

SEQUENCE LISTING

<110> Astellas Pharma Inc.

<120> anti-human NR1 antibody derivatives

<130> A21009A00

<150> JP2020-092105

<151> 2020-05-27

<160> 50

<170> PatentIn version 3.5

<210> 1

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized

<220>

<221> CDS

<222> (1)..(360)

<400> 1

cag gtc cag ctg caa gag tct ggc cct gga ctg gtc aag cct tct ggc	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly	
1 5 10 15	

acc ctg tct ctg aca tgt gct gtg tcc ggc ggc tcc atc tcc tcc tct	96
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser	
20 25 30	

aat tgg tgg tct tgg gtc cga cag cct cct ggc aaa gga ctg gaa tgg	144
Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp	
35 40 45	

atc ggc gag atc tac cac tcc ggc aac acc aac tac aac ccc agc ctg	192
Ile Gly Glu Ile Tyr His Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu	
50 55 60	

aag tcc aga gtg acc gtg tcc gtg gac aag tcc aag aac cag ttc tcc	240
Lys Ser Arg Val Thr Val Ser Val Asp Lys Ser Lys Asn Gln Phe Ser	
65 70 75 80	

ctg aag ctg acc tct gtg acc gct gcc gat acc gcc gtg tac tac tgt	288
Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gct	aga	gat	gtg	tct	ggc	gga	gtg	aat	tgg	ttc	gat	cct	tgg	ggc	cag	336
Ala	Arg	Asp	Val	Ser	Gly	Gly	Val	Asn	Trp	Phe	Asp	Pro	Trp	Gly	Gln	
			100					105					110			

ggc	aca	ctg	gtt	acc	gtg	tcc	tct									360
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115					120									

<210> 2
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 2

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

Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Ser
			20					25					30		

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

Ile	Gly	Glu	Ile	Tyr	His	Ser	Gly	Asn	Thr	Asn	Tyr	Asn	Pro	Ser	Leu
	50					55					60				

Lys	Ser	Arg	Val	Thr	Val	Ser	Val	Asp	Lys	Ser	Lys	Asn	Gln	Phe	Ser
65					70					75					80

Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

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

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120								

<210> 3
 <211> 330
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<220>
 <221> CDS
 <222> (1)..(330)

<400> 3
 aac ttt atg ctg acc cag cct cac tcc gtg tcc gag tct cca ggc aag 48
 Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15
 acc gtg acc atc tcc tgt acc aga tcc tcc ggc tct atc gcc tcc aac 96
 Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30
 tac gtg cag tgg tat cag cag agg cct ggc tct gct cct acc acc gtg 144
 Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
 35 40 45
 atc tac gag gac aac cag agg cct tct ggc gtg ccc gat agg ttc tct 192
 Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 ggc tcc atc gac tcc tct tcc aac tcc gcc tct ctg acc atc agc ggc 240
 Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80
 ctg aaa acc gag gac gag gcc gac tac tac tgc cag tcc tac gac tct 288
 Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
 85 90 95
 tcc acc gtg gtg ttt ggc ggc gga aca aag ctg aca gtg ctg 330
 Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105 110

<210> 4
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 4
 Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15
 Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30

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

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

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

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

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

<210> 5
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse antibody/ humanized

<220>
<221> CDS
<222> (1)..(363)

<400> 5
gaa gtt cag ctg gtt cag tct ggc gcc gaa gtg aag aag cct ggc gag 48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
tcc ctg aag atc tcc tgc aaa ggc tcc ggc tac acc tac acc agc tac 96
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Tyr Thr Ser Tyr
20 25 30
tgg atg aac tgg gtc cga cag atg cct ggc aaa ggc ctg gaa tgg atg 144
Trp Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
ggc aga atc gac ccc tac gac tcc gag aca cac tac gac cag aaa ttc 192
Gly Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asp Gln Lys Phe
50 55 60
aag gac caa gtg acc ctg agc gtg gac aag tcc atc tcc acc gct tac 240
Lys Asp Gln Val Thr Leu Ser Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

ctg	cag	tgg	tcc	tct	ctg	aag	gcc	tct	gac	acc	gcc	atg	tac	tac	tgt	288
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	
			85						90					95		

gct	ggc	ggc	atc	acc	acc	atc	ctc	ggc	ggc	tac	ttt	gat	tac	tgg	ggc	336
Ala	Gly	Gly	Ile	Thr	Thr	Ile	Leu	Gly	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	
			100					105					110			

cag	ggc	aca	ctg	gtc	acc	gtt	tct	tcc								363
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120									

<210> 6
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

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

Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Tyr	Thr	Ser	Tyr
		20					25						30		

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

Gly	Arg	Ile	Asp	Pro	Tyr	Asp	Ser	Glu	Thr	His	Tyr	Asp	Gln	Lys	Phe
	50					55				60					

Lys	Asp	Gln	Val	Thr	Leu	Ser	Val	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65				70					75					80	

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

Ala	Gly	Gly	Ile	Thr	Thr	Ile	Leu	Gly	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly
			100					105					110		

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
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115

120

<210> 7
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS
 <222> (1)..(327)

<400> 7
 gac atc cag atg acc cag tct cca tcc tct ctg tcc gcc tct gtg ggc 48
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 gac aga gtg acc atc acc tgt aga gcc agc cag gac atc tcc aac tac 96
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 ctg aac tgg tat cag cag aag ccc ggc aag gcc cct aag ctg ctg atc 144
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 tac tac acc tct cgg ctg cac tct ggc gtg ccc tct aga ttt tct ggc 192
 Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 tcc ggc tct ggc acc gac tat acc ctg aca atc tcc agc ctg cag cct 240
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 gag gac ttc gcc acc tac tat tgc cag cag ggc aac acc ctg cct cca 288
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro
 85 90 95
 tac aca ttt ggc cag ggc acc aag gtg gaa atc aag cgt 327
 Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

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

<220>
 <223> Synthetic Construct

<400> 8

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

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

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

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

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

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

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

<210> 9

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> mouse antibody/ humanized

<220>

<221> CDS

<222> (1)..(366)

<400> 9

gaa gtg cag ctg gtt gaa tct ggc ggc gga ttg gtt cag cct ggc gga 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tct ctg aga ctg tcc tgc aag gct tct ggc tac gcc tac acc tcc tac 96
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Ala Tyr Thr Ser Tyr
20 25 30

tgg atg aac tgg gtc cga cag gct cct ggc aaa gga ctc gtg tgg gtc	144
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val	
35 40 45	

gga aga atc gac ccc tac gac tcc gag aca cac tac aac cag aag ttc	192
Gly Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe	
50 55 60	

aag gac cgg ttc acc ctg agc gtg gac aag gcc aag tct acc acc tac	240
Lys Asp Arg Phe Thr Leu Ser Val Asp Lys Ala Lys Ser Thr Thr Tyr	
65 70 75 80	

ctg cag atg aac tcc ctg aga gcc gag gac acc gcc gtg tac tat tgc	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gct acc ctg atc acc aca ctg aga ggc gag ggc gcc atg gaa tat tgg	336
Ala Thr Leu Ile Thr Thr Leu Arg Gly Glu Gly Ala Met Glu Tyr Trp	
100 105 110	

gga cag gga acc ctg gtc acc gtg tcc tct	366
Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120	

