

SEQUENCE LISTING

<110> The Board of Trustees of the Leland Stanford Junior University

<120> THERAPEUTIC ANTIBODIES AGAINST OSTEOPONTIN

<130> STAN-1658 (S19-253)

<150> 62/884,818

<151> 2019-08-09

<160> 47

<170> PatentIn version 3.5

<210> 1

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin epitope

<400> 1

Ser Val Val Gly Leu Arg
1 5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin epitope

<400> 2

Ser Lys Ser Lys Lys Phe
1 5

<210> 3

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin epitope

<400> 3

Ser Val Val Tyr Gly Leu Arg
1 5

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

<220>
<223> osteopontin epitope

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Ser Lys Ser Lys Lys Phe Arg Arg
1 5

<210> 5
<211> 7
<212> PRT
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<220>
<223> immunogenic peptide

<400> 5

Ser Leu Ala Tyr Gly Leu Arg
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<210> 6
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> immunogenic peptide

<400> 6

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

<210> 7
<211> 9
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<213> Artificial Sequence

<220>
<223> immunogenic peptide

<400> 7

Ser Lys Ser Arg Ser Phe Gln Val Ser
1 5

<210> 8

<211> 314

<212> PRT

<213> Homo sapiens

<300>

<308> NCBI/NP_001035147

<309> 2019-06-18

<313> (1)..(314)

<400> 8

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

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

Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
50 55 60

Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
65 70 75 80

Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
85 90 95

Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100 105 110

Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115 120 125

Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130 135 140

Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly
145 150 155 160

Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg
165 170 175

Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His
180 185 190

Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
195 200 205

Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
210 215 220

Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His
225 230 235 240

Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
245 250 255

His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
260 265 270

Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp
275 280 285

Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His
290 295 300

Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
305 310

<210> 9

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> osteopontin thrombin cleavage site

<400> 9

Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
 1 5 10

<210> 10
 <211> 10
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 <213> Artificial Sequence

<220>
 <223> OPN-CTF region

<400> 10

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 1 5 10

<210> 11
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> immunogenic peptide

<400> 11

Tyr Gly Leu Arg Ser Lys Ser
 1 5

<210> 12

<400> 12
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<210> 13
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 <213> Artificial Sequence

<220>
 <223> clone encoding A2 monoclonal antibody heavy chain 3

<220>
 <221> CDS
 <222> (1)..(1383)

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 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
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gtc cag tgt cag tcg gtg aag gag tcc gag gga ggt ctc ttc aag cca	96
Val Gln Cys Gln Ser Val Lys Glu Ser Glu Gly Gly Leu Phe Lys Pro	
20 25 30	
acg gat acc ctg aca ctc acc tgc aaa gcc tct gga ttc acc gtc agt	144
Thr Asp Thr Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Thr Val Ser	
35 40 45	
agt tac gac atg ggc tgg ctc cgc cag gct cca ggg aac ggg ctt gaa	192
Ser Tyr Asp Met Gly Trp Leu Arg Gln Ala Pro Gly Asn Gly Leu Glu	
50 55 60	
tct atc gga gcc att ggt agt gat ggt agt gag tac tat gtg agc tgg	240
Ser Ile Gly Ala Ile Gly Ser Asp Gly Ser Glu Tyr Tyr Val Ser Trp	
65 70 75 80	
gcg aga ggc cga acc gcc atc acc aga aac acc aac cag aac acg gtg	288
Ala Arg Gly Arg Thr Ala Ile Thr Arg Asn Thr Asn Gln Asn Thr Val	
85 90 95	
act ctg aaa atg acc agt ctg aca gcc gcg gac acg gcc acc tat ttc	336
Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe	
100 105 110	
tgt gcg aga gac tca cac tat agc tat ggc tat gat tat gat atc tgg	384
Cys Ala Arg Asp Ser His Tyr Ser Tyr Gly Tyr Asp Tyr Asp Ile Trp	
115 120 125	
ggc cca ggc acc ctg gtc acc gtc tcc tca ggg caa cct aag gct cca	432
Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro	
130 135 140	
tca gtc ttc cca ctg gcc ccc tgc tgc ggg gac aca ccc agc tcc acg	480
Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr	
145 150 155 160	
gtc acc ctg ggt tgt ctt gtg aag gga tac ctc ccg gaa ccc gtg acc	528
Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr	
165 170 175	
gtg acc tgg aac tcc ggc acc ctg acc aat gga gtg cgg acc ttc ccg	576
Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro	
180 185 190	
agc gtc agg cag tcc tcc ggg ttg tac agc ttg tct agc gtg gtg tcc	624
Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser	
195 200 205	
gtg acg tcg tca agc cag cct gtg act tgc aat gtg gcc cat ccg gcc	672
Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala	
210 215 220	
acc aac acc aag gtc gac aag acc gtg gcg cct tcc acc tgt tcc aag	720

