

caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cttctggagg caccttcagc agttatgctc ttagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaacg cggccgccga cctcccggac agcaagctac 180
 gcacagaaat ttcagggcag agtcacgatt accgtggacg aatccacgag cacaggctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gtcaaacgac 300
 ttctgtgtacg ggagttatcg tttctggggc caagggacca cggtcaccgt ctcctcagcg 360

<210> 16
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "AM40_VL"

<400> 16
 aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60
 tcctgcaccc gcaccagtgg gaacattgcc ggctactttg tgcagtggta ccagcagcgc 120
 ccgggcagtt cccccaccac tgtgatctat gaggattacc aacgaccctc tggggtcctt 180
 gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga 240
 ctgaagactg aggacgaggc tgactactat tgtcagtcct atgatgacta ccggcgggcg 300
 gcgttcggcg gagggaccaa gctgaccgtc cta 333

<210> 17
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "SC4017_VH"

<400> 17
 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cttctggagg caccttcagc agttatgctc ttagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaacg cggccgccga cctcccggac agcaagctac 180
 gcacagaaat ttcagggcag agtcacgatt accgtggacg aatccacgag cacaggctac 240
 atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gtcaaacgac 300
 ttctgtgtacg ggagttatcg tttctggggc caagggacca cggtcaccgt ctcctca 357

<210> 18
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>

<223> "SC4017_VL"

<400> 18

aatttttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60

tcctgcaccc gcaccagtgg gtggattgcc ggctactttg tgcagtggta ccagcagcgc 120

ccgggcagtt cccccaccac tgtgatctat gaggattacc aacgaccctc tggggtcctt 180

gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga 240

ctgaagactg aggacgaggc tgactactat tgtcagtctt atgatgacta ccggcgggcg 300

gcgttcggcg gagggaccaa gctgaccgtc cta 333

<210> 19

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> "CAT5D9_VH"

<400> 19

caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaaga tttctggagg caccttcagc agttatgctc ttagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatccctg tctttcggac agcaagctac 180

gcacagaaat ttcagggcag agtcacgatt accgtggacg aatccgcgag cacaggctac 240

atagaactga gcagcctgaa atctgaggac acggccacat attactgtgc gtcaaataat 300

tacgtttggg ggagttatcg tttctggggc caggggacca cggtcaccgt ctctca 357

<210> 20

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> "CAT5D9_VL"

<400> 20

aatttttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtcaccatc 60

tcctgcaccc gcaccagtgg gaacattgcc ggctactttg tgcagtggta ccagcagcgc 120

ccgggcagtt cccccaccac tgtgatctat gaggattacc aacgaccctc tggggtcctt 180

gatcggttct ctggctccat cgacagggtcc tccaactctg cctccctcac catctctgga	240
ctgaagcctg acgacgaggc tgactactat tgtcagtcctt atgatgacac ctctcaaggt	300
gtgttcggcg cagggaccaa ggtcaccgtc cta	333

<210> 21
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "CAT8_VH"

<400> 21	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct	120
ccaggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagaagcagc	300
ggctactacg gggccaattt tgacttctgg gggcagggga ccacggtcac cgtctcgagt	360

<210> 22
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "CAT8_VL"

<400> 22	
cagtctgtgc tgacgcagcc gccctcagcg tccgggaccc ccgggcagag ggtcgccatc	60
tcttgttctg gaagcagctc caacatcgga agtggttatg tatactggta tcagcaggtc	120
ccaggaacgg cccccacact cctcatccat aggaataatc agcggccctc aggggtccct	180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg	240
tccgaggatg aggctgatta ttactgtgca gcgtgggatg acagcctgag tggttatgtc	300
ttcggaactg ggaccaaggt caccgtc	327

<210> 23
 <211> 369
 <212> DNA

<213> Artificial Sequence

<220>

<223> "CAT26_VH"

<400> 23

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctctggatt cacctttagc agctatgccg tgagctgggt ccgccaggct	120
ccaggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgt gaaagacgca	300
tatggcagca gctgggtactt ttactacttt gactactggg gccaaaggac aatggtcacc	360
gtctcgagt	369

<210> 24

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> "CAT26_VL"

