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- (54) **ANTIGEN BINDING PROTEINS TO PROPROTEIN CONVERTASE SUBTILISIN KEXIN TYPE 9 (PCSK9)**
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(57) **ABSTRACT**

Antigen binding proteins that interact with Proprotein Convertase Subtilisin Kexin Type 9 (PCSK9) are described. Methods of treating hypercholesterolemia and other disorders by administering a pharmaceutically effective amount of an antigen binding protein to PCSK9 are described. Methods of detecting the amount of PCSK9 in a sample using an antigen binding protein to PCSK9 are described.

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QEDEDGDYEELVLALRSEEDGLAEAPEHGTATFHRCAKDPWRLPGTYVVVLKEETHL
SQSERTARRLQAQAARRGYLTKILHVFHGLLPGFLVKMSGDLLELALKLPHVDYIEEDS
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VPEEDGTRFHRQASKCDSHGTHLAGVVSGRDAGVAKGASMRSLRVLNCQGKGTVSgt
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LYSPASAPENVITVGATNAQDQPVTLGTNGRCVDLFAPGEDIIGASSDCSTCFVSQS
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LTGCSSHWEVEDLGTHKPPVLRPRGQPNQCVGHREASIHASCCHAPGLECKVKEHGIPA
PQQQVTVACEEGWTLTGCALPGTSHVLGAYAVDNTCVVRSRDVSTTGSTSEEAVTAV
AICCRSRHLAQASQELQ

SEQ ID NO:1

FIG. 1A

```

          10      20      30      40      50
          -----|-----|-----|-----|-----|
Query  : atgggcaccgtcagctccaggcggtccctggtgccgctgcactgctgct SEQ ID NO:2
Frame1 : M G T V S S R R S W W P L P L L SEQ ID NO:3

          60      70      80      90      100
          -----|-----|-----|-----|-----|
Query  : gctgctgctgctgctctggtccccggggccccgtgcgcaggaggacg
Frame1 : L L L L L G P A G A R A Q E D E

          110     120     130     140     150
          -----|-----|-----|-----|-----|
Query  : aggacggcactacgaggagctggtgctagcctgcgcctcgaggaggac
Frame1 : D G D Y E E L V L A L R S E E D

          50      160     170     180     190     200
          -----|-----|-----|-----|-----|
Query  : ggccctggccgaagcaccgcggacacggaaaccacagccacccatccaccgcgtg
Frame1 : G L A E A P E H G T T A T F H R C

          210     220     230     240     250
          -----|-----|-----|-----|-----|
Query  : cggcaaggatccgtggagggtgcctggcacctacgtggtgctgaagg
Frame1 : A K D P W R L P G T Y V V V L K E

          50      260     270     280     290     300
          -----|-----|-----|-----|-----|
Query  : aggagaccacaccttcgcagtcaagagcgcactgcccggccctgcaggcc
Frame1 : E T H L S Q S E R T A R R L Q A

          310     320     330     340     350
          -----|-----|-----|-----|-----|
Query  : caggctgcccggggatacctcaccaagatcctgcattgtcttcatgg
Frame1 : Q A A R R G Y L T K I L H V F H G

          50      360     370     380     390     400
          -----|-----|-----|-----|-----|
Query  : ccttcttcctggcttcgttgaaagatgagtggtggcaccctgctggagctgg
Frame1 : L L P G F L V K M S G D L L E L A

          410     420     430     440     450
          -----|-----|-----|-----|-----|
Query  : ccttgaagttccccatgtcgactacatcgaggaggactcctgtcttt
Frame1 : L K L P H V D Y I E E D S S V F

          50      460     470     480     490     500
          -----|-----|-----|-----|-----|
Query  : gcccagagcatcccggtggAACCTGGAGCGGATTACCCCTCGCGGTACCG
Frame1 : A Q S I P W N L E R I T P P R Y R

          510     520     530     540     550
          -----|-----|-----|-----|-----|
Query  : ggccggatgaataccagccccccgacggaggcagcctggtgaggtgtatc
Frame1 : A D E Y Q P P D G G S L V E V Y L

```

FIG. 1B₁

Query :	tcctagacaccaggatacagagtgaccaccggaaatcgagggcagggtc
Frame1 :	L D T S I Q S D H R E I E G R V
----- ----- ----- ----- -----	
Query :	atggtcaccgacttcgagaatgtgcccgaggaggacgggaccgcgttcca
Frame1 :	M V T D F E N V P E E D G T R F H
----- ----- ----- ----- -----	
Query :	cagacaggccagcaagtgtgacagtcatggcacccacctggcaggggtgg
Frame1 :	R Q A S K C D S H G T H L A G V V
----- ----- ----- ----- -----	
Query :	tcagcgccggatgccggcgtggccaagggtgccagcatgcgcagctg
Frame1 :	S G R D A G V A K G A S M R S L
----- ----- ----- ----- -----	
Query :	cgcgtgctcaactgccaagggaagggcacggtagcggcacccatcatagg
Frame1 :	R V L N C Q G K G T V S G T L I G
----- ----- ----- ----- -----	
Query :	cctggagttattcgaaaagccagctgggtccagcctgtggggccactgg
Frame1 :	L E F I R K S Q L V Q P V G P L V
----- ----- ----- ----- -----	
Query :	tgggtgctgctccccctgggggtgggtacagccgcgtcctaacgcgc
Frame1 :	V L L P L A G G Y S R V L N A A
----- ----- ----- ----- -----	
Query :	tgcgcgcctggcgagggtgggtcgctgtgtcaccgcgtccggcaa
Frame1 :	C Q R L A R A G V V L V T A A G N
----- ----- ----- ----- -----	
Query :	cttcgggacgtgcctgcctactccccagcctcagctcccaggta
Frame1 :	F R D D A C L Y S P A S A P E V I
----- ----- ----- ----- -----	
Query :	tcacagttggggccaccaatgcccaggaccagccgtgaccctggggact
Frame1 :	T V G A T N A Q D Q P V T L G T
----- ----- ----- ----- -----	
Query :	ttggggaccaacttggccgtgtgtggacctttgcccaggggagga
Frame1 :	L G T N F G R C V D L F A P G E D

100	1110	1120	1130	1140	1150													
----- ----- ----- ----- -----																		
Query :	catcattgggtgcctccagcgactgcagcacctgcttgtgtcacagagtg																	
Frame1 :	I	I	G	A	S	S	D	C	S	T	C	F	V	S	Q	S	G	
150	1160	1170	1180	1190	1200													
----- ----- ----- ----- -----																		
Query :	ggacatcacaggctgctgccacgtggctggcattgcagccatgtgctg																	
Frame1 :	T	S	Q	A	A	A	H	V	A	G	I	A	A	M	M	L		
200	1210	1220	1230	1240	1250													
----- ----- ----- ----- -----																		
Query :	tctgccgagccggagctcacccctggccgagttgaggcagagactgatcca																	
Frame1 :	S	A	E	P	E	L	T	L	A	E	L	R	Q	R	L	I	H	
250	1260	1270	1280	1290	1300													
----- ----- ----- ----- -----																		
Query :	cttctctgccaaagatgtcatcaatgaggcctgggttcctgaggaccgc																	
Frame1 :	F	S	A	K	D	V	I	N	E	A	W	F	P	E	D	Q	R	
300	1310	1320	1330	1340	1350													
----- ----- ----- ----- -----																		
Query :	gggtactgaccccaacctggccgcctgcccccagcaccatgg																	
Frame1 :	V	L	T	P	N	L	V	A	A	L	P	P	S	T	H	G		
350	1360	1370	1380	1390	1400													
----- ----- ----- ----- -----																		
Query :	gcaggttggcagctgtttgcaggactgtgtggtcagcacactcggggcc																	
Frame1 :	A	G	W	Q	L	F	C	R	T	V	W	S	A	H	S	G	P	
400	1410	1420	1430	1440	1450													
----- ----- ----- ----- -----																		
Query :	tacacggatggccacagccatcgcccgctgcgcggccagatgaggagctgc																	
Frame1 :	T	R	M	A	T	A	I	A	R	C	A	P	D	E	E	L	L	
450	1460	1470	1480	1490	1500													
----- ----- ----- ----- -----																		
Query :	tgagctgtccaggcttctccaggagtggaaagcggcggggcgagcgcgt																	
Frame1 :	S	C	S	S	F	S	R	S	G	K	R	R	G	E	R	M		
500	1510	1520	1530	1540	1550													
----- ----- ----- ----- -----																		
Query :	gaggcccaaggggcaagctggctgccggcccacaacgtttgggg																	
Frame1 :	E	A	Q	G	G	K	L	V	C	R	A	H	N	A	F	G	G	
550	1560	1570	1580	1590	1600													
----- ----- ----- ----- -----																		
Query :	tgagggtgtctacgcattgccagggtctgcctgtcacccaggccaact																	
Frame1 :	E	G	V	Y	A	I	A	R	C	C	L	L	P	Q	A	N	C	
600	1610	1620	1630	1640	1650													
----- ----- ----- ----- -----																		
Query :	gcagcgtccacacagctccaccaggctgaggccagcatggggaccgtgtc																	
Frame1 :	S	V	H	T	A	P	P	A	E	A	S	M	G	T	R	V		

FIG. 1B₃

Query : cactgccaccaacaggggccacgtcctcacaggctgcagctcccactggga	650 1660 1670 1680 1690 1700
Frame1 : H C H Q Q G H V L T G C S S H W E	----- ----- ----- ----- ----- -----
Query : ggtggaggaccctggcaccacaagccgctgtgctgaggccacgaggtc	700 1710 1720 1730 1740 1750
Frame1 : V E D L G T H K P P V L R P R G Q	----- ----- ----- ----- -----
Query : agcccaaccagtgcgtggccacaggagggccacatccacgcttcctgc	750 1760 1770 1780 1790 1800
Frame1 : P N Q C V G H R E A S I H A S C	----- ----- ----- ----- -----
Query : tgccatccccaggctcgaaatgcaaagtcaaggagcatgaatccggc	800 1810 1820 1830 1840 1850
Frame1 : C H A P G L E C K V K E H G I P A	----- ----- ----- ----- -----
Query : ccctcaggggcaggctcgaccgtggccctgcgaggaggctggaccctgactg	850 1860 1870 1880 1890 1900
Frame1 : P Q G Q V T V A C E E G W T L T G	----- ----- ----- ----- -----
Query : gctgcagccccctccctggacacctccacgtcctggggcctacgcccata	900 1910 1920 1930 1940 1950
Frame1 : C S A L P G T S H V L G A Y A V	----- ----- ----- ----- -----
Query : gacaacacgtgttagtcaggagccggacgtcagcacatcaggcagcac	950 1960 1970 1980 1990 2000
Frame1 : D N T C V V R S R D V S T T G S T	----- ----- ----- ----- -----
Query : cagcgaagaggccgtgacagccgttgcacatctgtgcgcggagccggacc	2010 2020 2030 2040 2050
Frame1 : S E E A V T A V A I C C R S R H L	----- ----- ----- ----- -----
Query : tggcgccaggccctccaggagctccag	50 2060 2070 2080 2090 2100
Frame1 : A Q A S Q E L Q	----- ----- ----- ----- -----

FIG. 1B₄

Seq ID No.	LINE	GERMLINE	V	D	J	FR1		CDR1		FR2	
4	30A4	A3				DIVMTQSPLSLPVTPGEPASTIC	RSSQSLLHSNGNYILD	WYLQKPGQSPQLIY			
5	3C4	O2				--S-----P-----	--F-N-----				
6	23B5	O2				DIQMTQSPSSLSASVGDRVTITC	RASQISSYLN	WYQQKPGKAPKLIIY			
7	25G4	O2				--L-----	--R--N--S	--L----I-----			
8	31H4	V1-13				DIQMTQSPSSLSASVGDRVTITC	RASQISSYLN	WYQQKPGKAPKLIIY			
9	27B2	V1-13				--L-----	--I-----	--V-----Y-----			
10											
11											
12											
13											
14											
15	25A7	V1-4				QSALTQPASVSGSPGQSITISC	TGTSSDDVGGYNYVS	WYQQHPGKAPKLMIY			
16	27H5	V1-4				--JL2-----	--R--S----	--H----V---			
17	26H5	V1-4				--JL2-----	--S-----	--P-----			
18	31D1	V1-4				--JL2-----	--S-----	--P-----			
19	20D10	V1-4				--JL2-----	--S-----	--Y---P---K--			
20	27E7	V1-4				--JL2-----	--S-----	--P-----			
21	30B9	V1-4				--JL2-----	--S-----	--P-----			
22	19H9	V1-4				--JL2-----	--N-----S-----	--P-----			
23	26E10	V1-4				--JL2-----	--S-----				
23	21B12	V1-4				--JL2-----	--S-----				
24	17C2	V1-4				--JL2-----	--A--S-----	--R-----			

FIG. 2A

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
25	Gemline				QSALTQPAVSVGSPGQSITISC	TGTSSDVGGYNVVS	WYQQHFGKAPKLMIV
26	23G1	V1-4	JL3	-	-	-S-	-
27	Gemline				QSALTQPAVSVGSPGQSITISC	TGTSSDVGSYNLVS	WYQQHPGKAPKLMIV
28	13H1	V1-7	JL3	L	-	-N-	-YS-
29	Gemline				QSVLTQPPSASGTPGQRVTISC	SGSSSNIGSNTVN	WYQQQLPGTAPKLLIV
30	9C9	V1-16	JL3	-	-	-K-	-V-
31	9H6	V1-16	JL3	P	-	-	-
32	31A4	V1-16	JL3	-	-	-	-
33	1A12	V1-16	JL3	-	-	-K-	-F-
34	Gemline				QSVLTQPPSVSAAPGQKVVTISC	SGSSSNIGNNNVVS	WYQQQLPGTAPKLLIV
35	16F12	V1-19	JL1	-	-	-F-	-
36	22E2	V1-19	JL1	-	-	-F-	-
37	27A6	V1-19	JL1	-	-	-F-	-F-
38	28B12	V1-19	JL1	-	-	-F-	-
39	28D6	V1-19	JL1	T	-	-F-	-
40	31G11	V1-19	JL1	-	-	-F-	-
41	Gemline				QSVLTQPPSVSAAPGQKVVTISC	SGSSSNIGNNNVVS	WYQQQLPGTAPKLLIV
42	13B5	V1-19	JL2	-	-	-N-	-
43	Gemline				SYELTQPPSVSPGQTASITC	SGDKLGDKYAC	WYQQKPGQSPVVLVIV
44	31B12	V2-1	JL2	-	-R-	-	-
45	Gemline				QFVLTQPPSASASLGASVTLIC	TLSSGYNSNYKVD	WYQQRGKGPRFVMR
46	3B6	V5-2	JL2	-LF-	-	-S-E-	-

FIG. 2B

FIG. 2C

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
4					
5	30A4	LGSNRAS	GVPDREFGSGSGTDFTLKISRVEAEDVGVYYC	MQALQTPET	FGFGTKVDIK
6					
7	3C4	AASSLQS	GVPSRFSGSGSGTDFLTISLQPEDFATYTC	QSYSTPLT	FGGGTKEVK
8					
9	23B5	AASSLQS	GVPSRFSGSGSGTDFLTISLQPEDFATYTC	QSYSTPLT	FGQSTIALEIK
10	25G4	--A--	--N--	--S--	--A--
11					
12	31H4	GNSNRES	GVDPDRFGSKSGTASLAIITGLOADEADYTC	QSYDSSLSSGV	FGGGTKLTVL
13	27B2	--TY--	--	--N--	--V--
14					
15	25A7	EVSNRES	GVSNRFSGSKSGNTASLITISGLOADEADYTC	SYTSSSSVV	FGGGTKLTVL
16	25A7v1	--	--T--	--	--
16	27H5	--	--P--	--	--
17	27H5v1	--	--I--	--	--
17	26H5	--	--I--	--	--
18	31D1	--	--I--	--	--
19	20D10	--	--I--	--	--
20	27E7	--	--F--	--	--
21	30B2	--	--F--	--	--
22	19H9	--	--I--	--	--
23	19H9v1	--	--I--	--	--
23	26E10	--	--F--	--	--
23	21B12	--	--F--	--	--
24	17C2	--	--F--	--	--

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
25		EVSNRPS	GVSNRFGSKSGNTASLTISGLQAEDADYYC	S SYTSSS V	FGGGTKLTVL
26	23G1	--T----	-----	N----T-M-	-----
27		EGSKRPS	GVSNRFGSKSGNTASLTISGLQAEDADYYC	CSYAGSST	FGGGTKLTVL
28	13H1	-V-----	-----	-----LV	-----
29		SNNQRPS	GVPDRESGSKSGTSASLAISGLQSEDEADYYC	AAWDDSLNV	FGGGTKLTVL
30	9C9	R-----L	-----	-----W-	-----
31	9H6	--R---	-----	-----W-	-----
32	31A4	-----	-----	-----V-----GWV	-----
33	1A12	--R---	-----	-----W-	--A-----
34		DNNKRPS	GIPDRESGSKSGTSATLGITGLQTGDEADYYC	GTWDSLSSAYV	FGTGTKVTVL
35	16F12	-Y-----	-----	-----	-----R-----
36	22E2	-Y-----	-----	-----G--	-----R-----
37	27A6	-Y-----	-----	-----S--	-----R-----
38	28B12	-Y-----	-----	-----G--	-----R-----
39	28D6	-Y-----	-----	-----G--	-----R-----
40	31G11	-S-----	D-----	-----	-----
41		DNNKRPS	GIPDRESGSKSGTSATLGITGLQTGDEADYYC	GTWDSLSSAWV	FGGGTKLTVL
42	13B5	--T-----	N-----	-----	-----
43		QDSKRPS	GIPERFESGSNSGNNTATLTISGTOAMDEADYYC	QAWDSSSTAWV	FGGGTKLTVL
44	31B12	-NT-W-L	K-----V-----	V-	-----
45		VGTGGIVGSKGD	GIPDRESVLGSGLNRYLTIKNIQEEDESDYHC	GADHGSGSNFVVV	FGGGTKLTVL
46	3B6	-D-----E	-----	-----T-----	-----
45		VGTGGIV	GSKGDGIPDRFSVLGSGLNRYLTIKNIQEED	SDYHCADHGSGSNFVVV	FGGGTKLTVL
46	3B6v1	-D-----	E-----	T-----	-----