Thr 225	Asn	Thr	Lys	Val	Asp 230	Lys	Thr	Val	Ala	Pro 235	Ser	Thr	Cys	Ser	Lys 240	
ccc Pro	act Thr	tgc Cys	ccg Pro	ccg Pro	cct Pro	gag Glu	ctc Leu	ctg Leu	gga Gly	gga Gly	ccg Pro	tcc Ser	gtg Val	ttc Phe	atc Ile	768
				245					250					255		
ttc Phe	cct Pro	cca Pro	aaa Lys	ccc Pro	aag Lys	gat Asp	acc Thr	ctg Leu	atg Met	att Ile	agc Ser	cgc Arg	act Thr	ccc Pro	gaa Glu	816
			260					265					270			
gtc Val	act Thr	tgc Cys	gtg Val	gtc Val	gtg Val	gac Asp	gtg Val	tcg Ser	cag Gln	gac Asp	gat Asp	cct Pro	gag Glu	gtg Val	cag Gln	864
		275					280					285				
ttc Phe	act Thr	tgg Trp	tac Tyr	atc Ile	aac Asn	aac Asn	gaa Glu	caa Gln	gtc Val	cgg Arg	aca Thr	gct Ala	aga Arg	cca Pro	ccg Pro	912
	290					295					300					
ctg Leu	cgc Arg	gag Glu	cag Gln	cag Gln	ttc Phe	aac Asn	tca Ser	act Thr	atc Ile	cgg Arg	gtg Val	gtg Val	tcc Ser	acc Thr	ctg Leu	960
305					310					315					320	
ccg Pro	atc Ile	gcg Ala	cat His	cag Gln	gat Asp	tgg Trp	ctg Leu	cgg Arg	ggg Gly	aag Lys	gag Glu	ttc Phe	aag Lys	tgc Cys	aaa Lys	1008
				325					330					335		
gtc Val	cac His	aac Asn	aag Lys	gcc Ala	ctg Leu	ccc Pro	gcc Ala	ccc Pro	atc Ile	gaa Glu	aag Lys	acc Thr	atc Ile	tcc Ser	aag Lys	1056
			340				345						350			
gct Ala	cgg Arg	ggc Gly	cag Gln	cct Pro	ctg Leu	gag Glu	ccc Pro	aaa Lys	gtg Val	tac Tyr	acc Thr	atg Met	ggc Gly	ccg Pro	cct Pro	1104
		355					360					365				
cgc Arg	gag Glu	gag Glu	ctc Leu	tcc Ser	tca Ser	cgc Arg	tcg Ser	gtg Val	tcg Ser	ctg Leu	act Thr	tgc Cys	atg Met	att Ile	aac Asn	1152
	370					375					380					
ggc Gly	ttc Phe	tac Tyr	cct Pro	tcc Ser	gac Asp	atc Ile	tcc Ser	gtg Val	gaa Glu	tgg Trp	gag Glu	aag Lys	aac Asn	gga Gly	aaa Lys	1200
385					390				395					400		
gcc Ala	gaa Glu	gat Asp	aac Asn	tac Tyr	aag Lys	acc Thr	acg Thr	ccc Pro	gcc Ala	gtg Val	ctg Leu	gac Asp	tcc Ser	gac Asp	gga Gly	1248
				405					410					415		
agc Ser	tat Tyr	ttc Phe	ctg Leu	tac Tyr	tcc Ser	aag Lys	ctc Leu	tcc Ser	gtc Val	ccc Pro	act Thr	tcg Ser	gaa Glu	tgg Trp	cag Gln	1296
			420					425					430			
agg Arg	ggg Gly	gac Asp	gtg Val	ttc Phe	act Thr	tgc Cys	tcc Ser	gtg Val	atg Met	cac His	gag Glu	gca Ala	ctc Leu	cac His	aac Asn	1344
		435					440					445				

cac tac acc caa aag agc att tcg cgg tca cct ggc aag taa
 His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
 450 455 460

1386

<210> 14
 <211> 461
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1 5 10 15

Val Gln Cys Gln Ser Val Lys Glu Ser Glu Gly Gly Leu Phe Lys Pro
 20 25 30

Thr Asp Thr Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Thr Val Ser
 35 40 45

Ser Tyr Asp Met Gly Trp Leu Arg Gln Ala Pro Gly Asn Gly Leu Glu
 50 55 60

Ser Ile Gly Ala Ile Gly Ser Asp Gly Ser Glu Tyr Tyr Val Ser Trp
 65 70 75 80

Ala Arg Gly Arg Thr Ala Ile Thr Arg Asn Thr Asn Gln Asn Thr Val
 85 90 95

Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
 100 105 110

Cys Ala Arg Asp Ser His Tyr Ser Tyr Gly Tyr Asp Tyr Asp Ile Trp
 115 120 125

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

Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr
 145 150 155 160

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr
165 170 175

Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro
180 185 190

Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser
195 200 205

Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala
210 215 220

Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys
225 230 235 240

Pro Thr Cys Pro Pro Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile
245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
260 265 270

Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln
275 280 285

Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro
290 295 300

Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu
305 310 315 320

Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys
325 330 335

Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
340 345 350

Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro
355 360 365

Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn
 370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys
 385 390 395 400

Ala Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly
 405 410 415

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln
 420 425 430

Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn
 435 440 445

His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
 450 455 460

<210> 15
 <211> 714
 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
 <221> CDS
 <222> (1)..(711)

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 ctc cca ggt gcc aca ttt gcc caa gtg ctg acc cag act cca tcc cct 96
 Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ser Pro
 20 25 30
 gtg tct gca gct gtg gga ggc aca gtc agc atc agt tgc cag tcc agt 144
 Val Ser Ala Ala Val Gly Gly Thr Val Ser Ile Ser Cys Gln Ser Ser
 35 40 45
 cag agt att tat agt aac tac tta tcc tgg tat cag cag aaa cca ggg 192
 Gln Ser Ile Tyr Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 50 55 60

cag cct ccc aag ctc ctg atc tat tat gca tcc act ctg gca tct ggg Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser Gly 65 70 75 80	240
gtc cct tcg cgg ttc aaa ggc agt gga tct ggg aca cag ttc act ctc Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu 85 90 95	288
acc atc agc ggc gtg cag tgt gat gat gct gcc act tac tac tgt caa Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln 100 105 110	336
ggc act tat tat gtc act ggt tgg tac gac gct ttc ggc gga ggg acc Gly Thr Tyr Tyr Val Thr Gly Trp Tyr Asp Ala Phe Gly Gly Gly Thr 115 120 125	384
gag gtg gtg gtc aaa ggt gat cca gtt gca cct act gtc ctc atc ttc Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe 130 135 140	432
cca cca gct gct gat cag gtg gca act gga aca gtc acc atc gtg tgc Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys 145 150 155 160	480
gtg gct aac aag tac ttc ccg gac gtg acc gtg acc tgg gaa gtc gac Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp 165 170 175	528
gga acc act cag acc act ggt atc gag aac agc aag acg ccc cag aac Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn 180 185 190	576
tcc gcc gat tgt act tat aac ctg tcc tcc aca ctg acc ctc acc tcg Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser 195 200 205	624
acc cag tac aat tcc cac aag gag tac act tgc aaa gtc acc cag gga Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly 210 215 220	672
acc act tca gtg gtg cag agc ttc aac cgg ggg gat tgc tga Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys 225 230 235	714