<210> 10
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

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 Lys Ala Ser Gly Tyr Ala Tyr Thr Ser Tyr
20 25 30

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

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

Lys Asp Arg Phe Thr Leu Ser Val Asp Lys Ala Lys Ser Thr Thr Tyr
65 70 75 80

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

Ala Thr Leu Ile Thr Thr Leu Arg Gly Glu Gly Ala Met Glu Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 11

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> mouse antibody/ humanized

<220>

<221> CDS

<222> (1)..(324)

<400> 11

gac	ctg	cag	atg	acc	cag	tct	cct	tcc	agc	ctg	tct	gcc	tct	gtg	ggc	48
Asp	Leu	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		

gac	aga	gtg	acc	atc	aca	tgc	aag	gcc	agc	cag	gac	gtg	aac	acc	gcc	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	
			20					25					30			

gtt	gct	tgg	tat	cag	cag	aag	cct	ggc	aag	gcc	cct	aag	ctg	ctg	atc	144
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				

tac	tgg	gcc	tcc	acc	aga	cat	acc	ggc	gtg	ccc	tct	aga	ttc	tcc	ggc	192
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						

tct	ggc	tct	ggc	acc	gac	tat	acc	ctg	aca	atc	tcc	agc	ctg	cag	cct	240
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65					70				75					80		

gag	gac	ttc	gcc	acc	tac	tac	tgc	cag	cag	cac	tac	agc	acc	cct	ttc	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Ser	Thr	Pro	Phe	
				85					90					95		

acc	ttt	ggc	cag	ggc	acc	aag	gtg	gaa	atc	aag	cgt					324
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 12
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

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

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 13
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse antibody/ humanized

<220>
<221> CDS

<222> (1)..(357)

<400> 13

cag	gtt	cag	ctg	caa	gag	tct	ggc	cct	ggc	ctg	gtc	aag	cct	tcc	gaa	48
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	
1				5					10					15		

aca	ctg	tcc	ctg	acc	tgc	agc	gtg	acc	ggc	tac	tct	atc	acc	tcc	gac	96
Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Thr	Gly	Tyr	Ser	Ile	Thr	Ser	Asp	
			20					25					30			

tac	tac	tgg	cac	tgg	atc	aga	cag	cct	cca	ggc	aaa	ggc	ctg	gaa	tgg	144
Tyr	Tyr	Trp	His	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
		35					40					45				

atc	gcc	tac	atc	aga	tac	gac	ggc	cgg	aac	gac	tac	aac	ccc	agc	ctg	192
Ile	Ala	Tyr	Ile	Arg	Tyr	Asp	Gly	Arg	Asn	Asp	Tyr	Asn	Pro	Ser	Leu	
	50					55					60					

aag	aac	aga	gtg	acc	atc	agc	cgg	gac	acc	tcc	aag	aac	cag	ttc	tcc	240
Lys	Asn	Arg	Val	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	
65					70					75					80	

ctg	aag	ctg	tcc	tcc	gtg	acc	gct	gct	gat	acc	gcc	gtg	tac	tac	tgc	288
Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		

gcc	aga	gag	gac	tac	ggc	tcc	tcc	tcc	ttt	gat	tac	tgg	ggc	cag	ggc	336
Ala	Arg	Glu	Asp	Tyr	Gly	Ser	Ser	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	
			100					105					110			

acc	ctg	gtc	acc	gtt	agt	tct										357
Thr	Leu	Val	Thr	Val	Ser	Ser										
				115												

<210> 14

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 14

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

Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Thr	Gly	Tyr	Ser	Ile	Thr	Ser	Asp
			20					25					30		

Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Thr Leu Val Thr Val Ser Ser
 115

<210> 15
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS
 <222> (1)..(324)

<400> 15
 gac atc cag atg acc cag tct cca tcc tct ctg tcc gcc tct gtg ggc 48
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

gac aga gtg acc atc acc tgt cgg gcc tcc gag aac atc tac tcc aac 96
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asn
 20 25 30

ctg gcc tgg tat cag cag aag cct ggc aag gct cct aag ctg ctg gtg 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
 35 40 45

tac gcc gct acc aat ctg gct gat ggc gtg ccc tct aga ttc tcc ggc 192
 Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly

50				55				60								
tct	ggc	tct	ggc	acc	gac	tat	acc	ctg	aca	atc	tcc	agc	ctg	cag	cct	240
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
				70				75				80				
gag	gac	ttc	gcc	acc	tac	tac	tgc	cag	cac	ttc	tgg	gac	agc	cct	cca	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Asp	Ser	Pro	Pro	
				85				90				95				
acc	ttt	ggc	cag	ggc	acc	aag	gtg	gaa	atc	aag	cgt					324
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
				100				105								

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

<220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS
 <222> (1)..(357)

<400> 17
 cag gtt cag ctg caa gag tct ggc cct ggc ctg gtc aag cct tct cag 48
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 acc ctg tct ctg acc tgc agc gtg acc ggc tac tcc atc acc tcc gac 96
 Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp
 20 25 30
 tac tac tgg cac tgg atc aga cag cct cca ggc aaa ggc ctg gaa tgg 144
 Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 atc gcc tac atc aga tac gac ggc cgg aac gac agc aac ccc agc ctg 192
 Ile Ala Tyr Ile Arg Tyr Asp Gly Arg Asn Asp Ser Asn Pro Ser Leu
 50 55 60
 aag aac aga gtg acc atc agc cgg gac acc tcc aag aac cag ttc tcc 240
 Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80
 ctg aag ctg tcc tcc gtg acc gct gct gat acc gcc gtg tac tac tgc 288
 Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcc aga gag gac tac gcc tcc tcc tcc ttt gat tac tgg ggc cag ggc 336
 Ala Arg Glu Asp Tyr Ala Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 acc ctg gtc acc gtt agt tct 357
 Thr Leu Val Thr Val Ser Ser
 115

<210> 18
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

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

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Thr Leu Val Thr Val Ser Ser
115

<210> 19

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> mouse antibody/ humanized

<220>

<221> CDS

<222> (1)..(324)

<400> 19

gac atc cag atg acc cag tct cca tcc tct ctg tcc gcc tct gtg ggc
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

48

gac	aga	gtg	acc	atc	acc	tgt	cgg	cct	tcc	gag	aac	atc	tac	tcc	aac	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Pro	Ser	Glu	Asn	Ile	Tyr	Ser	Asn	
			20					25					30			

ctg	gcc	tgg	tat	cag	cag	aag	cct	ggc	aag	gct	cct	aag	ctg	ctg	gtg	144
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Val	
		35					40					45				

tac	gcc	gct	acc	aat	ctg	gct	gat	ggc	gtg	ccc	tct	aga	ttc	tcc	ggc	192
Tyr	Ala	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						

tct	ggc	tct	ggc	acc	gac	tat	acc	ctg	aca	atc	tcc	agc	ctg	cag	cct	240
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65					70					75					80	

gag	gat	atc	gcc	acc	tac	tac	tgc	cag	cac	ttc	tgg	gac	agc	cct	cca	288
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Asp	Ser	Pro	Pro	
				85					90					95		

acc	ttt	ggc	cag	ggc	acc	aag	ctg	gaa	atc	aag	cgt					324
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg					
			100					105								

