

SEQUENCE LISTING

<110> AGENSYS, INC.
SEAGEN INC.

<120> TREATMENT OF CANCERS WITH ANTIBODY DRUG CONJUGATES (ADC) THAT
BIND TO 191P4D12 PROTEINS

<130> 14369-252-228

<140>

<141>

<150> US 62/944,890

<151> 2019-12-06

<150> US 62/940,209

<151> 2019-11-25

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3464

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (264)...(1796)

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<221> misc_feature

<222> (1)...(3464)

<223> 191P4D12

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tcccctagtg gagacccaag tgcgagaggc aagaactctg cagcttctg ccttctgggt 180
cagttccta ttcaagtctg cagccggctc ccagggagat ctggtggaa cttcagaaac 240
gctgggcagt ctgccattca acc atg ccc ctg tcc ctg gga gcc gag atg tgg 293

Met Pro Leu Ser Leu Gly Ala Glu Met Trp

1 5 10

ggg cct gag gcc tgg ctg ctg ctg cta ctg ctg gca tca ttt aca 341

Gly Pro Glu Ala Trp Leu Leu Leu Leu Leu Leu Leu Ala Ser Phe Thr

15 20 25

ggc cgg tgc ccc gcg ggt gag ctg gag acc tca gac gtg gta act gtg 389

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

30 35 40

gtg ctg ggc cag gac gca aaa ctg ccc tgc ttc tac cga ggg gac tcc 437

Val Leu Gly Gln Asp Ala Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser

45 50 55

ggc gag caa gtg ggg caa gtg gca tgg gct cgg gtg gac gcg ggc gaa 485

Gly Glu Gln Val Gly Gln Val Ala Trp Ala Arg Val Asp Ala Gly Glu

60 65 70

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Gly Ala Gln Glu Leu Ala Leu Leu His Ser Lys Tyr Gly Leu His Val
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agc ccg gct tac gag ggc cgc gtg gag cag ccg ccg ccc cca cgc aac 581
Ser Pro Ala Tyr Glu Gly Arg Val Glu Gln Pro Pro Pro Pro Arg Asn
95      100     105

ccc ctg gac ggc tca gtg ctc ctg cgc aac gca gtg cag gcg gat gag 629
Pro Leu Asp Gly Ser Val Leu Leu Arg Asn Ala Val Gln Ala Asp Glu
110     115     120

ggc gag tac gag tgc cgg gtc agc acc ttc ccc gcc ggc agc ttc cag 677
Gly Glu Tyr Glu Cys Arg Val Ser Thr Phe Pro Ala Gly Ser Phe Gln
125     130     135

gcg cgg ctg cgg ctc cga gtg ctg gtg cct ccc ctg ccc tca ctg aat 725
Ala Arg Leu Arg Leu Arg Val Leu Val Pro Pro Leu Pro Ser Leu Asn
140     145     150

cct ggt cca gca cta gaa gag ggc cag ggc ctg acc ctg gca gcc tcc 773
Pro Gly Pro Ala Leu Glu Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser
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tgc aca gct gag ggc agc cca gcc ccc agc gtg acc tgg gac acg gag 821
Cys Thr Ala Glu Gly Ser Pro Ala Pro Ser Val Thr Trp Asp Thr Glu
175     180     185

gtc aaa ggc aca acg tcc agc cgt tcc ttc aag cac tcc cgc tct gct 869
Val Lys Gly Thr Thr Ser Ser Arg Ser Phe Lys His Ser Arg Ser Ala
190     195     200

gcc gtc acc tca gag ttc cac ttg gtg cct agc cgc agc atg aat ggg 917
Ala Val Thr Ser Glu Phe His Leu Val Pro Ser Arg Ser Met Asn Gly
205     210     215

cag cca ctg act tgt gtg gtg tcc cat cct ggc ctg ctc cag gac caa 965
Gln Pro Leu Thr Cys Val Val Ser His Pro Gly Leu Leu Gln Asp Gln
220     225     230