FIG. 2D

Seq ID No.	LINE	V	D	J	FR1	CDR1	CDR2
47		GermLine			QVQLVQSGAEVVKPGASVKVSCKAS	GYTFTSYGIS	WVRQAPGQGLEWMG
48	20D10	VH1-18			JH6B -I-----	--PL--	
49	26E10	VH1-18			JH6B -----L-	--L-	
49	21B12	VH1-18			JH6B -----L-	--L-	
50	23G1	VH1-18			JH6B -----L-	--L-	
51	26H5	VH1-18			JH6B -----L-	--L-	
52	27H5	VH1-18			JH6B -----L-	--L-	
53	31D1	VH1-18			JH6B -I-----L-	--L-	
54	27E7	VH1-18			JH6B -----L-	--SL--	
55	30B9	VH1-18			JH6B -----PL--	--PL--	
56	19H9	VH1-18			JH6B -----AL--	--AL--	
57	17C2	VH1-18			JH6B -----S-----P	--P--	
58	25A7	VH1-18			JH6B -----S-----P	--P--	
59		GermLine			QVQLVQSGAEVVKPGASVKVSCKAS	GYTFTSYGIS	WVRQAPGQGLEWMG
60	3B6	VH1-18			JH4B -----		
61		GermLine			EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYWS	WVRQAPGKGLEWVA
62	9H6	VH3-7	D7-27	JH3A	-----R-----	--R--	
63		GermLine			EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYWS	WVRQAPGKGLEWVA
64	9C9	VH3-7	D7-27	JH3B	-----VV-----	--L---NF---	
65	1A12	VH3-7	D7-27	JH3B	EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYSMN	WVRQAPGKGLEWVS
66		GermLine			EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYSMN	WVRQAPGKGLEWVS
67	31H4	VH3-21	D3-3	JH3A	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPGKGLEWVS
68		GermLine			EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPGKGLEWVS
69	13B5	VH3-23		JH4B	-----	-----	

FIG. 3A

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
70		Germline			EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPGKGLEWVS
71	23B5	VH3-23	D2-8	JH4B	-----	-----N	-----
72	25G4	VH3-23	D2-8	JH4B	-----	-----N	-----
73		Germline			QVQLVESGGGVVQPGRSRLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
74	30A4	VH3-33		JH6B	-----	-----	-----
75		Germline	D6-6	JH6B	-----	GFTFSSYGMH	WVRQAPGKGLEWVA
76	27A6	VH3-33	D6-6	JH6B	---H---	---N-F---	-----
77	28B12	VH3-33	D6-6	JH6B	-----	-----F---	-----
289	28B12v1	VH3-33	D6-6	JH6B	---H---	-----F---	-----
78	28D6	VH3-33	D6-6	JH6B	-----	-----F---	-----
79	16F12	VH3-33	D6-6	JH6B	---H---	-----N-F---	-----
80	22E2	VH3-33	D6-6	JH6B	-----	-----F---	-----
81	31B12	VH3-33	D6-6	JH6B	-----	-----	-----
290	31B12v1	VH3-33	D6-6	JH6B	-----	-----	-----C--
82		Germline			QVQLVESGGGVVQPGRSRLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
83	31G11	VH3-33	D6-19	JH6B	-----	-----R---	-----
84		Germline			QVQLQESGPGLVKPSQTLSLTCTVS	GGSISSGGYWS	WIRQHPGKGLEWIG
85	3C4	VH4-31		JH6B	-----	-----SD---	-----
86		Germline			QVQLQESGPGLVKPSQTLSLTCTVS	GGSISSGGYWS	WIRQHPGKGLEWIG
87	27B2	VH4-31	D5-5	JH4B	-----	-----	-----
88		Germline			QVQLQQWAGILLKPSETLSLTCAVY	GGSFSGYYWS	WIRQPPGKGLEWIG
89	31A4	VH4-34	D6-6	JH4B	-----	-----A--N	-----
90		Germline			QVQLQQSGPGLVKPSQTLSLTCATIS	GDSVSSNSAAWN	WIRQSPSRGLEWLIG
91	13H1			JH4B	-----	-----	-----
		VH6-1					

FIG. 3B

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
				YGMDV	WGQGTTVTVSS
47		WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMELLRSRSDDTAVYYCAR		
48	20D10	-V-----V--	S-----V-----	G-----	
49	26E10	-V-F-	-G-----P-	G-----	
49	21B12	-V-F-	-G-----P-	G-----	
50	23G1	-V-F-	-G-----P-	G-----	
50	26H5	-F-----V--	V-----V-----	G-----	
51	27H5	-V-----V--	V-----S-----	G-----	
52	31D1	-F-----V--	V-----V-----F-----	G-----	
53	31D1	-F-----V--	V-----V-----F-----	G-----	
54	27E7	-V-----V--	V-----V-----V-----	G-----	
55	30B9	-V-----V--	V-----V-----V-----	G-----	
55	19H9	-V-----V--	V-----V-----V-----	G-----	
56	17C2	-V-----F-----	V-----V-----V-----	G-V-----	
58	25A7	-E-----	V-----F-----	G-V-----	
59		WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMELLRSRSDDTAVYYCAR	GY DY	WGQGTLVTVSS
60	3B6	NIKQDGSEKYYDSVKG	RFTISRDNAKNNSLYLQMNSLRAEDTAVYYCAR	NWG AFDV	WGQGTMVTVSS
61	9H6	---T-----V--	---	--TR--	--H-----
62		NIKQDGSEKYYDSVKG	RFTISRDNAKNNSLYLQMNSLRAEDTAVYYCAR	NWG AFDI	WGQGTMVTVSS
63	9C9	---	---	ES ----- F -----	
64	1A12	---	---	ES ----- F -----	
65		SISSSSYYADSVKG	RFTISRDNAKNNSLYLQMNSLRAEDTAVYYCAR	DYDFWSGGYYTAFFDV	WGQGTMVTVSS
66	31H4	S-----	F-----	--A---D-----	
67		AISGGGGSTYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	FDY	WGQGTLVTVSS
68	13B5	T-----R-----	---	EVGSP-----	

FIG. 3C

FIG. 3D

Seq ID No.	LINE	CDR2	CDR3	FR3	FR4
70		RISGGCSTYADSVKS	RFTISRDNSKNTLYQMNSLRAEDTAVYYCAR	VLMVYAKDY	WCGSTLVTVSS
71	23B5	T-----DN-----	KF-----ML-----		
72	25G4	T-----N-----	KF-----ML-----		
73		VIVYDGSNKYADSVKS	RFTISRDNSKNTLYQMNSLRAEDTAVYYCAR	YYYMDDV	WCGSTLVTVSS
74	30A4	-----D-----	-----	-----	
75		VIVYDGSNKYADSVKS	RFTISRDNSKNTLYQMNSLRAEDTAVYYCAR	ERAZIKL-----	WCGSTLVTVSS
76	27A6	I----S----D-----	IRAA-----	GMDV	WCGSTLVTVSS
77	28B12	I----N-----	AIAA-----		
78	28D6	I----N-----	AIAA-----		
79	16F12	I----S----DE-----	AIAA-----		
80	22E2	I----N-----	AIAA-----		
291	22E2v1	I----N-----	AIAA-----		
81	31B12	I----N-----	AIAA-----		
290	31B12v1	I----N-----	AIAA-----		
82		VIVYDGSNKYADSVKS	RFTISRDNSKNTLYQMNSLRAEDTAVYYCAR	PGGL---PG-----	WCGSTLVTVSS
83	31G11	I----E----T----Y-----	GTAVAYYYYYGMDV		
84		YIYXGSSTYNNPLKS	RVTISVDTSKNQESLKLSSVTAADTAVYYCAR	-----	WCGSTLVTVSS
85	3C4	-----R-----	GGVTP-----A-----		
86		YIYXGSSTYNNPLKS	RVTISVDTSKNQESLKLSSVTAADTAVYYCAR	EDPAMV YFDY	WCGSTLVTVSS
87	27B2	-----R-----	-----P-----		
88		EINHGSSTYNNPLKS	RVTISVDTSKNQESLKLSSVTAADTAVYYCAR	GQLV FDX	WCGSTLVTVSS
89	31A4	-----R-----	-----P-----		
90		RTYYRSKWWNYAAYSVKS	RITIN2DTSKNQESLQMNVSVPEDTAVYYCAR	FXY	WCGSTLVTVSS
91	13H1	-----KN-----G-----	GSPTAA-----		

31H4**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGCTGGGGGAGGCCTGGTCAAGCCTGGGGGTCCTGA
GACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATAGCATGAACCTGGTCC
GCCAGGGCTCCAGGGAAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGT
TACATTTCCCTACGCAGACTCAGTGAAGGGCCGATTACCACATCTCCAGAGACAACGCC
AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGA
TTTCTGTGCGAGAGATTACGATTTGGAGTGCTTAATGATGCTTTGATGTCTGG
GGCCAAGGGACAATGGTCACCGTCTCTCA3' (**SEQ ID NO: 152**)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVKPGSLRLSCAASGFTSSYSMNWVRQAPGKGLEWVSSISSSSYISY
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYFCARDYDFWSAYYDAFDVWGQGT
MVTVSS (**SEQ ID NO: 67**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA
CCATCTCCTGCACTGGGAGCAGCTCAACATCGGGCAGGTTATGATGTACACTGGT
ACCAGCAGCTTCCAGGAACAGCCCCAAACTCCTCATCTGGTAACAGCAATCGGC
CCTCAGGGGTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACA
GCAGCCTGAGTGGTTCGGTATCGCGGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ
ID NO: 153**)

Amino acid sequence of light chain variable region:

QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDVHWYQQLPGTAPKLLISGNNSRPSGV
PDRFSGSKSGTSASLAITGLQAEDAYYCQSYDSSLGSVFGGGTKLTVL (**SEQ ID
NO: 12**)

FIG. 3E

20D10**Nucleotide sequence of heavy chain variable region:**

5'CAGATTCAAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTTCTGGTTACCCCTGACCAGCTATGGTATCAGCTGGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCGCTTACAATGGT
AACACAAACTATGCACAGAAGGTCCAGGGCAGCGTCACCATGACCACAGACACATC
CACGAGCACAGTCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
ATTACTGTGCGAGAGGGCTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' (**SEQ ID NO: 92**)

Amino acid sequence of heavy chain variable region:

QIQLVQSGAEVKPGASVKVSCKASGYPLTSYGISWVRQAPGQGLEWMGWISA YNGN
TNYAQKVQGSVTMTDTSTSTVYMELRSLSRSDDTAVYYCARGYGM DVWGQGTTVTV
SS (**SEQ ID NO: 48**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGC ACTGGAACCAGCAGTGACGTTGGTTATAACTCTGTCTCCTGGTA
CCAACAGTACCCAGGCAAACCCCCCAA ACTCAAGATTATGAGGTCAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATACAA
GCACCAGCATGGTCTCGCGGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO: 93**)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSWYQQYPGKPPKLKIYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGGTKLTVL (**SEQ ID NO:**
19)

FIG. 3F

26E10**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTCTGGTTACACCTAACAGCTATGGTATCAGCTGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGGTAGTTTATAATGGT
AACACAAACTATGCACAGAACGCTCCAGGGCAGAGGCACCATGACCACAGACCCATC
CACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGCCGTGT
ATTACTGTGCGAGAGGCTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' (**SEQ ID NO: 94**)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMGWVSYNG
NTNYAQKLQGRGTMTDPSTSTAYMELRSLSDDTAVYYCARGYGMDVWGQGTTVT
VSS (**SEQ ID NO: 49**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTCAGTGA CGTTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAAGCCCCAAACTCATGATTATGAGGTAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTGGCTCCAAGTCTGGCAACACGCCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAATTCAATACAA
GCACCAGCATGGTATTGGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO: 95**)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPKLMIYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYYCNSYTSTSMVFGGGTKLTVL (**SEQ ID NO: 23**)

Alternative Nucleotide sequence of light chain variable region (26E10v1):

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTCAGTGA CGTTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAAGCCCCAAACTCATGATTATGAGGTAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTGGCTCCAAGTCTGGCAACACGCCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAACTCAATACAA
GCACCAGCATGGTATTGGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO: 293**)

FIG. 3G

26H5**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAAGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTTCTGGTTACACCTTGACCAGCTATGGTATCAGCTGGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCTTACAATGGT
AACACAAACTATGCACAGAACGGTCCAGGGCAGAGTCACCATGACACAGACACATC
CACGAGCACAGTCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
ATTACTGTGCGAGAGGGCTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' (**SEQ ID NO: 96**)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMGWISFYNGN
TNYAQKVQGRVTMTDTSTSTVYMELRSLSDDTAVYYCARGYGMDVWGQGTTVTV
SS (**SEQ ID NO: 51**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTCAGTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAACCCCCCAAACATGATTATGAGGTCAAGTAATCGGC
CCTCAGGGGTTTCTATTCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGAC
CATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATACAAG
CACCAAGCATGGTCTCGCGGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO: 97**)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSWYQQHPGKPPKLMIYEVSNRPSGV
SIRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGGTKLTVL (**SEQ ID NO:**
17)

FIG. 3H

31D1**Nucleotide sequence of heavy chain variable region:**

5'CAGATTCAAGCTGGTGCAGTCAGTGAGCTGAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTCTGGTTACACCTTGACCAGCTATGGTATCAGCTGGTGC
GACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCTTTACAATGGT
AACACAAACTATGCACAGAAGGTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGTCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
ATTCTGTGCGAGAGGTTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' (SEQ ID NO: 98)

Amino acid sequence of heavy chain variable region:

QIQLVQSGAEVKPGASVKVSCKASGYLTTSYGISWVRQAPGQGLEWMGWISFYNGNT
NYAQKVQGRVTMTDTSTSTVYMELRSLRSDDTAVYFCARGYGMDVWGQGTTVTVS
S (SEQ ID NO: 53)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCCTCGTCTGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTCAGTGCAGTTGGTGGTTATAACTCTGTCTCGTGGTA
CCAACAGCACCCAGGCAAACCCCCAAACTCATGATTATGAGGTCAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTCAGCTCATATACAA
GCACCAGCATGGCTTCGGCGGAGGGACCAAGCTGGCCGTCTA3' (SEQ ID NO: 99)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDADYFCSSYTSTSMVFGGGTLAVL (SEQ ID NO:
18)

FIG. 3I

23G1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTCTGTTACACCTAACCGAGCTATGGTATCAGCTGGTGC
GACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGATGGTCAGTTTATAATGGT
AACACAAACTATGCACAGAACGCTCCAGGGCAGAGGCACCATGACCACAGACCCATC
CACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
ATTACTGTGCGAGAGGGTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' (SEQ ID NO: 100)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMGWVSYFNG
NTNYAQKLQGRGTMTDPSTSTAYMELRSRSDDTAVYYCARGYGMDVWGQGTTVT
VSS (SEQ ID NO: 50)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTGACGTTGGTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAAGCCCCAAACTCATGATTATGAGGTCACTAATCGGC
CCTCAGGGTTCTAATCGCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CCATCTCTGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAACTCATACAA
GCACCAGCATGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO:
101)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPKLMIYEVNRPNG
SNRFSGSKSGNTASLTISGLQAEDeadYYCNSYTSTSMVFGGGTKLTVL (SEQ ID NO:
26)

FIG. 3J

27B2**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTCACAGACCCGT
CCCTCACCTGCACTGTCTCTGGCTCCATCAGCAGTGGTGTTACTACTGGAGCT
GGATCCGCCAGCACCCAGGGAAAGGGCCTGGAGTGGATTGGGTACATATAACAGT
GGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACAC
GTCTAAGAACCAAGTCTCCCTGAAGCTGAGCTGTGACTGCCCGGACACGGCCGT
GTATTACTGTGCGAGAGAGGATAACAGCTATGGTCTTACTTTGACTACTGGGCCA
GGGAACCCTGGTCACCGTCTCCTCA3' (**SEQ ID NO: 102**)

Amino acid sequence of heavy chain variable region:

QVQLQESGPLVKPSQTLSLTCTVSGGISSGGYYWSWIRQHPGKGLEWIGYIYNSGSTY
YNPSLKSRTVTISVDTSKNQFSLKLSSVTAADTA VYYCAREDTAMVPYFDYWGQGTLVT
VSS (**SEQ ID NO: 87**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTACTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA
CCATCTCCTGCACTGGAGCAGCTCCAACATCGGGCACATTATGATGTGCACTGGT
ACCAAGCAGGTTCCAGGAACAGCCCCAAACTCCTCATCTATGGTAACACCTATCGGC
CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACA
ACAGCCTGAGTGGTGTGGTATTGGCAGGGACCAAGCTGACCGTCCTA3' (**SEQ
ID NO: 103**)

Amino acid sequence of light chain variable region:

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAHYDVHWYQQVPGTAPKLLIYGNTYRPSG
VPDRFSGSKSGTSASLAITGLQAEDAYYCQSYDNSLSGVVFGGTKLTVL (**SEQ ID
NO: 13**)

FIG. 3K

16F12**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCACCTGGTGGAGTCTGGGGGAGGCCGTGGTCCAGCCTGGGAGGTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTCAACAGCTTGCACTGGTCC
GCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCACTTATCTGGTCTGATGGAAGT
GATGAATACTATGCAGACTCCGTGAAGGGCCGATTCAACCCTCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTA
TTACTGTGCGAGAGCCATAGCAGCCCTCTACTACTACTACGGTATGGACGTCTGGGG
CCAAGGGACCACGGTCACCGTCTCCTCA3' (**SEQ ID NO: 104**)