<210> 16
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16

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

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ser Pro
20 25 30

Val Ser Ala Ala Val Gly Gly Thr Val Ser Ile Ser Cys Gln Ser Ser
35 40 45

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

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

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu
85 90 95

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

Gly Thr Tyr Tyr Val Thr Gly Trp Tyr Asp Ala Phe Gly Gly Gly Thr
115 120 125

Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe
130 135 140

Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys
145 150 155 160

Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp
165 170 175

Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn
180 185 190

Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser
195 200 205

Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly

210

215

220

Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
 225 230 235

<210> 17

<211> 1386

<212> DNA

<213> Artificial Sequence

<220>

<223> clone encoding A6 monoclonal antibody heavy chain 1

<220>

<221> CDS

<222> (1)..(1383)

<400> 17

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 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
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gtc cag tgt cag tcg gtg aag gag tcc gag gga ggt ctc ttc aag cca 96
 Val Gln Cys Gln Ser Val Lys Glu Ser Glu Gly Gly Leu Phe Lys Pro
 20 25 30

acg gat acc ctg aca ctc acc tgc aaa gcc tct gga ttc acc gtc agt 144
 Thr Asp Thr Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Thr Val Ser
 35 40 45

agt tac gac atg ggc tgg ctc cgc cag gct cca ggg aac ggg ctt gaa 192
 Ser Tyr Asp Met Gly Trp Leu Arg Gln Ala Pro Gly Asn Gly Leu Glu
 50 55 60

tct atc gga gcc att ggt agt gat ggt agt gag tac tat gtg agc tgg 240
 Ser Ile Gly Ala Ile Gly Ser Asp Gly Ser Glu Tyr Tyr Val Ser Trp
 65 70 75 80

gcg aga ggc cga acc acc atc acc aga aac acc aac cag aac acg gtg 288
 Ala Arg Gly Arg Thr Thr Ile Thr Arg Asn Thr Asn Gln Asn Thr Val
 85 90 95

act ctg aaa atg acc agt ctg aca gcc gcg gac acg gcc acc tat ttc 336
 Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
 100 105 110

tgt gcg aga gac tca cac tat agc tat ggc tat gat tat gat atc tgg 384
 Cys Ala Arg Asp Ser His Tyr Ser Tyr Gly Tyr Asp Tyr Asp Ile Trp
 115 120 125

ggc cca ggc acc ctg gtc acc gtc tcc tca ggg caa cct aag gct cca 432

Gly 130	Pro	Gly	Thr	Leu	Val	Thr 135	Val	Ser	Ser	Gly	Gln 140	Pro	Lys	Ala	Pro	
tca Ser 145	gtc Val	ttc Phe	cca Pro	ctg Leu	gcc Ala 150	ccc Pro	tgc Cys	tgc Cys	ggg Gly	gac Asp 155	aca Thr	ccc Pro	agc Ser	tcc Ser	acg Thr 160	480
gtc Val	acc Thr	ctg Leu	ggg Gly	tgt Cys 165	ctt Leu	gtg Val	aag Lys	gga Gly	tac Tyr 170	ctc Leu	ccg Pro	gaa Glu	ccc Pro	gtg Val 175	acc Thr	528
gtg Val	acc Thr	tgg Trp	aac Asn 180	tcc Ser	ggc Gly	acc Thr	ctg Leu	acc Thr 185	aat Asn	gga Gly	gtg Val	cgg Arg	acc Thr 190	ttc Phe	ccg Pro	576
agc Ser	gtc Val	agg Arg 195	cag Gln	tcc Ser	tcc Ser	ggg Gly	ttg Leu 200	tac Tyr	agc Ser	ttg Leu	tct Ser	agc Ser 205	gtg Val	gtg Val	tcc Ser	624
gtg Val 210	acg Thr	tcg Ser	tca Ser	agc Ser	cag Gln	cct Pro 215	gtg Val	act Thr	tgc Cys	aat Asn	gtg Val 220	gcc Ala	cat His	ccg Pro	gcc Ala	672
acc Thr 225	aac Asn	acc Thr	aag Lys	gtc Val	gac Asp 230	aag Lys	acc Thr	gtg Val	gcg Ala	cct Pro 235	tcc Ser	acc Thr	tgt Cys	tcc Ser	aag Lys 240	720
ccc Pro	act Thr	tgc Cys	ccg Pro	ccg Pro	cct Pro	gag Glu	ctc Leu	ctg Leu	gga Gly 250	gga Gly	ccg Pro	tcc Ser	gtg Val	ttc Phe 255	atc Ile	768
ttc Phe	cct Pro	cca Pro	aaa Lys 260	ccc Pro	aag Lys	gat Asp	acc Thr	ctg Leu 265	atg Met	att Ile	agc Ser	cgc Arg	act Thr 270	ccc Pro	gaa Glu	816
gtc Val	act Thr	tgc Cys 275	gtg Val	gtc Val	gtg Val	gac Asp	gtg Val 280	tcg Ser	cag Gln	gac Asp	gat Asp	cct Pro 285	gag Glu	gtg Val	cag Gln	864
ttc Phe	act Thr 290	tgg Trp	tac Tyr	atc Ile	aac Asn	aac Asn 295	gaa Glu	caa Gln	gtc Val	cgg Arg	aca Thr 300	gct Ala	aga Arg	cca Pro	ccg Pro	912
ctg Leu 305	cgc Arg	gag Glu	cag Gln	cag Gln	ttc Phe 310	aac Asn	tca Ser	act Thr	atc Ile	cgg Arg 315	gtg Val	gtg Val	tcc Ser	acc Thr	ctg Leu 320	960
ccg Pro	atc Ile	gcg Ala	cat His	cag Gln 325	gat Asp	tgg Trp	ctg Leu	cgg Arg	ggg Gly 330	aag Lys	gag Glu	ttc Phe	aag Lys	tgc Cys 335	aaa Lys	1008
gtc Val	cac His	aac Asn 340	aag Lys	gcc Ala	ctg Leu	ccc Pro	gcc Ala	ccc Pro 345	atc Ile	gaa Glu	aag Lys	acc Thr 350	atc Ile	tcc Ser	aag Lys	1056

gct	cgg	ggc	cag	cct	ctg	gag	ccc	aaa	gtg	tac	acc	atg	ggc	ccg	cct	1104
Ala	Arg	Gly	Gln	Pro	Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	
		355					360					365				