agg atc acc cac atc ctc cac gtg tcc ttc ctt gct gag gcc tct gtg 1013
Arg Ile Thr His Ile Leu His Val Ser Phe Leu Ala Glu Ala Ser Val
235     240     245     250

agg ggc ctt gaa gac caa aat ctg tgg cac att ggc aga gaa gga gct 1061
Arg Gly Leu Glu Asp Gln Asn Leu Trp His Ile Gly Arg Glu Gly Ala
255     260     265

atg ctc aag tgc ctg agt gaa ggg cag ccc cct ccc tca tac aac tgg 1109
Met Leu Lys Cys Leu Ser Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp
270     275     280

aca cgg ctg gat ggg cct ctg ccc agt ggg gta cga gtg gat ggg gac 1157
Thr Arg Leu Asp Gly Pro Leu Pro Ser Gly Val Arg Val Asp Gly Asp
285     290     295

act ttg ggc ttt ccc cca ctg acc act gag cac agc ggc atc tac gtc 1205
Thr Leu Gly Phe Pro Pro Leu Thr Thr Glu His Ser Gly Ile Tyr Val
300     305     310

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 315 320 325 330

gat gtt ctt gac ccc cag gaa gac tct ggg aag cag gtg gac cta gtg 1301
 Asp Val Leu Asp Pro Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val
 335 340 345

tca gcc tcg gtg gtg gtg ggt gtg atc gcc gca ctc ttg ttc tgc 1349
 Ser Ala Ser Val Val Val Val Gly Val Ile Ala Ala Leu Leu Phe Cys
 350 355 360

ctt ctg gtg gtg gtg gtg ctc atg tcc cga tac cat cgg cgc aag 1397
 Leu Leu Val Val Val Val Val Leu Met Ser Arg Tyr His Arg Arg Lys
 365 370 375

gcc cag cag atg acc cag aaa tat gag gag gag ctg acc ctg acc agg 1445
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 380 385 390

gag aac tcc atc cgg agg ctg cat tcc cat cac acg gac ccc agg agc 1493
 Glu Asn Ser Ile Arg Arg Leu His Ser His His Thr Asp Pro Arg Ser
 395 400 405 410

cag ccg gag gag agt gta ggg ctg aga gcc gag ggc cac cct gat agt 1541
 Gln Pro Glu Glu Ser Val Gly Leu Arg Ala Glu Gly His Pro Asp Ser
 415 420 425

ctc aag gac aac agt agc tgc tct gtg atg agt gaa gag ccc gag ggc 1589
 Leu Lys Asp Asn Ser Ser Cys Ser Val Met Ser Glu Glu Pro Glu Gly
 430 435 440

cgc agt tac tcc acg ctg acc acg gtg agg gag ata gaa aca cag act 1637
 Arg Ser Tyr Ser Thr Leu Thr Thr Val Arg Glu Ile Glu Thr Gln Thr
 445 450 455

gaa ctg ctg tct cca ggc tct ggg cgg gcc gag gag gag gaa gat cag 1685
 Glu Leu Leu Ser Pro Gly Ser Gly Arg Ala Glu Glu Glu Glu Asp Gln
 460 465 470

gat gaa ggc atc aaa cag gcc atg aac cat ttt gtt cag gag aat ggg 1733
 Asp Glu Gly Ile Lys Gln Ala Met Asn His Phe Val Gln Glu Asn Gly
 475 480 485 490

acc cta cgg gcc aag ccc acg ggc aat ggc atc tac atc aat ggg cgg 1781
 Thr Leu Arg Ala Lys Pro Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg
 495 500 505

gga cac ctg gtc tga cccaggcctg cctccctcc ctaggcctgg ctcttctgt 1836
 Gly His Leu Val
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<223> 191P4D12

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Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala
35 40 45
Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
50 55 60
Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
65 70 75 80
Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
85 90 95
Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
100 105 110
Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
115 120 125
Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
130 135 140
Val Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu
145 150 155 160
Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser
165 170 175
Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser
180 185 190
Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe
195 200 205
His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val
210 215 220
Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu
225 230 235 240

