

SEQUENCE LISTING

<110> Jiangsu Hengrui Pharmaceuticals Co., Ltd.
Shanghai Hengrui Pharmaceutical Co., Ltd.

<120> PHARMACEUTICAL COMPOSITION COMPRISING ANTI-CONNECTIVE TISSUE GROWTH FACTOR ANTIBODY

<130> 721132CPCT

<150> 202011405490.5

<151> 2020-12-03

<150> 202111366667.X

<151> 2021-11-18

<160> 104

<170> SIPOSequenceListing 1.0

<210> 1

<211> 323

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<223> Full-length human CTGF protein

<400> 1

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

<210> 2
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 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <223> CTGF-his

<400> 2

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1				5				10						15	
Val	Gln	Cys	Gln	Asn	Cys	Ser	Gly	Pro	Cys	Arg	Cys	Pro	Asp	Glu	Pro
			20					25					30		
Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser	Leu	Val	Leu	Asp	Gly	Cys	Gly
		35				40						45			
Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu	Gly	Glu	Leu	Cys	Thr	Glu	Arg
	50					55				60					
Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu	Phe	Cys	Asp	Phe	Gly	Ser	Pro
65					70				75					80	
Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys
				85					90					95	
Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser
		100					105						110		
Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro
	115					120						125			
Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro
	130					135					140				
Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp
145					150					155					160
Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg

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

<210> 3
 <211> 575
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <223> mCTGF-Fc

<400> 3

Met	Glu	Phe	Gly	Leu	Ser	Trp	Leu	Phe	Leu	Val	Ala	Ile	Leu	Lys	Gly		
1				5				10					15				
Val	Gln	Cys	Gln	Asp	Cys	Ser	Ala	Gln	Cys	Gln	Cys	Ala	Ala	Glu	Ala		
		20					25					30					
Ala	Pro	His	Cys	Pro	Ala	Gly	Val	Ser	Leu	Val	Leu	Asp	Gly	Cys	Gly		
	35					40					45						
Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu	Gly	Glu	Leu	Cys	Thr	Glu	Arg		
	50					55				60							
Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu	Phe	Cys	Asp	Phe	Gly	Ser	Pro		
65				70					75						80		
Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys		
			85					90					95				
Val	Phe	Gly	Gly	Ser	Val	Tyr	Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser		
	100						105					110					
Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Val	Pro		
	115					120					125						
Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro		
	130					135					140						

Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	145	150	155	160
Glu	Pro	Lys	Asp	Arg	Thr	Ala	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	165	170		175
Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro	Thr	Met	Met	Arg	Ala	Asn	Cys	180	185		190
Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala	Cys	Ser	Lys	Thr	Cys	Gly	Met	195	200		205
Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Thr	Phe	Cys	Arg	Leu	Glu	210	215		220
Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg	Pro	Cys	Glu	Ala	Asp	Leu	Glu	225	230		235
Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys	Ile	Arg	Thr	Pro	Lys	Ile	Ala	245	250		255
Lys	Pro	Val	Lys	Phe	Glu	Leu	Ser	Gly	Cys	Thr	Ser	Val	Lys	Thr	Tyr	260	265		270
Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr	Asp	Gly	Arg	Cys	Cys	Thr	Pro	275	280		285
His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu	Phe	Lys	Cys	Pro	Asp	Gly	Glu	290	295		300
Ile	Met	Lys	Lys	Asn	Met	Met	Phe	Ile	Lys	Thr	Cys	Ala	Cys	His	Tyr	305	310		315
Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe	Glu	Ser	Leu	Tyr	Tyr	Arg	Lys	325	330		335
Met	Tyr	Gly	Asp	Met	Ala	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	340	345		350
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	355	360		365
Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	370	375		380
Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	385	390		395
Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	405	410		415
Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	420	425		430
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	435	440		445
Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	450	455		460
Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	465	470		475
Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	485	490		495
Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	500	505		510
Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	515	520		525
Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	530	535		540
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	545	550		555
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys					

565

570

575

<210> 4
 <211> 348
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <223> Mouse CTGF protein-His tag

