

SEQUENCE LISTING

<110> BeiGene
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<120> Anti-Tim-3 Antibodies and Use Thereof

<130> BGB110

<160> 43

<170> PatentIn version 3.5

<210> 1

<211> 301

<212> PRT

<213> Homo sapiens

<400> 1

Met	Phe	Ser	His	Leu	Pro	Phe	Asp	Cys	Val	Leu	Leu	Leu	Leu	Leu	Leu
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Leu	Leu	Thr	Arg	Ser	Ser	Glu	Val	Glu	Tyr	Arg	Ala	Glu	Val	Gly	Gln
			20					25					30		

Asn	Ala	Tyr	Leu	Pro	Cys	Phe	Tyr	Thr	Pro	Ala	Ala	Pro	Gly	Asn	Leu
		35					40					45			

Val	Pro	Val	Cys	Trp	Gly	Lys	Gly	Ala	Cys	Pro	Val	Phe	Glu	Cys	Gly
	50					55					60				

Asn	Val	Val	Leu	Arg	Thr	Asp	Glu	Arg	Asp	Val	Asn	Tyr	Trp	Thr	Ser
65					70					75					80

Arg	Tyr	Trp	Leu	Asn	Gly	Asp	Phe	Arg	Lys	Gly	Asp	Val	Ser	Leu	Thr
				85					90					95	

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

Gln	Ile	Pro	Gly	Ile	Met	Asn	Asp	Glu	Lys	Phe	Asn	Leu	Lys	Leu	Val
		115					120					125			

Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
 130 135 140

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160

Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175

Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190

Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
 195 200 205

Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
 210 215 220

Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
 225 230 235 240

Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
 245 250 255

Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
 260 265 270

Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
 275 280 285

Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
 290 295 300

<210> 2
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
 1 5 10 15

Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
 20 25 30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
 35 40 45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
 50 55 60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
 65 70 75 80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
 85 90 95

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

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
 115 120 125

Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
 130 135 140

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160

Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175

Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190

Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly
 195 200

<210> 3
 <211> 5
 <212> PRT
 <213> Mus musculus

<400> 3

Arg Tyr Ala Met Ser
 1 5

<210> 4
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<212> PRT
<213> Mus musculus

<400> 4

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

<210> 5
<211> 11
<212> PRT
<213> Mus musculus

<400> 5

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

<210> 6
<211> 15
<212> PRT
<213> Mus musculus

<400> 6

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

<210> 7
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<213> Mus musculus

<400> 7

Ala Ala Ser Asn Val Glu Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> Mus musculus

<400> 8

Gln Gln Ser Met Lys Val Pro Leu Thr
1 5

<210> 9
<211> 119
<212> PRT
<213> Mus musculus

<400> 9

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

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

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

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

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

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

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

Thr Thr Leu Thr Val Ser Ser
115

<210> 10

<211> 357

<212> DNA

<213> Mus musculus

<400> 10

gaagtgaagc tgggtggagtc tggggggaggc ttagtgaagc ctggaggggc cctgaaactc
60

tcctgtgcag cctctggatt cactttcagt aggtatgccca tgtcttgggt tcgccagatt
120

ccagagaaga ggctggagtg ggtcgcagcc attagtagtg gtggtagttt atactttcca
180

gacagtgtga agggccgatt caccatctcc agagataatg ccaggaacat ctgctacctg
240

caaatgaaca gtctgaggtc tgacgacacg gccatgtatt actgtgcaag aggccgggag
300

gccgacggag gctactttga ctactggggc caaggcacca ctctcacagt ctctca
357

<210> 11
 <211> 111
 <212> PRT
 <213> Mus musculus

<400> 11

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

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

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

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala
 50 55 60

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

Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Met
 85 90 95

Lys Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105 110

<210> 12
 <211> 333
 <212> DNA
 <213> Mus musculus

<400> 12

gacattgtgc tcaccaatc tccagcttct ttggctgtgt ctctagggca gagagccacc
 60

atctcctgca gagccagtga aagtgttgaa tattatggca caagtttaat gcagtggtag
 120

caacagaaac caggacaacc acccaaactc ctcatctatg ctgcatccaa cgtagaatct
 180

ggggtccctg ccaggttttag tggcagtggg tctgggacag acttcagcct caacatccat
 240

cctgtggagg aggatgatat tgcaatgtat ttctgtcagc aaagtatgaa ggttcctctc
 300

acgttcggtg ctgggaccaa gctggagctg aaa
333

<210> 13
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> ch425 heavy chain pro

