

spec.txt
SEQUENCE LISTING

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<110>  BeiGene
        Zhang, Tong
        Xue, Liu
        Liu, Qi
        Peng, Hao
        Wei, Min
        Liu, Qi
        Li, Kang

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

<130>  SP100716SGM

<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
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

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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 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

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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
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<213> Mus musculus

<400> 3

Arg Tyr Ala Met Ser
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<210> 4
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<400> 4

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

<210> 5
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Gly Arg Glu Ala Asp Gly Gly Tyr Phe Asp Tyr
1 5 10

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

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<210> 7
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<400> 7

Ala Ala Ser Asn Val Glu Ser
 1 5

<210> 8
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 <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
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<210> 10
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 <213> Mus musculus

<400> 10

spec.txt

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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	ctcctca	357

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

<400> 11

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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
			100					105					110	

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 <212> DNA
 <213> Mus musculus

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caacagaaac	caggacaacc	acccaaactc	ctcatctatg	ctgcatccaa	cgtagaatct	180
ggggtccctg	ccaggtttag	tggcagtggg	tctgggacag	acttcagcct	caacatccat	240
cctgtggagg	aggtatgat	tgcaatgtat	ttctgtcagc	aaagtatgaa	ggttcctctc	300
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<210> 13

spec.txt

<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

spec.txt

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
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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>
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ccagagaaga ggctggagtg ggtcgcagcc attagtagtg gtggtagttt atactttcca 180

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                                spec.txt
gacagtgtga agggccgatt caccatctcc agagataatg ccaggaacat ctgctacctg      240
caaatgaaca gtctgaggtc tgacgacacg gccatgtatt actgtgcaag aggccgggag      300
gccgacggag gctactttga ctactggggc caaggcacca ctctcacagt ctctcagcc      360
tccaccaagg gcccatcggg cttccccctg gcaccctcct ccaagagtac ttctgggggc      420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      480
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga      540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac      600
atctgcaacg tgaatcacia gccagcaac accaagggtg acaagaaagt tgagcccaaa      660
tcttgtgaca aaactcacac atgccaccg tgcccagcac ctctgtctgc cggaccgtca      720
gtcttctct tcccccaaa acccaaggac acctcatga tctccggac ccctgaggtc      780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg      900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac      960
aagtgcaagg tctccaacia agccctcgcc gccccatcg agaaaaccat ctccaaagcc     1020
aaagggcagc cccgagaacc acaggtgtac acctgcccc catcccggga tgagctgacc     1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg     1140
gagtgaggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac     1200
tccgacggct ctttcttct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag     1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cagcagaag     1320
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<210> 15
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<212> PRT
<213> Artificial Sequence

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<220>
<223> ch425 light chain pro
<400> 15

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

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

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```

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

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```

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

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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
                                Page 8

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

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<211> 657
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caacagaaac	caggacaacc	acccaaactc	ctcatctatg	ctgcatccaa	cgtagaatct		180
ggggtccctg	ccaggtttag	tggcagtg	tctgggacag	acttcagcct	caacatccat		240
cctgtggagg	aggatgat	tgcaatgtat	ttctgtcagc	aaagtatgaa	ggttcctctc		300
acgttcggtg	ctgggaccaa	gctggagctg	aaacgggctg	atgctgcacc	aactgtatcc		360
atcttccac	catccagtga	gcagttaaca	tctggagg	cctcagtcgt	gtgttcttg		420
aacaacttct	accccaaaga	catcaatgtc	aagtggaaga	ttgatggcag	tgaacgacaa		480
aatggcgctc	tgaacagttg	gactgatcag	gacagcaaag	acagcaccta	cagcatgagc		540
agcaccctca	cgttgaccaa	ggacgagtat	gaacgacata	acagctatac	ctgtgaggcc		600

spec.txt
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
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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
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<212> DNA
<213> Artificial Sequence

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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 gtctagc 357

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 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
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 cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt 180
 ggcgtcccag cacgcttcag tggctcaggg agcggaacag actttaccct gacaattagc 240
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<210> 21
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 <213> Artificial Sequence

<220>
 <223> IgG1mf pro

<400> 21

spec.txt

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
245 250 255

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
260 265 270

spec.txt

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
275 280 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
290 295 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 22
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<212> PRT
<213> Artificial Sequence

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

<400> 22

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 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

Gln Ser Ser Gly₁₈₀ Leu Tyr Ser Leu Ser₁₈₅ Ser Val Val Thr Val₁₉₀ Pro Ser

Ser Ser Leu₁₉₅ Gly Thr Gln Thr Tyr₂₀₀ Ile Cys Asn Val Asn₂₀₅ His Lys Pro

Ser Asn₂₁₀ Thr Lys Val Asp Lys₂₁₅ Lys Val Glu Pro Lys₂₂₀ Ser Cys Asp Lys

Thr₂₂₅ His Thr Cys Pro Pro₂₃₀ Cys Pro Ala Pro Pro₂₃₅ Ala Ala Gly Pro Ser₂₄₀

Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg

Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro

Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala

Lys Thr₂₉₀ Lys Pro Arg Glu Glu₂₉₅ Gln Tyr Asn Ser Thr₃₀₀ Tyr Arg Val Val

Ser₃₀₅ Val Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀

Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Ala₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr

Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu

Pro Pro Ser₃₅₅ Arg Asp Glu Leu Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys

Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser

Asn₃₈₅ Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀

Ser Asp Gly Ser₄₀₅ Phe Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp Lys₄₁₅ Ser

Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

435

440

445

<210> 23
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 <213> Artificial Sequence

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 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 ctaaateccac ctctggcggc 420
 acagccgctc tgggctgtct ggtgaaggat tacttcccag agcccgtgac agtgtcttgg 480
 aacagcggcg ccctgacctc cggcgtgcac acatttcctg ctgtgctgca gagctccggc 540
 ctgtacagcc tgtctagcgt ggtgaccgtg ccacccctta gcctgggcac ccagacatat 600
 atctgcaacg tgaatcacia gccagcaat acaaagggtg ataagaagggt ggagccaaag 660
 tcctgtgaca agaccacac atgccccctt tgtcctgctc caccagctgc aggaccaagc 720
 gtgttcctgt ttccaccaa gcccaaggat accctgatga tctctcggac ccagagggtg 780
 acatgcgtgg tgggtggatgt gagccacgag gaccccgagg tgaagttcaa ctggtatgtg 840
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 aagtgcagg tgtccaataa ggccctggcc gtcctatcg agaagaccat ctctaaggcc 1020
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 tccgacggct ctttctttct gtatagcaag ctgaccgtgg acaagtcccg gtggcagcag 1260
 ggcaacgtgt tcagctgttc cgtgatgcac gaagctctgc ataataccta tactcagaaa 1320
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<210> 24
 <211> 218
 <212> PRT
 <213> Artificial Sequence

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

<400> 24

spec.txt

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 ctgtcagtg gcccaggaga gcgagctacc

60

spec.txt

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cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt 180
ggcgtcccag cacgcttcag tggctcaggg agcgggaacag actttaccct gacaattagc 240
tccctgcaga gtgaagattt cgccgtgtac tattgccagc agagcatgaa ggtccccctg 300
acatttggcg ggggaactaa ggtggagatc aaacgaacag tggcagcccc ttccgtcttc 360
atttttcccc cttctgacga acagctgaaa tcaggaactg ctagcgtggt ctgtctgctg 420
aacaatttct accccagaga ggccaagggt 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> 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
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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
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 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
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50

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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
gagatcg tca 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

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
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 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 gtctagcgct 360
 agcaccaaag gccccagcgt gtttcctctg gctccatcct ctaaattccac ctctggcggc 420
 acagccgctc tgggctgtct ggtgaaggat tacttcccag agcccgtgac agtgtcttgg 480
 aacagcggcg ccctgacctc cggcgtgcac acatttcctg ctgtgctgca gagctccggc 540
 ctgtacagcc tgtctagcgt ggtgaccgtg ccattcctta gcctgggcac ccagacatat 600
 atctgcaacg tgaatcacia gccagcaat acaaagggtg ataagaagggt ggagccaaag 660
 tcctgtgaca agaccacac atgccccct tgtcctgctc caccagctgc aggaccaagc 720
 gtgttcctgt ttccaccaa gcccaaggat accctgatga tctctcggac ccagagggtg 780
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 gacggcgtgg aggtgcacia tgctaagacc aagcccaggg aggagcagta caactccacc 900
 tatagagtgg tgtctgtgct gacagtgtg caccaggatt ggctgaacgg caaggagtat 960
 aagtgcagg tgtccaataa ggccctggcc gtcctatcg agaagaccat ctctaaggcc 1020
 aagggccagc ccagagagcc tcaggtgtac aactgcctc catcccggga tgagctgacc 1080

spec.txt

aagaaccagg tgtctctgac atgtctggtc aagggcttct atccctctga catcgccgtg	1140
gagtgggaga gcaatggcca gcctgagaac aattacaaga ccacaccccc tgtgctggat	1200
tccgacggct ctttctttct gtatagcaag ctgaccgtgg acaagtcccg gtggcagcag	1260
ggcaacgtgt tcagctgttc cgtgatgcac gaagctctgc ataatcacta 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

spec.txt

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
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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 ggccaagggt 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

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
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 cagcagaagc cagggcaggc tcccaggctg ctgatctatg ccgcttctaa cgtggagagt 180
 ggcatcccag cacgcttcag tggctcaggg agcggaaacag agttttaccct 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 ggccaagggt 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> 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
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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