cgc	gag	gag	ctc	tcc	tca	cgc	tcg	gtg	tcg	ctg	act	tgc	atg	att	aac	1152
Arg	Glu	Glu	Leu	Ser	Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	
	370						375				380					

ggc	ttc	tac	cct	tcc	gac	atc	tcc	gtg	gaa	tgg	gag	aag	aac	gga	aaa	1200
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	
385					390				395						400	

gcc	gaa	gat	aac	tac	aag	acc	acg	ccc	gcc	gtg	ctg	gac	tcc	gac	gga	1248
Ala	Glu	Asp	Asn	Tyr	Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	
			405						410					415		

agc	tat	ttc	ctg	tac	tcc	aag	ctc	tcc	gtc	ccc	act	tcg	gaa	tgg	cag	1296
Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	
			420					425					430			

agg	ggg	gac	gtg	ttc	act	tgc	tcc	gtg	atg	cac	gag	gca	ctc	cac	aac	1344
Arg	Gly	Asp	Val	Phe	Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	
		435					440					445				

cac	tac	acc	caa	aag	agc	att	tcg	cgg	tca	cct	ggc	aag	taa			1386
His	Tyr	Thr	Gln	Lys	Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys				
	450					455					460					

<210> 18
 <211> 461
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5					10					15	

Val	Gln	Cys	Gln	Ser	Val	Lys	Glu	Ser	Glu	Gly	Gly	Leu	Phe	Lys	Pro
			20					25					30		

Thr	Asp	Thr	Leu	Thr	Leu	Thr	Cys	Lys	Ala	Ser	Gly	Phe	Thr	Val	Ser
		35					40					45			

Ser	Tyr	Asp	Met	Gly	Trp	Leu	Arg	Gln	Ala	Pro	Gly	Asn	Gly	Leu	Glu
	50					55					60				

Ser Ile Gly Ala Ile Gly Ser Asp Gly Ser Glu Tyr Tyr Val Ser Trp
65 70 75 80

Ala Arg Gly Arg Thr Thr Ile Thr Arg Asn Thr Asn Gln Asn Thr Val
85 90 95

Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
100 105 110

Cys Ala Arg Asp Ser His Tyr Ser Tyr Gly Tyr Asp Tyr Asp Ile Trp
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr
145 150 155 160

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr
165 170 175

Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro
180 185 190

Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser
195 200 205

Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala
210 215 220

Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys
225 230 235 240

Pro Thr Cys Pro Pro Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile
245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
260 265 270

Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln
275 280 285

Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro
290 295 300

Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu
305 310 315 320

Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys
325 330 335

Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
340 345 350

Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro
355 360 365

Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn
370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys
385 390 395 400

Ala Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly
405 410 415

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln
420 425 430

Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
450 455 460

<210> 19

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> clone encoding A6 monoclonal antibody light chain 4

<220>

<221> CDS

<222> (1)..(711)

<400> 19

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

ctc	cca	ggg	gcc	aca	ttt	gcc	caa	gtg	ctg	acc	cag	act	cca	tcc	cct	96
Leu	Pro	Gly	Ala	Thr	Phe	Ala	Gln	Val	Leu	Thr	Gln	Thr	Pro	Ser	Pro	
			20					25					30			

gtg	tct	gca	gct	gtg	gga	ggc	aca	gtc	agc	atc	agt	tgc	cag	tcc	agt	144
Val	Ser	Ala	Ala	Val	Gly	Gly	Thr	Val	Ser	Ile	Ser	Cys	Gln	Ser	Ser	
		35					40					45				

cag	agt	att	tat	agt	aac	tac	tta	tcc	tgg	tat	cag	cag	aaa	cca	ggg	192
Gln	Ser	Ile	Tyr	Ser	Asn	Tyr	Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	
	50					55					60					

cag	cct	ccc	aag	ctc	ctg	atc	tat	tat	gca	tcc	act	ctg	gca	tct	ggg	240
Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Ala	Ser	Thr	Leu	Ala	Ser	Gly	
65					70				75						80	

gtc	cct	tcg	cgg	ttc	aaa	ggc	agt	gga	tct	ggg	aca	cag	ttc	act	ctc	288
Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Thr	Leu	
			85					90						95		

acc	atc	agc	ggc	gtg	cag	tgt	gat	gat	gct	gcc	act	tac	tac	tgt	caa	336
Thr	Ile	Ser	Gly	Val	Gln	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	
			100					105					110			

ggc	act	tat	tat	gtc	act	ggg	tgg	tac	gac	gct	ttc	ggc	gga	ggg	acc	384
Gly	Thr	Tyr	Tyr	Val	Thr	Gly	Trp	Tyr	Asp	Ala	Phe	Gly	Gly	Gly	Thr	
		115					120					125				

gag	gtg	gtg	gtc	aaa	ggg	gat	cca	gtt	gca	cct	act	gtc	ctc	atc	ttc	432
Glu	Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Ile	Phe	
	130					135					140					

cca	cca	gct	gct	gat	cag	gtg	gca	act	gga	aca	gtc	acc	atc	gtg	tgc	480
Pro	Pro	Ala	Ala	Asp	Gln	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val	Cys	
145					150				155						160	

gtg	gct	aac	aag	tac	ttc	ccg	gac	gtg	acc	gtg	acc	tgg	gaa	gtc	gac	528
Val	Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Val	Thr	Val	Thr	Trp	Glu	Val	Asp	
				165					170					175		

gga	acc	act	cag	acc	act	ggg	atc	gag	aac	agc	aag	acg	ccc	cag	aac	576
Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ile	Glu	Asn	Ser	Lys	Thr	Pro	Gln	Asn	

180							185					190					
tcc	gcc	gat	tgt	act	tat	aac	ctg	tcc	tcc	aca	ctg	acc	ctc	acc	tcg	624	
Ser	Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Ser		
	195						200				205						
acc	cag	tac	aat	tcc	cac	aag	gag	tac	act	tgc	aaa	gtc	acc	cag	gga	672	
Thr	Gln	Tyr	Asn	Ser	His	Lys	Glu	Tyr	Thr	Cys	Lys	Val	Thr	Gln	Gly		
	210					215					220						
acc	act	tca	gtg	gtg	cag	agc	ttc	aac	cgg	ggg	gat	tgc	tga			714	
Thr	Thr	Ser	Val	Val	Gln	Ser	Phe	Asn	Arg	Gly	Asp	Cys					
225					230					235							