<400> 13

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

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

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

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

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

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

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

Thr Thr Leu 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 Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Ala Ala Gly Pro Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 14
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> ch425 heavy chain DNA

<400> 14
gaagtgaagc tgggtggagtc tgggggaggc ttagtgaagc ctggaggggc cctgaaactc
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tcctgtgcag cctctggatt cactttcagt aggtatgcca tgtcttgggt tcgccagatt
120

ccagagaaga ggctggagtg ggtcgcagcc attagtagtg gtggtagttt atactttcca
180

gacagtgtga agggccgatt caccatctcc agagataatg ccaggaacat ctgctacctg
240

caaatgaaca gtctgaggtc tgacgacacg gccatgtatt actgtgcaag aggccgggag
300

gccgacggag gctactttga ctactggggc caaggcacca ctctcacagt ctctcagcc
360

tccaccaagg gcccatcggc cttccccctg gcaccctcct ccaagagtac ttctgggggc
420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg
480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga
540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac
600

atctgcaacg tgaatcaca gccagcaac accaagggtg acaagaaagt tgagcccaaa
660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctctgtctgc cggaccgtca
720

gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc
780

acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg
840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg
900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac
960

aagtgcaagg tctccaacaa agccctcgcc gcccccatcg agaaaaccat ctccaaagcc
1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc
1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg
1140

gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac
1200

tccgacggct ccttcttctc ctacagcaag ctcaccgtgg acaagagcag gtggcagcag
1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag
1320

agcctctccc tgtctccggg taaatga
1347

<210> 15
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> ch425 light chain pro

<400> 15

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

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

Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Val	Glu	Ser	Gly	Val	Pro	Ala
	50					55					60				

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His

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

<210> 16
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ch425 light chain DNA

<400> 16
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 60
 atctcctgca gagccagtga aagtgttgaa tattatggca caagtttaat gcagtggtag
 120
 caacagaaac caggacaacc acccaaactc ctcatctatg ctgcatccaa cgtagaatct
 180

ggggtccctg ccaggttttag tggcagtggg tctgggacag acttcagcct caacatccat
240

cctgtggagg aggatgatat tgcaatgtat ttctgtcagc aaagtatgaa ggttcctctc
300

acgttcggtg ctgggaccaa gctggagctg aaacgggctg atgctgcacc aactgtatcc
360

atcttccac catccagtga gcagttaaca tctggagggtg cctcagtcgt gtgcttcttg
420

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa
480

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc
540

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc
600

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttag
657

<210> 17
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> hu425-1-1 VH pro

<400> 17

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 18
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> hu425-1-1 VH DNA

<400> 18
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60

tcctgcgccg cttctggctt caccttttagc agatacgcca tgtcctgggt gcggcaggct
120

cctggcaagg gactggagtg ggtggccgct atcagctccg gcggctccct gtacttcccc
180

gattccgtga agggccgggt caccatcagc agggacaacg ccaagaacag ctgctatctg
240

cagatgaact ctctgagggc cgaggataca gccgtgtact attgcgctcg gggcagagaa
300

gcagatggcg gctacttcga ctattggggc cagggcaccc tggtgacagt gtctagc
357

<210> 19
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> hu425-1-1 VK pro

<400> 19

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

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

Arg Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala
 50 55 60

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

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

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

<210> 20
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hu425-1-1 VK DNA

<400> 20
 gacatcgtcc tgactcagtc ccctgccact ctgtcagtga gccaggaga gcgagctacc
 60

ctgtcctgca gagcatccga gtctgtcgaa tactatggca cctctctgat gcagtggtag
 120

cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt
 180

ggcgtcccag cacgcttcag tggctcaggg agcggaacag actttaccct gacaattagc
 240

tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcatgaa ggtccccctg
 300

acatttggcg ggggaactaa ggtggagatc aaa
 333

<210> 21
 <211> 329
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1mf pro

<400> 21

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 130 135 140

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 165 170 175

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 180 185 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 195 200 205

Ala Leu Ala Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 210 215 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 225 230 235 240

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

			100					105					110		
Thr	Leu	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	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys
	210					215					220				
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Ala	Ala	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Ala	Ala	Pro	Ile	Glu	Lys	Thr
				325					330					335	

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

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

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

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

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

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

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

<210> 23
 <211> 1347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hu425-1-1 heavy chain DNA

