

SEQUENCE LISTING

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<120> COMPOSITION AND USE OF ENGINEERED
 MONOCLONAL ANTIBODIES REFRACTORY TO TUMOR IMMUNO-SUPPRESSIVE
 FACTORS

<130> 008966.00005

<160> 50

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1663

<212> PRT

<213> Homo sapiens

<400> 1

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Ile	Leu	Arg	Leu	Glu	Ser	Glu	Glu	Thr	Met	Val	Leu	Glu	Ala	His	Asp
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Ala	Gln	Gly	Asp	Val	Pro	Val	Thr	Val	Thr	Val	His	Asp	Phe	Pro	Gly
	50					55					60				
Lys	Lys	Leu	Val	Leu	Ser	Ser	Glu	Lys	Thr	Val	Leu	Thr	Pro	Ala	Thr
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Asn	His	Met	Gly	Asn	Val	Thr	Phe	Thr	Ile	Pro	Ala	Asn	Arg	Glu	Phe
				85					90					95	
Lys	Ser	Glu	Lys	Gly	Arg	Asn	Lys	Phe	Val	Thr	Val	Gln	Ala	Thr	Phe
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Gly	Thr	Gln	Val	Val	Glu	Lys	Val	Val	Leu	Val	Ser	Leu	Gln	Ser	Gly
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Tyr	Leu	Phe	Ile	Gln	Thr	Asp	Lys	Thr	Ile	Tyr	Thr	Pro	Gly	Ser	Thr
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Val	Leu	Tyr	Arg	Ile	Phe	Thr	Val	Asn	His	Lys	Leu	Leu	Pro	Val	Gly
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Arg	Thr	Val	Met	Val	Asn	Ile	Glu	Asn	Pro	Glu	Gly	Ile	Pro	Val	Lys
				165					170					175	
Gln	Asp	Ser	Leu	Ser	Ser	Gln	Asn	Gln	Leu	Gly	Val	Leu	Pro	Leu	Ser
			180					185					190		
Trp	Asp	Ile	Pro	Glu	Leu	Val	Asn	Met	Gly	Gln	Trp	Lys	Ile	Arg	Ala
		195					200					205			
Tyr	Tyr	Glu	Asn	Ser	Pro	Gln	Gln	Val	Phe	Ser	Thr	Glu	Phe	Glu	Val

210		215		220
Lys Glu Tyr Val Leu Pro Ser Phe Glu Val Ile Val Glu Pro Thr Glu				
225		230		235
Lys Phe Tyr Tyr Ile Tyr Asn Glu Lys Gly Leu Glu Val Thr Ile Thr				
	245		250	255
Ala Arg Phe Leu Tyr Gly Lys Lys Val Glu Gly Thr Ala Phe Val Ile				
	260		265	270
Phe Gly Ile Gln Asp Gly Glu Gln Arg Ile Ser Leu Pro Glu Ser Leu				
	275		280	285
Lys Arg Ile Pro Ile Glu Asp Gly Ser Gly Glu Val Val Leu Ser Arg				
	290		295	300
Lys Val Leu Leu Asp Gly Val Gln Asn Pro Arg Ala Glu Asp Leu Val				
305		310		315
Gly Lys Ser Leu Tyr Val Ser Ala Thr Val Ile Leu His Ser Gly Ser				
	325		330	335
Asp Met Val Gln Ala Glu Arg Ser Gly Ile Pro Ile Val Thr Ser Pro				
	340		345	350
Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met				
	355		360	365
Pro Phe Asp Leu Met Val Phe Val Thr Asn Pro Asp Gly Ser Pro Ala				
	370		375	380
Tyr Arg Val Pro Val Ala Val Gln Gly Glu Asp Thr Val Gln Ser Leu				
385		390		395
Thr Gln Gly Asp Gly Val Ala Lys Leu Ser Ile Asn Thr His Pro Ser				
	405		410	415
Gln Lys Pro Leu Ser Ile Thr Val Arg Thr Lys Lys Gln Glu Leu Ser				
	420		425	430
Glu Ala Glu Gln Ala Thr Arg Thr Met Gln Ala Leu Pro Tyr Ser Thr				
	435		440	445
Val Gly Asn Ser Asn Asn Tyr Leu His Leu Ser Val Leu Arg Thr Glu				
	450		455	460
Leu Arg Pro Gly Glu Thr Leu Asn Val Asn Phe Leu Leu Arg Met Asp				
465		470		475
Arg Ala His Glu Ala Lys Ile Arg Tyr Tyr Thr Tyr Leu Ile Met Asn				
	485		490	495
Lys Gly Arg Leu Leu Lys Ala Gly Arg Gln Val Arg Glu Pro Gly Gln				
	500		505	510
Asp Leu Val Val Leu Pro Leu Ser Ile Thr Thr Asp Phe Ile Pro Ser				
	515		520	525
Phe Arg Leu Val Ala Tyr Tyr Thr Leu Ile Gly Ala Ser Gly Gln Arg				
	530		535	540
Glu Val Val Ala Asp Ser Val Trp Val Asp Val Lys Asp Ser Cys Val				
545		550		555
Gly Ser Leu Val Val Lys Ser Gly Gln Ser Glu Asp Arg Gln Pro Val				
	565		570	575
Pro Gly Gln Gln Met Thr Leu Lys Ile Glu Gly Asp His Gly Ala Arg				
	580		585	590
Val Val Leu Val Ala Val Asp Lys Gly Val Phe Val Leu Asn Lys Lys				
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Asn Lys Leu Thr Gln Ser Lys Ile Trp Asp Val Val Glu Lys Ala Asp				