<400> 24

cagtctgtgt tgacgcagcc gccttcagcg tctgggaccc ccgggcagag ggtcaccatc	60
tcttgttctg gaagcagctc caacatcgga atcaatcctg tgaactggta ccaacaactc	120
cccggaacgg cccccaagt cctcatttat agtgataaat accggccctc aggggtcgt	180
gaccgcttct ctggctccaa gtctggaacc tcagcctccc tggccatcag tggcctccag	240
tctgaggatg aggctgatta cttctgtgca gcatgggatg acagcctgaa tggtcgcgtc	300
ttcggaactg ggaccaagct gaccgtccta	330

<210> 25

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> "DYAX3_VH"

<400> 25

gaagttcaat tgttagagtc tggtagcggt cttgttcagc ctggtgggtc tttacgtctt	60
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tcttgcgctg cttccggatt cactttctct atgtacgaga tgcgttgggt tcgccaagct	120
cctggtaaag gtttggagtg ggtttctgtt atcccttctg gtggcaagac tttttatgct	180
gactccgtta aaggctgcctt cactatctct agagacaact ctaagaatac tctctacttg	240
cagatgaaca gcttaagggc tgaggacacg gccgtgtatt actgtgcgag atacagcaga	300
tggttcgggc agctaggggt ttactcccac tacgctatgg acgtctggag ccaagggacc	360
acggtcaccg tctcaagc	378

<210> 26
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "DYAX3_VL"

<400> 26	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcgcc	60
atcacttgcc gcgcaagtca gagcatcgac acctatttaa attggtatca gcagaaacca	120
gggaaagccc ctaaactcct gatctatgct gcatccaagt tggaagacgg ggtcccatca	180
agattcagtg gcagtggaac tgggacagat ttcactctca ccatcagaag tctgcaacct	240
gaagattttg caagttatth ctgtcaacag agctactcta gtccagggat cactttcggc	300
cctgggacca aggtggagat caaa	324

<210> 27
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "DYAX5_VH"

<400> 27	
gaagttcaat tgtagagtc tggtagcgt cttgttcagc ctggtggttc tttacgtctt	60
tcttgcgctg cttccggatt cactttctct tcttacatta tggtttgggt tcgccaagct	120
cctggtaaag gtttggagtg ggtttcttct atctattctt ctggtggctc tacttcttat	180
gctgactccg ttaaaggctg cttcactatc tctagagaca actctaagaa tactctctac	240
ttgcagatga acagcttaag ggctgaggac acagccgtgt attactgtac gagatacagc	300

agatggttcg ggcagctagg gttttactcc cactacgcta tggacgtctg gagccaaggg 360
accacggtca ccgtctcaag c 381

<210> 28
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> "DYAX5_VL"

<400> 28
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgtg gacgttcggc 300
caagggacca aggtggaaat caaa 324

<210> 29
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> "AM40 & SC4017 & CAT5D9_HCDR1"

<400> 29

Ser Tyr Ala Leu Ser
1 5

<210> 30
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> AM40 & SC4017_HCDR2"

<400> 30

Thr Arg Pro Pro Thr Ser Arg Thr Ala Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 31
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> "AM40 & SC4017_HCDR3"

<400> 31

Asn	Asp	Phe	Val	Tyr	Gly	Ser	Tyr	Arg	Phe
1				5					10

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> "AM40 & CAT5D9_LCDR1"

<400> 32

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

<210> 33
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> "AM40 & SC4017 & CAT5D9_LCDR2"

<400> 33

Glu	Asp	Tyr	Gln	Arg	Pro	Ser
1				5		

<210> 34
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> "AM40 & SC4017_LCDR3"

<400> 34

Gln Ser Tyr Asp Asp Tyr Arg Arg Ala Ala
1 5 10

<210> 35

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> "SC4017_LCDR1"

<400> 35

Thr Arg Thr Ser Gly Trp Ile Ala Gly Tyr Phe Val Gln
1 5 10

<210> 36

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT5D9_HCDR2"

<400> 36

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

Gly

<210> 37

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT5D9_HCDR3"

<400> 37

Asn Asn Tyr Val Trp Gly Ser Tyr Arg Phe
1 5 10

<210> 38

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

<220>
<223> "CAT5D9_LCDR3"

<400> 38

Gln Ser Tyr Asp Asp Thr Ser Gln Gly Val
1 5 10

<210> 39
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_HCDR1"