Amino acid sequence of heavy chain variable region:

QVHLVESGGVVQPGRSRLSCAASGFTFNSFGMHWVRQAPGKGLEWVALIWSDGSD
EYYADSVVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAIAALYYYYGMDVWGQ
GTTVTVSS (**SEQ ID NO: 79**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGGCCCCAGGACAGAAGGTCA
CCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTGGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACTATAATAAGCGACCCT
CAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAAGCCACCCCTGGGCA
TCACCGGACTCCAGACTGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGC
AGCCTGAGTGCTTATGTCTCGGAACTGGGACCAGGGTCACCGTCCTA3' (**SEQ ID
NO: 105**)

Amino acid sequence of light chain variable region:

QSVLTQPPSVAAPGQKVТИСГСССНИГНФСВYQQLPGTAPKLLIYDYNKRPSGIPD
RFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAYVFGTGRVTVL (**SEQ ID NO:
35**)

FIG. 3L

22E2**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGA
GAECTCTCTGTGCAGCGTCTGGATTACCTTCAGCAGCTTGGCATGCAGCTGGTCC
GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATGGAATGATGGAAGT
AATAAAACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTA
TTACTGTGCGAGAGCCATAGCAGCCCTCTACTACTACGGTATGGACGTCTGGGG
CCAAGGGACCACGGTCACCGTCTCCTCA3' (**SEQ ID NO: 106**)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQPGRSLRLSCAASGFTSSFGMHWVRQAPGKGLEWVALIWNDGSN
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAIAALYYYYGMDVWGQ
GTTVTVSS (**SEQ ID NO: 80**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAACGGTCA
CCATCTCCTGCTCTGGAAAGCAGCTCCAACATTGGAATAATTGTATCCTGGTACC
AGCAGCTCCAGGAACAGCCCCAAACTCCTCATTATGACTATAATAAGCGACCC
CAGGGATTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAAGCCACCC
TCACCGGACTCCAGACTGGGGACGAGGCCGATTACTGCGGAACATGGGATAGC
AGTCTGAGTGGTTATGTCTCGGAACTGGGACCAGGGTCACCGTCCTA3' (**SEQ ID
NO: 107**)

Amino acid sequence of light chain variable region:

QSVLTQPPSVAAPGQKVTCGSSSNIGNNFWSYQQLPGTAPKLLIYDYNKRPSGIPD
RFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLGYVFGTGTRTVL (**SEQ ID NO:
36**)

FIG. 3M

27A6**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCACCTGGTGGAGCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTACCTCAACAGCTTGGCATGCACTGGTCC
GCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCACCTATATGGTCTGATGGAAGT
GATAAACTATGCAGACTCCGTGAAGGGCCGATTACCACATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGAACACGGCTGTGA
TTACTGTGCGAGAGCCATAGCAGCCCTACTACTACTACGGTATGGACGTCCTGGGG
CCAAGGGACCACGGTCACCGTCTCCTCA3' (**SEQ ID NO: 108**)

Amino acid sequence of heavy chain variable region:

QVHLVESGGGVVQPGRSLRLSCAASGFTFNSFGMHWVRQAPGKGLEWVALIWSDGSD
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAIAALYYYYGMDVWGQ
GTTVTVSS (**SEQ ID NO: 76**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCAGGACAGAAGGTCA
CCATCTCCTGCTCTGGAAAGCAGTCCAACATTGGAATAATTGTATCCTGGTACC
AGCAGTTCCCAGGAACAGCCCCAAACTCCTCATTATGACTATAATAAGCGACCCT
CAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCCTGGCA
TCACCGGACTCCAGACTGGGACGAGGCCGATTACTGCGGAACATGGGATAGC
AGCCTGAGTTCTTATGTCTCGGAACTGGACCAGGGTACCGTCCTA3' (**SEQ ID NO: 109**)

Amino acid sequence of light chain variable region:

QSVLTQPPSVSAAPGQKVТИСГСССНИГНФВСУQQFPGTAPKLLIYDYNKRPSGIPD
RFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSSYVFGTGRVTVL (**SEQ ID NO: 37**)

FIG. 3N

28B12**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGAGGCCTGGTCCAGCCTGGAGGTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTACCTTCAGCAGCTTGGCATGCAGCTGGTCC
GCCAGGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATGGAATGATGGAAGT
AATAAAACTATGCAGACTCCGTGAAGGGCCGATTACCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCGAGGACACGGCTGTGTA
TTACTGTGCGAGAGCCATAGCAGCCCTCTACTACTACTACGGTATGGACGTCCTGGGG
CCACGGGACCACGGTCACCGTCTCCTCA3' (**SEQ ID NO: 110**)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTSSFGMHWVRQAPGKGLEWVALIWNDGSN
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAIAALYYYYGMDVWGH
GTTVTVSS (**SEQ ID NO: 77**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGGGCCAGGACAGAACGGTCA
CCATCTCCTGCTCTGGAAAGCAGCTCCAACATTGGGAATAATTGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACTATAATAAGCGACCCT
CAGGGATTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCCTGGCA
TCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGC
AGCCTGAGTGGTTATGTCTCGGAACCTGGGACCAGGGTACCGTCCTA3' (**SEQ ID
NO: 111**)

Amino acid sequence of light chain variable region:

QSVLTPPPSVAAPGQKVTVTISCGSSSNIGNNFVSWYQQLPGTAPKLLIYDYNKRPSGIPD
RFSGSKSGTSATLGITGLQTGDEADYYCGTWDSLGSYVF GTGTRTVL (**SEQ ID NO:
38**)

FIG. 3O

28D6**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTACCTTCAGCAGCTTGGCATGCACGGTCC
GCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCACTTATATGGAATGATGGAAGT
AATAAAATACTATGCAGACTCCGTGAAGGGCGATTACCACATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCAGGACACGGCTGTGTA
TTACTGTGCGAGAGCCATAGCAGCCCTACTACTACTACCGTATGGACGTCTGGGG
CCAAGGGACCACGGTCACCGTCTCCTCA3' (**SEQ ID NO: 112**)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTSSFGMHWVRQAPGKGLEWVALIWNDGSN
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAIAALYYYYGMDVWGQ
GTTVTVSS (**SEQ ID NO: 78**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCACAGTGTCTGCGGCCAGGACAGAACGGTCA
CCATCTCCTGCTCTGGAAGCAGCTCAAACATTGGAATAATTGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTATGACTATAATAAGCGACCC
CAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCCTGGCA
TCACCGGACTCCAGACTGGGGACGAGGCCGATTACTACTGCGGAACATGGGATAGC
AGCCTGAGTGGTTATGTCTCGGAACTGGGACCAGGGTACCGTCCTA3' (**SEQ ID
NO: 113**)

Amino acid sequence of light chain variable region:

QSVLTVPPPTVSAAPGQKVТИСГСССНИГНФВШYQQLPGTAPKLLIYDYNKRPSGIPD
RFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLGYVFGTGTRVTVL (**SEQ ID NO:
39**)

FIG. 3P

31G11**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGCTGGGGGGAGCGTGGTCCAGCCTGGGAGGTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTACCTTCAGGAGCTATGGCATGCACGTGGTCC
GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATGGCATGATGGAAGT
AATACATACTATGTAGACTCCGTGAAGGGCCATTACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCAGGACACGGCTGTGTA
TTACTGTGCGAGAGGTATAGCAGTGGCTTACTACTACCGTATGGACGTCTGGGG
CCAAGGGACCACGGTCACCGTCTCCTCA3' (**SEQ ID NO: 114**)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFRSYGMHWVRQAPGKGLEWVALIWHDSN
TYYVDSVKRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGIAVAYYYYGMDVWGQ
GTTVTVSS (**SEQ ID NO: 83**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTCGGGCCCCAGGACAGAAGGTCA
CCATCTCCTGCTCTGGAAAGCAGCTCCAACATTGGAATAATTGTATCTGGTACCC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACAGTAATAAGCGACCC
CAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAAGCCACCTGGACA
TCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGC
AGCCTGAGTGCTTATGTTTCGGAACTGGGACCAAGGTACCGTCCTA3' (**SEQ ID
NO: 115**)

Amino acid sequence of light chain variable region:

QSVLTQPPSVAAPGQKVTCGSSSNIGNNFVSWYQQLPGTAPKLLIYDSNKRPSGIPD
RFSGSKSGTSATLDITGLQTGDEADYYCGTWDSL SAYVFGTGTKVTVL (**SEQ ID NO:
40**)

FIG. 3Q

23B5**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGTCCCTGA
GACTCTCCTGTGCAGCCTCTGGATTACCTTACAGCTATGCCATGAACCTGGTCC
GCCAGGCTCCAGGGAAAGGGGCTGGAGTGGTCTCAACTATTAGTGGTAGTGGTGAT
AACACATACTACGCAGACTCCGTGAAGGGCCGGTCACCATCTCAGAGACAATT
CAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGCCGTAT
ATTACTGTGCGAAAAAGTTGTACTAATGGTGTATGCTATGCTTACTACTGGGCC
AGGAACCTGGTACCGTCTCCTCA3' (**SEQ ID NO: 116**)

Amino acid sequence of heavy chain variable region:

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWWSTISGSDNT
YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKKFVLMVYAMLDYWQGQG
TLTVSS (**SEQ ID NO: 71**)

Nucleotide sequence of light chain variable region:

5'GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGGAGACAGAGT
CACCATCACTGCCGGCAAGTCAGAGCATTAGCAGTTATTAAATTGGTATCAGCA
GAAACCAGGGAAAGCCCCTAACGGTCTGATCTATGCTGCCCTCAGTTGCAAAGTGG
GGTCCCATCAAGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAA
CAGTCTGCAACCTGAAGATTGCAACTTACTACTGTCAACAGAGTTACAGTTCCCC
CATCACCTCGGCCAAGGGACACGACTGGAGATTAAA3' (**SEQ ID NO: 117**)

Amino acid sequence of light chain variable region:

DILMTQSPSSLASVGDRVTITCRASQSISSYLNWYQQKPGKAPKVLIVYASSLQSGVPSR
FSGSGSGTDFTLTINSQPEDFATYYCQQSYSSPITFGQGTRLEIK (**SEQ ID NO: 9**)

FIG. 3R

25G4**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGAGCTGGGGAGGCTGGTACAGCCGGGGGGTCCCTGA
GAECTCCTGTGCAGCCTCTGGATTACCTTAGCAGCTATGCCATGAACTGGGTCC
GCCAGGCTCCAGGGAAGGGGCTGGAGTGGTCTCAACTATTAGTGGTAGTGGTGGT
AACACATACTACGCAGACTCCGTGAAGGGCCGTTACCACATCTCCAGAGACAATT
CAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCAGGACACGGCCGTAT
ATTACTGTGCGAAAAAGTTGTACTAATGGTGTATGCTATGCTTGACTACTGGGCC
AGGAACCTGGTACCGTCTCCTCA3' (**SEQ ID NO: 118**)

Amino acid sequence of heavy chain variable region:

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISSGGNT
YYADSVKGRFTISRDN SKNTL YLQMNSLRAEDTA VYYCAKKFVLMVYAMLDYWQGQ
TLTVVSS (**SEQ ID NO: 72**)

Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGT
CACCATCACTGCCGGCAAGTCAGAGCATTAGCATCTATTAAATTGGTATCAGCA
GAAGCCAGGGAAAGCCCCCTAACCTCCTGATCTATGCTGCAGCCAGTTGCAAAGTGG
GGTCCCCTCAAGGTTCAAGTGGCAGTGGATCTGGGACAGATTCACTCTACCATCAG
CAGTCTGCAACCTGAAGATTGCAACTTACTACTGTCAACAGAGTTACAGTGC
CATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA3' (**SEQ ID NO: 119**)

Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQSISIYLNWYQQKPGKAPYLLIYAASLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCQQSYSAPITFGQGTRLEIK (**SEQ ID NO: 10**)

FIG. 3S

27E7

Nucleotide sequence of heavy chain variable region:

5'CAGGTTCAGCTGGTCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGCCTCACTGA
AGGTCTCTGCAAGGCTTCTGGTTACAGTTGACCAGCTATGGTATCAGCTGGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCGCTTACAATGGT
AACACAAACTATGCACAGAACGGTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGTCTACATGGAGGTGAGGAGTCTGAGATCTGACGACACGGCCGTGT
ATTACTGTGCGAGAGGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' (**SEQ ID NO: 120**)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASLKVSKASGYSLTSYGISWVRQAPGQGLEWMGWISAYNGN
TNYAQKVQGRVTMTTDSTSTVYMEVRSLSDDTAVYYCARGYGMGVWGQGTTV
SS (**SEQ ID NO: 54**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAACCCCCCAAACATGATTATGAGGTCAAGTAATCGGC
CCTCAGGGGTTTCTAATCGCTCTGGCTCCAAGTCTGGCAATACGGCCTCCCTGA
CCATCTCTGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATACAA
GCACCAGCATGGTCTCGCCGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO: 121**)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSWSYQQHPGKPPKLMIYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDADYFCSSYTSTSMVFGGTKLTVL (**SEQ ID NO: 20**)

FIG. 3T

27H5**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCACTGGTGCAGTCTGGAGCTGAGGTGAAGAGGCCCTGGGCCTCAGTGA
AGGTCTCTGCAAGGCTCTGGTACACCTGACCAGCTATGGTATCAGCTGGTGC
GACAGGGCCCTGACAAGGGCTTGAGTGGATGGATGGATCAGCGTTACAATGGT
AACACAAACTATGACAGAAGGTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGTCTACATGGAGCTGAGGAGCCTGAGCTCTGACGACACGCCGTGT
ATTACTGTGCGAGAGGCTACGGTATGGACGTCTGGGCCAAGGGACACGGTCACC
GTCTCCTCA3' (SEQ ID NO: 122)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKRPGASVKVSCKASGYLT SYGISWVRQAPGQGLEWMGWISVYNGN
TNYAQKVQGRVTMTDTSTVYMELRSLSDDTAVYYCARGYGM DVWGQQGTTVTV
SS (SEQ ID NO: 52)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGTCTCCTGGACAGTCGATCAC
CATCTCTGCACTGGAACCAGCAGTGCAGTTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAACCCCCCAAACATGATTATGAGGTCAGTAATCGGC
CCTCAGGGTTCTATTGCTCTGGCTCAAGTCTGGCAACACGCCCTCCCTGAC
CATCTCTGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATACAAG
CACCAGCATGGTCTCGCGCGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO: 123)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGSITISCTGTSSDVGGYNSVWYQQHPGKPPKLMIYEVSNRPSGV
SIRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGGTKLTVL (SEQ ID NO:
16)

FIG. 3U

30B9**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCAGCTGGAGCTGAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTCTGGTTACCCCTGACCAGCTATGGTATCAGCTGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCGCTAACATGGT
AACACAAACTATGCACAGAAGGTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGTCTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGCCGTGT
ATTACTGTGCGAGAGGCTACGGTATGGACGTCTGGGCAAGGGACCACGGTCACC
GTCTCCTCA3' (SEQ ID NO: 124)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYPLTSYGISWVRQAPGQGLEWMGWISAYNGN
TNYAQKVQGRVTMTDTSTVYMELRSLSRSDDTAVYYCARGYGMDVWGQGTTVTV
SS (SEQ ID NO: 55)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAACCCCCCAAACATGATTATGAGGTCAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTCTGGCTCCAAGTCTGGCAATACGCCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATAACAA
GCACCAGCATGGTCTCGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO:
125)

Alternative Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAACCCCCCAAACATGATTATGAGGTCAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTCTGGCTCCAAGTCTGGCAACACGCCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATAACAA
GCACCAGCATGGTCTCGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO:
294)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDADYFCSSYTSTSMVFGGGTKLTVL (SEQ ID NO:
21)

FIG. 3V

19H9**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAAGTGGTGCAGTCAGCTGGAGCTGAGGTGAAGAACGCTGGGGCTCAGTGA
AGGTCTCCTGCAAGGCTCTGGTTACGCCCTGACCAGCTATGGTATCAGCTGGGTGC
GACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCGCTTACAATGGT
AACACAAACTATGCACAGAAGGTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGTCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
ATTACTGTGCGAGAGGGTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' (**SEQ ID NO: 126**)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYALTSYGISWVRQAPGQGLEWMGWISAYNGN
TNYAQKVQGRVTMTDTSTVYMELRSLSDDTAVYYCARGYGMDVWGQGTTVTV
SS (**SEQ ID NO: 56**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAACAGTGACGTTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAACCCCCCAAACATGATTATGAGGTAGTAATCGGC
CCTCAGGGATTCTAATCGCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CCATCTCTGGCTCCAGGCTGAGGACGAGGCTGATTATTCTGCAGCTCATATACAA
GCACCAGCATGGCTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO:**
127)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTNSDVGGYNSVSWYQQHPGKPPKLMYEVSNRPSGI
SNRFSGSKSGNTASLTISGLQAEDeadyFCSSYTSTSMVFGGGTKLTVL (**SEQ ID NO:**
22)

FIG. 3W

17C2**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTTCTGGTACAGCTTACAGCTATGGTATCAGCTGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGGTACCGCTTACAATGGT
AACACAAACTATGCACAGAACGTTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGCCTACATGGAAC TGAGGAGCCTGAGATCTGACGACACGCCGTGT
ATTACTGTGCGAGAGGGTACGTTATGGACGTCTGGGCAAGGGACCACGGTCACC
GTCTCCTCA3' (SEQ ID NO: 128)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWVSAVNG
NTNYAQKFQGRVTMTDTSTSTAYMELRSRSDDTAVYYCARGYVMDVWGQGTVT
VSS (SEQ ID NO: 57)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTTCTGGTCTCCTGGACAGTCGATCAC
CATCTCCTGC ACTGGAAC CAGCAGTGACGTTGGT GCTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAAGCCCCAAACGCATGATTATGAGGTCAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTCTGGCTCCAAGTCTGGCAACACGCCCTCCCTGA
CCATCTCTGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATACAA
GCACCAACATGGTATCGCGGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO:
129)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVAYNSVSWYQQHPGKAPKRMIVEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDADYYCSSYTSTMVFGGGTKLTVL (SEQ ID NO:
24)