<210> 20
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20

Met	Asp	Thr	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
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Leu	Pro	Gly	Ala	Thr	Phe	Ala	Gln	Val	Leu	Thr	Gln	Thr	Pro	Ser	Pro
			20				25						30		

Val	Ser	Ala	Ala	Val	Gly	Gly	Thr	Val	Ser	Ile	Ser	Cys	Gln	Ser	Ser
		35					40					45			

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

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

Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Thr	Leu
			85					90						95	

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

Gly	Thr	Tyr	Tyr	Val	Thr	Gly	Trp	Tyr	Asp	Ala	Phe	Gly	Gly	Gly	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe
130 135 140

Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys
145 150 155 160

Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp
165 170 175

Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn
180 185 190

Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser
195 200 205

Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly
210 215 220

Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225 230 235

<210> 21
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> clone encoding E5 monoclonal antibody heavy chain 1

<220>
<221> CDS
<222> (1)..(1368)

<220>
<221> misc_feature
<222> (54)..(54)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (58)..(59)
<223> n is a, c, g, or t

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Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly		
1				5				10						15			
gtc	can	tgt	nng	tcg	gtg	aag	gag	tcc	gag	gga	ggg	ctc	ttc	aag	cca	96	
Val	Xaa	Cys	Xaa	Ser	Val	Lys	Glu	Ser	Glu	Gly	Gly	Leu	Phe	Lys	Pro		
			20				25						30				
acg	gct	acc	ctg	aca	ctc	acc	tgc	aca	gtc	tct	gga	ttc	tcc	ctc	agt	144	
Thr	Ala	Thr	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser		
		35					40				45						
agc	tac	gac	atg	agt	tgg	gtc	cgc	cag	gct	cca	ggg	aac	ggg	ctg	gaa	192	
Ser	Tyr	Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Asn	Gly	Leu	Glu		
50						55				60							
tgg	atc	gga	tac	ctt	agt	agt	gat	ggg	cgc	gca	tac	tac	gcg	agc	tgg	240	
Trp	Ile	Gly	Tyr	Leu	Ser	Ser	Asp	Gly	Arg	Ala	Tyr	Tyr	Ala	Ser	Trp		
65				70						75			80				
gcg	aaa	agc	cga	tcc	acc	atc	acc	aga	aac	acc	aac	ctg	aac	acg	gtg	288	
Ala	Lys	Ser	Arg	Ser	Thr	Ile	Thr	Arg	Asn	Thr	Asn	Leu	Asn	Thr	Val		
				85				90						95			
act	ctg	aaa	atg	acc	agt	ctg	aca	gcc	gcg	gac	acg	gcc	acc	tat	ttc	336	
Thr	Leu	Lys	Met	Thr	Ser	Leu	Thr	Ala	Ala	Asp	Thr	Ala	Thr	Tyr	Phe		
			100				105						110				
tgt	gcg	aga	ggg	gat	aat	act	gct	gac	atc	tgg	ggc	cca	ggc	acc	ctg	384	
Cys	Ala	Arg	Gly	Asp	Asn	Thr	Ala	Asp	Ile	Trp	Gly	Pro	Gly	Thr	Leu		
		115					120				125						
gtc	acc	gtc	tcc	tca	ggg	caa	cct	aag	gct	cca	tca	gtc	ttc	cca	ctg	432	
Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu		
130						135			140								
gcc	ccc	tgc	tgc	ggg	gac	aca	ccc	agc	tcc	acg	gtc	acc	ctg	ggg	tgt	480	
Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys		
145				150						155			160				
ctt	gtg	aag	gga	tac	ctc	ccg	gaa	ccc	gtg	acc	gtg	acc	tgg	aac	tcc	528	
Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser		
				165				170						175			
ggc	acc	ctg	acc	aat	gga	gtg	cgg	acc	ttc	ccg	agc	gtc	agg	cag	tcc	576	
Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser		
			180				185						190				
tcc	ggg	ttg	tac	agc	ttg	tct	agc	gtg	gtg	tcc	gtg	acg	tcg	tca	agc	624	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser		
		195					200				205						
cag	cct	gtg	act	tgc	aat	gtg	gcc	cat	ccg	gcc	acc	aac	acc	aag	gtc	672	

Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val		
210						215					220						
gac	aag	acc	gtg	gcg	cct	tcc	acc	tgt	tcc	aag	ccc	act	tgc	ccg	ccg	720	
Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	240	
225					230					235							
cct	gag	ctc	ctg	gga	gga	ccg	tcc	gtg	ttc	atc	ttc	cct	cca	aaa	ccc	768	
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	255	
				245					250					255			
aag	gat	acc	ctg	atg	att	agc	cgc	act	ccc	gaa	gtc	act	tgc	gtg	gtc	816	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	270	
			260					265					270				
gtg	gac	gtg	tcg	cag	gac	gat	cct	gag	gtg	cag	ttc	act	tgg	tac	atc	864	
Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	285	
		275					280					285					
aac	aac	gaa	caa	gtc	cgg	aca	gct	aga	cca	ccg	ctg	cgc	gag	cag	cag	912	
Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	300	
	290					295											
ttc	aac	tca	act	atc	cgg	gtg	gtg	tcc	acc	ctg	ccg	atc	gcg	cat	cag	960	
Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	320	
305					310					315							
gat	tgg	ctg	cgg	ggg	aag	gag	ttc	aag	tgc	aaa	gtc	cac	aac	aag	gcc	1008	
Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	335	
				325					330					335			
ctg	ccc	gcc	ccc	atc	gaa	aag	acc	atc	tcc	aag	gct	cgg	ggc	cag	cct	1056	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro	350	
			340					345					350				
ctg	gag	ccc	aaa	gtg	tac	acc	atg	ggc	ccg	cct	cgc	gag	gag	ctc	tcc	1104	
Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser	365	
		355					360										
tca	cgc	tcg	gtg	tcg	ctg	act	tgc	atg	att	aac	ggc	ttc	tac	cct	tcc	1152	
Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser	380	
	370					375					380						
gac	atc	tcc	gtg	gaa	tgg	gag	aag	aac	gga	aaa	gcc	gaa	gat	aac	tac	1200	
Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr	400	
385					390					395							
aag	acc	acg	ccc	gcc	gtg	ctg	gac	tcc	gac	gga	agc	tat	ttc	ctg	tac	1248	
Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	415	
				405					410								
tcc	aag	ctc	tcc	gtc	ccc	act	tcg	gaa	tgg	cag	agg	ggg	gac	gtg	ttc	1296	
Ser	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe	430	
			420					425					430				

act tgc tcc gtg atg cac gag gca ctc cac aac cac tac acc caa aag 1344
Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
435 440 445