<210> 20
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Pro	Ser	Glu	Asn	Ile	Tyr	Ser	Asn
			20					25					30		

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

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

Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65		70		75		80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Phe Trp Asp Ser Pro Pro						
		85		90		95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 21
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified antibody

<220>
 <221> CDS
 <222> (1)..(1350)

<400> 21	
cag gtc cag ctg caa gag tct ggc cct gga ctg gtc aag cct tct ggc	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly	
1 5 10 15	
acc ctg tct ctg aca tgt gct gtg tcc ggc ggc tcc atc tcc tcc tct	96
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser	
20 25 30	
aat tgg tgg tct tgg gtc cga cag cct cct ggc aaa gga ctg gaa tgg	144
Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp	
35 40 45	
atc ggc gag atc tac cac tcc ggc aac acc aac tac aac ccc agc ctg	192
Ile Gly Glu Ile Tyr His Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu	
50 55 60	
aag tcc aga gtg acc gtg tcc gtg gac aag tcc aag aac cag ttc tcc	240
Lys Ser Arg Val Thr Val Ser Val Asp Lys Ser Lys Asn Gln Phe Ser	
65 70 75 80	
ctg aag ctg acc tct gtg acc gct gcc gat acc gcc gtg tac tac tgt	288
Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gct aga gat gtg tct ggc gga gtg aat tgg ttc gat cct tgg ggc cag	336
Ala Arg Asp Val Ser Gly Gly Val Asn Trp Phe Asp Pro Trp Gly Gln	
100 105 110	

ggc aca ctg gtt acc gtg tcc tct gct tct acc aag gga ccc tct gtg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val 115 120 125	384
ttc cct ctg gct cct tcc agc aag tct acc tct ggt gga acc gct gct Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 130 135 140	432
ctg ggc tgc ctg gtc aag gat tac ttt cct gag cct gtg aca gtg tcc Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 145 150 155 160	480
tgg aac tct ggt gct ctg aca tcc ggc gtg cac acc ttt cca gct gtg Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 165 170 175	528
ctg cag tcc tct ggc ctg tac tct ctg tcc tct gtc gtg acc gtg cct Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 180 185 190	576
tct agc tct ctg ggc acc cag acc tac atc tgc aac gtg aac cac aag Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 195 200 205	624
cct tcc aac acc aag gtg gac aag aag gtg gaa ccc aag tcc tgc gac Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 210 215 220	672
aag acc cac acc tgt cct cca tgt cct gct cca gaa gct gct ggc ggt Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly 225 230 235 240	720
ccc tcc gtt ttc ctg ttt cca cct aag cct aag gac acc ctg atg atc Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile 245 250 255	768
tct cgg acc cct gaa gtg aca tgc gtg gtg gtg gat gtg tcc cac gag Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu 260 265 270	816
gat ccc gaa gtg aag ttc aat tgg tac gtg gac ggc gtg gaa gtg cac Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His 275 280 285	864
aac gcc aag acc aag cct aga gag gaa cag tac aac tcc acc tac aga Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg 290 295 300	912
gtg gtg tcc gtg ctg acc gtg ctg cac cag gat tgg ctg aac ggc aaa Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys 305 310 315 320	960
gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gct cct atc gaa	1008

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu	
325 330 335	
aag acc atc tcc aag gct aag ggc cag cct cgg gaa cct cag gtt tac	1056
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr	
340 345 350	
aca ctg cct cca tct cgg gac gag ctg acc aag aat cag gtg tcc ctg	1104
Thr Leu Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu	
355 360 365	
tct tgc gcc gtg aag ggc ttc tac cct tct gat atc gcc gtg gaa tgg	1152
Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	
370 375 380	
gag tcc aac ggc cag cct gag aac aac tac aag aca acc cct cct gtg	1200
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	
385 390 395 400	
ctg gac tcc gac ggc tca ttc ttc ctg gtg tcc aag ctg aca gtg gat	1248
Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp	
405 410 415	
aag tct cgg tgg cag cag ggc aac gtg ttc tcc tgt tct gtg atg cac	1296
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	
420 425 430	
gag gcc ctg cac aac cac tac acc cag aag agt ctg tct ctg tcc cct	1344
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	
435 440 445	
ggc aag	1350
Gly Lys	
450	

<210> 22
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

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

Ile Gly Glu Ile Tyr His Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Val Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys

450

<210> 23
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified antibody

<220>
 <221> CDS
 <222> (1)..(648)

<400> 23
 aac ttt atg ctg acc cag cct cac tcc gtg tcc gag tct cca ggc aag 48
 Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15
 acc gtg acc atc tcc tgt acc aga tcc tcc ggc tct atc gcc tcc aac 96
 Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30
 tac gtg cag tgg tat cag cag agg cct ggc tct gct cct acc acc gtg 144
 Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
 35 40 45
 atc tac gag gac aac cag agg cct tct ggc gtg ccc gat agg ttc tct 192
 Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 ggc tcc atc gac tcc tct tcc aac tcc gcc tct ctg acc atc agc ggc 240
 Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80
 ctg aaa acc gag gac gag gcc gac tac tac tgc cag tcc tac gac tct 288
 Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
 85 90 95
 tcc acc gtg gtg ttt ggc ggc gga aca aag ctg aca gtg ctg ggc cag 336
 Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 cct aag gcc aat cct acc gtg aca ctg ttc cct cca tcc tcc gag gaa 384
 Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 ctg cag gct aac aag gct acc ctc gtg tgc ctg atc tcc gat ttt tac 432
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140

cct ggc gct gtg acc gtg gct tgg aag gct gat gga tct cct gtg aag 480
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160

gcc ggc gtg gaa acc acc aag cct agc aag cag tcc aac aac aaa tac 528
Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

gcc gcc tcc tcc tac ctg tct ctg acc cct gaa cag tgg aag tcc cac 576
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

cgg tcc tac tct tgc caa gtg acc cat gag ggc agc acc gtg gaa aag 624
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

aca gtg gcc cct acc gag tgc tct 648
Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210>	24
<211>	216
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 25
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse antibody/ humanized

<220>
<221> CDS
<222> (1)..(1353)

<400> 25
gaa gtt cag ctg gtt cag tct ggc gcc gaa gtg aag aag cct ggc gag 48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

tcc ctg aag atc tcc tgc aaa ggc tcc ggc tac acc tac acc agc tac 96

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

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

ccc ggc aag
Pro Gly Lys
450

1353

<210> 26
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Tyr Thr Ser Tyr
20 25 30