	610					615					620				
Ile 625	Gly	Cys	Thr	Pro	Gly 630	Ser	Gly	Lys	Asp	Tyr 635	Ala	Gly	Val	Phe	Ser 640
Asp	Ala	Gly	Leu	Thr 645	Phe	Thr	Ser	Ser	Ser 650	Gly	Gln	Gln	Thr	Ala 655	Gln
Arg	Ala	Glu	Leu 660	Gln	Cys	Pro	Gln	Pro 665	Ala	Ala	Arg	Arg	Arg 670	Arg	Ser
Val	Gln	Leu 675	Thr	Glu	Lys	Arg	Met 680	Asp	Lys	Val	Gly 685	Lys	Tyr	Pro	Lys
Glu	Leu 690	Arg	Lys	Cys	Cys	Glu 695	Asp	Gly	Met	Arg	Glu 700	Asn	Pro	Met	Arg
Phe 705	Ser	Cys	Gln	Arg	Arg 710	Thr	Arg	Phe	Ile	Ser 715	Leu	Gly	Glu	Ala 720	Cys
Lys	Lys	Val	Phe 725	Leu	Asp	Cys	Cys	Asn	Tyr 730	Ile	Thr	Glu	Leu	Arg 735	Arg
Gln	His	Ala	Arg 740	Ala	Ser	His	Leu	Gly 745	Leu	Ala	Arg	Ser	Asn 750	Leu	Asp
Glu	Asp	Ile 755	Ile	Ala	Glu	Glu	Asn 760	Ile	Val	Ser	Arg 765	Ser	Glu	Phe	Pro
Glu	Ser 770	Trp	Leu	Trp	Asn 775	Val	Glu	Asp	Leu	Lys	Glu 780	Pro	Pro	Lys	Asn
Gly 785	Ile	Ser	Thr	Lys	Leu 790	Met	Asn	Ile	Phe	Leu 795	Lys	Asp	Ser	Ile 800	Thr
Thr	Trp	Glu	Ile 805	Leu	Ala	Val	Ser	Met	Ser 810	Asp	Lys	Lys	Gly	Ile 815	Cys
Val	Ala	Asp	Pro 820	Phe	Glu	Val	Thr	Val 825	Met	Gln	Asp	Phe	Phe 830	Ile	Asp
Leu	Arg	Leu 835	Pro	Tyr	Ser	Val	Val 840	Arg	Asn	Glu	Gln	Val	Glu 845	Ile	Arg
Ala	Val 850	Leu	Tyr	Asn	Tyr	Arg 855	Gln	Asn	Gln	Glu	Leu 860	Lys	Val	Arg	Val
Glu 865	Leu	Leu	His	Asn	Pro	Ala 870	Phe	Cys	Ser	Leu	Ala 875	Thr	Thr	Lys	Arg
Arg	His	Gln	Gln 885	Thr	Val	Thr	Ile	Pro	Pro 890	Lys	Ser	Ser	Leu	Ser 895	Val
Pro	Tyr	Val	Ile 900	Val	Pro	Leu	Lys	Thr 905	Gly	Leu	Gln	Glu	Val	Glu 910	Val
Lys	Ala	Ala 915	Val	Tyr	His	His	Phe 920	Ile	Ser	Asp	Gly	Val 925	Arg	Lys	Ser
Leu	Lys 930	Val	Val	Pro	Glu	Gly 935	Ile	Arg	Met	Asn	Lys 940	Thr	Val	Ala	Val
Arg 945	Thr	Leu	Asp	Pro	Glu 950	Arg	Leu	Gly	Arg	Glu 955	Gly	Val	Gln	Lys	Glu
Asp	Ile	Pro	Pro 965	Ala	Asp	Leu	Ser	Asp	Gln 970	Val	Pro	Asp	Thr	Glu 975	Ser
Glu	Thr	Arg	Ile 980	Leu	Leu	Gln	Gly	Thr 985	Pro	Val	Ala	Gln	Met	Thr	Glu
Asp	Ala	Val 995	Asp	Ala	Glu	Arg	Leu 1000	Lys	His	Leu	Ile	Val 1005	Thr	Pro	Ser
Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	Gly	Met	Thr	Pro	Thr	Val	Ile	Ala