<400> 4
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1 5 10 15
 Val Gln Cys Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Ala Glu Ala
 20 25 30
 Ala Pro His Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly
 35 40 45
 Cys Cys Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg
 50 55 60
 Asp Pro Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro
 65 70 75 80
 Ala Asn Arg Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys
 85 90 95
 Val Phe Gly Gly Ser Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser
 100 105 110
 Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro
 115 120 125
 Leu Cys Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro
 130 135 140
 Arg Arg Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp
 145 150 155 160
 Glu Pro Lys Asp Arg Thr Ala Val Gly Pro Ala Leu Ala Ala Tyr Arg
 165 170 175
 Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys
 180 185 190
 Leu Val Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met
 195 200 205
 Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu
 210 215 220
 Lys Gln Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu
 225 230 235 240
 Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala
 245 250 255
 Lys Pro Val Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr
 260 265 270
 Arg Ala Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro
 275 280 285
 His Arg Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu
 290 295 300
 Ile Met Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr
 305 310 315 320

Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe	Glu	Ser	Leu	Tyr	Tyr	Arg	Lys
				325					330					335	
Met	Tyr	Gly	Asp	Met	Ala	His	His	His	His	His	His				
			340					345							

<210> 5
 <211> 574
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <223> Cynomolgus monkey CTGF-Fc

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

290	295	300
Val Met Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr		
305	310	315
Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys		
	325	330
Met Tyr Gly Asp Met Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr		
	340	345
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe		
	355	360
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro		
	370	375
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val		
385	390	395
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr		
	405	410
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val		
	420	425
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys		
	435	440
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser		
	450	455
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro		
465	470	475
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val		
	485	490
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly		
	500	505
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp		
	515	520
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp		
	530	535
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His		
545	550	555
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	565	570

<210> 6
 <211> 116
 <212> PRT
 <213> Mus musculus

<220>
 <221> DOMAIN
 <223> mab147 VH

<400> 6
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Glu Gly
 1 5 10 15
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala	Arg	Ile	Arg	Thr	Lys	Ser	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp
50					55					60					
Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Glu	Ser	Met
65					70				75						80
Leu	Tyr	Leu	Gln	Met	Asn	Asn	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Met	Tyr
				85				90						95	
Tyr	Cys	Val	Glu	Thr	Gly	Phe	Ala	Tyr	Trp	Asp	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ala												
			115												

<210> 7
 <211> 106
 <212> PRT
 <213> Mus musculus

<220>
 <221> DOMAIN
 <223> mab147 VL

Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5				10						15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met
			20					25					30		
His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			
Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
		50				55					60				
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu
65					70				75						80
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Leu	Thr
				85				90						95	
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys						
			100					105							

<210> 8
 <211> 114
 <212> PRT
 <213> Mus musculus

<220>
 <221> DOMAIN
 <223> mab164 VH

Gln	Val	Gln	Leu	Lys	Gln	Ser	Gly	Pro	Gly	Leu	Val	Gln	Pro	Ser	Gln
1				5				10						15	
Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Thr	Phe
			20					25					30		
Gly	Val	His	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu

<211> 19
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab147 HCDR2

<400> 11
Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15
Val Lys Asp

<210> 12
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab147 HCDR3

<400> 12
Thr Gly Phe Ala Tyr
1 5

<210> 13
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab147 LCDR1

<400> 13
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 14
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab147 LCDR2

<400> 14
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 15
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab147 LCDR3

<400> 15
Gln Gln Arg Ser Ser Tyr Pro Leu Thr
1 5

<210> 16
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab164 HCDR1

<400> 16
Thr Phe Gly Val His
1 5

<210> 17
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN
<223> mab164 HCDR2

<400> 17
Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met Ser
1 5 10 15

<210> 18
<211> 6
<212> PRT
<213> Mus musculus

<220>
<221> DOMAIN

<223> mab164 HCDR3

<400> 18

Asp Gly Gly Phe Asp Tyr
1 5

<210> 19

<211> 14

<212> PRT

<213> Mus musculus

<220>

<221> DOMAIN

<223> mab164 LCDR1

<400> 19

Arg Ser Ser Ile Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 20

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> DOMAIN

<223> mab164 LCDR2

<400> 20

Gly Thr Ser Asn Arg Ala Pro
1 5

<210> 21

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> DOMAIN

<223> mab164 LCDR3

<400> 21

Ala Leu Trp Tyr Ser Thr His Tyr Val
1 5

<210> 22

<211> 106

<212> PRT

<213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu147-VL1

<400> 22
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 23
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu147-VL2

<400> 23
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 24
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu147-VL3

<400> 24
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Trp Ile Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 25
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu147-VL4

<400> 25
 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 Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 26
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>