$\langle 210 \rangle$	22
$\langle 211 \rangle$	456
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

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<220>
<221> misc_feature
<222> (20)..(20)
<223> The 'Xaa' at location 20 stands for Lys, Arg, Thr, Met, Glu, Gly,
Ala, Val, Gln, Pro, Leu, Trp, or Ser.
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<400> 22

Val	Xaa	Cys	Xaa	Ser	Val	Lys	Glu	Ser	Glu	Gly	Gly	Leu	Phe	Lys	Pro
			20					25					30		

Thr Ala Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45

Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu
50 55 60

Trp Ile Gly Tyr Leu Ser Ser Asp Gly Arg Ala Tyr Tyr Ala Ser Trp
65 70 75 80

Ala Lys Ser Arg Ser Thr Ile Thr Arg Asn Thr Asn Leu Asn Thr Val
85 90 95

Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
100 105 110

Cys Ala Arg Gly Asp Asn Thr Ala Asp Ile Trp Gly Pro Gly Thr Leu
115 120 125

Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
130 135 140

Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
145 150 155 160

Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
165 170 175

Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
180 185 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
195 200 205

Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
210 215 220

Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro
225 230 235 240

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
245 250 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
260 265 270

Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
275 280 285

Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
290 295 300

Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln

305 310 315 320
 Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
 325 330 335
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
 340 345 350
 Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
 355 360 365
 Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
 370 375 380
 Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
 385 390 395 400
 Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
 405 410 415
 Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
 420 425 430
 Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 435 440 445
 Ser Ile Ser Arg Ser Pro Gly Lys
 450 455

<210> 23
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> clone encoding E5 monoclonal antibody light chain 3

<220>
 <221> CDS
 <222> (1)..(708)

<400> 23
 atg gac acg agg gcc ccc act cag ctg ctg ggg ctc ctg ctg ctc tgg

Met	Asp	Thr	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	
1				5					10					15		
ctc	cca	ggt	gcc	aca	ttt	gct	caa	gtg	ctg	acc	cag	act	cca	tcc	tcc	96
Leu	Pro	Gly	Ala	Thr	Phe	Ala	Gln	Val	Leu	Thr	Gln	Thr	Pro	Ser	Ser	
			20					25					30			
gtg	tct	gca	gct	gtg	gga	ggc	aca	gtc	acc	atc	aat	tgc	cag	tcc	agt	144
Val	Ser	Ala	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Asn	Cys	Gln	Ser	Ser	
		35					40					45				
cag	agt	gtt	tat	aag	aac	aac	gac	tta	gcc	tgg	tat	cag	cag	aaa	cta	192
Gln	Ser	Val	Tyr	Lys	Asn	Asn	Asp	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Leu	
	50					55					60					
ggg	cag	cct	ccc	aag	ctc	ctg	atc	tat	ttt	gca	tcc	act	ctg	gca	tct	240
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Phe	Ala	Ser	Thr	Leu	Ala	Ser	
65				70						75					80	
ggg	gtc	cca	tcg	cgg	ttc	aaa	ggc	agt	gga	tct	ggg	aca	cag	ttc	act	288
Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Thr	
				85				90						95		
ctc	acc	atc	agc	gac	ctg	gag	tgt	gac	gat	gct	gcc	act	tat	tac	tgt	336
Leu	Thr	Ile	Ser	Asp	Leu	Glu	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	
			100					105					110			
gca	ggc	ggt	tat	agt	ggt	cct	gtt	ggt	gct	ttc	ggc	gga	ggg	acc	gag	384
Ala	Gly	Gly	Tyr	Ser	Gly	Pro	Val	Gly	Ala	Phe	Gly	Gly	Gly	Thr	Glu	
		115					120					125				
gtg	gtg	gtc	aag	agt	gat	cca	gtt	gca	cct	act	gtc	ctc	atc	ttc	cca	432
Val	Val	Val	Lys	Ser	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Ile	Phe	Pro	
	130					135					140					
cca	gct	gct	gat	cag	gtg	gca	act	gga	aca	gtc	acc	atc	gtg	tgc	gtg	480
Pro	Ala	Ala	Asp	Gln	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val	Cys	Val	
145					150					155					160	
gct	aac	aag	tac	ttc	ccg	gac	gtg	acc	gtg	acc	tgg	gaa	gtc	gac	gga	528
Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Val	Thr	Val	Thr	Trp	Glu	Val	Asp	Gly	
				165					170					175		
acc	act	cag	acc	act	ggt	atc	gag	aac	agc	aag	acg	ccc	cag	aac	tcc	576
Thr	Thr	Gln	Thr	Thr	Gly	Ile	Glu	Asn	Ser	Lys	Thr	Pro	Gln	Asn	Ser	
			180					185					190			
gcc	gat	tgt	act	tat	aac	ctg	tcc	tcc	aca	ctg	acc	ctc	acc	tcg	acc	624
Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Ser	Thr	
		195					200					205				
cag	tac	aat	tcc	cac	aag	gag	tac	act	tgc	aaa	gtc	acc	cag	gga	acc	672
Gln	Tyr	Asn	Ser	His	Lys	Glu	Tyr	Thr	Cys	Lys	Val	Thr	Gln	Gly	Thr	
	210					215					220					

act tca gtg gtg cag agc ttc aac cgg ggg gat tgc tga
 Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
 225 230 235

<210> 24
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

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

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ser Ser
 20 25 30

Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
 35 40 45

Gln Ser Val Tyr Lys Asn Asn Asp Leu Ala Trp Tyr Gln Gln Lys Leu
 50 55 60

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

Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
 85 90 95

Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
 100 105 110

Ala Gly Gly Tyr Ser Gly Pro Val Gly Ala Phe Gly Gly Gly Thr Glu
 115 120 125

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

Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
 145 150 155 160

Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
165 170 175

Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
180 185 190

Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
195 200 205

Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
210 215 220

Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225 230 235

<210> 25
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<223> clone encoding G7 monoclonal antibody heavy chain 1