<400> 23
 gaagtgcagc tggtcgaatc aggggggggg ctggtgcagc ctggaggcag cctgagactg
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tcctgcgccg cttctggctt cacctttagc agatacgcca tgtcctgggt gcggcaggct
 120

cctggcaagg gactggagtg ggtggccgct atcagctccg gcggctccct gtacttcccc
 180

gattccgtga agggccggtt caccatcagc agggacaacg ccaagaacag ctgctatctg
 240

cagatgaact ctctgagggc cgaggataca gccgtgtact attgcgctcg gggcagagaa
 300

gcagatggcg gctacttcga ctattggggc cagggcaccc tggtgacagt gtctagcgct
 360

agcaccaaag gccccagcgt gtttcctctg gctccatcct ctaaatccac ctctggcggc
 420

acagccgctc tgggctgtct ggtgaaggat tacttcccag agcccgtgac agtgtcttgg
480

aacagcggcg ccctgacctc cggcgtgcac acatttcctg ctgtgctgca gagctccggc
540

ctgtacagcc tgtctagcgt ggtgaccgtg ccatacctcta gcctggggcac ccagacatat
600

atctgcaacg tgaatcacao gccagcaat acaaagggtg ataagaagggt ggagccaaag
660

tcctgtgaca agaccacac atgccccct tgtcctgctc caccagctgc aggaccaagc
720

gtgttcctgt ttccacccaa gcccaaggat accctgatga tctctcggac ccagaggtg
780

acatgcgtgg tgggtggatgt gagccacgag gaccccgagg tgaagttcaa ctggtatgtg
840

gacggcgtgg aggtgcacaa tgctaagacc aagcccaggg aggagcagta caactccacc
900

tatagagtgg tgtctgtgct gacagtgctg caccaggatt ggctgaacgg caaggagtat
960

aagtgcgaagg tgtccaataa ggccctggcc gtcctatcg agaagaccat ctctaaggcc
1020

aagggccagc ccagagagcc tcaggtgtac aactgcctc catcccggga tgagctgacc
1080

aagaaccagg tgtctctgac atgtctggtc aagggttct atccctctga catcgccgtg
1140

gagtgggaga gcaatggcca gcctgagaac aattacaaga ccacaccccc tgtgctggat
1200

tccgacggct ctttctttct gtatagcaag ctgaccgtgg acaagtcccg gtggcagcag
1260

ggcaacgtgt tcagctgttc cgtgatgcac gaagctctgc ataatacta tactcagaaa
1320

tcctgtcac tgtcacctgg taaatga
1347

<210> 24

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> hu425-1-1 light chain pro

<400> 24

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

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

Arg Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala
50 55 60

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

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

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

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

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

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

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

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

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

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

<210> 25
 <211> 657
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hu425-1-1 light chain DNA