<400> 39

Ser Tyr Ala Met Ser
1 5

<210> 40
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8 & CAT26_HCDR2"

<400> 40

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 41
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_HCDR3"

<400> 41

Ser Ser Gly Tyr Tyr Gly Ala Asn Phe Asp Phe
1 5 10

<210> 42
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_LCDR1"

<400> 42

Ser Gly Ser Ser Ser Asn Ile Gly Ser Gly Tyr Val Tyr
1 5 10

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_LCDR2"

<400> 43

Arg Asn Asn Gln Arg Pro Ser
1 5

<210> 44
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT8_LCDR3"

<400> 44

Ala Ala Trp Asp Asp Ser Leu Ser Gly Tyr Val
1 5 10

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> "CAT26_HCDR1"

<400> 45

Ser Tyr Ala Val Ser
1 5

<210> 46

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT26_HCDR3"

<400> 46

Asp Ala Tyr Gly Ser Ser Trp Tyr Phe Tyr Tyr Phe Asp Tyr
1 5 10

<210> 47

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT26_LCDR1"

<400> 47

Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn Pro Val Asn
1 5 10

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT26_LCDR2"

<400> 48

Ser Asp Lys Tyr Arg Pro Ser
1 5

<210> 49

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT26_LCDR3"

<400> 49

Ala Ala Trp Asp Asp Ser Leu Asn Gly Arg Val
1 5 10

<210> 50

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> "DYAX3_HCDR1"

<400> 50

Met Tyr Glu Met Arg
1 5

<210> 51

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> "DYAX3_HCDR2"

<400> 51

Val Ile Pro Ser Gly Gly Lys Thr Phe Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 52

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> "DYAX3 & DYAX5_HCDR3"

<400> 52

Tyr Ser Arg Trp Phe Gly Gln Leu Gly Phe Tyr Ser His Tyr Ala Met
1 5 10 15

Asp Val

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

<220>
<223> "DYAX3_LCDR1"

<400> 53

Arg Ala Ser Gln Ser Ile Asp Thr Tyr Leu Asn
1 5 10

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

<220>
<223> "DYAX3_LCDR2"

<400> 54

Ala Ala Ser Lys Leu Glu Asp
1 5

<210> 55
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> "DYAX3_LCDR3"

<400> 55

Gln Gln Ser Tyr Ser Ser Pro Gly Ile Thr
1 5 10

<210> 56
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> "DYAX5_HCDR1"

<400> 56

Ser Tyr Ile Met Val

1 5

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> "DYAX5_HCDR2"

<400> 57

Ser Ile Tyr Ser Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 58
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> "DYAX5_LCDR1"

<400> 58

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

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> "DYAX_LCDR2"

<400> 59

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> "DYAX_LCDR3"

<400> 60

Gln Gln Ser Tyr Ser Thr Pro Pro Trp Thr
1 5 10

<210> 61

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> "AM40_HC"

<400> 61

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

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

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

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

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

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

Ala Ser Asn Asp Phe Val Tyr Gly Ser Tyr Arg Phe Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

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

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

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

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

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

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr

355

360

365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

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

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

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

Lys

<210> 62

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> "AM40_LC"

<400> 62

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15

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

Phe Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
 35 40 45

Ile Tyr Glu Asp Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly

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

<210> 63
 <211> 1347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "AM40_HC"

<400> 63	
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cttctggagg caccttcagc agttatgctc ttagctgggt gcgacaggcc	120
cctggacaag ggcttgagtg gatgggaacg cggccgccga cctcccgac agcaagctac	180

gcacagaaat ttcagggcag agtcacgatt accgtggacg aatccacgag cacaggctac	240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gtcaaacgac	300
ttcgtgtacg ggagttatcg tttctggggc caagggacca cggtcaccgt ctctcagcg	360
tcgaccaagg gcccatccgt cttccccctg gcaccctcct ccaagagcac ctctgggggc	420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcctgg	480
aactcaggcg ctctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga	540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac	600
atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagagagt tgagcccaaa	660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaattcga ggggggaccg	720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag	780
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac	840
gtggacggcg tggagggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc	900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	960
tacaagtgca aggtctccaa caaagccctc ccagcctcca tcgagaaaac catctccaaa	1020
gccaaagggc agccccgaga accacaggctc tacaccctgc ccccatcccg ggaggagatg	1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc	1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1200
gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag cagggtggcag	1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	1320
aagagcttaa gcctgtctcc gggtaaa	1347