1010	1015	1020
Val His Tyr Leu Asp Glu Thr Glu Gln Trp Glu Lys Phe Gly Leu Glu		
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Lys Arg Gln Gly Ala Leu Glu Leu Ile Lys Lys Gly Tyr Thr Gln Gln		1040
	1045	1050
Leu Ala Phe Arg Gln Pro Ser Ser Ala Phe Ala Ala Phe Val Lys Arg		1055
	1060	1065
Ala Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys Val Phe Ser Leu		1070
	1075	1080
Ala Val Asn Leu Ile Ala Ile Asp Ser Gln Val Leu Cys Gly Ala Val		1085
	1090	1095
Lys Trp Leu Ile Leu Glu Lys Gln Lys Pro Asp Gly Val Phe Gln Glu		1100
1105	1110	1115
Asp Ala Pro Val Ile His Gln Glu Met Ile Gly Gly Leu Arg Asn Asn		1120
	1125	1130
Asn Glu Lys Asp Met Ala Leu Thr Ala Phe Val Leu Ile Ser Leu Gln		1135
	1140	1145
Glu Ala Lys Asp Ile Cys Glu Glu Gln Val Asn Ser Leu Pro Gly Ser		1150
	1155	1160
Ile Thr Lys Ala Gly Asp Phe Leu Glu Ala Asn Tyr Met Asn Leu Gln		1165
	1170	1175
Arg Ser Tyr Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala Gln Met Gly		1180
1185	1190	1195
Arg Leu Lys Gly Pro Leu Leu Asn Lys Phe Leu Thr Thr Ala Lys Asp		1200
	1205	1210
Lys Asn Arg Trp Glu Asp Pro Gly Lys Gln Leu Tyr Asn Val Glu Ala		1215
	1220	1225
Thr Ser Tyr Ala Leu Leu Ala Leu Leu Gln Leu Lys Asp Phe Asp Phe		1230
	1235	1240
Val Pro Pro Val Val Arg Trp Leu Asn Glu Gln Arg Tyr Tyr Gly Gly		1245
	1250	1255
Gly Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe Gln Ala Leu Ala		1260
1265	1270	1275
Gln Tyr Gln Lys Asp Ala Pro Asp His Gln Glu Leu Asn Leu Asp Val		1280
	1285	1290
Ser Leu Gln Leu Pro Ser Arg Ser Ser Lys Ile Thr His Arg Ile His		1295
	1300	1305
Trp Glu Ser Ala Ser Leu Leu Arg Ser Glu Glu Thr Lys Glu Asn Glu		1310
	1315	1320
Gly Phe Thr Val Thr Ala Glu Gly Lys Gly Gln Gly Thr Leu Ser Val		1325
	1330	1335
Val Thr Met Tyr His Ala Lys Ala Lys Asp Gln Leu Thr Cys Asn Lys		1340
1345	1350	1355
Phe Asp Leu Lys Val Thr Ile Lys Pro Ala Pro Glu Thr Glu Lys Arg		1360
	1365	1370
Pro Gln Asp Ala Lys Asn Thr Met Ile Leu Glu Ile Cys Thr Arg Tyr		1375
	1380	1385
Arg Gly Asp Gln Asp Ala Thr Met Ser Ile Leu Asp Ile Ser Met Met		1390
	1395	1400
Thr Gly Phe Ala Pro Asp Thr Asp Asp Leu Lys Gln Leu Ala Asn Gly		1405

1410	1415	1420
Val Asp Arg Tyr Ile Ser Lys Tyr Glu Leu Asp Lys Ala Phe Ser Asp		
1425	1430	1435
Arg Asn Thr Leu Ile Ile Tyr Leu Asp Lys Val Ser His Ser Glu Asp		1440
	1445	1450
Asp Cys Leu Ala Phe Lys Val His Gln Tyr Phe Asn Val Glu Leu Ile		1455
	1460	1465
Gln Pro Gly Ala Val Lys Val Tyr Ala Tyr Tyr Asn Leu Glu Glu Ser		1470
	1475	1480
Cys Thr Arg Phe Tyr His Pro Glu Lys Glu Asp Gly Lys Leu Asn Lys		1485
	1490	1495
Leu Cys Arg Asp Glu Leu Cys Arg Cys Ala Glu Glu Asn Cys Phe Ile		1500
1505	1510	1515
Gln Lys Ser Asp Asp Lys Val Thr Leu Glu Glu Arg Leu Asp Lys Ala		1520
	1525	1530
Cys Glu Pro Gly Val Asp Tyr Val Tyr Lys Thr Arg Leu Val Lys Val		1535
	1540	1545
Gln Leu Ser Asn Asp Phe Asp Glu Tyr Ile Met Ala Ile Glu Gln Thr		1550
	1555	1560
Ile Lys Ser Gly Ser Asp Glu Val Gln Val Gly Gln Gln Arg Thr Phe		1565
	1570	1575
Ile Ser Pro Ile Lys Cys Arg Glu Ala Leu Lys Leu Glu Glu Lys Lys		1580
1585	1590	1595
His Tyr Leu Met Trp Gly Leu Ser Ser Asp Phe Trp Gly Glu Lys Pro		1600
	1605	1610
Asn Leu Ser Tyr Ile Ile Gly Lys Asp Thr Trp Val Glu His Trp Pro		1615
	1620	1625
Glu Glu Asp Glu Cys Gln Asp Glu Glu Asn Gln Lys Gln Cys Gln Asp		1630
	1635	1640
Leu Gly Ala Phe Thr Glu Ser Met Val Val Phe Gly Cys Pro Asn		1645
1650	1655	1660

<210> 2

<211> 1744

<212> PRT

<213> Homo sapiens

<400> 2

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	20
Leu Gly Val Pro Leu Ser Val Gly Val Gln Leu Gln Asp Val Pro Arg	25
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Gly Gln Val Val Lys Gly Ser Val Phe Leu Arg Asn Pro Ser Arg Asn	40
	45
	50
Asn Val Pro Cys Ser Pro Lys Val Asp Phe Thr Leu Ser Ser Glu Arg	55
65	60
	65
Asp Phe Ala Leu Leu Ser Leu Gln Val Pro Leu Lys Asp Ala Lys Ser	70
	75
	80
	85
	90
	95