<221> DOMAIN
<223> Hu147-VL5

<400> 26
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
His Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Trp Ile Tyr
35 40 45
Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
85 90 95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 27
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Hu147-VH1

<400> 27
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60
Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Val Glu Thr Gly Phe Ala Tyr Trp Asp Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 28
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu147-VH2

<400> 28
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Val Glu Thr Gly Phe Ala Tyr Trp Asp Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 29
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu147-VH3

<400> 29
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Glu Ser Ser
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Val Glu Thr Gly Phe Ala Tyr Trp Asp Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 30
 <211> 109

<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Hu164-VL7

<400> 30
Glu Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr Ser
20 25 30
Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45
Leu Ile Gly Gly Thr Ser Asn Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80
Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Thr
85 90 95
His Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 31
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Hu164-VL8

<400> 31
Glu Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr Ser
20 25 30
Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Phe Arg Gly
35 40 45
Leu Ile Gly Gly Thr Ser Asn Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60
Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80
Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Thr
85 90 95
His Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 32
<211> 109
<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<223> Hu164-VL9

<400> 32

```
Glu Ser Val Val Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1          5          10          15
Arg Val Thr Ile Ser Cys Arg Ser Ser Ile Gly Ala Val Thr Thr Ser
          20          25          30
Asn Tyr Ala Asn Trp Val Gln Gln Leu Pro Gly Thr Ala Phe Lys Gly
          35          40          45
Leu Ile Gly Gly Thr Ser Asn Arg Ala Pro Gly Val Pro Asp Arg Phe
          50          55          60
Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65          70          75          80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Thr
          85          90          95
His Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
          100          105
```

<210> 33

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<223> Hu164-VH5

<400> 33

```
Glu Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1          5          10          15
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Thr Phe
          20          25          30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
          35          40          45
Ala Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
          50          55          60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Val Leu
65          70          75          80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
          85          90          95
Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
          100          105          110
Ser Ser
```

<210> 34

<211> 114

<212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu164-VH6

<400> 34
 Glu Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Val Phe
 65 70 75 80
 Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser

<210> 35
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu164-VH7

<400> 35
 Glu 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 Thr Val Ser Gly Phe Ser Ile Ser Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser

<210> 36
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Hu164-VH8

<400> 36
 Glu 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 Thr Val Ser Gly Phe Ser Ile Ser Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Phe
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser

<210> 37
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Heavy chain constant region w

<400> 37
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
			100					105					110			
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
		115					120					125				
Lys	Pro	Lys	Asp	Thr	Leu	Tyr	Ile	Thr	Arg	Glu	Pro	Glu	Val	Thr	Cys	
	130					135					140					
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
145					150					155					160	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
			165						170					175		
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
			180					185					190			
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
		195					200					205				
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
	210					215					220					
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	
225					230					235					240	
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	
			245						250					255		
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	
			260					265					270			
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	
		275					280					285				
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	
	290					295					300					
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	
305					310					315					320	
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
			325						330							

<210> 39
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Humanized antibody light chain kappa constant region

<400>	39															
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	
1				5				10						15		
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	
			20					25					30			
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	
	35						40					45				
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	
	50					55					60					
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
65					70					75				80		
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	

				85					90				95
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
			100					105					

<210> 40
 <211> 105
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> DOMAIN
 <223> Humanized antibody light chain lambda constant region

<400> 40

Gly	Gln	Pro	Lys	Ala	Asn	Pro	Thr	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser
1				5					10					15	
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp
			20					25					30		
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Gly	Ser	Pro
		35					40					45			
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Lys	Pro	Ser	Lys	Gln	Ser	Asn	Asn
	50					55					60				
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys
65					70					75					80
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val
			85						90					95	
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys							
			100					105							

<210> 41
 <211> 446
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> CHAIN
 <223> Heavy chain of Ch147

<400> 41

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Glu	Gly
1				5					10					15	
Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Asn	Thr	Tyr
			20					25					30		
Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40						45			
Ala	Arg	Ile	Arg	Thr	Lys	Ser	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp
	50					55					60				
Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Glu	Ser	Met
65					70					75					80
Leu	Tyr	Leu	Gln	Met	Asn	Asn	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Met	Tyr
			85						90					95	