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His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln
 245 250 255
 Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser
 260 265 270
 Glu Gly Gln Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
 275 280 285
 Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
 290 295 300
 Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
 305 310 315 320
 Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Asp Pro Gln
 325 330 335
 Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Val Val Val
 340 345 350
 Val Gly Val Ile Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val Val
 355 360 365
 Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr Gln
 370 375 380
 Lys Tyr Glu Glu Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg Arg
 385 390 395 400
 Leu His Ser His His Thr Asp Pro Arg Ser Gln Pro Glu Glu Ser Val
 405 410 415
 Gly Leu Arg Ala Glu Gly His Pro Asp Ser Leu Lys Asp Asn Ser Ser
 420 425 430
 Cys Ser Val Met Ser Glu Glu Pro Glu Gly Arg Ser Tyr Ser Thr Leu
 435 440 445
 Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu Leu Ser Pro Gly
 450 455 460
 Ser Gly Arg Ala Glu Glu Glu Asp Gln Asp Glu Gly Ile Lys Gln
 465 470 475 480
 Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu Arg Ala Lys Pro
 485 490 495
 Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His Leu Val
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 Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu
 10 15 20

gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga ctc 148
 Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

14369-252-228_SEQ_LISTING

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30

35

tcc tgt gca gcc tct gga ttc acc ttc agt agc tat aac atg aac tgg 196
 Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asn Met Asn Trp
 40 45 50 55

gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt tca tac att agt 244
 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser
 60 65 70

agt agt agt agt acc ata tac tac gca gac tct gtg aag ggc cga ttc 292
 Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
 75 80 85

acc atc tcc aga gac aat gcc aag aac tca ctg tct ctg caa atg aac 340
 Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Ser Leu Gln Met Asn
 90 95 100

agc ctg aga gac gag gac acg gct gtg tat tac tgt gcg aga gca tac 388
 Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Tyr
 105 110 115

tac tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc 436
 Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 120 125 130 135

tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc 484
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 140 145 150

aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac 532
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 155 160 165

tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc 580
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 170 175 180

agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac 628
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 185 190 195

tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag 676
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 200 205 210 215

acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac 724
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 220 225 230

aag aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg 772
 Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 235 240 245

tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc 820
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 250 255 260

cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca 868
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 265 270 275

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 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 280 285 290 295

tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg 964
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 300 305 310

gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc 1012
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 315 320 325

ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc 1060
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 330 335 340

aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa 1108
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 345 350 355

ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag 1156
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 360 365 370 375

gag atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc 1204
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 380 385 390

tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag 1252
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 395 400 405

aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc 1300
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 410 415 420

ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg 1348
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 425 430 435

aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac 1396
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
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<210> 4

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<212> PRT

<213> Homo sapiens

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<222> (1)...(466)

<223> Ha22-2(2,4)6.1 heavy chain

<400> 4

14369-252-228_SEQ_LISTING

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 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95
 Ser Leu Ser Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ala Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
 115 120 125
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 130 135 140
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 145 150 155 160
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 165 170 175
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 180 185 190
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 195 200 205
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 210 215 220
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 225 230 235 240
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 245 250 255
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 260 265 270
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 275 280 285
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 290 295 300
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 305 310 315 320
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 340 345 350
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 355 360 365
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 370 375 380
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 385 390 395 400
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 405 410 415
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 420 425 430
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
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 Gly Lys
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14369-252-228_SEQ_LISTING

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 Leu Gly Leu Leu Leu Trp Phe Pro Gly Ser Arg Cys Asp Ile Gln
 10 15 20 25

atg acc cag tct cca tct tcc gtg tct gca tct gtt gga gac aga gtc 147
 Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val
 30 35 40

acc atc act tgt cgg gcg agt cag ggt att agc ggc tgg tta gcc tgg 195
 Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Gly Trp Leu Ala Trp
 45 50 55

tat cag cag aaa cca ggg aaa gcc cct aag ttc ctg atc tat gct gca 243
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile Tyr Ala Ala
 60 65 70

tcc act ttg caa agt ggg gtc cca tca agg ttc agc ggc agt gga tct 291
 Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 75 80 85

ggg aca gat ttc act ctc acc atc agc agc ctg cag cct gaa gat ttt 339
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 90 95 100 105

gca act tac tat tgt caa cag gct aac agt ttc cct ccc act ttc ggc 387
 Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro Thr Phe Gly
 110 115 120

gga ggg acc aag gtg gag atc aaa cga act gtg gct gca cca tct gtc 435
 Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
 125 130 135

ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct 483
 Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 140 145 150

gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag 531
 Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 155 160 165

tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc 579

14369-252-228_SEQ_LISTING

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 170 175 180 185

aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg 627
 Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
 190 195 200

acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa 675
 Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 205 210 215

gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg 723
 Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 220 225 230

gga gag tgt tag 735
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 <221> misc_feature
 <222> (1)...(236)
 <223> Ha22-2(2,4)6.1 light chain

<400> 6
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15
 Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Gly Ile Ser Gly Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Phe Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Ala Asn Ser Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

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<210> 7
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(466)
 <223> Ha22-2(2,4)6.1 heavy chain

<400> 7
 Met Glu Leu Gly Leu Cys Trp Val Phe Leu Val Ala Ile Leu Glu Gly
 1 5 10 15
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95
 Ser Leu Ser Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ala Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
 115 120 125
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 130 135 140
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 145 150 155 160
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 165 170 175
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 180 185 190
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 195 200 205
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 210 215 220
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 225 230 235 240
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 245 250 255
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 260 265 270
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 275 280 285
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 290 295 300
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 305 310 315 320
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 340 345 350
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 355 360 365
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 370 375 380

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Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 385 390 395 400
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 405 410 415
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 420 425 430
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 435 440 445
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 450 455 460
 Gly Lys
 465

<210> 8

<211> 236

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(236)

<223> Ha22-2(2,4)6.1 light chain

<400> 8

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15
 Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Gly Ile Ser Gly Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Phe Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Ala Asn Ser Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 9

<211> 5

<212> PRT

<213> Homo sapiens

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<220>

<223> CDR1 of heavy chain

<400> 9

Ser Tyr Asn Met Asn

1 5

<210> 10

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<223> CDR2 of heavy chain

<400> 10

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 11

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> CDR3 of heavy chain

<400> 11

Ala Tyr Tyr Tyr Gly Met Asp Val

1 5

<210> 12

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<223> CDR1 of light chain

<400> 12

Arg Ala Ser Gln Gly Ile Ser Gly Trp Leu Ala

1 5 10

<210> 13

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<223> CDR2 of light chain

14369-252-228_SEQ_LISTING

<400> 13

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 14

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> CDR3 of light chain

<400> 14

Gln Gln Ala Asn Ser Phe Pro Pro Thr
1 5

<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 15

Gly Phe Leu Gly
1

<210> 16

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> VH CDR1 according to IMGT

<400> 16

Gly Phe Thr Phe Ser Ser Tyr Asn
1 5

<210> 17

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> VH CDR2 according to IMGT

<400> 17

Ile Ser Ser Ser Ser Ser Thr Ile
1 5

14369-252-228_SEQ_LISTING

<210> 18
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH CDR3 according to IMGT

<400> 18

Ala Arg Ala Tyr Tyr Tyr Gly Met Asp Val
 1 5 10

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

<220>
 <223> VL CDR1 according to IMGT

<400> 19

Gln Gly Ile Ser Gly Trp
 1 5

<210> 20
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL CDR2 according to IMGT

<400> 20

Ala Ala Ser
 1

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

<220>
 <223> VL CDR3 according to IMGT

<400> 21

Gln Gln Ala Asn Ser Phe Pro Pro Thr
 1 5

<210> 22
 <211> 117
 <212> PRT

14369-252-228_SEQ_LISTING

<213> Artificial Sequence

<220>

<223> heavy chain variable region (VH), the 20th amino acid (glutamic acid) to the 136th amino acid (serine) of SEQ ID NO:7

<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 Ser Tyr
20 25 30

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 23

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable region (VL), the 23rd amino acid (aspartic acid) to the 130th amino acid (arginine) of SEQ ID NO:8

<400> 23

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

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

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

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

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

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

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