Cys	Gly	Leu	His	Gln	Leu	Leu	Arg	Gly	Pro	Glu	Val	Gln	Leu	Val	Ala		
			100					105					110				
His	Ser	Pro	Trp	Leu	Lys	Asp	Ser	Leu	Ser	Arg	Thr	Thr	Asn	Ile	Gln		
		115					120					125					
Gly	Ile	Asn	Leu	Leu	Phe	Ser	Ser	Arg	Arg	Gly	His	Leu	Phe	Leu	Gln		
	130					135					140						
Thr	Asp	Gln	Pro	Ile	Tyr	Asn	Pro	Gly	Gln	Arg	Val	Arg	Tyr	Arg	Val		
145				150						155					160		
Phe	Ala	Leu	Asp	Gln	Lys	Met	Arg	Pro	Ser	Thr	Asp	Thr	Ile	Thr	Val		
			165					170						175			
Met	Val	Glu	Asn	Ser	His	Gly	Leu	Arg	Val	Arg	Lys	Lys	Glu	Val	Tyr		
		180						185					190				
Met	Pro	Ser	Ser	Ile	Phe	Gln	Asp	Asp	Phe	Val	Ile	Pro	Asp	Ile	Ser		
	195						200					205					
Glu	Pro	Gly	Thr	Trp	Lys	Ile	Ser	Ala	Arg	Phe	Ser	Asp	Gly	Leu	Glu		
	210				215						220						
Ser	Asn	Ser	Ser	Thr	Gln	Phe	Glu	Val	Lys	Lys	Tyr	Val	Leu	Pro	Asn		
225				230					235					240			
Phe	Glu	Val	Lys	Ile	Thr	Pro	Gly	Lys	Pro	Tyr	Ile	Leu	Thr	Val	Pro		
			245					250						255			
Gly	His	Leu	Asp	Glu	Met	Gln	Leu	Asp	Ile	Gln	Ala	Arg	Tyr	Ile	Tyr		
	260							265					270				
Gly	Lys	Pro	Val	Gln	Gly	Val	Ala	Tyr	Val	Arg	Phe	Gly	Leu	Leu	Asp		
	275						280					285					
Glu	Asp	Gly	Lys	Lys	Thr	Phe	Phe	Arg	Gly	Leu	Glu	Ser	Gln	Thr	Lys		
	290				295						300						
Leu	Val	Asn	Gly	Gln	Ser	His	Ile	Ser	Leu	Ser	Lys	Ala	Glu	Phe	Gln		
305				310					315					320			
Asp	Ala	Leu	Glu	Lys	Leu	Asn	Met	Gly	Ile	Thr	Asp	Leu	Gln	Gly	Leu		
			325					330						335			
Arg	Leu	Tyr	Val	Ala	Ala	Ala	Ile	Ile	Glu	Ser	Pro	Gly	Gly	Glu	Met		
	340							345					350				
Glu	Glu	Ala	Glu	Leu	Thr	Ser	Trp	Tyr	Phe	Val	Ser	Ser	Pro	Phe	Ser		
	355					360						365					
Leu	Asp	Leu	Ser	Lys	Thr	Lys	Arg	His	Leu	Val	Pro	Gly	Ala	Pro	Phe		
	370					375					380						
Leu	Leu	Gln	Ala	Leu	Val	Arg	Glu	Met	Ser	Gly	Ser	Pro	Ala	Ser	Gly		
385				390					395					400			
Ile	Pro	Val	Lys	Val	Ser	Ala	Thr	Val	Ser	Ser	Pro	Gly	Ser	Val	Pro		
			405					410						415			
Glu	Val	Gln	Asp	Ile	Gln	Gln	Asn	Thr	Asp	Gly	Ser	Gly	Gln	Val	Ser		
	420							425					430				
Ile	Pro	Ile	Ile	Ile	Pro	Gln	Thr	Ile	Ser	Glu	Leu	Gln	Leu	Ser	Val		
	435					440						445					
Ser	Ala	Gly	Ser	Pro	His	Pro	Ala	Ile	Ala	Arg	Leu	Thr	Val	Ala	Ala		
	450					455					460						
Pro	Pro	Ser	Gly	Gly	Pro	Gly	Phe	Leu	Ser	Ile	Glu	Arg	Pro	Asp	Ser		
465				470						475				480			
Arg	Pro	Pro	Arg	Val	Gly	Asp	Thr	Leu	Asn	Leu	Asn	Leu	Arg	Ala	Val		
			485					490						495			