Tyr	Cys	Val	Glu	Thr	Gly	Phe	Ala	Tyr	Trp	Asp	Gln	Gly	Thr	Leu	Val	100	105	110
Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	115	120	125
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	130	135	140
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	145	150	155
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	165	170	175
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	180	185	190
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	195	200	205
Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	210	215	220
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	225	230	235
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	245	250	255
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	260	265	270
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	275	280	285
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	290	295	300
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	305	310	315
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	325	330	335
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	340	345	350
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	355	360	365
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	370	375	380
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	385	390	395
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	405	410	415
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	420	425	430
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			435	440	445

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

<220>
 <221> CHAIN
 <223> Light chain of Ch147

<400> 42

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

<210> 43

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Heavy chain of Hu147-11wk

<400> 43

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60
Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	85	90	95
Tyr	Cys	Val	Glu	Thr	Gly	Phe	Ala	Tyr	Trp	Asp	Gln	Gly	Thr	Leu	Val	100	105	110
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	115	120	125
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	130	135	140
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	145	150	155
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	165	170	175
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	180	185	190
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	195	200	205
Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	210	215	220
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	225	230	235
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	245	250	255
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	260	265	270
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	275	280	285
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	290	295	300
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	305	310	315
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	325	330	335
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	340	345	350
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	355	360	365
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	370	375	380
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	385	390	395
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	405	410	415
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	420	425	430
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			435	440	445