 <400> 25
 gacatcgtcc tgactcagtc ccctgccact ctgtcagtga gcccaggaga gcgagctacc
 60

 ctgtcctgca gagcatccga gtctgtcgaa tactatggca cctctctgat gcagtggtag
 120

 cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt
 180

 ggcgtcccag cacgcttcag tggctcaggg agcggaacag actttaccct gacaattagc
 240

 tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcatgaa ggtccccctg
 300

 acatttggcg ggggaactaa ggtggagatc aaacgaacag tggcagcccc ttccgtcttc
 360

 atttttcccc cttctgacga acagctgaaa tcaggaactg ctagcgtggg ctgtctgctg
 420

 aacaatttct accccagaga ggccaagggt cagtggaaaag tcgataacgc tctgcagtcc
 480

 ggcaattctc aggagagtgt gaccgaacag gactcaaagg atagcacata ttccctgtct
 540

 agtactctga ccctgagcaa agcagactac gagaagcaca aagtgtatgc ctgtgaagtc
 600

 acacaccagg ggctgagttc accagtcacc aagagtttca acagagggga atgctaa
 657

<210> 26
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu425-2-2 HCDR2

<400> 26

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

<210> 27

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

<220>
<223> hu425-2-2 LCDR3

<400> 27

Gln Gln Ser Leu Lys Val Pro Leu Thr
1 5

<210> 28
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> hu425-2-2 VH pro

<400> 28

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 29
<211> 357
<212> DNA

<213> Artificial Sequence

<220>

<223> hu425-2-2 VH DNA

<400> 29

gaagtgcagc tggtcgaatc aggggggggg ctggtgcagc ctggaggcag cctgagactg
60

tcctgcgccg cttctggctt caccttttagc agatacgcca tgtcctgggt gcggcaggct
120

cctggcaagg gactggagtg ggtggccgct atcagctccg gcggctccct gtactatccc
180

gattccgtga agggccggtt caccatcagc agggacaacg ccaagaacac actgtatctg
240

cagatgaact ctctgagggc cgaggataca gccgtgtact attgcgctcg gggcagagaa
300

gcagatggcg gctacttcga ctattggggc cagggcaccc tggtgacagt gtctagc
357

<210> 30

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> hu425-2-2 VK pro

<400> 30

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

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

Arg Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
65 70 75 80

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

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

<210> 31
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> hu425-2-2 VK DNA

<400> 31
gagatcgtca tgactcagtc ccctgccact ctgtcagtga gcccaggaga gcgagctacc
60

ctgtcctgca gagcatccga gtctgtcgaa tactatggca cctctctgat gcagtggtag
120

cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt
180

ggcatcccag cacgcttcag tggctcaggg agcggaacag agtttaccct gacaattagc
240

tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcctgaa ggtccccctg
300

acatttggcg ggggaactaa ggtggagatc aaa
333

<210> 32
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> hu425-2-2 heavy chain pro

<400> 32

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

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

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

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

Thr Leu 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 Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Ala Ala Gly Pro Ser
225 230 235 240

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

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

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

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

290	295	300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr 305 310 315 320		
Lys Cys Lys Val Ser Asn Lys Ala Leu Ala Ala Pro Ile Glu Lys Thr 325 330 335		
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu 340 345 350		
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys 355 360 365		
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser 370 375 380		
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp 385 390 395 400		
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser 405 410 415		
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala 420 425 430		
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 435 440 445		

<210> 33
 <211> 1347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hu425-2-2 heavy chain DNA

<400> 33
 gaagtgcagc tggtcgaatc aggggggggg ctggtgcagc ctggaggcag cctgagactg
 60
 tcctgcgccg cttctggctt caccttttagc agatacgcca tgtcctgggt gcggcaggct
 120
 cctggcaagg gactggagtg ggtggccgct atcagctccg gcggctccct gtactatccc
 180

gattccgtga agggccgggtt caccatcagc agggacaacg ccaagaacac actgtatctg
240
cagatgaact ctctgagggc cgaggataca gccgtgtact attgcgctcg gggcagagaa
300
gcagatggcg gctacttcga ctattggggc cagggcaccc tggtgacagt gtctagcgct
360
agcaccaaag gccccagcgt gtttcctctg gctccatcct ctaaateccac ctctggcggc
420
acagccgctc tgggctgtct ggtgaaggat tacttcccag agcccgtgac agtgtcttgg
480
aacagcggcg ccctgacctc cggcgtgcac acatttcctg ctgtgctgca gagctccggc
540
ctgtacagcc tgtctagcgt ggtgaccgtg ccatcctcta gcctgggcac ccagacatat
600
atctgcaacg tgaatcacia gccagcaat acaaagggtg ataagaagggt ggagccaaag
660
tcctgtgaca agaccacac atgccccctt tgtcctgctc caccagctgc aggaccaagc
720
gtgttcctgt ttccacccaa gcccaaggat accctgatga tctctcggac ccagaggtg
780
acatgcgtgg tggatggatgt gagccacgag gaccccgagg tgaagttcaa ctggtatgtg
840
gacggcgtgg aggtgcacia tgctaagacc aagcccaggg aggagcagta caactccacc
900
tatagagtgg tgtctgtgct gacagtgtg caccaggatt ggctgaacgg caaggagtat
960
aagtgcagg tgtccaataa ggcctggcc gtcctatcg agaagaccat ctctaaggcc
1020
aagggccagc ccagagagcc tcaggtgtac aactgcctc catcccggga tgagctgacc
1080
aagaaccagg tgtctctgac atgtctggtc aagggttct atccctctga catcgccgtg
1140
gagtgggaga gcaatggcca gcctgagaac aattacaaga ccacaccccc tgtgctggat
1200
tccgacggct ctttctttct gtatagcaag ctgaccgtgg acaagtcccg gtggcagcag
1260
ggcaacgtgt tcagctgttc cgtgatgcac gaagctctgc ataataccta tactcagaaa
1320

tccctgtcac tgtcacctgg taaatga
1347

<210> 34
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> hu425-2-2 light chain pro