Gly	Ser	Gly	Ala	Thr	Phe	Ser	His	Tyr	Tyr	Tyr	Met	Ile	Leu	Ser	Arg
			500					505					510		
Gly	Gln	Ile	Val	Phe	Met	Asn	Arg	Glu	Pro	Lys	Arg	Thr	Leu	Thr	Ser
		515					520					525			
Val	Ser	Val	Phe	Val	Asp	His	His	Leu	Ala	Pro	Ser	Phe	Tyr	Phe	Val
	530					535					540				
Ala	Phe	Tyr	Tyr	His	Gly	Asp	His	Pro	Val	Ala	Asn	Ser	Leu	Arg	Val
545					550					555					560
Asp	Val	Gln	Ala	Gly	Ala	Cys	Glu	Gly	Lys	Leu	Glu	Leu	Ser	Val	Asp
			565						570					575	
Gly	Ala	Lys	Gln	Tyr	Arg	Asn	Gly	Glu	Ser	Val	Lys	Leu	His	Leu	Glu
			580					585					590		
Thr	Asp	Ser	Leu	Ala	Leu	Val	Ala	Leu	Gly	Ala	Leu	Asp	Thr	Ala	Leu
		595					600					605			
Tyr	Ala	Ala	Gly	Ser	Lys	Ser	His	Lys	Pro	Leu	Asn	Met	Gly	Lys	Val
	610					615					620				
Phe	Glu	Ala	Met	Asn	Ser	Tyr	Asp	Leu	Gly	Cys	Gly	Pro	Gly	Gly	Gly
625					630					635					640
Asp	Ser	Ala	Leu	Gln	Val	Phe	Gln	Ala	Ala	Gly	Leu	Ala	Phe	Ser	Asp
			645						650					655	
Gly	Asp	Gln	Trp	Thr	Leu	Ser	Arg	Lys	Arg	Leu	Ser	Cys	Pro	Lys	Glu
		660						665					670		
Lys	Thr	Thr	Arg	Lys	Lys	Arg	Asn	Val	Asn	Phe	Gln	Lys	Ala	Ile	Asn
		675					680					685			
Glu	Lys	Leu	Gly	Gln	Tyr	Ala	Ser	Pro	Thr	Ala	Lys	Arg	Cys	Cys	Gln
	690					695					700				
Asp	Gly	Val	Thr	Arg	Leu	Pro	Met	Met	Arg	Ser	Cys	Glu	Gln	Arg	Ala
705					710					715					720
Ala	Arg	Val	Gln	Gln	Pro	Asp	Cys	Arg	Glu	Pro	Phe	Leu	Ser	Cys	Cys
			725						730					735	
Gln	Phe	Ala	Glu	Ser	Leu	Arg	Lys	Lys	Ser	Arg	Asp	Lys	Gly	Gln	Ala
		740						745					750		
Gly	Leu	Gln	Arg	Ala	Leu	Glu	Ile	Leu	Gln	Glu	Glu	Asp	Leu	Ile	Asp
		755					760					765			
Glu	Asp	Asp	Ile	Pro	Val	Arg	Ser	Phe	Phe	Pro	Glu	Asn	Trp	Leu	Trp
	770					775					780				
Arg	Val	Glu	Thr	Val	Asp	Arg	Phe	Gln	Ile	Leu	Thr	Leu	Trp	Leu	Pro
785					790					795					800
Asp	Ser	Leu	Thr	Thr	Trp	Glu	Ile	His	Gly	Leu	Ser	Leu	Ser	Lys	Thr
			805						810					815	
Lys	Gly	Leu	Cys	Val	Ala	Thr	Pro	Val	Gln	Leu	Arg	Val	Phe	Arg	Glu
		820						825					830		
Phe	His	Leu	His	Leu	Arg	Leu	Pro	Met	Ser	Val	Arg	Arg	Phe	Glu	Gln
	835						840					845			
Leu	Glu	Leu	Arg	Pro	Val	Leu	Tyr	Asn	Tyr	Leu	Asp	Lys	Asn	Leu	Thr
	850					855					860				
Val	Ser	Val	His	Val	Ser	Pro	Val	Glu	Gly	Leu	Cys	Leu	Ala	Gly	Gly
865					870					875					880
Gly	Gly	Leu	Ala	Gln	Gln	Val	Leu	Val	Pro	Ala	Gly	Ser	Ala	Arg	Pro
			885						890					895	

Val	Ala	Phe	Ser	Val	Val	Pro	Thr	Ala	Ala	Thr	Ala	Val	Ser	Leu	Lys
			900					905					910		
Val	Val	Ala	Arg	Gly	Ser	Phe	Glu	Phe	Pro	Val	Gly	Asp	Ala	Val	Ser
		915					920					925			
Lys	Val	Leu	Gln	Ile	Glu	Lys	Glu	Gly	Ala	Ile	His	Arg	Glu	Glu	Leu
	930					935					940				
Val	Tyr	Glu	Leu	Asn	Pro	Leu	Asp	His	Arg	Gly	Arg	Thr	Leu	Glu	Ile
945					950					955					960
Pro	Gly	Asn	Ser	Asp	Pro	Asn	Met	Ile	Pro	Asp	Gly	Asp	Phe	Asn	Ser
				965					970					975	
Tyr	Val	Arg	Val	Thr	Ala	Ser	Asp	Pro	Leu	Asp	Thr	Leu	Gly	Ser	Glu
			980					985					990		
Gly	Ala	Leu	Ser	Pro	Gly	Gly	Val	Ala	Ser	Leu	Leu	Arg	Leu	Pro	Arg
		995					1000					1005			
Gly	Cys	Gly	Glu	Gln	Thr	Met	Ile	Tyr	Leu	Ala	Pro	Thr	Leu	Ala	Ala
	1010					1015					1020				
Ser	Arg	Tyr	Leu	Asp	Lys	Thr	Glu	Gln	Trp	Ser	Thr	Leu	Pro	Pro	Glu
1025					1030					1035					1040
Thr	Lys	Asp	His	Ala	Val	Asp	Leu	Ile	Gln	Lys	Gly	Tyr	Met	Arg	Ile
			1045						1050					1055	
Gln	Gln	Phe	Arg	Lys	Ala	Asp	Gly	Ser	Tyr	Ala	Ala	Trp	Leu	Ser	Arg
			1060					1065					1070		
Gly	Ser	Ser	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Val	Leu	Ser	Leu
		1075					1080					1085			
Ala	Gln	Glu	Gln	Val	Gly	Gly	Ser	Pro	Glu	Lys	Leu	Gln	Glu	Thr	Ser
	1090					1095					1100				
Asn	Trp	Leu	Leu	Ser	Gln	Gln	Gln	Ala	Asp	Gly	Ser	Phe	Gln	Asp	Leu
1105					1110					1115					1120
Ser	Pro	Val	Ile	His	Arg	Ser	Met	Gln	Gly	Gly	Leu	Val	Gly	Asn	Asp
			1125						1130					1135	
Glu	Thr	Val	Ala	Leu	Thr	Ala	Phe	Val	Thr	Ile	Ala	Leu	His	His	Gly
			1140					1145					1150		
Leu	Ala	Val	Phe	Gln	Asp	Glu	Gly	Ala	Glu	Pro	Leu	Lys	Gln	Arg	Val
		1155					1160					1165			
Glu	Ala	Ser	Ile	Ser	Lys	Ala	Ser	Ser	Phe	Leu	Gly	Glu	Lys	Ala	Ser
	1170					1175					1180				
Ala	Gly	Leu	Leu	Gly	Ala	His	Ala	Ala	Ala	Ile	Thr	Ala	Tyr	Ala	Leu
1185					1190					1195					1200
Thr	Leu	Thr	Lys	Ala	Pro	Ala	Asp	Leu	Arg	Gly	Val	Ala	His	Asn	Asn
			1205						1210					1215	
Leu	Met	Ala	Met	Ala	Gln	Glu	Thr	Gly	Asp	Asn	Leu	Tyr	Trp	Gly	Ser
		1220						1225					1230		
Val	Thr	Gly	Ser	Gln	Ser	Asn	Ala	Val	Ser	Pro	Thr	Pro	Ala	Pro	Arg
		1235					1								