<210> 44

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN
 <223> Heavy chain of Hu147-21wk

```

<400> 44
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1      5      10      15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20      25      30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35      40      45
Ala Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50      55      60
Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65      70      75      80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85      90      95
Tyr Cys Val Glu Thr Gly Phe Ala Tyr Trp Asp Gln Gly Thr Leu Val
100     105     110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115     120     125
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130     135     140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145     150     155     160
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165     170     175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180     185     190
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195     200     205
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210     215     220
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225     230     235     240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245     250     255
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260     265     270
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275     280     285
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290     295     300
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305     310     315     320
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325     330     335
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340     345     350
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355     360     365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370     375     380

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

<210> 45
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu147-31wk

<400> 45
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Glu Ser Ser
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Val Glu Thr Gly Phe Ala Tyr Trp Asp Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
145					150					155					160
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
				165					170						175
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
			180					185					190		
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr
		195					200					205			
Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
	210					215					220				
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
225					230					235					240
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Tyr	Ile	Thr	Arg	Glu	Pro
				245					250					255	
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
			260					265					270		
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
		275					280					285			
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
	290					295					300				
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
305					310					315					320
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
				325					330					335	
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
			340					345					350		
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
		355					360					365			
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
	370					375					380				
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
385					390					395					400
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
			405						410					415	
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
			420					425					430		
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
		435					440					445			

<210> 47

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Heavy chain of Hu147-21yk

<400> 47

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Thr	Tyr

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<210> 48
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu147-31yk

<400> 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Arg Thr Lys Ser Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Glu Ser Ser
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Val Glu Thr Gly Phe Ala Tyr Trp Asp Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser

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

<210> 49
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Hu147-11wk

<400> 49

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

Asn Arg Gly Glu Cys
210

<210> 50
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<221> CHAIN
<223> Light chain of Hu147-12wk

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

<210> 51
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<221> CHAIN
<223> Light chain of Hu147-13wk

<400> 51
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Trp Ile Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 52
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Hu147-14wk

<400> 52
 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 Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
 85 90 95

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

<210> 53
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Hu147-15wk

<400> 53

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

	195	200	205
Asn Arg Gly Glu Cys			
210			

<210> 54
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Ch164

<400> 54
 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Arg Ser His Val Phe Phe
 65 70 75 80
 Lys Met Thr Ser Leu Gln Thr Asp Asp Ser Ala Ile Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
 100 105 110
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 145 150 155 160
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 165 170 175
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 180 185 190
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 195 200 205
 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300

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

<210> 55
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Ch164

<400> 55

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

			180					185				190			
Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys	Thr
		195					200					205			
Val	Ala	Pro	Thr	Glu	Cys										
	210														

<210> 56
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu164-57w1

<400> 56
 Glu Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
 35 40 45
 Ala Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Val Leu
 65 70 75 80
 Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 145 150 155 160
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 165 170 175
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 180 185 190
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 195 200 205
 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285

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

<210> 57

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Heavy chain of Hu164-67w1

<400> 57

Glu	Val	Thr	Leu	Lys	Glu	Ser	Gly	Pro	Val	Leu	Val	Lys	Pro	Thr	Glu
1			5					10					15		
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Phe
			20				25					30			
Gly	Val	His	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu
		35				40						45			
Gly	Val	Ile	Trp	Arg	Arg	Gly	Gly	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Met
50						55				60					
Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Ser	Gln	Val	Val	Phe
65				70					75						80
Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala
			85					90						95	
Arg	Asp	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
		100					105						110		
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser
		115				120						125			
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
130					135					140					
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
145				150					155						160
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu

Gly	Val	Ile	Trp	Arg	Arg	Gly	Gly	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Met
50						55					60				
Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu
65					70					75					80
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Asp	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
			100					105					110		
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser
		115					120					125			
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
	130					135					140				
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
145					150					155					160
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
				165					170					175	
Tyr	Ser	Leu	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
		180					185					190			
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
	195					200						205			
Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
	210					215					220				
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235					240
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
		260					265						270		
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
	275						280					285			
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290					295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305					310					315					320
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
			340					345						350	
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
	355						360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
		420						425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
		435					440								

<210> 59
<211> 444

<212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu164-87w1

<400> 59
 Glu 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 Thr Val Ser Gly Phe Ser Ile Ser Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Phe
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 145 150 155 160
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 165 170 175
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 180 185 190
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 195 200 205