FIG. 3X

13H1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTACAGTTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCT
CACTCACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGTGCTTGGAACT
GGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGG
TCCAAGTGGTATAAAAATTATTCAAGTATCTGTAAAAGTCGAATAACCATCAACCCA
GACACATCCAAGAACCAAGTTCTCTGCAACTGAACACTCTGTGACTCCCAGGACACG
GCTGTGTATTACTGTGCAAGAGGGGGCCAACTGCTGCTTTGACTACTGGGGCCAG
GGAACCCTGGTCACCGTCTCCTCA3' (**SEQ ID NO: 130**)

Amino acid sequence of heavy chain variable region:

QVQLQQSGPGLVKPSQTLSTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRYYRSK
WYKNYSVSVKSRTINPDTSKNQFSLQLNSVTPGDTAVYYCARGGPTAAF DYWGQGTL
VTVSS (**SEQ ID NO: 91**)

Nucleotide sequence of light chain variable region:

5'CTTCTGCCCTGACTCAGCCTGCCTCCGTCTGGGCTCCTGGACAGTCGATCAC
CATCTCCTGCCTGAAACCAGCAGTGATGTTGGGAATTATAACCTTGCTCCTGGTA
CCAACAGTATTCAAGGCAAAGCCCCAAACTCATGATTATGAGGTCAAGTAAGCGGC
CCTCAGGGTTCTAATCGCTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CAATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCTGCTCATATGCAG
GTAGTAGCACTTGGTTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID
NO: 131**)

Amino acid sequence of light chain variable region:

LSALTQPASVSGSPGQSITISCTGTSSDVGNYNLVSWYQQYSGKAPKLMYEVSKRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTLVFGGGTKLTVL (**SEQ ID NO:
28**)

FIG. 3Y

9C9**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGTTGGTGGAGCTGGGGAGGCTTGGTCCAGCCTGGGGGTCCTGA
GAECTCCTGTGTAGTCTCTGGATTACCTTAGTAGCTATTGGATGAGCTGGTCCG
CCAGGCTCCAGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGT
GAGAAATACTATGTGGACTCTGTGAAGGGCCGATTACCACCATCTCCAGAGACAACGC
CAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTAT
ATTACTGTGCGAGAGAGTCAAACACTGGGATTGCTTGATATCTGGGCCAAGGGA
CAATGGTCACCGTCTCTTCA3' (**SEQ ID NO: 132**)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGVQPGGSLRLSCVSVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSE
KYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARESNWGFAFDIWGQGTM
VTVSS (**SEQ ID NO: 64**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGACCCCCGGCAGAGGGTCA
CCATCTCTGTTCTGGAAGCAGCTCCAACATCGGAAGTAAGACTGTAAACTGGTACC
AACAGGTCCCAGGAACGGCCCCAAACTCCTCATCTATAGGAATAATCAGCGGCC
TTAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCC
ATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTATTGTGCAGCATGGGATGAC
AGCCTGAATTGGGTGTTCGCGGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID NO: 133**)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQVPGTAPKLLIYRNNQRPLGVP
DRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWVFGGGTKLTVL (**SEQ ID NO: 30**)

FIG. 3Z

9H6**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCCAGCCTGGGGGTCCCTGA
GACTCTCCTGTGCAGCCTCTGGATTCACCTTAGTCGCTATTGGATGAGCTGGTCCG
CCAGGCTCCAGGGAAAGGGCTGGAGTGGTGCCAACATAAGCATGATGGAAGTG
AGAAATACTATGTGGACTCTGTGAAGGGCGATTCAACCATTCCAGAGACAACGCC
AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGGCCGAGGACACGGCTGTGA
TTACTGTGCGAGAGAGTCAAACACTGGGATTGCTTTGATGTCTGGGCCACGGGAC
AATGGTCACCGTCTCTCA3' (SEQ ID NO: 134)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKHDGSE
KYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARESNWGFADFVWGHGT
MVTVSS (SEQ ID NO: 62)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCTCAGCGCTGGGCCCGGACAGAGGGTCA
CCATCTCTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGTAAACTGGTACC
AGCAGCTCCCAGGAACGGCCCCAAACTCCTCATCTATAGTAATAATCGGCGGCCCT
CAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCA
TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACA
GCCTGAATTGGGTGTTGGCGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO:
135)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGPPGQRVTISCSGSSNIGSNTVNWYQQLPGTAPKLLIYSNNRRPSGV
RFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWVFGGKLT
V (SEQ ID NO:
31)

FIG. 3AA

13B5**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGTCCCTGA
GACTCTCTGTGCAGCCTCTGGATTACCTTAGCAGCTATGCCATGAGCTGGTCC
GCCAGGCTCCAGGGAAAGGGCTGGAGTGGTCTCACTATTAGTGGTAGTGGTGGT
AGGACATATTACGCAGACTCCGTGAAGGGCCGTTCACCATCTCCAGAGACAATT
CAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGGCCGAGGACACGCCGTAT
ATTACTGTGCGAAAGAAGTTGGCAGTCCTTGAECTACTGGGCCAGGGAACCTGG
TCACCGTCTCCTCA3' (SEQ ID NO: 136)

Amino acid sequence of heavy chain variable region:

EVQLLESGGGLVQPGGLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGRTY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEVGSPFDYWQGTLTVSS
(SEQ ID NO: 69)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCAGGACAGAACGGTCA
CCATCTCTGCTCTGGAAGCAACTCCAACATTGGGAATAATTATGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTATGACAATAATAAGCGACCC
CAGGGATTCTTGACCGATTCTCTGGCTCCAACTCTGGCACGTCAGCCACCCCTGGCA
TCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGC
AGCCTGAGTGCTGTGGTATTCCGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID
NO: 137)

Amino acid sequence of light chain variable region:

QSVLTQPPSVSAAPGQKVТИСSGSNSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP
DRFSGSNSGTSATLGITGLQTGDEADYYCGTWDSLAVVFGGGTKLTVL (SEQ ID
NO: 42)

FIG. 3BB

31B12**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGA
GAECTCTCTGTGCAGCGTCTGGATTCACCTCAGTAGCTATGGCATGCACGGTCC
GCCAGGCTCAGGCAAGGGCTGGAGTGGTGGCAATTATATGGTATGATGGAAGT
AATAAAACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC
AAGAACACACTGTATCTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGA
TTACTGTGCGAGGAGGGGGGCTGGCAGCTCGTCCGGCGGTATGGACGTCTGGG
GCCAAGGGACCACGGTCACCGTCTCCTCA3' (SEQ ID NO: 138)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWYDGSN
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRGGLAARPGGMDVWG
QGTTTVSS (SEQ ID NO: 81)

Nucleotide sequence of light chain variable region:

5'TCCTATGAGCTGACTCAGCCACCCTCAGTGTCTGTGTCCCCAGGACAGACAGCCAG
AATCACCTGCTCTGGAGATAAAATTGGGGATAAAATATGCTTGCTGGTATCAGCAGAA
ACCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAAATACCAAGTGGCCCTTAGGGAT
CCCTGAGCGATTCTCTGGCTCCAAGTCTGGGAACACAGTCACTCTGACCATCAGCGG
GACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTG
TGGTATTGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO: 139)

Amino acid sequence of light chain variable region:

SYELTQPPSVSVPQTARITCSGDKLGDKYACWYQQKPGQSPVLVIYQNTKWPLGIPE
RFSGSKSGNTVTLTISGTQAMDEADYYCQAWDSSVVFGGGTKLTVL (SEQ ID NO:
44)

Alternative Nucleotide sequence of light chain variable region:

5'TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCA
GAATCACCTGCTCTGGAGATAAAATTGGGGATAAAATATGCTTGCTGGTATCAGCAGA
AGCCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAAATACCAAGTGGCCCTTAGGGA
TCCCTGAGCGATTCTCTGGCTCCAAGTCTGGGAACACAGTCACTCTGACCATCAGCG
GGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACT
GTGGTATTGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO: 295)

FIG. 3CC

3C4**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTCACAGACCCGT
CCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTATTACTACTGGAGCT
GGATCCGCCAGCACCCAGGAAAGGGCCTGGAGTGGATTGGTACATCTATTACAGT
GGGAGCACCTACTACAACCCGTCCTCAAGAGTCGAATTACCATATCAGTAGACAC
GTCTAAGAACCTGTTCTCCCTGAAGTTGAGCTCTGTGACTGCCGCGGACACGGCCGT
GTATTACTGTGCAGAGAGGGGGGTGACTACGTACTACTACGCTATGGACGTCTGGG
GCCAAGGGACCACGGTCACCGTCTCCTCA3' (SEQ ID NO: 140)

Amino acid sequence of heavy chain variable region:

QVQLQESGPLVKPSQLTSLTCTVSGGSISSSDYYWSWIRQHPGKGLEWIGYIYYSGSTY
YNPSLKSRTISVDTSKNLFSKLSSVTAADTAVYYCARGGVTTYYAMDVGQGTTV
TVSS (SEQ ID NO: 85)

Nucleotide sequence of light chain variable region:

5'GACATACAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTTAGGAGACAGAGT
CACCATCACTGCCGGCAAGTCAGCGCATTAGCAACTATTTAAGTTGGTATCTGCA
GAAACCAGGGATTGCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTGCAGAGTGG
GGTCCCCTCAAGGTTCACTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAG
CAGTCTGCAATCTGAAGATTGCAACTACTACTGTCAACAGAGTTACAGTACCCCC
GCTCATTTCGGCGGAGGGACCAAGGTGGAGATCAA3' (SEQ ID NO: 141)

Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQRISNYLSWYLQKPGIAPKLLIYAASSLQSGVPSR
FSGSGSGTDFTLTISLQSEDFATYYCQQSYTPLIFGGGTKEIK (SEQ ID NO: 7)

FIG. 3DD

30A4**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCACGGTCC
GCCAGGCTCAGGCAAGGGCTGGAGTGGGTGGCAGTTATGGTATGGAAGT
GATAAAATACTATGCAGACTCCGTGAAGGGCCGATTACCACATCTCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTA
TTACTGTGCGAGAGAGACTGGTCCCTGAAACTCTACTACTACGGTATGGACGTCTG
GGCCAAGGGACCACGGTCACCGTCTCCTCA3' (SEQ ID NO: 142)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIVYDGSD
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARETGPLKLYYYGMDVWG
QGTTVTVSS (SEQ ID NO: 74)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGTCCGTACCCCTGGAGAGCCGCC
CTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATACAACTTTTG
AATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCTGATCTATTGGTTCT
CATCGGGCCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTT
ACACTGGAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCA
AGTTCTACAAACTCCATTCACTTCCGGCCCTGGGACCAAAGTGGATATCAA3'
(SEQ ID NO: 143)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLSVTPGEPPSISCRSSQSLLHSNGYNFLNWYLQKPGQSPQLLIYLGSHRAS
GVPDFRSGSGSGTDFTLEISRVEAEDVGVYYCMQVLQTPFTFGPGTKVDIK (SEQ ID
NO: 5)

FIG. 3EE

1A12**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGA
GACTCTCCTGTGCAGCCTCTGGACTCACCTTAGTAACTTGGATGAGCTGGTCCG
CCAGGCTCCAGGGAAAGGGGCTGGAGTGGGTGCCAACATAAGCAAGATGGAAGT
GAGAAATACTATGTGGACTCTGTGAAGGGCCGATTACCACATCTCCAGAGACAAACGC
CAAGAATTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGT
ATTCCCTGTACGAGAGAGTCAAACACTGGGATTGCTTTGATATCTGGGCCAAGGGA
CAATGGTCACCGTCTTCA3' (SEQ ID NO: 144)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGLTFSNFWMSWVRQAPGKGLEWVANIKQDGSE
KYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVSCTRESNWGFADIWGQGTM
VTVSS (SEQ ID NO: 65)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTGGACCCCCGGCAGAGGGTCA
CCATCTCTGTTCTGGAAGCAGCTCCAACATCGGAAGTAAAATGTAAACTGGTACC
AGCAGTTCCCAGGAACGGCCCCAAACTCCTCATCTATAGTAATAATCGGCGGCCCT
CAGGGGTCCCTGACCATTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCA
TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGATGACA
GCCTGAATTGGGTGTTGGCCAGGGACCAAGCTGACCGTCATA3' (SEQ ID NO:
145)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQFPGTAPKLLIYSNNRPSGVPD
RFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWVFGAGTKLTVL (SEQ ID NO:
33)

FIG. 3FF

3B6**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAACGCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTTCTGGTTACACCTTACAGCTATGGTATCAGCTGGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCACTTACAATGGT
AACACAAACTATGCACAGAACGGTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTT
ATTACTGTGCGAGAGGGTATACTCGGGACTACTGGGCCAGGGAACCTGGTCACC
GTCTCCTCA3' (SEQ ID NO: 146)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYFTSYGISWVRQAPGQGLEWMGWISTYNGN
TNYAQKVQGRVTMTDTSTSTAYMELRSLSDDTAVYYCARGYTRDYWGQGTLTVS
S (SEQ ID NO: 60)

Nucleotide sequence of light chain variable region:

5'CAGCCTGTGCTGACTCAGCCACTTTGCATCAGCCTCCCTGGAGCCTCGGTAC
ACTCACCTGCACCCCTGAGCAGCGGCTACAGTAGTTATGAAGTGGACTGGTATCAGCA
GAGACCAGGGAAGGGCCCCCGGTTGTCATGCGAGTGGACACTGGTGGATTGTGG
GATCCAAGGGGGAAAGGCATCCCTGATCGCTTCTCAGTTTGGGCTCAGGCCTGAATC
GGTATCTGACCATCAAGAACATCCAGGAAGAGGATGAGAGTGACTACCACTGTGGG
GCAGACCATGGCAGTGGACCAACTCGTGGTATTGGCGGAGGGACCAAGCT
GACCGTCCTA3' (SEQ ID NO: 147)

Amino acid sequence of light chain variable region:

QPVLQPLFASASLGSVLTCTLSSGYSSYEVDWYQQRPGKGPRFVMRVDTGGIVGSK
GEGIPDRFSVLGGLNRYLTIKNIQEEDESDYHCGADHSGTNFVVFGGGTKLTVL
(SEQ ID NO: 46)

FIG. 3GG

31A4**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTACAGCAGTGGGCGCAGGACTGTTGAAGCCTCGGAGACCCTGT
CCCTCACCTGCGCTGTCTATGGTGGTCCTCACTGCCTACTACTGGAACTGGATCC
GCCAGCCCCAGGGAAGGGCTGGAGTGGATTGGGAAATCAATCATAGTGGAAAGA
ACCGACTACAACCCGTCCTCAAGAGTCGAGTCACCATACTAGTAGACACCGTCAA
GAAGCAGTCTCCCTGAAGCTGAACTCTGTGACCGCCGGACACGGCTGTATT
CTGTGCGAGAGGGCAGCTCGTCCCTTGACTACTGGGCCAGGGAACCCCTGGTCAC
CGTCTCTTCA3' (**SEQ ID NO: 148**)

Amino acid sequence of heavy chain variable region:

QVQLQQWGAGLLKPSETSLTCAVYGGFSAYYWNIWIRQPPGKGLEWIGEINHSGRTD
YNPSLKSRTVTISVDTSKKQFSLKLNSVTAADTAVYYCARGQLVPFDYWGQGTLTVSS
(**SEQ ID NO: 89**)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCTCAGCGCTGGGACCCCCGGCAGAGGGTCA
CCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGTAAATTGGTATC
AGCAACTCCCAGGAACGGCCCCAAACTCCTCATCTATAGTAATAATCAGCGGCCCT
CAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCA
TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATGGGATGACA
GCCTGAATGGTTGGGTGTTGGCGGAGGGACCAAGCTGACCGTCCTA3' (**SEQ ID
NO: 149**)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVWYQQLPGTAPKLLIYSNNQRPSGVPD
RFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL (**SEQ ID NO:
32**)

FIG. 3HH

25A7**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTTCTGGTACACCTTCCCAGCTATGGTATCAGCTGGGTGC
GACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCGCTTACAATGGT
AACACAAACTATGCAGAGAAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATC
CACGAGCACAGCCTACATGGAGGTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
TTTACTGTGCGAGAGGCTACGTTATGGACGTCTGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' (SEQ ID NO: 150)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGISWVRQAPGQGLEWMGWISAYNGN
TNYAEKLQGRVTMTDTSTSTAYMEVRSLSDDTAVFYCARGYVMDVWGQGTTVTS
S (SEQ ID NO: 58)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAAGCAGTCAGTGA
CAACACCAACCCAGGCAAAGCCCCAAAGTCATGATTATGAGGTCA
CTCAGGGGTTCTACTCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGAC
CATCTCTGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATA
CAGCAGCGITGTATTGGCGGAGGGACAAACTGACCGTCCTA3' (SEQ ID NO:
151)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGRYNSVSWYQHHPGKAPKVMITYEVSNRPSGV
STRFSGSKSGNTASLTISGLQAEDADYYCSSYTSSSVFGGGTKLTVL (SEQ ID NO:
15)

FIG. 3II

21B12**Nucleotide sequence of heavy chain variable region:**

5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGA
AGGTCTCCTGCAAGGCTTCTGGTTACACCTTAACCAGCTATGGTATCAGCTGGTGC
GACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGATGGTCAGTTTTATAATGGT
AACACAAACTATGCACAGAACGCTCCAGGGCAGAGGCACCATGACCACAGACCCATC
CACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGT
ATTACTGTGCGAGAGGGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' (SEQ ID NO: 94)