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

Gly Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asp Gln Lys Phe
50 55 60

Lys Asp Gln Val Thr Leu Ser Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Gly Gly Ile Thr Thr Ile Leu Gly Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145		150		155		160									
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
			180					185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			

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

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

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

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

Pro Gly Lys
 450

<210> 27
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS
 <222> (1)..(645)

<400> 27
 gac atc cag atg acc cag tct cca tcc tct ctg tcc gcc tct gtg ggc 48
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

gac aga gtg acc atc acc tgt aga gcc agc cag gac atc tcc aac tac 96
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

ctg aac tgg tat cag cag aag ccc ggc aag gcc cct aag ctg ctg atc 144
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

tac tac acc tct cgg ctg cac tct ggc gtg ccc tct aga ttt tct ggc 192

Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly		
50						55					60						
tcc	ggc	tct	ggc	acc	gac	tat	acc	ctg	aca	atc	tcc	agc	ctg	cag	cct		240
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro		
65					70					75					80		
gag	gac	ttc	gcc	acc	tac	tat	tgc	cag	cag	ggc	aac	acc	ctg	cct	cca		288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Pro		
				85					90					95			
tac	aca	ttt	ggc	cag	ggc	acc	aag	gtg	gaa	atc	aag	cgt	acg	gtg	gcc		336
Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala		
			100					105					110				
gct	cct	tcc	gtg	ttc	atc	ttc	cca	cct	tcc	gac	gag	cag	ctg	aag	tcc		384
Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser		
		115					120					125					
ggc	aca	gct	tct	gtc	gtg	tgc	ctg	ctg	aac	aac	ttc	tac	cct	cgg	gaa		432
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu		
	130					135					140						
gcc	aag	gtg	cag	tgg	aag	gtg	gac	aat	gcc	ctg	cag	tcc	ggc	aac	tcc		480
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser		
145					150				155						160		
caa	gag	tct	gtg	acc	gag	cag	gac	tcc	aag	gac	agc	acc	tac	agc	ctg		528
Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu		
				165					170					175			
tcc	tcc	aca	ctg	acc	ctg	tcc	aag	gcc	gac	tac	gag	aag	cac	aag	gtg		576
Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val		
			180					185					190				
tac	gcc	tgc	gaa	gtg	acc	cat	cag	ggc	ctg	tct	agc	cct	gtg	acc	aag		624
Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys		
		195					200					205					
tct	ttc	aac	cgg	ggc	gag	tgc											645
Ser	Phe	Asn	Arg	Gly	Glu	Cys											
	210					215											

<210> 28
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 28

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

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 29
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS
 <222> (1)..(1356)

<400> 29
 gaa gtg cag ctg gtt gaa tct ggc ggc gga ttg gtt cag cct ggc gga 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tct ctg aga ctg tcc tgc aag gct tct ggc tac gcc tac acc tcc tac 96
 Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Ala Tyr Thr Ser Tyr
 20 25 30
 tgg atg aac tgg gtc cga cag gct cct ggc aaa gga ctc gtg tgg gtc 144
 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
 35 40 45
 gga aga atc gac ccc tac gac tcc gag aca cac tac aac cag aag ttc 192
 Gly Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
 50 55 60
 aag gac cgg ttc acc ctg agc gtg gac aag gcc aag tct acc acc tac 240
 Lys Asp Arg Phe Thr Leu Ser Val Asp Lys Ala Lys Ser Thr Thr Tyr
 65 70 75 80
 ctg cag atg aac tcc ctg aga gcc gag gac acc gcc gtg tac tat tgc 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gct acc ctg atc acc aca ctg aga ggc gag ggc gcc atg gaa tat tgg 336
 Ala Thr Leu Ile Thr Thr Leu Arg Gly Glu Gly Ala Met Glu Tyr Trp
 100 105 110
 gga cag gga acc ctg gtc acc gtg tcc tct gct agc acc aag gga ccc 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 tct gtg ttc cct ctg gct cct tcc agc aag tcc acc tct ggt gga aca 432
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

gct gct ctg ggc tgc ctg gtc aag gac tac ttt cct gag cct gtg acc Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 145 150 155 160	480
gtg tct tgg aac tct ggc gct ctg aca tct ggc gtg cac acc ttt cca Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 165 170 175	528
gct gtg ctg cag tcc tcc ggc ctg tac tct ctg tcc tct gtc gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr 180 185 190	576
gtg cct tcc agc tct ctg gga acc cag acc tac atc tgc aat gtg aac Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 195 200 205	624
cac aag cct tcc aac acc aag gtc gac aag aag gtg gaa ccc aag tcc His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser 210 215 220	672
tgc gac aag acc cac acc tgt cct cca tgt cct gct cca gaa gct gct Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 225 230 235 240	720
ggc ggc cct tcc gtg ttt ctg ttc cct cca aag cct aag gac acc ctg Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 245 250 255	768
atg atc tct cgg acc cct gaa gtg acc tgc gtg gtg gtg gat gtg tct Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 260 265 270	816
cac gag gat ccc gaa gtg aag ttc aat tgg tac gtg gac ggc gtg gaa His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 275 280 285	864
gtg cac aac gcc aag acc aag cct aga gag gaa cag tac aac tcc acc Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 290 295 300	912
tac aga gtg gtg tcc gtg ctg acc gtg ctg cac cag gat tgg ctg aac Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 305 310 315 320	960
ggc aaa gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gct cct Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 325 330 335	1008
atc gaa aag acc atc tct aag gcc aag ggc cag cct cgg gaa cct cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 340 345 350	1056

gtt	tac	acc	ttg	cct	cca	tct	cgg	gac	gag	ctg	acc	aag	aac	cag	gtg	1104
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
		355					360					365				

tcc	ctg	tct	tgt	gcc	gtg	aag	ggc	ttc	tac	ccc	tcc	gat	atc	gct	gtg	1152
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	
	370					375					380					

gaa	tgg	gag	agc	aat	ggc	cag	cct	gag	aac	aac	tac	aag	aca	acc	cct	1200
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	
	385				390					395					400	

cct	gtg	ctg	gac	tcc	gac	ggc	tca	ttc	ttc	ctg	gtg	tcc	aag	ctg	aca	1248
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	
			405					410						415		

gtg	gac	aag	tcc	aga	tgg	cag	cag	ggc	aac	gtg	ttc	tcc	tgc	agc	gtg	1296
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	
			420					425					430			

atg	cac	gag	gcc	ctg	cac	aat	cac	tat	acc	cag	aag	tct	ctg	tct	ctg	1344
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	
		435				440						445				

agc	ccc	ggc	aag													1356
Ser	Pro	Gly	Lys													
		450														

<210> 30
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30

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	Lys	Ala	Ser	Gly	Tyr	Ala	Tyr	Thr	Ser	Tyr	
			20					25					30			

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

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

Lys Asp Arg Phe Thr Leu Ser Val Asp Lys Ala Lys Ser Thr Thr Tyr
65 70 75 80

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

Ala Thr Leu Ile Thr Thr Leu Arg Gly Glu Gly Ala Met Glu Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