 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 340 345 350

Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
			420					425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
		435					440								

<210> 60

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Heavy chain of Hu164-57yl

<400> 60

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

225					230					235				240
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Tyr	Ile	Thr	Arg	Glu	Pro	Glu
				245					250					255
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
			260					265					270	Phe
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
		275					280					285		Pro
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
	290					295					300			Thr
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
305					310					315				320
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys
				325					330					335
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
			340					345					350	Arg
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
	355					360						365		Gly
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
	370				375					380				Pro
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
385					390				395					400
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
				405					410					415
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
		420					425					430		His
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
		435					440							

<210> 61
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu164-67y1

<400>	61													
Glu	Val	Thr	Leu	Lys	Glu	Ser	Gly	Pro	Val	Leu	Val	Lys	Pro	Thr
1				5				10					15	
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser	Thr
			20				25					30		Phe
Gly	Val	His	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp
		35				40						45		Leu
Gly	Val	Ile	Trp	Arg	Arg	Gly	Gly	Thr	Asp	Tyr	Asn	Ala	Ala	Phe
	50					55				60				Met
Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Ser	Gln	Val	Val
65					70			75						80
Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys
			85					90					95	Ala
Arg	Asp	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr
			100					105					110	Val

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 145 150 155 160
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 165 170 175
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 180 185 190
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 195 200 205
 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 340 345 350
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 355 360 365
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 405 410 415
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440

<210> 62

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Heavy chain of Hu164-77y1

<400> 62
 Glu 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 Thr Val Ser Gly Phe Ser Ile Ser Thr Phe
 20 25 30
 Gly Val His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 145 150 155 160
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 165 170 175
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 180 185 190
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 195 200 205
 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 340 345 350
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 355 360 365
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 63
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<221> CHAIN
<223> Heavy chain of Hu164-87y1

<400> 63
Glu 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 Thr Val Ser Gly Phe Ser Ile Ser Thr Phe
20 25 30
Gly Val His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Arg Arg Gly Gly Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Phe
65 70 75 80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
195 200 205
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
210 215 220
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240
Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
245 250 255
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
260 265 270
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

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

<210> 64

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Light chain of Hu164-57w1

<400> 64

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

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205
Val Ala Pro Thr Glu Cys
210

<210> 65
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> CHAIN
<223> Light chain of Hu164-58w1

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

<210> 66
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<221> CHAIN
 <223> Light chain of Hu164-59w1

<400> 66
 Glu Ser Val Val Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Arg Ser Ser Ile Gly Ala Val Thr Thr Ser
 20 25 30
 Asn Tyr Ala Asn Trp Val Gln Gln Leu Pro Gly Thr Ala Phe Lys Gly
 35 40 45
 Leu Ile Gly Gly Thr Ser Asn Arg Ala Pro Gly Val Pro Asp Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Thr
 85 90 95
 His Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
 130 135 140
 Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala
 145 150 155 160
 Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
 165 170 175
 Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
 180 185 190
 Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
 195 200 205
 Val Ala Pro Thr Glu Cys
 210

<210> 67
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of mAb1

<400> 67
 Glu Gly Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Gly Thr Gly Gly Gly Thr Tyr Ser Thr Asp Ser Val Lys
 50 55 60

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	65	70	75	80
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Met	Ala	Val	Tyr	Tyr	Cys	Ala	85	90	95	
Arg	Gly	Asp	Tyr	Tyr	Gly	Ser	Gly	Ser	Phe	Phe	Asp	Cys	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	Arg	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	Glu	Glu	Met	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> 68
 <211> 214

<212> PRT
<213> Artificial Sequence

<220>
<221> CHAIN
<223> Light chain of mAb1

<400> 68
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 Gly Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr 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> 69
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> CHAIN
<223> mab95 VH

<400> 69
Glu Val Leu Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Pro
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
20 25 30

Asp	Ile	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile
		35					40				45				
Gly	Leu	Val	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe
	50					55					60				
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Phe	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr
65					70					75				80	
Met	Glu	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Trp	Gly	Leu	Ile	Pro	Gly	Thr	Thr	Ser	Tyr	Phe	Asp	Val	Trp
			100					105					110		
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser						
		115					120								

<210> 70
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> mab95 VL

Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Pro	Ile	Leu	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Arg	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu
65					70					75				80	
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Asn	Ser	Asn	Pro	Trp	Thr
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Arg	Leu	Glu	Ile	Lys						
			100					105							

<210> 71
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> mab95 HCDR1

Asn	Tyr	Asp	Ile	His
1				5

<210> 72
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> mab95 HCDR2

<400> 72
Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys
1 5 10 15
Asp

<210> 73
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> mab95 HCDR3

<400> 73
Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val
1 5 10

<210> 74
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> mab95 LCDR1

<400> 74
Arg Ala Ser Ser Ser Val Ser Tyr Ile His
1 5 10

<210> 75
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> mab95 LCDR2

<400> 75
 Ala Thr Ser Asn Leu Ala Ser
 1 5

<210> 76
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> mab95 LCDR3

<400> 76
 Gln Gln Trp Asn Ser Asn Pro Trp Thr
 1 5

<210> 77
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VL1

<400> 77
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr
 35 40 45
 Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Trp Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 78
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VL2

<400> 78
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Pro Trp Ile Tyr
 35 40 45
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Trp Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 79
 <211> 105
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VL3

<400> 79
 Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His
 20 25 30
 Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Pro Trp Ile Tyr Ala
 35 40 45
 Thr Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys
 50 55 60
 Ser Gly Thr Ser Tyr Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp
 65 70 75 80
 Glu Ala Asp Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Trp Thr Phe
 85 90 95
 Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 80
 <211> 105
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VL4

<400> 80
 Glu Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His
 20 25 30
 Trp Tyr Gln Gln Leu Pro Gly Thr Ser Pro Lys Pro Trp Ile Tyr Ala
 35 40 45
 Thr Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys
 50 55 60
 Ser Gly Thr Ser Tyr Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp
 65 70 75 80
 Glu Ala Asp Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Trp Thr Phe
 85 90 95
 Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 81
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VH1

<400> 81
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Val Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 82
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VH2

<400> 82