<220>
<221> CDS
<222> (1)..(1380)

<400> 25
atg gag act ggg ctg cgc tgg ctt ctc ctg gtc gct gtg ctc aaa ggt 48
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

gtc cag tgt cag tcg gtg aag gag tcc gag gga ggt ctc ttc aag cca 96
Val Gln Cys Gln Ser Val Lys Glu Ser Glu Gly Gly Leu Phe Lys Pro
20 25 30

acg gat acc ctg aca ctc acc tgc aca gtc tct gga ttc tcc ctc agt 144
Thr Asp Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45

agt tat gga gtg agc tgg gtc cgc cag gct cca ggg aac ggg ctg gag 192
Ser Tyr Gly Val Ser Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu
50 55 60

tgg atc gga ttc att gac aag tat gga cgc aca cac tac gcg agc tgg 240
Trp Ile Gly Phe Ile Asp Lys Tyr Gly Arg Thr His Tyr Ala Ser Trp

65		70		75		80										
gcg	aaa	agc	cga	tcc	acc	atc	acc	aga	aat	acc	aac	gag	aac	acg	gtg	288
Ala	Lys	Ser	Arg	Ser	Thr	Ile	Thr	Arg	Asn	Thr	Asn	Glu	Asn	Thr	Val	
			85						90					95		
act	ctg	aaa	atg	acc	agt	ctg	aca	gcc	gcg	gac	acg	gcc	acc	ttt	ttg	336
Thr	Leu	Lys	Met	Thr	Ser	Leu	Thr	Ala	Ala	Asp	Thr	Ala	Thr	Phe	Leu	
			100					105					110			
tgt	gcg	aga	gat	gac	tat	cgt	cct	gct	tat	ggg	ttc	gac	atc	tgg	ggc	384
Cys	Ala	Arg	Asp	Asp	Tyr	Arg	Pro	Ala	Tyr	Gly	Phe	Asp	Ile	Trp	Gly	
		115					120					125				
cca	ggc	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	caa	cct	aag	gct	cca	tca	432
Pro	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	
	130					135					140					
gtc	ttc	cca	ctg	gcc	ccc	tgc	tgc	ggg	gac	aca	ccc	agc	tcc	acg	gtc	480
Val	Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	
145					150					155					160	
acc	ctg	ggg	tgt	ctt	gtg	aag	gga	tac	ctc	ccg	gaa	ccc	gtg	acc	gtg	528
Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
acc	tgg	aac	tcc	ggc	acc	ctg	acc	aat	gga	gtg	cgg	acc	ttc	ccg	agc	576
Thr	Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	
			180					185					190			
gtc	agg	cag	tcc	tcc	ggg	ttg	tac	agc	ttg	tct	agc	gtg	gtg	tcc	gtg	624
Val	Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	
		195					200					205				
acg	tgc	tca	agc	cag	cct	gtg	act	tgc	aat	gtg	gcc	cat	ccg	gcc	acc	672
Thr	Ser	Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	
	210					215					220					
aac	acc	aag	gtc	gac	aag	acc	gtg	gcg	cct	tcc	acc	tgt	tcc	aag	ccc	720
Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	
225					230					235					240	
act	tgc	ccg	ccg	cct	gag	ctc	ctg	gga	gga	ccg	tcc	gtg	ttc	atc	ttc	768
Thr	Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	
				245					250					255		
cct	cca	aaa	ccc	aag	gat	acc	ctg	atg	att	agc	cgc	act	ccc	gaa	gtc	816
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
			260					265					270			
act	tgc	gtg	gtc	gtg	gac	gtg	tgc	cag	gac	gat	cct	gag	gtg	cag	ttc	864
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	
		275					280					285				

act tgg tac atc aac aac gaa caa gtc cgg aca gct aga cca ccg ctg	912
Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu	
290 295 300	
cgc gag cag cag ttc aac tca act atc cgg gtg gtg tcc acc ctg ccg	960
Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro	
305 310 315 320	
atc gcg cat cag gat tgg ctg cgg ggg aag gag ttc aag tgc aaa gtc	1008
Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val	
325 330 335	
cac aac aag gcc ctg ccc gcc ccc atc gaa aag acc atc tcc aag gct	1056
His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
340 345 350	
cgg ggc cag cct ctg gag ccc aaa gtg tac acc atg ggc ccg cct cgc	1104
Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg	
355 360 365	
gag gag ctc tcc tca cgc tcg gtg tcg ctg act tgc atg att aac ggc	1152
Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly	
370 375 380	
ttc tac cct tcc gac atc tcc gtg gaa tgg gag aag aac gga aaa gcc	1200
Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala	
385 390 395 400	
gaa gat aac tac aag acc acg ccc gcc gtg ctg gac tcc gac gga agc	1248
Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser	
405 410 415	
tat ttc ctg tac tcc aag ctc tcc gtc ccc act tcg gaa tgg cag agg	1296
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg	
420 425 430	
ggg gac gtg ttc act tgc tcc gtg atg cac gag gca ctc cac aac cac	1344
Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His	
435 440 445	
tac acc caa aag agc att tcg cgg tca cct ggc aag taa	1383
Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys	
450 455 460	

<210> 26
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ser Val Lys Glu Ser Glu Gly Gly Leu Phe Lys Pro
20 25 30

Thr Asp Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45

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

Trp Ile Gly Phe Ile Asp Lys Tyr Gly Arg Thr His Tyr Ala Ser Trp
65 70 75 80

Ala Lys Ser Arg Ser Thr Ile Thr Arg Asn Thr Asn Glu Asn Thr Val
85 90 95

Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Phe Leu
100 105 110

Cys Ala Arg Asp Asp Tyr Arg Pro Ala Tyr Gly Phe Asp Ile Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val
145 150 155 160

Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val
165 170 175

Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser
180 185 190

Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val
195 200 205

Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr

210

215

220

Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro
 225 230 235 240

Thr Cys Pro Pro Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe
 245 250 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270

Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe
 275 280 285

Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu
 290 295 300

Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro
 305 310 315 320

Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val
 325 330 335

His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350

Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg
 355 360 365

Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly
 370 375 380

Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala
 385 390 395 400

Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser
 405 410 415

Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg
 420 425 430

Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445

Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
 450 455 460

<210> 27
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> clone encoding G7 monoclonal antibody light chain 1

<220>
 <221> CDS
 <222> (1)..(717)

<400> 27
 atg gac acg agg gcc ccc act cag ctg ctg ggg ctc ctg ctg ctc tgg 48
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15
 ctc cca ggt gcc aca ttt gcc caa gtg ctg acc cag act gca tcg ccc 96
 Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro
 20 25 30
 gtg tct gca gct gtg gga agc aca gtc acc atc aat tgc cag gcc agt 144
 Val Ser Ala Ala Val Gly Ser Thr Val Thr Ile Asn Cys Gln Ala Ser
 35 40 45
 cag agt gtt tat aat aac aac tgg tta tcc tgg ttt cag cag aaa cca 192
 Gln Ser Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys Pro
 50 55 60
 ggg cag cct ccc aag caa ctg ata tat ggt gca tcc act ctg cca tct 240
 Gly Gln Pro Pro Lys Gln Leu Ile Tyr Gly Ala Ser Thr Leu Pro Ser
 65 70 75 80
 ggg gtc tca tcg cgg ttc aaa ggc agt gga tct ggg aca cag ttc act 288
 Gly Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
 85 90 95
 ctc acc atc agc gac gtg cag tgt gac gat gct gcc act tac tac tgt 336
 Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
 100 105 110
 ctg ggc ggt tat cat tgg agt act gct gat tgt aat gtt ttc ggc gga 384
 Leu Gly Gly Tyr His Trp Ser Thr Ala Asp Cys Asn Val Phe Gly Gly
 115 120 125

ggg acc gag gtg gtg gtc aaa ggt gat cca gtt gca cct act gtc ctc	432
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu	
130 135 140	

atc ttc cca cca gct gct gat cag gtg gca act gga aca gtc acc atc	480
Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile	
145 150 155 160	

gtg tgc gtg gct aac aag tac ttc ccg gac gtg acc gtg acc tgg gaa	528
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu	
165 170 175	

gtc gac gga acc act cag acc act ggt atc gag aac agc aag acg ccc	576
Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro	
180 185 190	

cag aac tcc gcc gat tgt act tat aac ctg tcc tcc aca ctg acc ctc	624
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu	
195 200 205	

acc tcg acc cag tac aat tcc cac aag gag tac act tgc aaa gtc acc	672
Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr	
210 215 220	

cag gga acc act tca gtg gtg cag agc ttc aac cgg ggg gat tgc tga	720
Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys	
225 230 235	

<210> 28
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 28

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

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro
20 25 30

Val Ser Ala Ala Val Gly Ser Thr Val Thr Ile Asn Cys Gln Ala Ser
35 40 45

Gln Ser Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys Pro
50 55 60

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

Gly Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
85 90 95

Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

Leu Gly Gly Tyr His Trp Ser Thr Ala Asp Cys Asn Val Phe Gly Gly
115 120 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
130 135 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145 150 155 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
165 170 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
180 185 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
195 200 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
210 215 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225 230 235

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H1 of A2 monoclonal antibody

<400> 29

Phe Thr Val Ser Ser Tyr Asp Met Gly
1 5

<210> 30

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H2 of A2 monoclonal antibody

<400> 30

Ser Ile Gly Ala Ile Gly Ser Asp Gly Ser Glu Tyr Tyr Val Ser Trp
1 5 10 15

Ala

<210> 31

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H3 of A2 monoclonal antibody

<400> 31

Ala Arg Asp Ser His Tyr Ser Tyr Gly Tyr Asp Tyr Asp Ile
1 5 10

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-L1 of A2 monoclonal antibody

<400> 32

Gln Ser Ile Tyr Ser Asn Tyr Leu Ser
1 5

<210> 33

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2 of A2 monoclonal antibody

<400> 33

Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser
1 5 10

<210> 34
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3 of A2 monoclonal antibody

<400> 34

Gln Gly Thr Tyr Tyr Val Thr Gly Trp Tyr Asp Ala
1 5 10

<210> 35
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1 of E5 monoclonal antibody

<400> 35

Phe Ser Leu Ser Ser Tyr Asp Met Ser
1 5

<210> 36
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2 of E5 monoclonal antibody

<400> 36

Trp Ile Gly Tyr Leu Ser Ser Asp Gly Arg Ala Tyr Tyr Ala Ser Trp
1 5 10 15

Ala

<210> 37
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3 of E5 monoclonal antibody

<400> 37

Ala Arg Gly Asp Asn Thr Ala Asp Ile
1 5

<210> 38
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1 of E5 monoclonal antibody

<400> 38

Gln Ser Val Tyr Lys Asn Asn Asp Leu Ala
1 5 10

<210> 39
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2 of E5 monoclonal antibody

<400> 39

Leu Leu Ile Tyr Phe Ala Ser Thr Leu Ala Ser
1 5 10

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3 of E5 monoclonal antibody

<400> 40

Ala Gly Gly Tyr Ser Gly Pro Val Gly Ala
1 5 10

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H1 of G7 monoclonal antibody

<400> 41

Phe Ser Leu Ser Ser Tyr Gly Val Ser
1 5

<210> 42

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H2 of G7 monoclonal antibody

<400> 42

Trp Ile Gly Phe Ile Asp Lys Tyr Gly Arg Thr His Tyr Ala Ser Trp
1 5 10 15

Ala

<210> 43

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-H3 of G7 monoclonal antibody

<400> 43

Ala Arg Asp Asp Tyr Arg Pro Ala Tyr Gly Phe Asp Ile
1 5 10

<210> 44

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1 of G7 monoclonal antibody

<400> 44

Gln Ser Val Tyr Asn Asn Asn Trp Leu Ser
1 5 10

<210> 45
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2 of G7 monoclonal antibody

<400> 45

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

<210> 46
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3 of G7 monoclonal antibody

<400> 46

Leu Gly Gly Tyr His Trp Ser Thr Ala Asp Cys Asn Val
1 5 10

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> immunogenic peptide

<400> 47

Tyr Arg Leu Lys Arg Ser Lys Ser
1 5