Amino acid sequence of heavy chain variable region:

QVQLVQSGAEVKPGASVKVSCKASGYLTTSYGISWVRQAPGQGLEWMGWVSYFNG
NTNYAQKLQGRGTMTTDPSTSTAYMELRSLSDDTAVYYCARGYGMDVWGQGTTVT
VSS (SEQ ID NO: 49)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGCTGGGTCTCCTGGACAGTCGATCAC
CATCTCCTGCACTGGAACCAGCAGTGCAGTGGTGGTTATAACTCTGTCTCCTGGTA
CCAACAGCACCCAGGCAAAGCCCCAAACTCATGATTATGAGGTCAGTAATCGGC
CCTCAGGGGTTCTAATCGCTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGA
CCATCTCTGGGCTCCAGGCTGAGGACGGAGGCTGATTATTACTGCAATTATACAA
GCACCAGCATGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA3' (SEQ ID NO:
296)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSWYQQHPGKAPKLMIYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYYCNSYTSTSMVFGGGTKLTVL (SEQ ID NO:
23)

FIG. 3JJ

Constant Domains

Human IgG2:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPPKDTLMisRTPEVTC
VVVDVSHEDPEVQFNWYVGVEVHNAKTKPREEQFNSTFRVSVLTvhQDWLNGKEYKCKVSNKGLP
APIEKTISKKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMULD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPGK (SEQ ID NO: 154)

Human IgG4:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVVT
VPSSSLGTQTYTCNVDHKPSNTKVDRVESKGPPCPSCPAPEFLGGPSVFLFPPPKDTLMisRTPEVTC
CVVVDVSQEDPEVQFNWYVGVEVHNAKTKPREEQFNSTYRVSVLHQLDWLNGKEYKCKVSNKGL
PSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVL
DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGK (SEQ ID NO: 155)

Human lambda:

QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNNKYAASSY
LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 156)

Human kappa:

TVAAPSVFIFPPSDEQLKSGTASVVCLLNFYPREAKVQW/KVDNALQSGNSQESVTEQDSKDSTYSLSS
TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 157)

FIG. 3KK

5H5.1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGGTGGTGCAGTCTGGGCTGAGGTGAAGAAGCCTGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTCACCGGCTACTATATAC
ACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAA
CCCTCACAGTGGTGGCGCAAACATATGCACAGAACAGTTCAAGGGCAGGGTCACC
ATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGAGCAGGCTGA
GATCTGACGACACGGCCGTATTACTGTGCGAGAGGCAACTGGAACTACGA
CTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACCGTCTCCTCA
3' (SEQ ID NO:418)

Amino acid sequence of heavy chain variable region:

QVQVVQSGAEVKPGASVKVSCKASGYTFTGYYIHWRQAPGQGLEWMGWIN
PHSGGANYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGNWNYD
YYGMDVWGQGTTVTVSS (SEQ ID NO:419)

Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
AGAGTCACCATCACTGCCGGCGAGTCAGGACATTAGCAATTATTAAGCCT
GGTATCAGCAGAAACCAGGGAAAGTTCTTAAGCTCTGATCTATGCTGCATC
CACTTGCAATCAGGGTCCCCTCGGTTAGTGGCAGTGGATCTGGGACA
GATTTCACTCTCACCATCAGCAGCCTACAGCCTGAAGATGTTGCAACTATT
CTGTCAAAGGTATCAGATTGCCCATTCACTTCGGCCCTGGGACCAAGGTGG
ATATAAA3' (SEQ ID NO:420)

Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVITCRASQDISNYLAWYQQKPGKVPKLLIYAASTLQ
SGVPSRFSGSGTDFTLTISSLQPEDVATYFCQRYQIAPFTFGPGTKVDIK (SEQ
ID NO:421)

FIG. 3LL

24F7.1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTCAGTAGCTATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAGGGCTGGAGTGGGTGGCAGTTATCTG
GTATGATGGAAGTACTAAATACTATGCAGACTCCGTGAAGGGCCGATCCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTATTACTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACCGTCTCC
TCA3' (SEQ ID NO:422)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQPGRLSLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSTKYYADSVKGRSTISRDNSKNTLYLQMNSLRAEDTAVYYCARSVAGYHY
YYGMDVWGQGTTVTVSS (SEQ ID NO: 423)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCCTGCTGTCTGGCCTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCATTATGCAACCTGGT
ACCAGCAGAAGCCAAGACAGGCCCTGTACTTGTATCTATGGTAAAAACTA
CCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCACCTCAGGAAACACA
GCTTCCTTGACCATCACTGGGCTCAGGCGAAGATGAGGCTGACTATTACT
GTAACTCCCGGGACAGCATTGTAACCATCTGGTGTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:424)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDLSLRGYYATWYQQKPRQAPVLVIYGKNYRP
SGIPDRFSGSTSGNTASLTITGAQAEDAEADYYCNSRDSIGNHLVFGGGTKLTVL
(SEQ ID NO:425)

FIG. 3MM

22B11.1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAGCTATGGCTTGC
ACTGGGTCCGCCAGGCTCCAGGCAGGGCTGGAGTGGGTGGCAGTTATATG
GTTAGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCATCCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACCGTCTCC
TCA3' (SEQ ID NO:426)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGLHWVRQAPGKGLEWVAVIWL
DGSNKYYADSVKGRSTISRDNSKNLTYLQMNSLRAEDTAVYYCARSVAGYHYY
YGMDFVWGQQGTTVTVSS (SEQ ID NO:427)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGGCCTTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGTTATTATGGAAGCTGGT
ACCAGCAGAACGCAAGACAGGCCCTGTACTTGTCTTGGTAAAAACAA
CCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCACCTCAGGAAACACA
GCTTCCITGACCATCACTGGGCTCAGGCGGAAGATGAGGCTGACTATTACT
GTAACTCACGGACATCATTGGTGACCATCTGCTGTTGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:428)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRSYYGSWYQQKPRQAPVLVIFGKNNRP
SGIPDRFSGSTSGNTASLTITGAQAEDeadYYCNSRDIIGDHLLFGGGTKLTVL
(SEQ ID NO:429)

FIG. 3NN

30F1.1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGAGGCCTGGTCCAGTCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGGAACATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATGG
TTTGATGGAAGTAATAAAATACTATGCAGACTCCGTGAAGGGCCGATCCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAG
AGCCGAGGACACGGCTGTATTACTGTGCGAGGTCACTGGCTGGTTACAC
TACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCT
CA3' (SEQ ID NO:430)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQSGRLSCLASGFTFRNYGMHWVRQAPGKGLEWVAVIWF
FDGSNKYYADSVKGRSTISRDNKNTLYLLMNSLRAEDTAVYYCARSVAGYHY
YYGMDVWGQGTTVTVSS (SEQ ID NO:431)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCCTGCTGTGTCCTGGCCTGGGACAGACA
GTCAGGATCACATGCCAGGGAGACAGCCTCAGAAGCTATTATGCAAGCTGGT
ACCAGCAGAAGCCAAGACAGGCCCTGTACTTGTATCTATGGTAAAACAA
CCGGCCCTCAGGGATCCCAGACCGAATCTCTGGCTCACCTCAGGAAACACA
GCTTCCTTGACCATCACTGGGCTCAGGCGGAAGATGAGGCTGACTATTACT
GTAAATCCGGGACATCATTGGTGACCATCTGGTGTTCGGCGGAGGGACCAA
ACTGACCGTCCTA3' (SEQ ID NO:432)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDLSRSYYASWYQQKPRQAPVLVIYGKNNRP
SGIPDRISGSTSGNTASLTITGAQAEDEADEYYCKSRDIIGDHLVFGGGTKLTVL
(SEQ ID NO:433)

FIG. 300

24B9.1**Nucleotide sequence of heavy chain variable region:**

5' CAGGTGCAGCTGGTGGAGTCTGGGGAGGCCTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAGCTATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATG
GTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCA
ATCTCCAGAGACAATTCCAAGAACACCGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTATTACTGTGTGAGAGATGGGGACTGGACTG
GGGCCAGGGACCCTGGTCACCGTCTCCTCA3' (SEQ ID NO:434)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRDRGLDW
GQGTLVTVSS (SEQ ID NO:435)

Nucleotide sequence of light chain variable region:

5' TCTTCTGAGCTGACTCAGGACCCTGCTGTGTGGCCTTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCTATTATGCAAGCTGGT
ACCAGCAGAACGCAAGACAGGCCCTGTACTTGTATCTATGGTAAAAACAA
CCGGCCCTCAGGGATCCAGCCGATTCTCTGGCTCCACCTCAGGAAACACA
GCTTCCTTGACCATCACTGGGCTCAGCGGAAGATGAGGCTGACTATTACT
GTAAGTCCCAGGACAGCAGTGGTGACCATCTGGTGTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:436)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRYYASWYQQKPRQAPVLVIYGKNRPS
SGIPDRFSGSTSGNTASLTITGAQAEDAEADYYCKSRDSSGDHLVFGGGTKLTVL
(SEQ ID NO:437)

FIG. 3PP

24B9.2**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAACATGGCATGC
ACTGGGTCCGCCAGGCTCAGGCAAGGGCTGGAGTGGGTGGCAGTTATTG
GTATGATGGAAGTAGTAAATACTATGCAGACTCCGTGAAGGGCCGATCCACC
ATCTCCAGAGACAATTCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACCGTCTCC
TCA3' (SEQ ID NO:438)

Amino acid sequence of heavy chain variable region:

QVQVESGGGVVQPGSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIW
YDGSSKYYADSVKGRSTISRDNSKNTVYLQMNSLRAEDTAVYYCARSVAGYHY
YYGMDVWGQGTTVTVSS (SEQ ID NO:439)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTCTGTGGCCTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCTATTATGCAAGCTGGT
ACCAGCAGAACCAAGACAGGCCCTGTACTTGTCTATGGTAAAAACAA
CCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCACCTCAGGAAACACA
GCTTCCTGACCATCACTGGGCTCAGGCGGAAGATGAGGCTGACTATTACT
GTAAGTCCCGGGACAGCAGTGGTACCATCTGGTGTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:440)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDLSRGYYASWYQQKPRQAPVLVIYGKNRPS
SGIPDRFSGSTSGNTASLTITGAQAEDAEADYYCKSRDSSGDHLVFGGGTKLTVL
(SEQ ID NO:441)

FIG. 3QQ

20A5.1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGGTGGTCCAGCCTGGGAGGTC
CCTGAGTCTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATG
GTATGATGGAAGTTATAAGACTATGCAGACTCCGTGAAGGGCCGATCCACC
ATCTCCAGAGACAACCTCCAAGAACACGCTGTATCTGCAAATGAACACGCTGA
GAGCCGAGGACACGGCTGTATTATTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGGCAAGGGACACGGTCACCGTCTCC
TCA3' (SEQ ID NO:442)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVVQPGRSLSLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWy
DGSYKDyADSVKGRSTISRDNSKNLTYLQMNSLRAEDTAVYYCARSVAGYHYY
YGMDVWGQGTTVTVSS (SEQ ID NO:443)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCCTGCTGTGTCTGGCCTTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAACCTATTATGCAAGCTGGT
ACCAGCAGAACCAAGACAGGCCCTATTCTTGTCATCTATGGTAAAAACAA
CCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCACCTCAGGAATCACA
GCTTCCTTGACCATCACTGGGCTCAGGCGGAAGATGAGGCTGACTATTACT
GTAAATCCCGGGACATCATTGGTAACCATCTGCTGTTGGCGGAGGGACTAA
GCTGACCGTCCTA3' (SEQ ID NO:444)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPRQAPILVYGNRPS
GIPDRFSGSTSGITASLTITGAQAEDAYYCKSRDIIGNHLLFGGGTKLTVL (SEQ
ID NO:445)

FIG. 3RR

20A5.2**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGCGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCCAGGGCTGGAGTGGGTGGCAGTCATATGG
TATGATGGAAGTAACAAATACTATGCAGCCTCCGTGAAGGGCCGATTACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGTCTGAG
AGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGGTGGTCCGGGAGT
CATCGCTACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCA
CCGTCTCCTCA3' (SEQ ID NO:446)

Amino acid sequence of heavy chain variable region:

QVQLVASGGGVVQPGRSLRLSCAASGFTLSSYGMHWVRQAPGQGLEWVAVIW
YDGSNKYYAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGGSGSH
YYYYYGMDVWGQGTVTVSS (SEQ ID NO:447)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCCTGCTGTGTCTGGCCTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAACCTATTATGCAAGCTGGT
ACCAGCAGAACGCAAGACAGGCCCTATTCTTGTCATCTATGGTAAAAACAA
CCGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCACCTCAGGAATCACA
GCTTCITGACCATCACTGGGCTCAGGCGGAAGATGAGGCTGACTATTACT
GTAAATCCCAGGACATCATTGGTAACCATCTGCTGTTGGCGGAGGGACTAA
GCTGACCGTCTCA3' (SEQ ID NO:448)

Amino acid sequence of light chain variable region:

SSELTDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPRQAPILVYKNNRPS
GIPDRFSGSTSGITASLTITGAQAEDAYYCKSRDIIGNHLLFGGGTKLTWL (SEQ
ID NO:449)

FIG. 3S

20E5.1 – version1 (v1)**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAAGTGGTGGAGTCTGGGGAGGCAGTCAGCCTGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAACATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATG
GTATGATGGAGGTAATAAACTATGCAGACTCCGTGAAGGGCCGATCCATC
ATCTCCAGAGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTTATTATTGTGCGAGGTCAGTGGCTGGTACCA
TTATTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACCGTCGCC
TCA3' (SEQ ID NO:450)

Amino acid sequence of heavy chain variable region:

QVQVVESGGVVQPGRSRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIW
YDGGNKYYADSVKGRSIISRDNSKSTLYLQMNSLRAEDTAVYYCARSKVAGYHY
YYGMDVWGQGTTTVVAS (SEQ ID NO:451)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCGTGTCTGGGTCTCCTGGACAGTCGA
TCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTTATAACTCTGTC
TCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACATCATGATTTATGAGG
TCAGTAATCGGCCCTCAGGGATTCTAATCGCTTCTCTGGCTCCAAGTCTGGC
AACACGGCCTCCCTGACCATCTCTGGCTCCAGGCTGAGGACGAGGCTGATT
ATTCTGCAGCTCATATACAAGCACAGCATGGTCTCGGCAGGGACCAA
GCTGGCCGTCTA3' (SEQ ID NO:452)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIYEVSN
RPSGISNRFSGSKSGNTASLTISGLQAEDAEADYFCSSYTSTSMVFGGGTLAVL
(SEQ ID NO:453)

FIG. 3TT

20E5.1 – version2 (v2)**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAACATGGCATGC
ACTGGGTCCGCCAGGCTCAGGCAAGGGCTGGAGTGGGTGGCAGTTATATG
GTATGATGGAGGTAATAAAACTATGCAGACTCCGTGAAGGGCCGATCCATC
ATCTCCAGAGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTTATTATTGTGCGAGGTCACTGGCTGGTACCA
TTATTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACCGTCGCC
TCA3' (SEQ ID NO:454)

Amino acid sequence of heavy chain variable region:

QVQVESGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIW
YDGGNKYYADSVKGRSIISRDNSKSTLYLQMNSLRAEDTAVYYCARSVAGYHY
YYGMDVWGQGTTVTVAS (SEQ ID NO:455)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTGGGACAGACA
GTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCTATTATGCAAGCTGGT
ACCAGCAGAACGCAAGACAGGCCCTGTACTTGTATCTATGGTAAAAACAA
CCGGCCCTCAGGGATCCAGACCGATTCTCTGGCTCCACGTCAAGGAAACACA
GCTTCCTTGACCATCACTGGGCTCAGGCAGGAAGATGAGGCTGACTATTACT
GTAACTCCCAGGACAACATTGGTGACCATCTGGTHTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:456)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALQTVRITCQGDSLRYYASWYQQKPRQAPVLVIYGKNRPS
SGIPDRFSGSTSGNTASLTITGAQAEDAEADYYCNSRDNIGDHLVFGGGTKLTVL
(SEQ ID NO:457)

FIG. 3UU

8A3.1**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCC
CTGAGACTCTCCTGTGCAGCCTCCGGATTCACTTAGTAGCTATTGGATGAG
CTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGTGCCAGCATAAA
ACAAGATGGAAGTGAGAAAATACTATGTGGACTCTGTGAAGGGCGATTCAAC
ATCTCCAGAGACAACGCCAGGAACACTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCTTGATTAATGGT
GTATGATATAGACTACTACGTATGGACGTCTGGGCCAAGGGACC
ACGGTCACCGTCTCCTCA3' (SEQ ID NO:458)

Amino acid sequence of heavy chain variable region:

EVQLVESGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVASIKQ
DGSEKYYVDSVKGRFTISRDNRNARNSLYLMQNSLRAEDTAVYYCARDLVLMLVD
IDYYYYGMDVGQGTTVTVSS (SEQ ID NO:459)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGC
CGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATAC
AACTATTGGATTGGTACCTGCAGAACGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCACTGGCAGT
GGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
TTGGGGTTATTACTGCATGCAAGCTACAAACTCCGCTCACITTCGGCGGA
GGGACCAAGGTAGAGATCAAA3' (SEQ ID NO:460)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQLIYLG
SNRASGVVPDRFSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKEI
K (SEQ ID NO:461)