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

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

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

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

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

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

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

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

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

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

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

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

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 31
<211> 642
<212> DNA
<213> Artificial Sequence

<220>

<223> mouse antibody/ humanized

<220>

<221> CDS

<222> (1)..(642)

<400> 31

gac	ctg	cag	atg	acc	cag	tct	cct	tcc	agc	ctg	tct	gcc	tct	gtg	ggc	48
Asp	Leu	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		

gac	aga	gtg	acc	atc	aca	tgc	aag	gcc	agc	cag	gac	gtg	aac	acc	gcc	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	
			20					25					30			

gtt	gct	tgg	tat	cag	cag	aag	cct	ggc	aag	gcc	cct	aag	ctg	ctg	atc	144
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				

tac	tgg	gcc	tcc	acc	aga	cat	acc	ggc	gtg	ccc	tct	aga	ttc	tcc	ggc	192
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						

tct	ggc	tct	ggc	acc	gac	tat	acc	ctg	aca	atc	tcc	agc	ctg	cag	cct	240
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65					70					75					80	

gag	gac	ttc	gcc	acc	tac	tac	tgc	cag	cag	cac	tac	agc	acc	cct	ttc	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Ser	Thr	Pro	Phe	
				85					90					95		

acc	ttt	ggc	cag	ggc	acc	aag	gtg	gaa	atc	aag	cgt	acg	gtg	gcc	gct	336
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	
			100					105					110			

cct	tcc	gtg	ttc	atc	ttc	cca	cct	tcc	gac	gag	cag	ctg	aag	tcc	ggc	384
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	
		115					120					125				

aca	gct	tct	gtc	gtg	tgc	ctg	ctg	aac	aac	ttc	tac	cct	cgg	gaa	gcc	432
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	
	130					135					140					

aag	gtg	cag	tgg	aag	gtg	gac	aat	gcc	ctg	cag	tcc	ggc	aac	tcc	caa	480
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	
145					150					155					160	

gag	tct	gtg	acc	gag	cag	gac	tcc	aag	gac	agc	acc	tat	agc	ctg	tcc	528
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	
				165					170					175		

tcc	aca	ctg	acc	ctg	tcc	aag	gcc	gac	tac	gag	aag	cac	aag	gtg	tac	576
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	
		180						185					190			

gcc	tgc	gaa	gtg	acc	cat	cag	ggc	ctg	tct	agt	ccc	gtg	acc	aag	tct	624
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	
		195					200					205				

ttc	aac	cgg	ggc	gag	tgc											642
Phe	Asn	Arg	Gly	Glu	Cys											
		210														

<210> 32
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32

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

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

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

Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
			100					105					110		

Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130	135	140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145	150	155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165	170	175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180	185	190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195	200	205
Phe Asn Arg Gly Glu Cys		
210		

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

 <220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS
 <222> (1)..(1347)

<400> 33	
cag gtt cag ctg caa gag tct ggc cct ggc ctg gtc aag cct tcc gaa	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	
1 5 10 15	
aca ctg tcc ctg acc tgc agc gtg acc ggc tac tct atc acc tcc gac	96
Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp	
20 25 30	
tac tac tgg cac tgg atc aga cag cct cca ggc aaa ggc ctg gaa tgg	144
Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp	
35 40 45	

atc gcc tac atc aga tac gac ggc cgg aac gac tac aac ccc agc ctg Ile Ala Tyr Ile Arg Tyr Asp Gly Arg Asn Asp Tyr Asn Pro Ser Leu 50 55 60	192
aag aac aga gtg acc atc agc cgg gac acc tcc aag aac cag ttc tcc Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser 65 70 75 80	240
ctg aag ctg tcc tcc gtg acc gct gct gat acc gcc gtg tac tac tgc Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
gcc aga gag gac tac ggc tcc tcc tcc ttt gat tac tgg ggc cag ggc Ala Arg Glu Asp Tyr Gly Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly 100 105 110	336
acc ctg gtc acc gtt agt tct gct agc acc aag gga ccc agc gtg ttc Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe 115 120 125	384
cct ctg gct cct tcc agc aag tct acc tct ggc gga aca gct gct ctg Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 130 135 140	432
ggc tgt ctg gtc aag gac tac ttc cct gag cct gtg acc gtg tcc tgg Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp 145 150 155 160	480
aac tct ggc gct ctg aca tct ggc gtg cac acc ttt cca gct gtg ctg Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 165 170 175	528
cag tcc tcc ggc ctg tac tct ctg tcc tct gtc gtg acc gtg cct tcc Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 180 185 190	576
agc tct ctg gga acc cag acc tac atc tgc aat gtg aac cac aag cct Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 195 200 205	624
agc aac acc aag gtg gac aag aag gtg gaa ccc aag tcc tgc gac aag Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys 210 215 220	672
acc cac acc tgt cct cca tgt cct gct cca gaa gct gct ggc ggc cct Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro 225 230 235 240	720
tcc gtg ttt ctg ttc cct cca aag cct aag gac acc ctg atg atc tct Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 245 250 255	768
cgg acc cct gaa gtg acc tgc gtg gtg gtg gat gtg tct cac gag gat	816

Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp		
			260					265					270				
ccc	gaa	gtg	aag	ttc	aat	tgg	tac	gtg	gac	ggc	gtg	gaa	gtg	cac	aac	864	
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn		
		275					280					285					
gcc	aag	acc	aag	cct	aga	gag	gaa	cag	tac	aac	tcc	acc	tac	aga	gtg	912	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val		
	290					295					300						
gtg	tcc	gtg	ctg	acc	gtg	ctg	cac	cag	gat	tgg	ctg	aac	ggc	aaa	gag	960	
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu		
305					310					315					320		
tac	aag	tgc	aag	gtg	tcc	aac	aag	gcc	ctg	cct	gct	cct	atc	gaa	aag	1008	
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys		
				325					330					335			
acc	atc	tcc	aag	gct	aag	ggc	cag	cct	cgg	gaa	cct	cag	gtg	tac	aca	1056	
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr		
			340					345					350				
ttg	cct	cca	tct	cgg	gac	gag	ctg	acc	aag	aat	cag	gtg	tcc	ctg	tct	1104	
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser		
		355					360					365					
tgc	gcc	gtg	aag	ggc	ttc	tac	cct	tcc	gat	atc	gcc	gtg	gaa	tgg	gag	1152	
Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu		
	370					375					380						
tcc	aat	ggc	cag	cca	gag	aac	aac	tac	aag	aca	acc	cct	cct	gtg	ctg	1200	
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu		
385					390					395					400		
gac	tcc	gac	ggc	tca	ttc	ttc	ctg	gtg	tcc	aag	ctg	aca	gtg	gac	aag	1248	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys		
				405					410					415			
tcc	aga	tgg	cag	cag	ggc	aac	gtg	ttc	tcc	tgc	tct	gtg	atg	cac	gag	1296	
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		
			420				425						430				
gcc	ctg	cac	aac	cac	tac	acc	cag	aag	tct	ctg	tct	ctg	agc	ccc	ggc	1344	
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly		
		435					440					445					
aag																1347	
Lys																	