<400> 34

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

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

Arg Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
65 70 75 80

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

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

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

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

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

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

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

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

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

<210> 35
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hu425-2-2 light chain DNA

<400> 35
 gagatcgtca tgactcagtc ccctgccact ctgtcagtga gcccaggaga gcgagctacc
 60

ctgtcctgca gagcatccga gtctgtcgaa tactatggca cctctctgat gcagtggtag
 120

cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt
 180

ggcatcccag cacgcttcag tggctcaggg agcggaacag agtttaccct gacaattagc
 240

tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcctgaa ggtccccctg
 300

acatttggcg ggggaactaa ggtggagatc aaacgaacag tggcagcccc ttccgtcttc
 360

atttttcccc cttctgacga acagctgaaa tcaggaactg ctagcgtggt ctgtctgctg
 420

aacaatttct accccagaga ggccaaggtg cagtggaaag tcgataacgc tctgcagtcc
 480

ggcaattctc aggagagtgt gaccgaacag gactcaaagg atagcacata ttccctgtct
 540

agtactctga ccctgagcaa agcagactac gagaagcaca aagtgtatgc ctgtgaagtc
 600

acacaccagg ggctgagttc accagtcacc aagagtttca acagagggga atgctaa
 657

<210> 36
 <211> 111
 <212> PRT

<213> Artificial Sequence

<220>

<223> hu425-2-3b VK pro

<400> 36

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

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

Arg Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
65 70 75 80

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

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

<210> 37

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> hu425-2-3b VK DNA

<400> 37

gagatcgctc tgactcagtc ccctgccact ctgtcagtga gcccaggaga gcgagctacc
60

ctgtcctgca gagcatccga gtctgtcgaa tactatggca cctctctgat gcagtggtag
120

cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt
180

ggcatcccag cagcgttcag tggctcaggg agcggaacag agtttaccct gacaattagc
240

tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcctgaa ggtccccctg
300

acatttggcg ggggaactaa ggtggagatc aaa
333

<210> 38
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> hu425-2-3b light chain pro

<400> 38

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

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

Arg Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
65 70 75 80

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

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

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

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

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

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

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

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

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

<210> 39
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> hu425-2-3b light chain DNA

<400> 39
gagatcgtcc tgactcagtc ccctgccact ctgtcagtga gcccaggaga gcgagctacc
60

ctgtcctgca gagcatccga gtctgtcgaa tactatggca cctctctgat gcagtgggtac
120

cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt
180

ggcatcccag cacgcttcag tggctcaggg agcggaacag agttttaccct gacaattagc
240

tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcctgaa ggtccccctg
300

acatttggcg ggggaactaa ggtggagatc aaacgaacag tggcagcccc ttccgtcttc
360

atttttcccc cttctgacga acagctgaaa tcaggaactg ctagcgtggg ctgtctgctg
420

aacaatttct accccagaga ggccaaggtg cagtggaaaag tcgataacgc tctgcagtcc
480

ggcaattctc aggagagtgt gaccgaacag gactcaaagg atagcacata ttccctgtct
540

agtactctga ccctgagcaa agcagactac gagaagcaca aagtgtatgc ctgtgaagtc
600

acacaccagg ggctgagttc accagtcacc aagagtttca acagagggga atgctaa
657

<210> 40
<211> 118

<212> PRT
<213> Artificial Sequences

<220>
<223> artificial sequences

<400> 40

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 Tyr Thr Phe Thr Ser Tyr
20 25 30

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

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

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Val 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 Arg Val Gly Gly Ala Phe Pro Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 41
<211> 111
<212> PRT
<213> Artificial Sequences

<220>
<223> artificial sequences

<400> 41

Ala Ile Gln Leu 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 Glu Ser Val Glu Tyr Tyr
20 25 30

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

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ser
 50 55 60

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

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

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

<210> 42
 <211> 114
 <212> PRT
 <213> Artificial Sequences

<220>
 <223> artificial sequences

<400> 42

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 Ala Ser Gly Phe Thr Phe Ser Ser
 20 25 30

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

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

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

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

Cys Ala Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 100 105 110

Ser Ala

<210> 43

<211> 108

<212> PRT

<213> Artificial Sequences

<220>

<223> artificial sequences

<400> 43

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 Arg Arg Tyr
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105