FIG. 3VV

11F1.1**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCCAGCCTGGGGGTCC
CTGAGACTCTCCTGTGCAGCCTCCGGATTCACCTTAGTAACATTGGATGAG
CTGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGGTGGCCAGCATAAA
ACAAGATGGAAGTGAGAAAATACTATGTGGACTCTGTGAAGGGCCGATCGCC
ATCTCCAGAGACAACGCCAAGAACACTCACTGTTCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCTGTACTAATGGT
GTATGATATAGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACC
ACGGTCACCGTCTCCTCA3' (SEQ ID NO:462)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMSVRQAPGKGLEWVASIKQ
DGSEKYVYDSVKRFAISRDNAKNSLFLQMNSLRAEDTAVYYCARDLVLVYD
IDYYYYGMDVWGQGTTVTVSS (SEQ ID NO:463)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCTGTCACCCCTGGAGAGC
CGGCCTCCATCTCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGGTAC
AACTATTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTGGGTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTAGTGGCAGT
GGATCAGGCACACATCTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
TTGGAGTTTATTACTGCATGCAAACACTCTACAAACTCCGCTCACTTCGGCGGA
GGGACCAAGGTGGAGATCAAA3' (SEQ ID NO:464)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLIYLG
SNRASGVPDFSGSGTHLTLKISRVEAEDVGVYYCMQLTQLTFGGGTKEI
K (SEQ ID NO:465)

FIG. 3WW

12H11.1**Nucleotide sequence of heavy chain variable region:**

5'CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGCCCAGCCTGGGAGGTC
CCTGAGACTCTCTGTGCAGCGTCTGGATTACCTCAGTAGCTATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCAGTTATATA
CTATGATGGAATTAATAAACACTATGCAGACTCCGTGAAGGGCCGATTCA
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGGACTGGACTG
GGGCCAGGGAACCTGGTCACCGTCTCCTCA3' (SEQ ID NO:466)

Amino acid sequence of heavy chain variable region:

QVQLVESGGVAQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIYY
DGINKHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGLDWGQ
GTLTVSS (SEQ ID NO:467)

Nucleotide sequence of light chain variable region:

5'GACATCGTATGACCCAGTCTCCAGACTCCCTGGCTGTCTGGCGAG
AGGGCCACCCTCAACTGCAAGTCCAGCCAGAGTGTTTATACAGCTCCAACA
GTAAGAACTACTTAGTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCT
GCTCATTTACTGGGCCTCTACCCGGGAATCCGGGTCCCTGACCGATTAGTG
GCAGCGGGTCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGGCTGA
AGATGTGGCAGTTTATTACTGTCAACAATATTATAGTACTCCGTGGACGTTCG
GCCAAGGGACCAAGGTGGAAATCAAA3' (SEQ ID NO:468)

Amino acid sequence of light chain variable region:

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLVWYQQKPGQPPKLLIY
WASTRESGVVPDRFSGSGSGTDFTLTSSLQAEDVAVYYCQQYYSTPWTFGQGTK
VEIK (SEQ ID NO:469)

FIG. 3XX

11H4.1**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGACTCACCTTAGTAACTTGGATGAG
CTGGTCCGCCAGGCTCAGGGAAAGGGCTGGAGTGGTGGCCAACATAAA
GCAAGATGAAATGATAAATACATGTGGACTCTGTGAAGGGCCGATTACC
ATCTCCAGAGACAACGCCAAGAATTCACTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGTCAAACTGGGGATT
TGCTTTGATATCTGGGCCAAGGGACAATGGTACCGTCTTCA3' (SEQ ID
NO:470)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGVQPGGSLRLSCAASGLTFSNFWMSWVRQAPGKGLEWVANIKQ
DGNDKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARESNWGFAF
DIWGQQGTMVTVSS (SEQ ID NO:471)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTGGACCCCCGGCAGAGG
GTCACCATCTCTTGTGGAAGCAGCTCAACATCGGAAGTAAAATGTAA
ACTGGTACCGAGCAGTCCCAGGAACGGCCCCAAACTCCTCATCTATAGTAA
TAATCGGCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCA
CCTCAGCCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGATTAT
TACTGTGCAGCATGGGATGACAGCCTGAATTGGGTGTTGGCGCAGGGACCA
AGCTGACCGTCCTA3' (SEQ ID NO:472)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQFPGTAPKLLIYSNNRRP
SGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWVFGAGTKLTVL
(SEQ ID NO:473)

FIG. 3YY

11H8.1**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGAGGTTGGTCCAGCCTGGGGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGACTCACCTTAGTAACCTTGATGAG
CTGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGTGGCCAACATAAA
GCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTGAAGGGCCGATTCA
ATCTCCAGAGACAACGCCAAGAATTCACTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGTCAAACGGGATT
TGCTTTGATATCTGGGCCAAGGGACAATGGTACCGTCTTC3' (SEQ ID
NO:474)

Amino acid sequence of heavy chain variable region:

EVQLVESGGLVQPGGSLRLSCAASGLTFSNFWMSWVRQAPGKGLEWVANIKQ
DGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARESNWGFAF
DIWGQGTMVTVSS (SEQ ID NO:475)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGACCCCCGGCAGAGG
GTCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAAAATGTAA
ACTGGTACCAAGCAGTTCCCAGGAACGGCCCCAAACTCCTCATCTATAGTAA
TAATCGCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCA
CCTCAGCCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGATTAT
TACTGTGCAACATGGGATGACAGACTGAATTGGGTGTTCGGCGCAGGGACCA
AGCTGACCGTCCTA3' (SEQ ID NO:476)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQFPGTAPKLLIYSNNRRP
SGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDRLNWVFGAGTKLTVL
(SEQ ID NO:477)

FIG. 3ZZ

11G1.5**Nucleotide sequence of heavy chain variable region:**

5'CAGGTACACCTGAAGGAGTCTGGTCCTGTGCTGGTCAAACCCACAGAGACC
CTCACGCTGACCTGCACCGTCTGGGTTCTCACTCAGCAATGTTAGAATGGG
TGTGAGCTGGATCCGTCAAGCCCCAGGGAAAGGCCCTGGAGTGGCTTGACAC
ATTTTTCAATGACGAAAATTCTACAGAACATCTCTGAAGAGCAGGCTCA
CCATCTCCAAGGACACCTCCAAAAGCCAGGTGGCTTACCATGACCAACAT
GGACCCCTGTGGACACAGCCACATATTACTGTGCACGGATAGTGGGAGCTACA
ACGGATGATGCTTTGATATCTGGGGCAAGGGACAATGGTCACCGTCTCTTC
A3' (SEQ ID NO:478)

Amino acid sequence of heavy chain variable region:

QVTLKESGPVLVKPTETLTLTCTVSGFSLNSVRMGVSWIRQPPGKALEWLAHIFS
NDENSYRTSLKSRLTISKDTSKSQVVLTMNMDPVDATYYCARIVGATTDDAF
DIWGQGTMVTVSS (SEQ ID NO:479)

Nucleotide sequence of light chain variable region:

5'TCCTATGTGCTGACTCAGCCACCCCTCGGTGTCAGTGGCCCCAGGACAGACG
GCCAGGATTACCTGTGGGGAAACAAACATTGGAAGTAAAAGTGTGCACTGGT
ACCAAGCAGAACGCCAGGCCAGGCCCTGTGCTGGTCGTCTATGATGATAAGCGA
CCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACCTCTGGAACACG
GCCACCCCTGACCATCAGCAGGGTCGAAGCCGGGATGAGGCCGACTTTACT
GTCAGGTGTGGGATAGTAGTAGTGATCCTGTGGTATTGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:480)

Amino acid sequence of light chain variable region:

SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRP
SGIPERFSGNSGNATLTISRVEAGDEADFYCQVWDSSDPVVFGGKLTQL
(SEQ ID NO:481)

FIG. 3AAA

8A1.2**Nucleotide sequence of heavy chain variable region:**

5'GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTAGTAACTATTGGATGAC
CTGGTCCGCCAGGCTCAGGGAAAGGGCTGGAGTGGTGGCCAGCATAAA
GCAAGATGGAAGTGAGAGATACTATGTGGAUTCTGTGAAGGGCCGATTCA
ATCTCCCAGACACCGCCAAGAACACTCTGTATCTCAAATGAACAGCCTGC
GAGCCGAGGACACGGCTGTATTACTGTGCGAGACCTCTGTACTAATGGT
GTATGCTCTACACTACTACGGTATGGACGTCTGGGCCACGGGACC
ACGGTCACCGTCTCCTCA3' (SEQ ID NO:482)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMTWVRQAPGKGLEWVASIKQ
DGSERYYVDSDKRFTISRDTAKNSLYLQMNSLRAEDTAVYYCARPLVLMVYA
LHYYYYGMDVWGHGTTVTVSS (SEQ ID NO:483)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGC
CGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATAC
AACTATTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTGGGTCTAATCGGGCCTCCGGGTCCCTGACAGGTTCACTGGCAGT
GGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
TTGGGGTTTATTACTGCATGCAAGCTACAAACTCCGCTCACTTCGGCGGA
GGGACCAAGGTGGAGATCAA3' (SEQ ID NO:484)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLIYLG
SNRASGPDRFSGSGTDFTLKISRVEADVGVYYCMQALQTPLTFGGGTKEI
K (SEQ ID NO:485)

FIG. 3BBB

FIG. 3CCC

Heavy variable	SEQ ID NO:	Germline	FR1	CDR1	FR2
	493	VH1 1-02	QVQLVQSGAEVKPPGASVKVSCKAS	GYTFTGYMH	WVRQAPGQGLEWMG
5H5.1G	419	VH1 1-02	JH6 ---V---	-----I-	-----
		Germline	FR1	CDR1	FR2
	494	VH3 3-33	QVQLVESGGGVQPPGRSLRLSCAAS	GFTFSYGMH	WVRQAPGKGLEWVA
24B9.1G	435	VH3 3-33	JH4 -----	-----	-----
		Germline	FR1	CDR1	FR2
	495	VH3 3-33	QVQLVESGGGVQPPGRSLRLSCAAS	GFTFSYGMH	WVRQAPGKGLEWVA
24F7.1G	423	VH3 3-33	JH6 -----	-----	-----
22B11.1G	427	VH3 3-33	JH6 -----	-----I-	-----
20A5.1G	443	VH3 3-33	JH6 -----S-----	-----	-----
20A5.2G	447	VH3 3-33	JH6 -----A-----	-----I-----	-----Q-----
30F1.1G	431	VH3 3-33	JH6 -----S-----	-----RN-----	-----
20E5.1GV1	451	VH3 3-33	JH6 -----V-----	-----N-----	-----
24B9.2G	439	VH3 3-33	JH6 -----V-----G-----	-----N-----	-----

FIG. 3DDD

Heavy variable	SEQ ID NO:	CDR2	FR3	CDR3	FR4
	493	WINPNSSGGTNYAQKFQG	RVTMTRDTISIATAYMELSRRLRSDDTAVYYCAR		
5H5.1G	419	----H---A----	-----	GNWNYDYYGMDV	WGQGTIVTVSS
		CDR2	FR3	CDR3	FR4
	494	VIWYDGSSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR		
24B9.1G	435	-----	-----V-	DRGLDWGQGTIVTVSS	
		CDR2	FR3	CDR3	FR4
	495	VIWYDGSSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR		
24F7.1G	423	-----T-----	-S-----	SVAGYHYYYGMDV	WGQGTIVTVSS
22B11.1G	427	---L-----	-S-----	SVAGYHYYYGMDV	WGQGTIVTVSS
20A5.1G	443	-----Y-D-----	-S-----	SVAGYHYYYGMDV	WGQGTIVTVSS
20A5.2G	447	-----A-----	-----	GGGSGSNSHRYYYYGMDV	WGQGTIVTVSS
30F1.1G	431	----F-----	-S-----L-----	SVAGYHYYYGMDV	WGQGTIVTVSS
20E5.1GV1	451	-----G-----	-SI-----S-----	SVAGYHYYYGMDV	WGQGTIVTVAS
24B9.2G	439	-----S-----	-S-----V-----	SVAGYHYYYGMDV	WGQGTIVTVSS

Kappa variable	SEQ ID NO:	Germline	FR1	CDR1	FR2
496	VK1 A20	DIQMTQSPSSLSASVGDRVTITC	RASQGINSYLA	WYQQKPGKVPKLLIY	
5H5.1K	421	VK1 A20	JK3	-----D-----	-----
Lambda variable					
		Germline	FR1	CDR1	FR2
497	VL2 2a2	QSALTQPASVSGSPQSIITISC	TGTSSDVGGYNYVS	WYQQHPGKAPKLMIV	
20E5.1L v1	453	VL2 2a2	JL2	-----S-----	-----P-----
		Germline	FR1	CDR1	FR2
498	VL3 3I	SSELTQDPAVSVALGQTIVRITC	QGDSLRSYAS	WYQQKPGQAPVLYIY	
30F1.1L	433	VL3 3I	JL2	-----	-----R-----
22B11.1L	429	VL3 3I	JL2	-----	-----R-----F
24B9.1L	437	VL3 3I	JL2	-----G-----	-----R-----
24B9.2L	441	VL3 3I	JL2	-----G-----	-----R-----
20E5.1L v2	457	VL3 3I	JL2	-----G-----	-----R-----
24F7.1L	425	VL3 3I	JL2	-----G-----T	-----R-----
20A5.1L	445	VL3 3I	JL2	-----T-----	-----R-----I-----
20A5.2L	449	VL3 3I	JL2	-----T-----	-----R-----I-----

FIG. 3EEE

Kappa Variable	SEQ ID NO:				
		CDR2	FR3	CDR3	FR4
5H5.1K	496 421	AASTLQS -----	GVPSRFSGSGSGTDFLTISLQPEDVATYYC -----F-	QRYQIAPEF FGPGTKVDIK	
Lambda_variable					
20E5.1L v1	497 453	EVSNRPS -----	GVSNRFSGSKSGNTASLTISGLOAEDEADYYC -----F-	SSYTSTSVM FGGGTKLAVL	
		CDR2	FR3	CDR3	FR4
30F1.1L	498 433	GKNNRPS -----	GIPDRFSGSSSGNTASLTISGLOAEDEADYYC -----	KSRDIIGDHIV FGGGTKLTVL	
22B11.1L	429	-----	-----	NSRDIIGDHLL FGGGTKLTVL	
24B9.1L	437	-----	-----	KSRSDDGDHLV FGGGTKLTVL	
24B9.2L	441	-----	-----	KSRDSSGDHLV FGGGTKLTVL	
20E5.1L v2	457	-----	-----	NSRDNIIGDHIV FGGGTKLTVL	
24F7.1L	425	---Y---	-----	NSRDSIGNHIV FGGGTKLTVL	
20A5.1L	445	-----	-----	KSRDIIGNHLL FGGGTKLTVL	
20A5.2L	449	-----	-----	KSRDIIGNHLL FGGGTKLTVL	

FIG. 3FFF

	SEQ ID NO:					
		Germline	Germline	FR1	CDR1	FR2
486	VH2 226			QVTIKESGPVIVKPTETLTCTVS	GFSLSNARMGVSVIROPPGKALEWLA	
11G1.5	479	VH2 226	JH3	-----	-----V-----	-----
		Germline	Germline	FR1	CDR1	FR2
487	VH3 307			EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYWNMS	WVRQAPGKGLEWVA
11H8.1	475	VH3 307	JH3	-----	-L-----NF-----	-----
11H4.1	471	VH3 307	JH3	-----	-L-----NF-----	-----
8A3.1	459	VH3 307	JH6	-----	-----	-----
11F1.1	463	VH3 307	JH6	-----	-----N-----	-----
8A1.2	483	VH3 307	JH6	-----	-----N-----T	-----
		Germline	Germline	FR1	CDR1	FR2
488	VH3 3-33			QVQLVESGGGVQPGRSILRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
12H11.1	467	VH3 3-33	JH4	-----A-----	-----	-----

FIG. 3GGG

SEQ ID NO:					
		CDR2	FR3	CDR3	FR4
486	HIFSNDEKSYSTSIKS	RLTISKDTSKSQVVLMTMDPVDTATYCAR			WGQGTMVTVSS
11G1.5 479	-----N---R-----	-----	-----	VGATTDDAFA DI	WGQGTMVTVSS
		CDR2	FR3	CDR3	FR4
487	NIKQDGSEKYYVDSVKG	RFTISRDNAKNSLYLQMNSLRAEDTA VYYCAR			
11H8.1 475	-----	-----	-----	ESNWGF AFDI	WGQGTMVTVSS
11H4.1 471	-ND-----	-	-	ESNWGF AFDI	WGQGTMVTVSS
8A3.1 459	S-----	-R-----	-	DLVLMVYDIDYYY GMDV	WGQGTTTVTVSS
11F1.1 463	S-----	-A-----	F-----	DLVLMVYDIDYYY GMDV	WGQGTTTVTVSS
8A1.2 483	S-----	-R-----	-T-----	PLVLMVYALHYYY GMDV	WGHTGTTTVTVSS
		CDR2	FR3	CDR3	FR4
488	VIWYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTA VYYCAR			
12H11.1 467	--Y---I---H-----	-----	-----	DRGLD	WGQGTLVTVSS

FIG. 3HHH

SEQ ID NO:	Germline	Germline	FR1	CDR1	FR2
489	VK2 A19		DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGNYNLD	WYLQKPGOSPQLIY
8A1.2	485	VK2 A19	JK4	-	-
8A3.1	461	VK2 A19	JK4	-	-
11F1.1	465	VK2 A19	JK4	-	-
Germline	Germline	FR1	CDR1	FR2	
490	VK4 B3		DIVMTQSPDSLAVSIGERATINC	KSSQSVLYYSSNNKNYIA	WYQQKPGQQPKLILY
12H11.1	469	VK4 B3	JK1	-	-
				\$-----V	-
Germline	Germline	FR1	CDR1	FR2	
491	VL1 1c		QSVLTOPPSASSGTPGQRVTISC	SGSSSNIGSNTVN	WYQOLPGTAKPLILY
11H4.1	473	VL1 1c	JL3b	-	-
11H8.1	477	VL1 1c	JL3b	-	-
				K-----	F-----
Germline	Germline	FR1	CDR1	FR2	
492	VL3 3h		SYVLTQPPSVSVAPGKTARITC	GGNNIGSKSVH	WYQQKPGQAPVLVY
11G1.5	481	VL3 3h	JL2	-	-
			Q-----	V-----	-