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Ala Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 83
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VH3

<400> 83
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Val Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 84
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VH4

<400> 84
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Ala Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 85
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-VH5

<400> 85
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Arg Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Ala Ile His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45
 Gly Leu Val Tyr Pro Tyr Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Val Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Met Ile Pro Gly Thr Asn Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 86
 <211> 452

<212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Ch95

<400> 86
 Glu Val Leu Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Pro
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Ala Thr Leu Thr Phe Asp Thr Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Thr Gly Thr Thr 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 Leu Leu
 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	Thr	Cys	Leu	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	Tyr	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> 87
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Ch95

<400> 87

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

210

<210> 88
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu95-11wk

<400> 88
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Val Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr 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 Leu Leu
 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	Thr	Cys	Leu	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	Tyr	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> 89

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Heavy chain of Hu95-21wk

<400> 89

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1			5					10					15			
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asn	Tyr	
		20					25					30				
Asp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Ile	
	35					40					45					
Gly	Leu	Val	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	
	50					55				60						
Lys	Asp	Arg	Ala	Thr	Leu	Thr	Phe	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	
65				70					75					80		
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
Ala	Arg	Trp	Gly	Leu	Ile	Pro	Gly	Thr	Thr	Ser	Tyr	Phe	Asp	Val	Trp	
		100					105						110			
Gly	Gln	Gly	Thr	Thr	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	

Gly	Leu	Val	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	50	55	60
Lys	Asp	Lys	Val	Thr	Leu	Thr	Phe	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	65	70	75
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95
Ala	Arg	Trp	Gly	Leu	Ile	Pro	Gly	Thr	Thr	Ser	Tyr	Phe	Asp	Val	Trp	100	105	110
Gly	Gln	Gly	Thr	Thr	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
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	Leu	Leu	225	230	235
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
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	Thr	Cys	Leu	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
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	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> 91
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu95-41wk

<400> 91
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Ala Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr 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 Leu Leu
 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	Thr	Cys	Leu	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	Tyr	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> 92
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu95-51wk

<400> 92															
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Arg	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asn	Tyr
			20				25						30		
Ala	Ile	His	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Met
		35				40					45				
Gly	Leu	Val	Tyr	Pro	Tyr	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe
	50					55				60					
Lys	Asp	Lys	Val	Thr	Leu	Thr	Phe	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Trp	Gly	Met	Ile	Pro	Gly	Thr	Asn	Ser	Tyr	Phe	Asp	Val	Trp
			100				105						110		
Gly	Gln	Gly	Thr	Thr	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

Lys Asp Arg Val Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr 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 Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Tyr Ile Thr Arg Glu 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 Thr Cys Leu 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 Tyr 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> 94

<211> 452

<212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu95-21yk

<400> 94
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Asp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
 35 40 45
 Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Ala Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Leu Ile Pro Gly Thr Thr Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr 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 Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Tyr Ile Thr Arg Glu 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	Thr	Cys	Leu	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	Tyr	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> 95
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Hu95-31yk

<400>	95														
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asn	Tyr
			20				25						30		
Asp	Ile	His	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Met
	35					40					45				
Gly	Leu	Val	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe
	50				55					60					
Lys	Asp	Lys	Val	Thr	Leu	Thr	Phe	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr
65				70					75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85				90						95		
Ala	Arg	Trp	Gly	Leu	Ile	Pro	Gly	Thr	Thr	Ser	Tyr	Phe	Asp	Val	Trp
			100				105						110		
Gly	Gln	Gly	Thr	Thr	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 Leu Leu		
225	230	235	240	
Gly Gly Pro Ser Val Phe	Leu Phe Pro Pro Lys	Pro Lys Asp Thr Leu		
	245	250	255	
Tyr Ile Thr Arg Glu 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 Thr Cys Leu 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	Tyr 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> 96
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu95-41yk

<400>	96
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1	5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asn Tyr	
	20 25 30
Asp Ile His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile	
	35 40 45
Gly Leu Val Tyr Pro Tyr Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe	
	50 55 60
Lys Asp Lys Ala Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr	
65	70 75 80

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Trp	Gly	Leu	Ile	Pro	Gly	Thr	Thr	Ser	Tyr	Phe	Asp	Val	Trp	
			100					105					110			
Gly	Gln	Gly	Thr	Thr	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	Leu	Leu	
225					230				235						240	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
			245					250						255		
Tyr	Ile	Thr	Arg	Glu	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	Thr	Cys	Leu	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	Tyr	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> 97
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of Hu95-51yk

<400> 97
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Arg Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30
 Ala Ile His Trp Val Lys Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45
 Gly Leu Val Tyr Pro Tyr Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Val Thr Leu Thr Phe Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Met Ile Pro Gly Thr Asn Ser Tyr Phe Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr 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 Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Tyr Ile Thr Arg Glu 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 Thr Cys Leu 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 Tyr 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> 98
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Hu95-11wk

<400> 98
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Trp Ile Tyr
 35 40 45
 Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Trp Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 99
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Hu95-12wk

<400> 99
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Pro Trp Ile Tyr
 35 40 45
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Trp Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 100
 <211> 212
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of Hu95-13wk

<400> 100
 Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15

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

<210> 101

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<221> CHAIN

<223> Light chain of Hu95-14wk

<400> 101

Glu	Ile	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1				5					10					15	
Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile	His
			20					25					30		
Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala
		35					40					45			
Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys
	50					55					60				
Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp
65					70					75					80
Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Gln	Trp	Asn	Ser	Asn	Pro	Trp	Thr	Phe
			85						90					95	
Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser
			100					105					110		
Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala

<400> 104
Trp Gly Met Ile Pro Gly Thr Asn Ser Tyr Phe Asp Val
1 5 10