<210> 64
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "AM40_LC"

<400> 64	
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc	60
tcctgcaccc gcaccagtgg gaacattgcc ggctactttg tgcaagggtg ccagcagcgc	120

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ccgggcagtt cccccaccac tgtgatctat gaggattacc aacgaccctc tggggtcctt      180
gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga      240
ctgaagactg aggacgaggc tgactactat tgtcagtcctt atgatgacta ccggcgggcg      300
gcgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggcggc gccctcggtc      360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc      540
agctacctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a                651

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```

<210> 65
<211> 449
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> "SC4017_HC"

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```

<400> 65

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```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Ser Asn Asp Phe Val Tyr Gly Ser Tyr Arg Phe Trp Gly Gln Gly

```

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

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

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

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

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

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

Lys

<210> 66
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> "SC4017_LC"

<400> 66

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys Thr Arg Thr Ser Gly Trp Ile Ala Gly Tyr
20 25 30

Phe Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asp
85 90 95

Tyr Arg Arg Ala Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

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

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 67
<211> 1486
<212> DNA
<213> Artificial Sequence

<220>

<223> "SC4017_HC"

<400> 67

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtaa ggggctcaca	60
gtagcaggct tgagggtctag acatatatat ggggtgacaat gacatccact ttgcctttct	120
ctccacaggt gtacactccc aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc	180
tgggtcctcg gtgaagggtct cctgcaaggc ttctggaggc accttcagca gttatgctct	240
tagctgggtg cgacaggccc ctggacaagg gcttgagtgg atgggaacgc ggccgccgac	300
ctcccggaca gcaagctacg cacagaaatt tcagggcaga gtcacgatta ccgtggacga	360
atccacgagc acaggctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta	420
ttactgtgcg tcaaacgact tcgtgtacgg gagttatcgt ttctggggcc aagggaccac	480
ggtcaccgtc tcctcagcgt cgaccaaggg cccatccgtc ttccccctgg caccctcctc	540
caagagcacc tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga	600
accggtgacg gtgtcctgga actcaggcgc tctgaccagc ggcgtgcaca cttccccggc	660
tgtcctacag tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag	720
cttgggcacc cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaaggtgga	780
caagagagtt gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc	840
tgaattcgag ggggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat	900
gatctcccgg acccctgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga	960
ggtcaagttc aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg	1020
ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga	1080
ctggctgaat ggcaaggagt acaagtgaac ggtctccaac aaagccctcc cagcctccat	1140
cgagaaaacc atctccaaag ccaaagggca gccccgagaa ccacagggtct acaccctgcc	1200
cccatcccgg gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt	1260
ctatcccagc gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa	1320
gaccacgcct cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt	1380
ggacaagagc aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct	1440
gcacaaccac tacacgcaga agagcttaag cctgtctccg ggtaaa	1486

<210> 68
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "SC4017_LC"

<400> 68
 aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60
 tcctgcaccc gcaccagtgg gtggattgcc ggctactttg tgcagtggta ccagcagcgc 120
 ccgggcagtt cccccaccac tgtgatctat gaggattacc aacgaccctc tggggtcctt 180
 gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga 240
 ctgaagactg aggacgaggc tgactactat tgtcagtctt atgatgacta ccggcgggcg 300
 gcgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggcggc gccctcggtc 360
 actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
 ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540
 agctacctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 69
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> "CAT5D9_HC"

<400> 69

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

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

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

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

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

Ile Glu Leu Ser Ser Leu Lys Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Ser Asn Asn Tyr Val Trp Gly Ser Tyr Arg Phe Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

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

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

260

265

270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

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

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
 325 330 335

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

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

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

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

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

Lys

<210> 70

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> "CAT5D9_LC"

<400> 70

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

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

Phe Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Arg Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

Leu Lys Pro Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asp
85 90 95

Thr Ser Gln Gly Val Phe Gly Ala Gly Thr Lys Val Thr Val Leu Gly
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

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

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> 71
 <211> 1346
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> "CAT5D9_HC"

<400> 71
 aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc tgggtcctcg gtgaaggtct 60
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