<210> 34

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

<220>
 <223> Synthetic Construct

<400> 34

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

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp
 20 25 30

Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Tyr Gly Ser Ser Ser 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 Glu Ala Ala Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu

gag gac ttc gcc acc tac tac tgc cag cac ttc tgg gac agc cct cca	288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Asp Ser Pro Pro	
85 90 95	

acc ttt ggc cag ggc acc aag gtg gaa atc aag cgt acg gtg gcc gct	336
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	

cct tcc gtg ttc atc ttc cca cct tcc gac gag cag ctg aag tcc ggc	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	

aca gct tct gtc gtg tgc ctg ctg aac aac ttc tac cct cgg gaa gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	

aag gtg cag tgg aag gtg gac aat gcc ctg cag tcc ggc aac tcc caa	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	

gag tct gtg acc gag cag gac tcc aag gac agc acc tac agc ctg tcc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	

tcc aca ctg acc ctg tcc aag gcc gac tac gag aag cac aag gtg tac	576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	

gct tgc gaa gtg acc cac cag ggc ctg tct agc cct gtg acc aag tcc	624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	

ttc aac cgg ggc gag tgc	642
Phe Asn Arg Gly Glu Cys	
210	

<210> 36
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 36

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 37
<211> 1347
<212> DNA

<213> Artificial Sequence

<220>

<223> mouse antibody/ humanized

<220>

<221> CDS

<222> (1)..(1347)

<400> 37

cag gtt cag ctg caa gag tct ggc cct ggc ctg gtc aag cct tct cag	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln	
1 5 10 15	

acc ctg tct ctg acc tgc agc gtg acc ggc tac tcc atc acc tcc gac	96
Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp	
20 25 30	

tac tac tgg cac tgg atc aga cag cct cca ggc aaa ggc ctg gaa tgg	144
Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp	
35 40 45	

atc gcc tac atc aga tac gac ggc cgg aac gac agc aac ccc agc ctg	192
Ile Ala Tyr Ile Arg Tyr Asp Gly Arg Asn Asp Ser Asn Pro Ser Leu	
50 55 60	

aag aac aga gtg acc atc agc cgg gac acc tcc aag aac cag ttc tcc	240
Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser	
65 70 75 80	

ctg aag ctg tcc tcc gtg acc gct gct gat acc gcc gtg tac tac tgc	288
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gcc aga gag gac tac gcc tcc tcc tcc ttt gat tac tgg ggc cag ggc	336
Ala Arg Glu Asp Tyr Ala Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly	
100 105 110	

acc ctg gtc acc gtt agt tct gct agc acc aag gga ccc agc gtg ttc	384
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe	
115 120 125	

cct ctg gct cct tcc agc aag tct acc tct ggc gga aca gct gct ctg	432
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu	
130 135 140	

ggc tgt ctg gtc aag gac tac ttc cct gag cct gtg acc gtg tcc tgg	480
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp	
145 150 155 160	

aac tct ggc gct ctg aca tct ggc gtg cac acc ttt cca gct gtg ctg	528
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu	

165	170	175	
cag tcc tcc ggc ctg tac tct ctg tcc tct gtc gtg acc gtg cct tcc Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 180 185 190			576
agc tct ctg gga acc cag acc tac atc tgc aat gtg aac cac aag cct Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 195 200 205			624
tcc aac acc aag gtg gac aag aag gtg gaa ccc aag tcc tgc gac aag Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys 210 215 220			672
acc cac acc tgt cct cca tgt cct gct cca gaa gct gct ggc ggc cct Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro 225 230 235 240			720
tcc gtg ttt ctg ttc cct cca aag cct aag gac acc ctg atg atc tct Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 245 250 255			768
cgg acc cct gaa gtg acc tgc gtg gtg gtg gat gtg tct cac gag gat Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp 260 265 270			816
ccc gaa gtg aag ttc aat tgg tac gtg gac ggc gtg gaa gtg cac aac Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn 275 280 285			864
gcc aag acc aag cct aga gag gaa cag tac aac tcc acc tac aga gtg Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val 290 295 300			912
gtg tcc gtg ctg acc gtg ctg cac cag gat tgg ctg aac ggc aaa gag Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu 305 310 315 320			960
tac aag tgc aag gtg tcc aac aag gcc ctg cct gct cct atc gaa aag Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys 325 330 335			1008
acc atc tcc aag gct aag ggc cag cct cgg gaa cct cag gtg tac aca Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr 340 345 350			1056
ttg cct cca tct cgg gac gag ctg acc aag aat cag gtg tcc ctg tcc Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser 355 360 365			1104
tgt gcc gtg aag ggc ttc tac cct tcc gat atc gcc gtg gaa tgg gag Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 370 375 380			1152

tcc aat ggc cag cca gag aac aac tac aag aca acc cct cct gtg ctg	1200
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu	
385 390 395 400	

gac tcc gac ggc tca ttc ttc ctg gtg tcc aag ctg aca gtg gac aag	1248
Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys	
405 410 415	

tcc aga tgg cag cag ggc aac gtg ttc tcc tgc tct gtg atg cac gag	1296
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu	
420 425 430	

gcc ctg cac aac cac tac acc cag aag agt ctg tct ctg tcc cct ggc	1344
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly	
435 440 445	

aag	1347
Lys	

<210> 38
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 38

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

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Tyr Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Glu Asp Tyr Ala Ser Ser Ser 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 Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 39
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> mouse antibody/ humanized

<220>
 <221> CDS

<222> (1)..(642)

<400> 39

gac	atc	cag	atg	acc	cag	tct	cca	tcc	tct	ctg	tcc	gcc	tct	gtg	ggc		48
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly		
1				5					10					15			

gac	aga	gtg	acc	atc	acc	tgt	cgg	cct	tcc	gag	aac	atc	tac	tcc	aac		96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Pro	Ser	Glu	Asn	Ile	Tyr	Ser	Asn		
			20					25					30				

ctg	gcc	tgg	tat	cag	cag	aag	cct	ggc	aag	gct	cct	aag	ctg	ctg	gtg		144
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Val		
		35					40					45					

tac	gcc	gct	acc	aat	ctg	gct	gat	ggc	gtg	ccc	tct	aga	ttc	tcc	ggc		192
Tyr	Ala	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly		
	50					55					60						

tct	ggc	tct	ggc	acc	gac	tat	acc	ctg	aca	atc	tcc	agc	ctg	cag	cct		240
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro		
65					70					75					80		

gag	gat	atc	gcc	acc	tac	tac	tgc	cag	cac	ttc	tgg	gac	agc	cct	cca		288
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Asp	Ser	Pro	Pro		
				85					90					95			

acc	ttt	ggc	cag	ggc	acc	aag	ctg	gaa	atc	aag	cgt	acg	gtg	gcc	gct		336
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala		
			100					105					110				

cct	tcc	gtg	ttc	atc	ttc	cca	cct	tcc	gac	gag	cag	ctg	aag	tcc	ggc		384
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly		
		115					120					125					

aca	gct	tct	gtc	gtg	tgc	ctg	ctg	aac	aac	ttc	tac	cct	cgg	gaa	gcc		432
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala		
	130					135					140						

aag	gtg	cag	tgg	aag	gtg	gac	aat	gcc	ctg	cag	tcc	ggc	aac	tcc	caa		480
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln		
145					150					155					160		

gag	tct	gtg	acc	gag	cag	gac	tcc	aag	gac	agc	acc	tac	agc	ctg	tcc		528
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser		
				165					170					175			

tcc	aca	ctg	acc	ctg	tcc	aag	gcc	gac	tac	gag	aag	cac	aag	gtg	tac		576
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr		
			180					185					190				

gct	tgc	gaa	gtg	acc	cac	cag	ggc	ctg	tct	agc	cct	gtg	acc	aag	tcc		624
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser		