Gly	Gly	Phe	Arg	Ser	Thr	Gln	Asp	Thr	Val	Ile	Ala	Leu	Asp	Ala	Leu		
			1300					1305					1310				
Ser	Ala	Tyr	Trp	Ile	Ala	Ser	His	Thr	Thr	Glu	Glu	Arg	Gly	Leu	Asn		
		1315					1320					1325					
Val	Thr	Leu	Ser	Ser	Thr	Gly	Arg	Asn	Gly	Phe	Lys	Ser	His	Ala	Leu		
		1330				1335					1340						
Gln	Leu	Asn	Asn	Arg	Gln	Ile	Arg	Gly	Leu	Glu	Glu	Glu	Leu	Gln	Phe		
1345					1350					1355					1360		
Ser	Leu	Gly	Ser	Lys	Ile	Asn	Val	Lys	Val	Gly	Gly	Asn	Ser	Lys	Gly		
			1365					1370						1375			
Thr	Leu	Lys	Val	Leu	Arg	Thr	Tyr	Asn	Val	Leu	Asp	Met	Lys	Asn	Thr		
		1380						1385					1390				
Thr	Cys	Gln	Asp	Leu	Gln	Ile	Glu	Val	Thr	Val	Lys	Gly	His	Val	Glu		
		1395					1400					1405					
Tyr	Thr	Met	Glu	Ala	Asn	Glu	Asp	Tyr	Glu	Asp	Tyr	Glu	Tyr	Asp	Glu		
	1410					1415				1420							
Leu	Pro	Ala	Lys	Asp	Asp	Pro	Asp	Ala	Pro	Leu	Gln	Pro	Val	Thr	Pro		
1425					1430					1435					1440		
Leu	Gln	Leu	Phe	Glu	Gly	Arg	Arg	Asn	Arg	Arg	Arg	Arg	Glu	Ala	Pro		
			1445					1450						1455			
Lys	Val	Val	Glu	Gln	Glu	Ser	Arg	Val	His	Tyr	Thr	Val	Cys	Ile			
	1460					1465					1470						
Trp	Arg	Asn	Gly	Lys	Val	Gly	Leu	Ser	Gly	Met	Ala	Ile	Ala	Asp	Val		
	1475					1480					1485						
Thr	Leu	Leu	Ser	Gly	Phe	His	Ala	Leu	Arg	Ala	Asp	Leu	Glu	Lys	Leu		
	1490					1495				1500							
Thr	Ser	Leu	Ser	Asp	Arg	Tyr	Val	Ser	His	Phe	Glu	Thr	Glu	Gly	Pro		
1505					1510					1515					1520		
His	Val	Leu	Leu	Tyr	Phe	Asp	Ser	Val	Pro	Thr	Ser	Arg	Glu	Cys	Val		
		1525						1530						1535			
Gly	Phe	Glu	Ala	Val	Gln	Glu	Val	Pro	Val	Gly	Leu	Val	Gln	Pro	Ala		
		1540						1545					1550				
Ser	Ala	Thr	Leu	Tyr	Asp	Tyr	Tyr	Asn	Pro	Glu	Arg	Arg	Cys	Ser	Val		
	1555					1560					1565						
Phe	Tyr	Gly	Ala	Pro	Ser	Lys	Ser	Arg	Leu	Leu	Ala	Thr	Leu	Cys	Ser		
	1570					1575					1580						
Ala	Glu	Val	Cys	Gln	Cys	Ala	Glu	Gly	Lys	Cys	Pro	Arg	Gln	Arg	Arg		
1585					1590					1595					1600		
Ala	Leu	Glu	Arg	Gly	Leu	Gln	Asp	Glu	Asp	Gly	Tyr	Arg	Met	Lys	Phe		
		1605						1610						1615			
Ala	Cys	Tyr	Tyr	Pro	Arg	Val	Glu	Tyr	Gly	Phe	Gln	Val	Lys	Val	Leu		
		1620						1625					1630				
Arg	Glu	Asp	Ser	Arg	Ala	Ala	Phe	Arg	Leu	Phe	Glu	Thr	Lys	Ile	Thr		
	1635						1640						1645				
Gln	Val	Leu	His	Phe	Thr	Lys	Asp	Val	Lys	Ala	Ala	Ala	Asn	Gln	Met		
	1650					1655					1660						
Arg	Asn	Phe	Leu	Val	Arg	Ala	Ser	Cys	Arg	Leu	Arg	Leu	Glu	Pro	Gly		
1665					1670					1675					1680		
Lys	Glu	Tyr	Leu	Ile	Met	Gly	Leu	Asp	Gly	Ala	Thr	Tyr	Asp	Leu	Glu		
			1685					1690						1695			