	195	200	205	
ttc aac cgg ggc gag tgc				642
Phe Asn Arg Gly Glu Cys				
210				
<210> 40				
<211> 214				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> Synthetic Construct				
<400> 40				
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly				
1 5 10 15				
Asp Arg Val Thr Ile Thr Cys Arg Pro Ser Glu Asn Ile Tyr Ser Asn				
20 25 30				
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val				
35 40 45				
Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly				
50 55 60				
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro				
65 70 75 80				
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Phe Trp Asp Ser Pro Pro				
85 90 95				
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala				
100 105 110				
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly				
115 120 125				
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala				
130 135 140				

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 41
 <211> 666
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified Fc fragment

<220>
 <221> CDS
 <222> (1)..(666)

<400> 41
 tgc cct cca tgt cct gct cca gaa gcc gct ggc gga ccc tct gtg ttt 48
 Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 1 5 10 15
 ctg ttc cct cca aag cct aag gac acc ctg atg atc tct cgg acc cct 96
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 20 25 30
 gaa gtg acc tgc gtg gtg gtg gat gtg tct cac gag gat ccc gaa gtg 144
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 35 40 45
 aag ttc aat tgg tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc 192
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 50 55 60
 aag cct aga gag gaa cag tac aac tcc acc tac aga gtg gtg tcc gtg 240
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 65 70 75 80

ctg acc gtg ctg cac cag gat tgg ctg aac ggc aaa gag tac aag tgc	288
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys	
85 90 95	
aag gtg tcc aac aag gcc ctg cct gct cct atc gaa aag acc atc tcc	336
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser	
100 105 110	
aag gct aag ggc cag cct cgg gaa cct cag gtt tac aca ctg cct cca	384
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro	
115 120 125	
tct cgg gac gag ctg acc aag aat cag gtg tcc ctg tgg tgc ctg gtc	432
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val	
130 135 140	
aag ggc ttc tac cct tcc gat atc gcc gtg gaa tgg gag tcc aat ggc	480
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	
145 150 155 160	
cag cct gag aac aac tac aag acc aca cct cct gtg ctg gac tcc gac	528
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp	
165 170 175	
ggc tca ttc ttc ctg tac tcc aag ctg aca gtg gac aag tct cgg tgg	576
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	
180 185 190	
cag cag ggc aac gtg ttc tcc tgt tct gtg atg cac gag gcc ctg cac	624
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His	
195 200 205	
aac cac tac acc cag aag tcc ctg tct ctg tcc cct ggc aaa	666
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
210 215 220	

<210> 42
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 42

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
1 5 10 15

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

20

25

30

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 35 40 45

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 50 55 60

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 65 70 75 80

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 85 90 95

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 100 105 110

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 115 120 125

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 130 135 140

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 145 150 155 160

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 165 170 175

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 180 185 190

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 195 200 205

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215 220

<210> 43

<211> 1176

<212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<220>
 <221> CDS
 <222> (1)..(1176)

<400> 43
 atg tca acg atg agg ctc ctg acc ctt gct ctg ctg ttc agc tgc tca 48
 Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1 5 10 15

gtt gcc agg gct gct tgt gac ccc aaa atc gtg aac att ggc gcc gtg 96
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
 20 25 30

ctg tct acc aga aag cac gag cag atg ttt agg gaa gcc gtg aac cag 144
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
 35 40 45

gca aac aag agg cat ggg tct tgg aaa att cag ctg aat gca acc tct 192
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
 50 55 60

gtg aca cac aag cca aat gcc att caa atg gca ctg tcc gtc tgc gag 240
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
 65 70 75 80

gac ttg att agc agc cag gtt tac gcc ata ctc gtg agc cat cct ccc 288
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
 85 90 95

acg ccc aat gac cac ttc act cca act cct gtt tcc tat acc gct ggc 336
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
 100 105 110

ttt tac cgg att cct gtc ttg ggc ctc acc aca aga atg agt atc tac 384
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
 115 120 125

agt gac aag agc ata cac ctg agt ttc ctc cgc act gtg cct ccc tat 432
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
 130 135 140

agt cac cag tcc tct gtg tgg ttc gaa atg atg agg gtc tac tcc tgg 480
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
 145 150 155 160

aat cac atc att ctg ttg gtg tcc gat gac cac gaa gga cgt gca gcc 528

Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala		
				165					170					175			
cag	aaa	agg	ctg	gaa	act	ctg	ctc	gaa	gaa	cga	gag	tca	aaa	gcg	gaa		576
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu		
			180					185					190				
aag	gtg	ctg	caa	ttc	gac	cca	gga	aca	aag	aac	gtc	act	gcg	ttg	ctg		624
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu		
		195					200					205					
atg	gag	gca	aaa	gag	ctg	gaa	gca	cgg	gtg	atc	atc	ctc	agc	gca	tca		672
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser		
	210					215					220						
gag	gac	gat	gcc	gcc	act	gtg	tat	cga	gct	gct	gcg	atg	ctg	aat	atg		720
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met		
225					230				235						240		
aca	ggg	tcc	ggc	tac	gtc	tgg	ctt	gtc	ggc	gag	aga	gag	att	agc	ggt		768
Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly		
				245					250					255			
aat	gct	ctg	cgg	tat	gct	ccc	gat	ggc	atc	ttg	ggg	ctt	cag	ctc	atc		816
Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile		
			260					265					270				
aat	ggc	aag	aac	gaa	agc	gcc	cat	att	tct	gac	gcc	gtt	ggg	gta	gta		864
Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val		
		275					280					285					
gcc	caa	gca	gtt	cac	gag	ctg	ctt	gag	aag	gag	aac	ata	acc	gat	cca		912
Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro		
	290					295					300						
cct	aga	ggg	tgt	gtg	ggg	aac	acc	aac	att	tgg	aaa	aca	gga	ccg	ctg		960
Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu		
305					310				315						320		
ttc	aaa	cga	gtt	ctg	atg	tct	agc	aag	tat	gct	gat	ggc	gtg	aca	ggc		1008
Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly		
				325					330					335			
aga	gtg	gag	ttc	aac	gag	gat	ggt	gat	cgg	aaa	ttt	gct	aac	tac	agc		1056
Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser		
			340					345					350				
att	atg	aat	ctg	caa	aat	cgc	aaa	ctg	gta	cag	gtt	ggg	ata	tac	aat		1104
Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn		
		355					360					365					
gga	acc	cac	gtg	atc	ccg	aac	gac	cgg	aag	ata	atc	tgg	cct	gga	ggc		1152
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly		