Gly	His	Pro	Gln	Tyr	Leu	Leu	Asp	Ser	Asn	Ser	Trp	Ile	Glu	Glu	Met
			1700					1705					1710		
Pro	Ser	Glu	Arg	Leu	Cys	Arg	Ser	Thr	Arg	Gln	Arg	Ala	Ala	Cys	Ala
		1715					1720					1725			
Gln	Leu	Asn	Asp	Phe	Leu	Gln	Glu	Tyr	Gly	Thr	Gln	Gly	Cys	Gln	Val
	1730					1735					1740				

<210> 3
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> rituximab heavy chain wild type

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

<210> 4
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> encoding mutant heavy chain

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgctgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gtgattggta	cttcgacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360

gccgcatcca	ccaagggccc	atcgggtcttc	tccctggcac	cctcctacaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggt	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaatctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgttacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	aaa			1353

<210> 5

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant heavy chain

<400> 5

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

			180				185				190						
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
		195					200					205					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
	210					215					220						
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly		
225					230					235					240		
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
			245						250					255			
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
			260					265					270				
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
		275					280					285					
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
	290					295					300						
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
305					310					315					320		
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile		
				325					330					335			
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
			340					345					350				
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser		
		355					360					365					
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu		
	370					375					380						
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
385					390					395					400		
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val		
				405				410						415			
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
			420					425					430				
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
		435					440					445					
Pro	Gly	Lys															
	450																

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

<220>
 <223> mutant heavy chain

<400> 6
 Gln Ile Val Leu Ser Gln Ser Pro Ala 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 Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr

35	40	45
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val 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
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr		
85	90	95
Phe Gly Gly 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
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> 7

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 7

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcgacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctt	cccctggcac	cctcctccaa	gagcacctct	420
gggggacacag	cggccctggg	ctgcctgggtc	aaggactact	tccccgaacc	ggtgacgggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctccccggacc	780
cctgaggcca	catgcgtggg	ggtggacgtg	agccacgaag	accctgagggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctcccggg aaa	1353

<210> 8

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 8

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

Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	275						280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			325						330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435						440					445			
Pro	Gly	Lys													
	450														

<210> 9

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 9

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaa	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagt	gattggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgctgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaaggggccc	atcggctctt	tccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tcccgaacc	ggtgacggtg	480
tcgtggaa	caggcgccct	gaccagcggc	gtgcacacct	tcccggtgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggt	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgaggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtag	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960

aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatacga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 10

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant heavy chain

<400> 10

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

	260		265		270
Glu Asp Pro	Glu Val Lys Phe Asn Trp Tyr Val	Asp Gly Val Glu Val			
	275		280		285
His Asn Ala	Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr				
	290		295		300
Arg Val Val	Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly				
305		310		315	320
Lys Glu Tyr	Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile				
	325		330		335
Glu Lys Thr	Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val				
	340		345		350
Tyr Thr Leu	Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser				
	355		360		365
Leu Thr Cys	Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu				
370		375		380	
Trp Glu Ser	Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro				
385		390		395	400
Val Leu Asp	Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val				
	405		410		415
Asp Lys Ser	Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met				
	420		425		430
His Glu Ala	Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser				
	435		440		445
Pro Gly Lys					
450					

<210> 11

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 11

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcgggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctc	cccctggcac	cctcctacaa	gagcacctct	420
gggggacacag	cggccctggg	ctgcctggtc	aaggactact	tcccgaacc	ggtgacggtg	480
tcgtggaaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtgggaaa	gaaaagttgag	660
cccaaactctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggg	gggtggacgtg	agccacgaag	accctgagggt	caagttcaac	840
tgttacgtgg	acggcgtgga	gggtgcataat	gccaagacaa	agccgcggga	ggagcagtag	900

aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 12
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant heavy chain

<400> 12

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 13

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 13

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtag	240
atgcagctga	gctcgtctgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcgacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctc	tccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggtg	480
tcgtggaaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtgggaaa	gaaagttgag	660
cccaaactct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgaggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840

tggtacgtgg	acggcgtgga	ggtgcataat	gccaaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 14

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant heavy chain

<400> 14

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

cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 16
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant heavy chain

<400> 16

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

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

<210> 17

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 17

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctc	tccctggcac	cctcctacaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720

ggaccgtcag	tcttcctctt	cccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	ccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atgcccggtg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 18

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant heavy chain

<400> 18

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

cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	aaa			1353

<210> 20

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 20

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

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	275						280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405				410						415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425				430			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435						440					445			
Pro	Gly	Lys													
	450														

<210> 21

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 21

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggtg	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggtcttc	cccctggcac	cctcctccaa	gagcacctct	420
ggggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600

acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 22

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 22

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

210	215	220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
225	230	235
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		240
	245	250
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		255
	260	265
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		270
	275	280
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		285
	290	295
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		300
305	310	315
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		320
	325	330
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		335
	340	345
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		350
	355	360
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		365
	370	375
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		380
385	390	395
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val		400
	405	410
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met		415
	420	425
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser		430
	435	440
Pro Gly Lys		445
450		