370

375

380

1176

gaa acg gag aaa ccc cgc ggt tat
 Glu Thr Glu Lys Pro Arg Gly Tyr
 385 390

<210> 44
 <211> 392
 <212> PRT
 <213> Homo sapiens

<400> 44

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
 20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
 35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
 50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
 65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
 85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
 100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
 115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
 130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
 145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
 370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr
 385 390

<210> 45
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pathogenic anti-human NR1 antibody

<220>
 <221> CDS
 <222> (1)..(1350)

<400> 45
 cag gtc cag ctg caa gag tct ggc cct gga ctg gtc aag cct tct ggc 48
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
 1 5 10 15

acc ctg tct ctg aca tgt gct gtg tcc ggc ggc tcc atc tcc tcc tct 96
 Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
 20 25 30

aat tgg tgg tct tgg gtc cga cag cct cct ggc aaa gga ctg gaa tgg 144
 Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 35 40 45

atc ggc gag atc tac cac tcc ggc aac acc aac tac aac ccc agc ctg 192
 Ile Gly Glu Ile Tyr His Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

aag tcc aga gtg acc gtg tcc gtg gac aag tcc aag aac cag ttc tcc 240
 Lys Ser Arg Val Thr Val Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
 65 70 75 80

ctg aag ctg acc tct gtg acc gct gcc gat acc gcc gtg tac tac tgt 288
 Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gct aga gat gtg tct ggc gga gtg aat tgg ttc gat cct tgg ggc cag 336
 Ala Arg Asp Val Ser Gly Gly Val Asn Trp Phe Asp Pro Trp Gly Gln
 100 105 110

ggc aca ctg gtt acc gtg tcc tct gct tct acc aag gga ccc tct gtg 384
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

ttc cct ctg gct cct tcc agc aag tct acc tct ggt gga acc gct gct Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 130 135 140	432
ctg ggc tgc ctg gtc aag gat tac ttt cct gag cct gtg aca gtg tcc Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 145 150 155 160	480
tgg aac tct ggt gct ctg aca tcc ggc gtg cac acc ttt cca gct gtg Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 165 170 175	528
ctg cag tcc tct ggc ctg tac tct ctg tcc tct gtc gtg acc gtg cct Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 180 185 190	576
tct agc tct ctg ggc acc cag acc tac atc tgc aac gtg aac cac aag Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 195 200 205	624
cct tcc aac acc aag gtg gac aag aag gtg gaa ccc aag tcc tgc gac Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 210 215 220	672
aag acc cac acc tgt cct cca tgt cct gct cca gaa ctg ctc ggc ggt Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 225 230 235 240	720
ccc tcc gtt ttc ctg ttt cca cct aag cct aag gac acc ctg atg atc Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile 245 250 255	768
tct cgg acc cct gaa gtg aca tgc gtg gtg gtg gat gtg tcc cac gag Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu 260 265 270	816
gat ccc gaa gtg aag ttc aat tgg tac gtg gac ggc gtg gaa gtg cac Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His 275 280 285	864
aac gcc aag acc aag cct aga gag gaa cag tac aac tcc acc tac aga Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg 290 295 300	912
gtg gtg tcc gtg ctg acc gtg ctg cac cag gat tgg ctg aac ggc aaa Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys 305 310 315 320	960
gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gct cct atc gaa Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu 325 330 335	1008

aag acc atc tcc aag gct aag ggc cag cct cgg gaa cct cag gtt tac	1056
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr	
340 345 350	
aca ctg cct cca tct cgg gac gag ctg acc aag aat cag gtg tcc ctg	1104
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu	
355 360 365	
acc tgc ctc gtg aag ggc ttc tac cct tct gat atc gcc gtg gaa tgg	1152
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	
370 375 380	
gag tcc aac ggc cag cct gag aac aac tac aag aca acc cct cct gtg	1200
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	
385 390 395 400	
ctg gac tcc gac ggc tca ttc ttc ctg tac tcc aag ctg aca gtg gat	1248
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp	
405 410 415	
aag tcc cgg tgg cag cag ggc aac gtg ttc tct tgt tct gtg atg cac	1296
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	
420 425 430	
gag gcc ctg cac aac cac tac acc cag aag agt ctg tct ctg tcc cct	1344
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	
435 440 445	
ggc aag	1350
Gly Lys	
450	

<210> 46
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 46

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

Ile Gly Glu Ile Tyr His Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Val Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 47
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Pathogenic anti-human NR1 antibody

<220>
 <221> CDS
 <222> (1)..(648)

<400> 47
 aac ttt atg ctg acc cag cct cac tcc gtg tcc gag tct cca ggc aag 48
 Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15
 acc gtg acc atc tcc tgt acc aga tcc tcc ggc tct atc gcc tcc aac 96
 Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30
 tac gtg cag tgg tat cag cag agg cct ggc tct gct cct acc acc gtg 144
 Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
 35 40 45
 atc tac gag gac aac cag agg cct tct ggc gtg ccc gat agg ttc tct 192
 Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 ggc tcc atc gac tcc tct tcc aac tcc gcc tct ctg acc atc agc ggc 240
 Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80
 ctg aaa acc gag gac gag gcc gac tac tac tgc cag tcc tac gac tct 288
 Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
 85 90 95
 tcc acc gtg gtg ttt ggc ggc gga aca aag ctg aca gtg ctg ggc cag 336
 Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 cct aag gcc aat cct acc gtg aca ctg ttc cct cca tcc tcc gag gaa 384
 Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 ctg cag gct aac aag gct acc ctc gtg tgc ctg atc tcc gat ttt tac 432
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 cct ggc gct gtg acc gtg gct tgg aag gct gat gga tct cct gtg aag 480
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
 145 150 155 160

gcc ggc gtg gaa acc acc aag cct agc aag cag tcc aac aac aaa tac	528
Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr	
165 170 175	

gcc gcc tcc tcc tac ctg tct ctg acc cct gaa cag tgg aag tcc cac	576
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His	
180 185 190	

cgg tcc tac tct tgc caa gtg acc cat gag ggc agc acc gtg gaa aag	624
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys	
195 200 205	

aca gtg gcc cct acc gag tgc tct	648
Thr Val Ala Pro Thr Glu Cys Ser	
210 215	

<210> 48
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 48

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

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

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

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

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

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

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln

100

105

110

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

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

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

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

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

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

Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> 49

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 49

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
 1 5 10 15

Val His Ser

<210> 50

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 50

Met	Ser	Val	Pro	Thr	Gln	Val	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Thr
1				5					10					15	

Asp	Ala	Arg	Cys
			20