<210> 23

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 23

caagtgcagc	tcagcagccc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtctgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccacatcca	ccaagggccc	atcggctctt	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctgggt	aaggactact	tccccgaacc	ggtgacgggt	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540

tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaactct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtgggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgggtacgtgg	acggcgtgga	ggtgcataat	gccaaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtgggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcctgggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 24

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 24

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

Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
210						215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			245						250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			325						330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
			405					410						415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425				430			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435						440					445			
Pro	Gly	Lys													
	450														

<210> 25

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 25

caagtgcagc	tcgagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgctgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactatggcg	gcgattggta	cttaaactgc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcgggtctac	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctgggtc	aaggactact	tccccgaacc	ggtgacggtg	480

tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggt	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaactct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgaggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcctgggtc	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	aaa			1353

<210> 26

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 26

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

	195		200		205										
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			245						250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	275						280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			325						330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	355						360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385				390						395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
			405					410						415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
		420					425					430			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435						440					445			
Pro	Gly	Lys													
	450														

<210> 27

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 27

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgttgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttaaactgc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcattcca	ccaagggccc	atcgggtcttc	cccctggcac	cctcctccaa	gagcacctct	420

gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaactct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcgaagg	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcctgggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 28

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 28

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

Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	195						200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			245						250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	275						280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			325						330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	355						360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435						440					445			
Pro	Gly	Lys													
	450														

<210> 29

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 29

caagtgcagc	tgacgcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaaag	ccagcggcta	caccttcacc	tcctacaaca	tgacttgggt	caagcaaact	120
cctggacgcg	gacttgagt	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360

gccgcatcca	ccaagggccc	atcgggtctac	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggt	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaatctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	ccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgttacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 30

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 30

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

tactactgcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctt	cccctggcat	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggta	aaggactact	tccccgaacc	ggtgacgggt	480
tcgtggaact	caggcgccct	gaccaccggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggt	accgtgccct	ccagccgctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaactct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcgaagg	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	aaa			1353

<210> 32

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 32

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

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		180					185					190			
Pro	Ser	Ser	Arg	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
		210				215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			245						250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
		370				375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
		435					440					445			
Pro	Gly	Lys													
		450													

<210> 33

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 33

caagtgcagc	tgacgcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgacttggtg	caagcaaact	120
cctggacgcg	gacttgagtg	gattggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240

atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactactgcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctt	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctgggt	aaggactact	tccccgaacc	ggtgacgggt	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggt	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaactct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgttacgtgg	acggcggtga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgaagggt	ctccaacaaa	gccctcccag	ccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	cagggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 34

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 34

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

				165					170					175			
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
			180					185					190				
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
		195					200					205					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
	210					215					220						
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly		
	225				230					235					240		
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
			245						250					255			
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
			260					265					270				
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
	275						280					285					
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
	290					295					300						
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
	305				310					315					320		
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile		
				325					330					335			
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
			340					345				350					
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser		
	355					360						365					
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu		
	370					375					380						
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
	385				390					395					400		
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val		
				405				410						415			
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
			420					425					430				
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
	435						440					445					
Pro	Gly	Lys															
	450																

<210> 35

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 35

caagtgcagc	tgcagcagcc	gggtgcagaa	ctcgtgaagc	caggggcctc	agtgaagatg	60
tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180

aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcgggtctt	cccctggcat	cctcctccaa	gagcacctct	420
ggggggcacag	cggcccctggg	ctgcctgggtc	aaggactact	tccccgaacc	ggtgacgggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaaagttgag	660
cccaaactctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgttacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcgaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 36

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 36

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 37

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 37

caagtgcagc tgcagcagcc ggggtgcagaa ctcgtgaagc caggggcctc agtgaagatg
 tcctgcaaag ccagcggcta caccttcacc tcctacaaca tgcactgggt caagcaaact

60

120

cctggacgcg	gacttgagtg	gattggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tacttcggcg	gcgattggtg	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcgggtctt	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcgaagg	ctccaacaaa	gccctcccag	ccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	cagggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcctgggtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 38

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 38

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

145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170						175
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
			180					185						190	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345				350			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435						440					445			
Pro	Gly	Lys													
	450														

<210> 39

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> encoding mutant heavy chain

<400> 39

caagtgcagc tgcagcagcc ggggtgcagaa ctcgtgaagc caggggcctc agtgaagatg

60

tcctgcaaag	ccagcggcta	caccttcacc	tcctacaaca	tgcactgggt	caagcaaact	120
cctggacgcg	gacttgagtg	gattgggtgct	atctaccccg	gaaacggcga	caccagctac	180
aatcagaagt	ttaaggggaa	ggccactctg	actgccgaca	agtcgtcctc	gacggcgtac	240
atgcagctga	gctcgtgac	ctccgaggac	tccgccgtgt	attactgtgc	tcggtccacc	300
tactacggcg	gcgattggta	cttcaacgtc	tggggagccg	gaaccactgt	gaccgtgtca	360
gccgcatcca	ccaagggccc	atcggctctc	cccctggcac	cctcctccaa	gagcacctct	420
gggggacacag	cggccctggg	ctgcctgggtc	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaact	caggcgccca	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaactctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	cccccaaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgagggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcccag	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	cagggtgtaca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctgacc	tgcctgggtca	aaggcttcta	tcccagcgac	1140
atgcccggtg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	tatagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctcccggg	aaa			1353

<210> 40

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain mutant

<400> 40

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

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

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1

5

10

15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20

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30

Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile

35

40

45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly

100

105

110

Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser

115

120

125

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