FIG. 3III

	SEQ ID NO:					
		CDR2	FR3	CDR3	FR4	
	489	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDGVYYC			
8A1.2	485	-----	-----	MQALQTPILT	FGGGTKVEIK	
8A3.1	461	-----	-----	MQALQTPILT	FGGGTKVEIK	
11F1.1	465	-----	-----HL-----	MQLQTPILT	FGGGTKVEIK	
	CDR2	FR3	CDR3	FR4		
490	WASTRES	GVPDRFSGSGSGTDFTLTISLQAEDVAVYCYC				
12H11.1	469	-----	-----	QQYYSTPWT	FGQGTTKVEIK	
	CDR2	FR3	CDR3	FR4		
491	SNNQRPS	GVPDRFSGSKSGTSASLAISSGLQSEDEADYYC				
11H4.1	473	---R---	-----	AAWDDSLNWV	FGAGTKLTVL	
11H8.1	477	---R---	-----	ATWDDRLNWV	FGAGTKLTVL	
	CDR2	FR3	CDR3	FR4		
492	YDSDRPS	GIPERFSGNSGNATLTISRVEAGDEADYYC				
11G1.5	481	D-----	F---	QWWDSSSDEVW	FGGGTKLTVL	

FIG. 3JJ

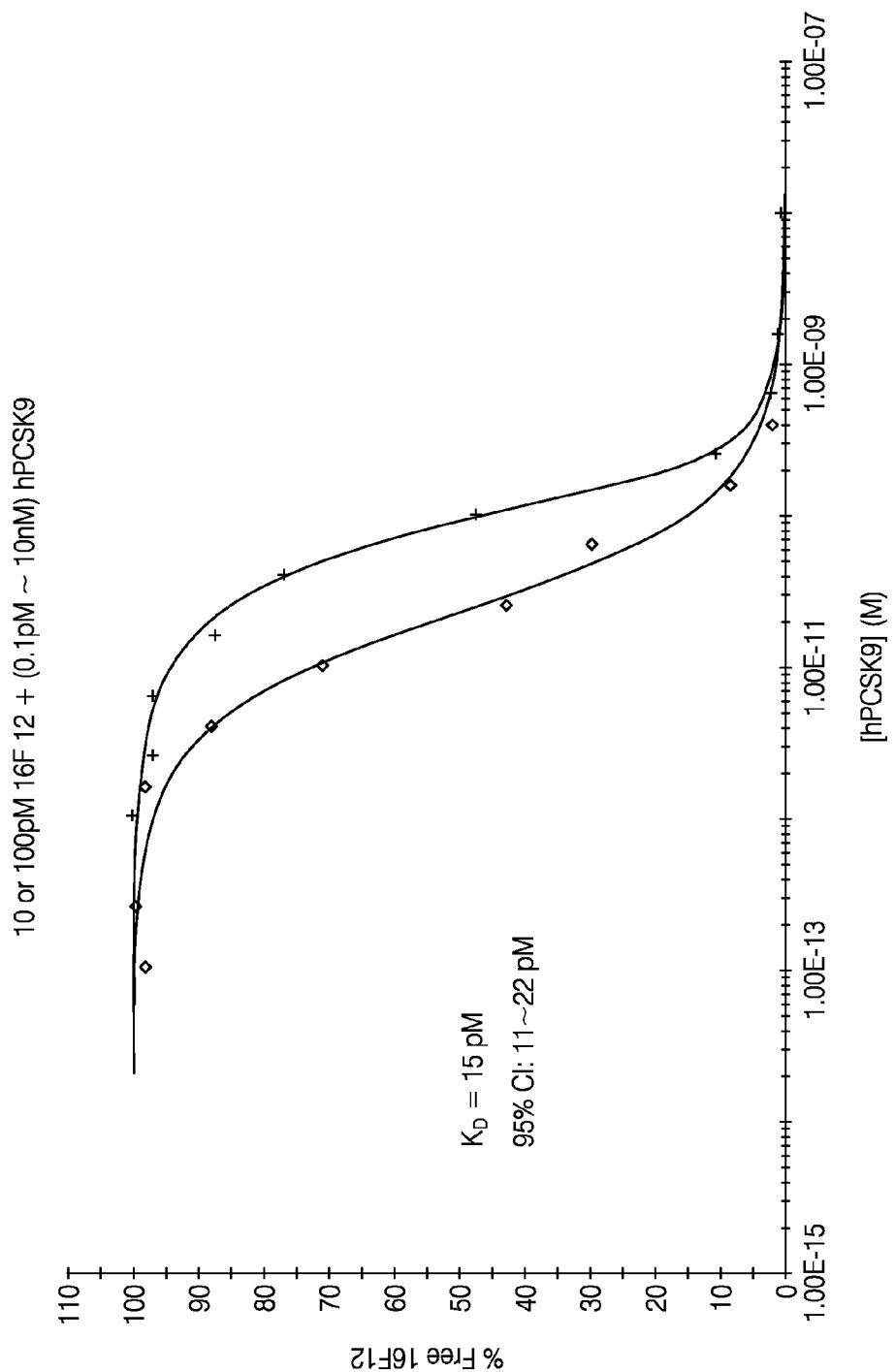


FIG. 4A

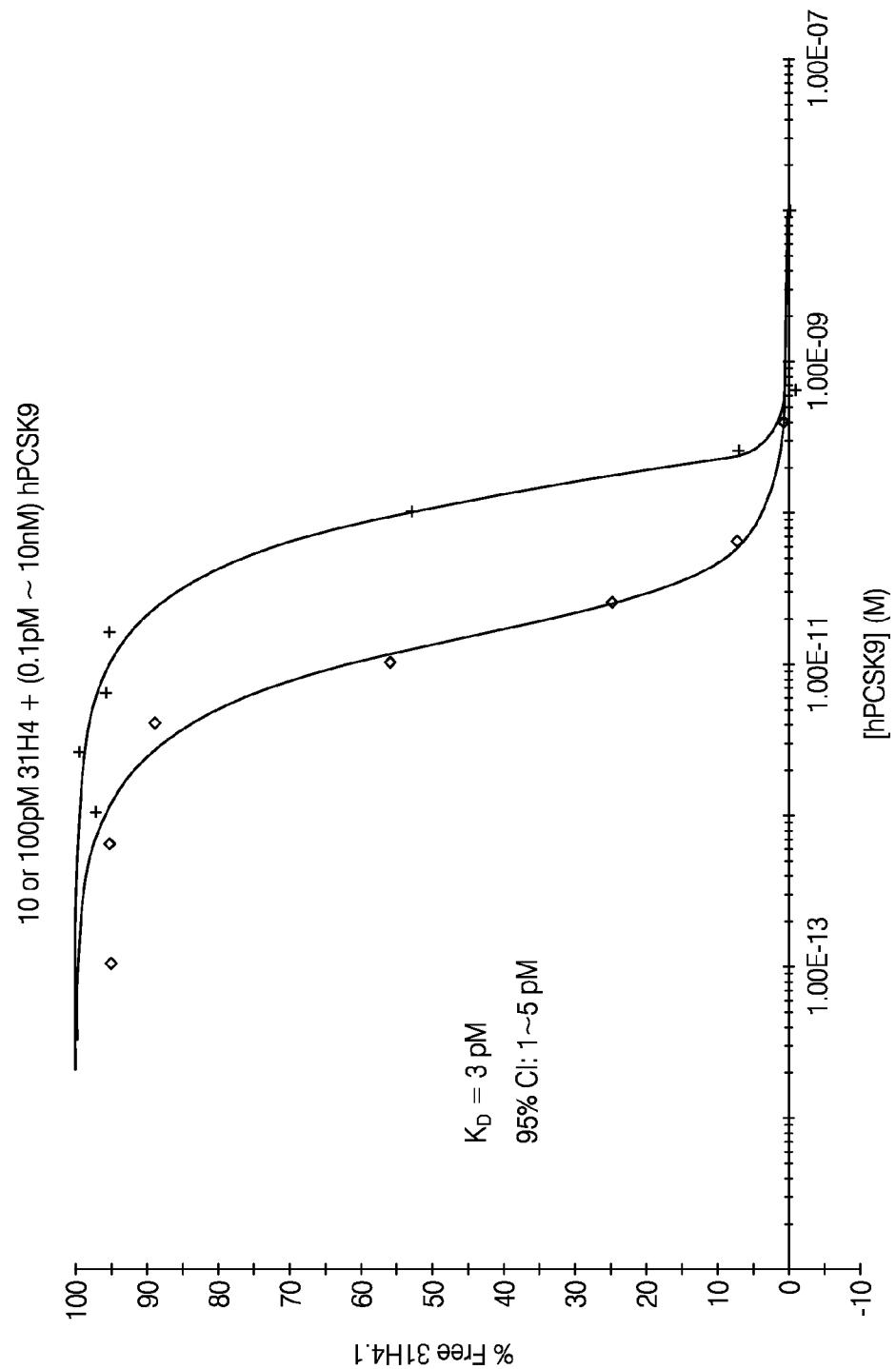


FIG. 4B

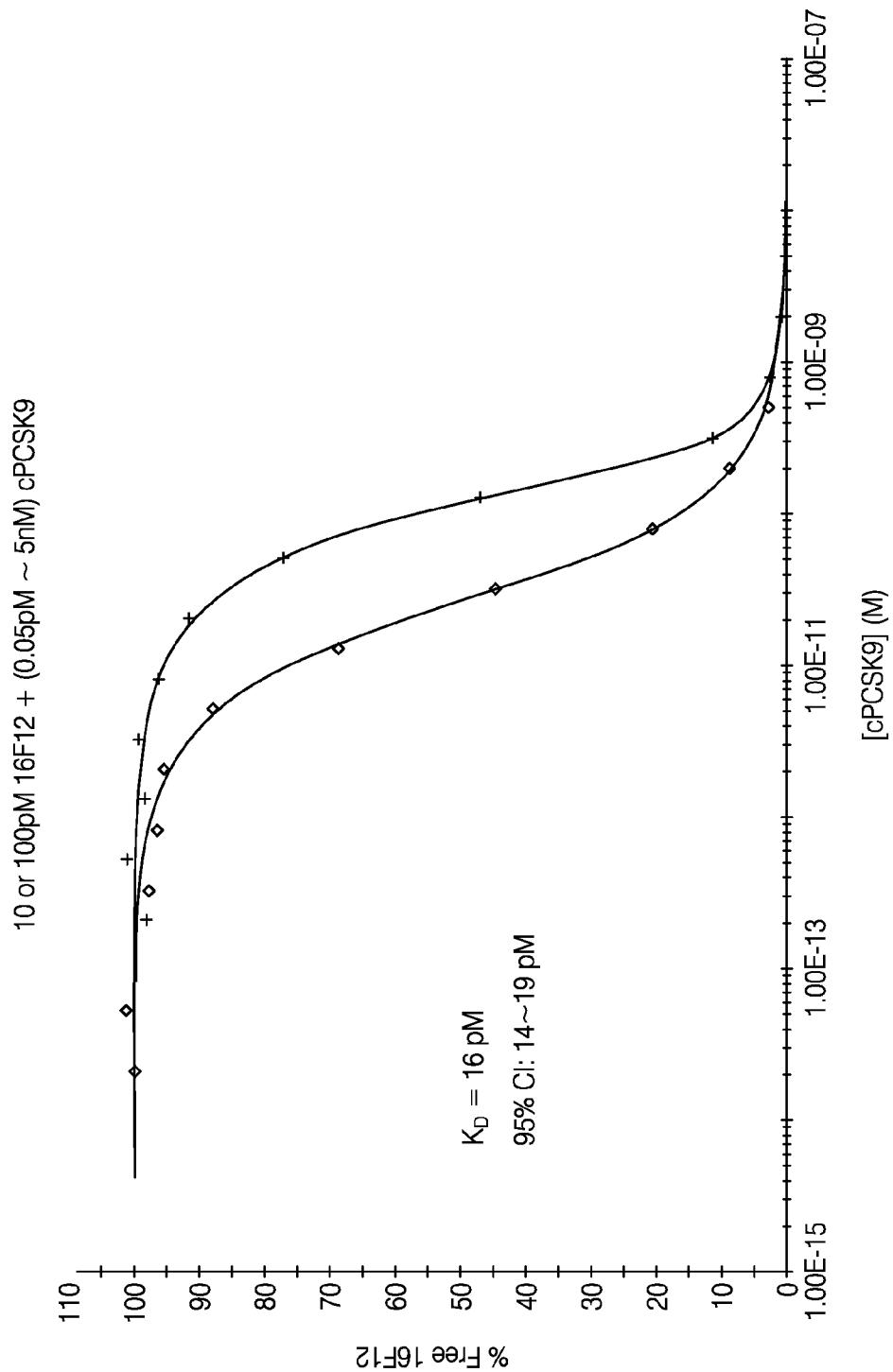


FIG. 4C

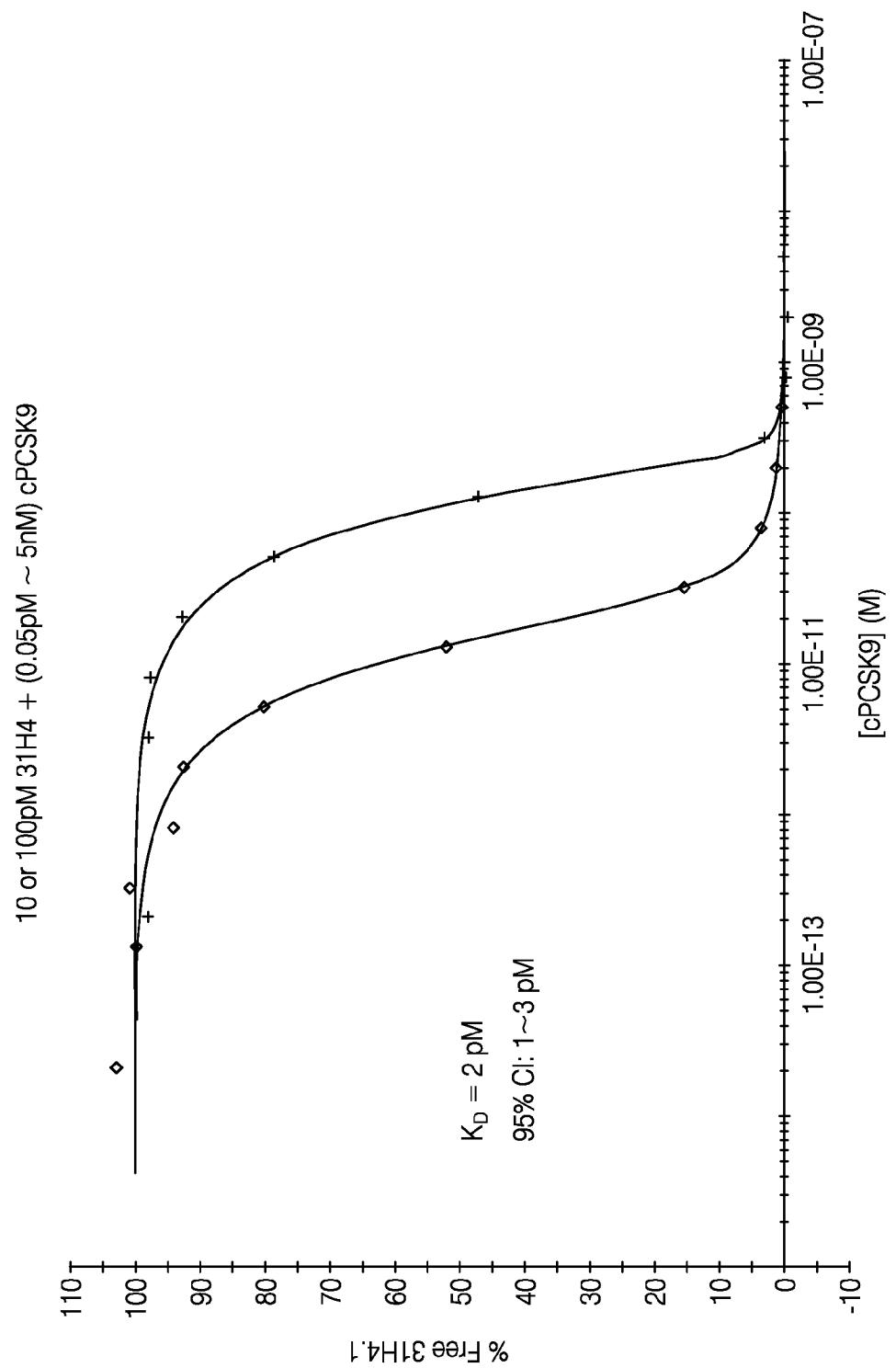


FIG. 4D

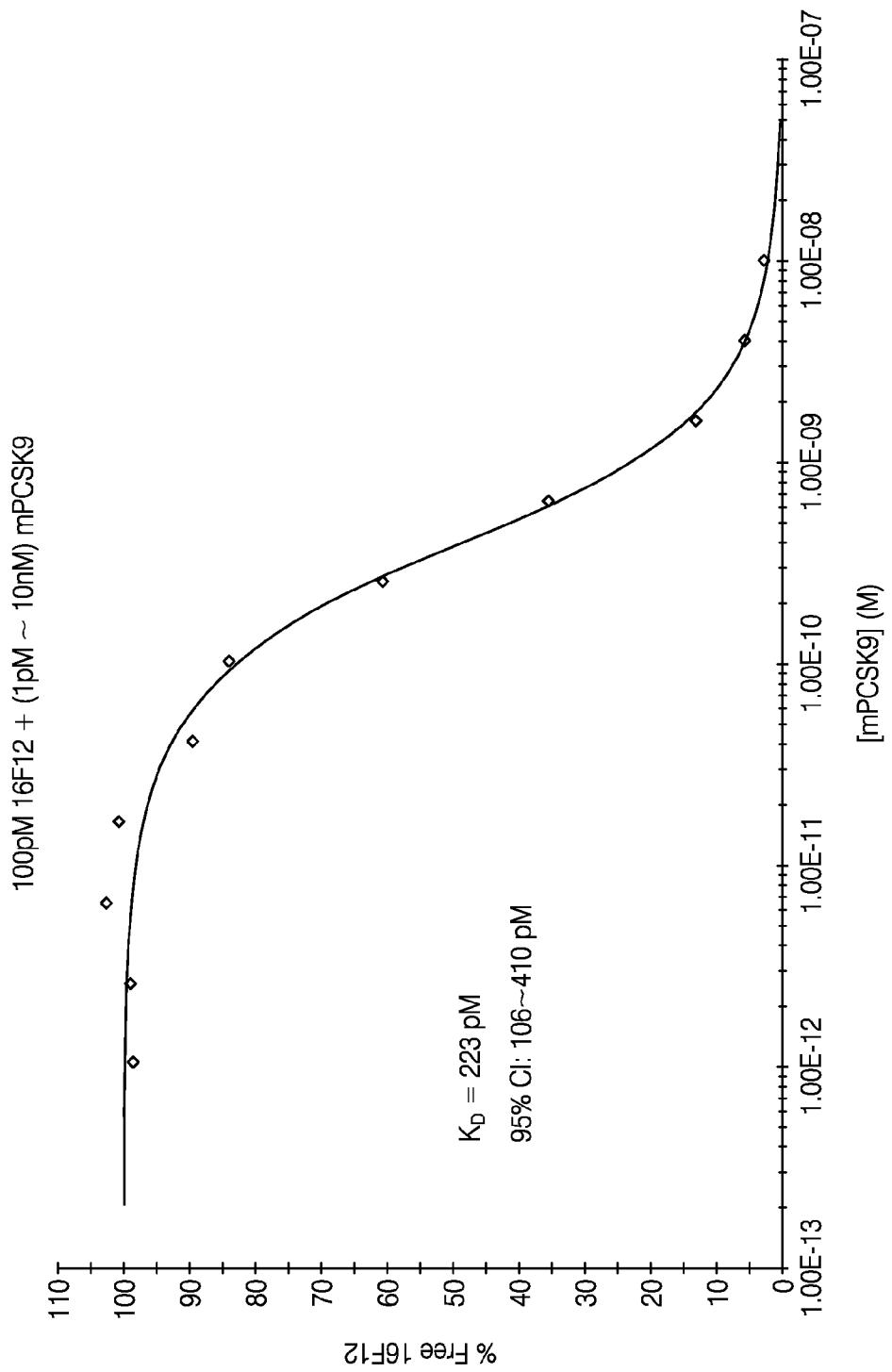


FIG. 4E

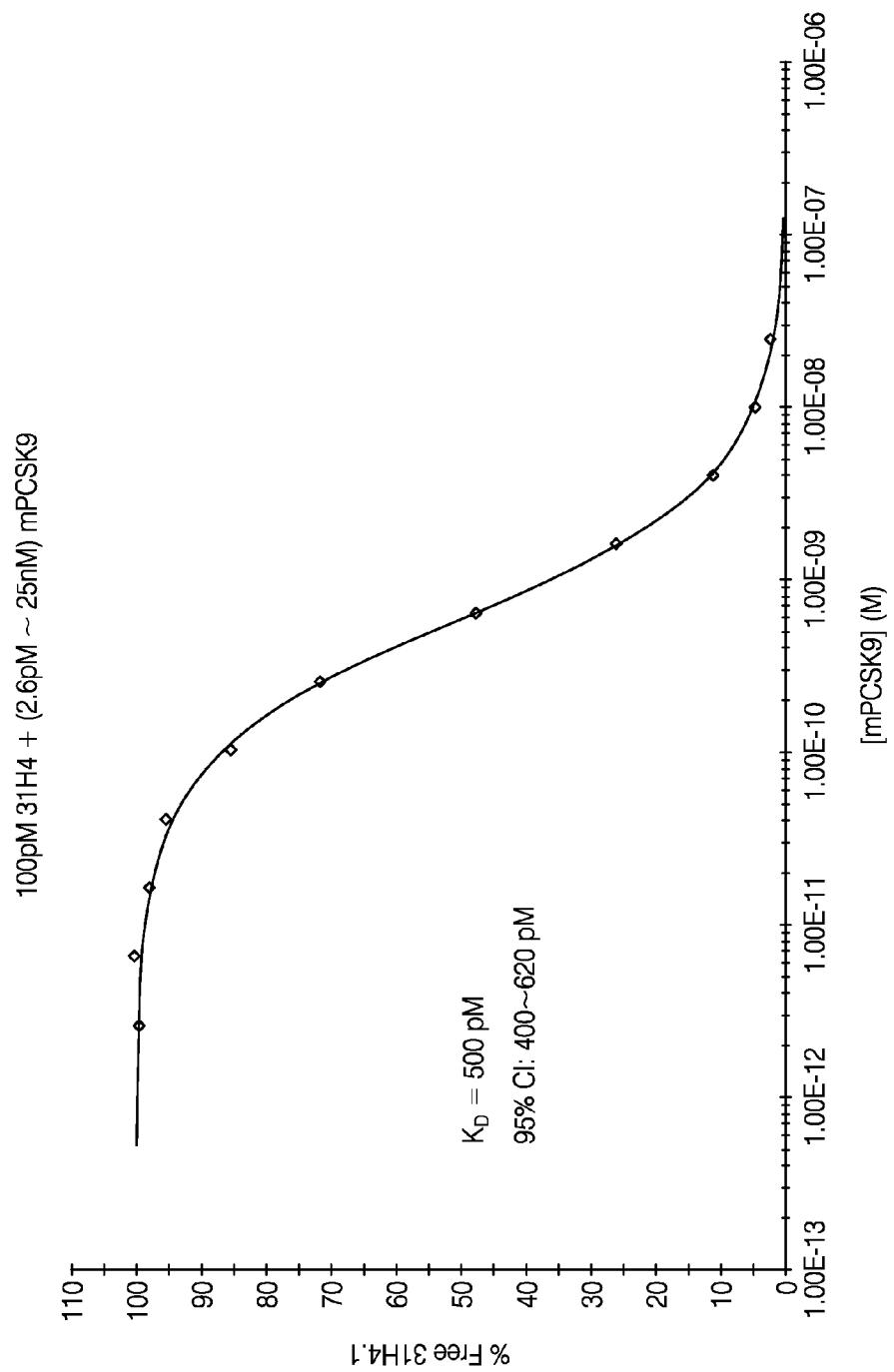


FIG. 4F

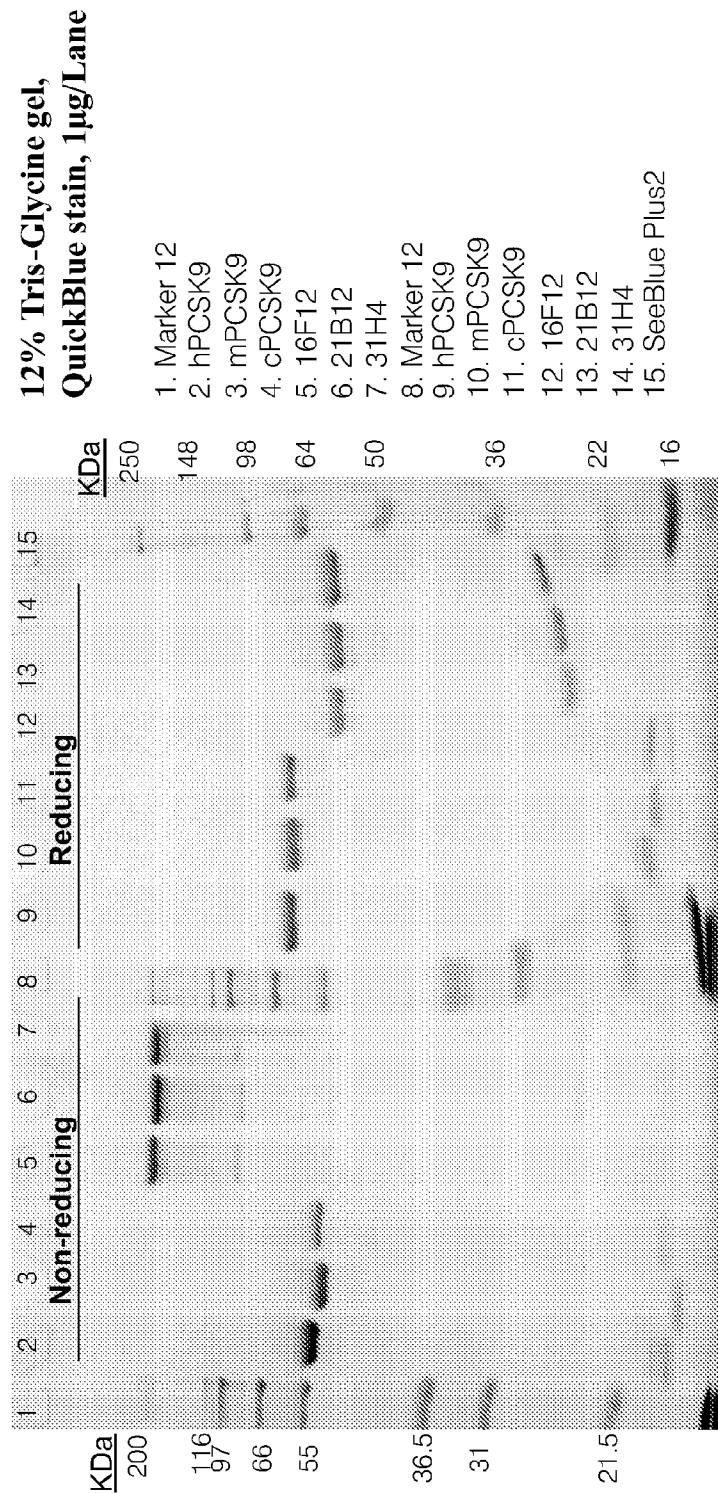


FIG. 5A

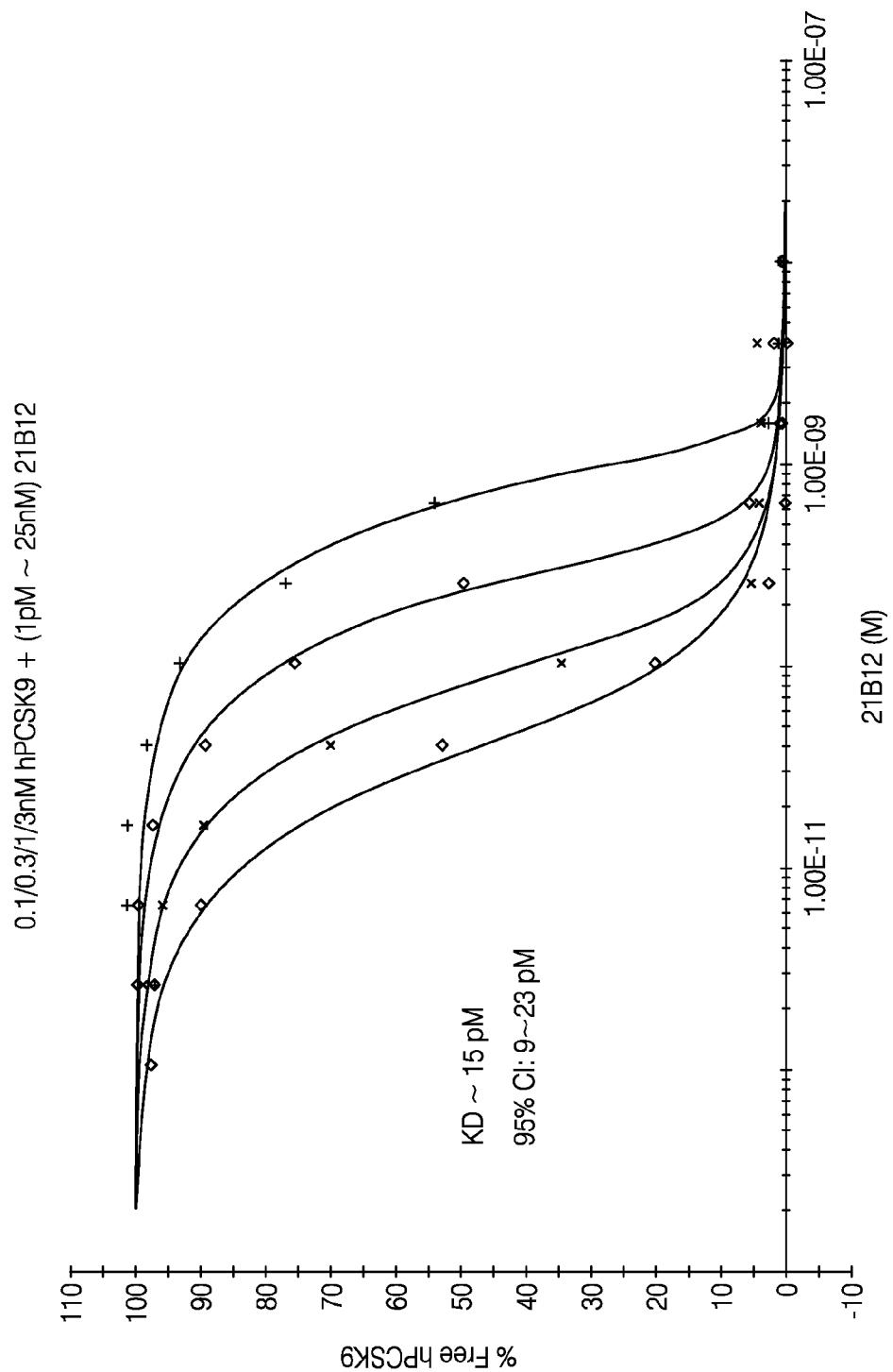


FIG. 5B

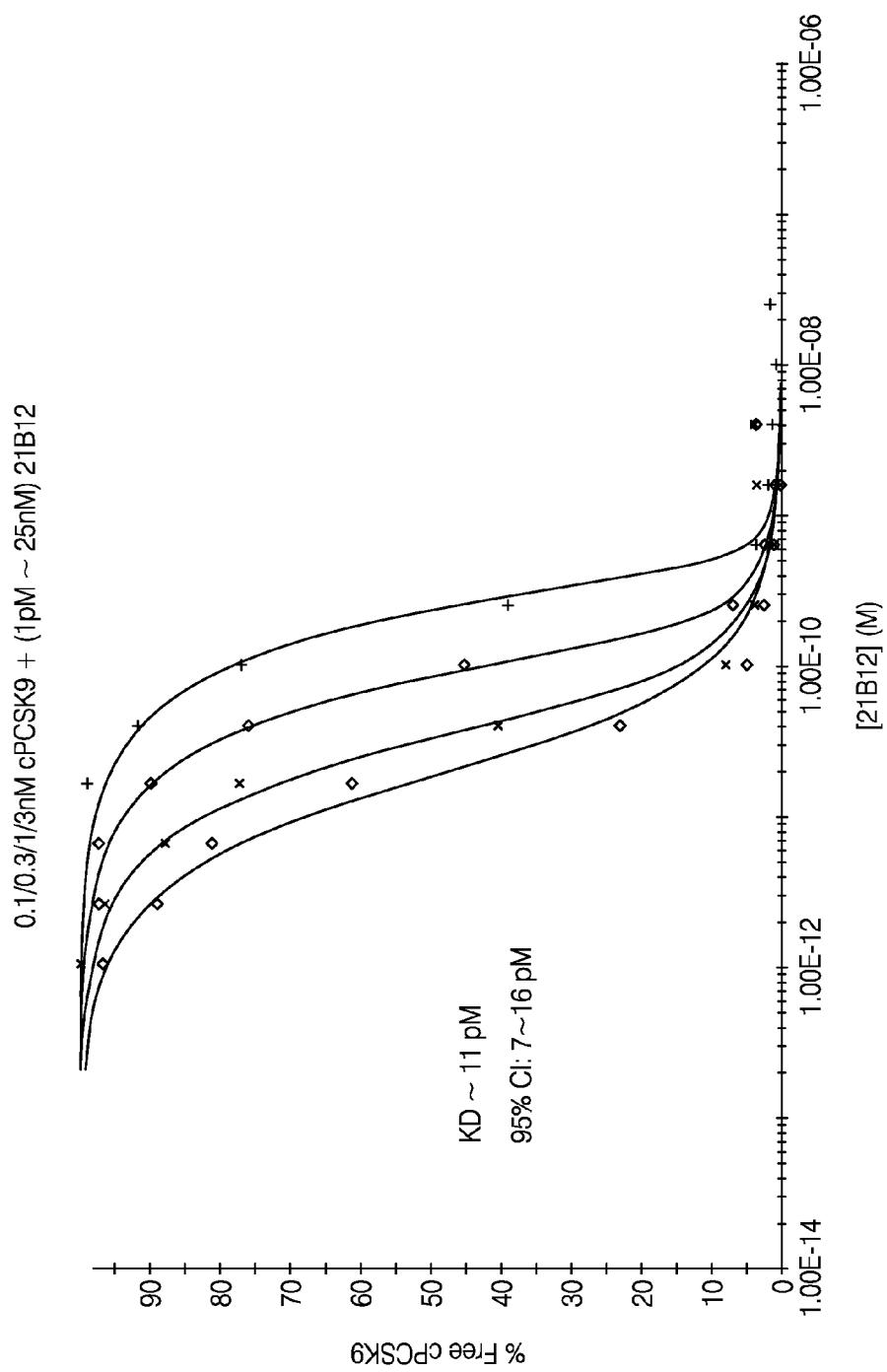


FIG. 5C

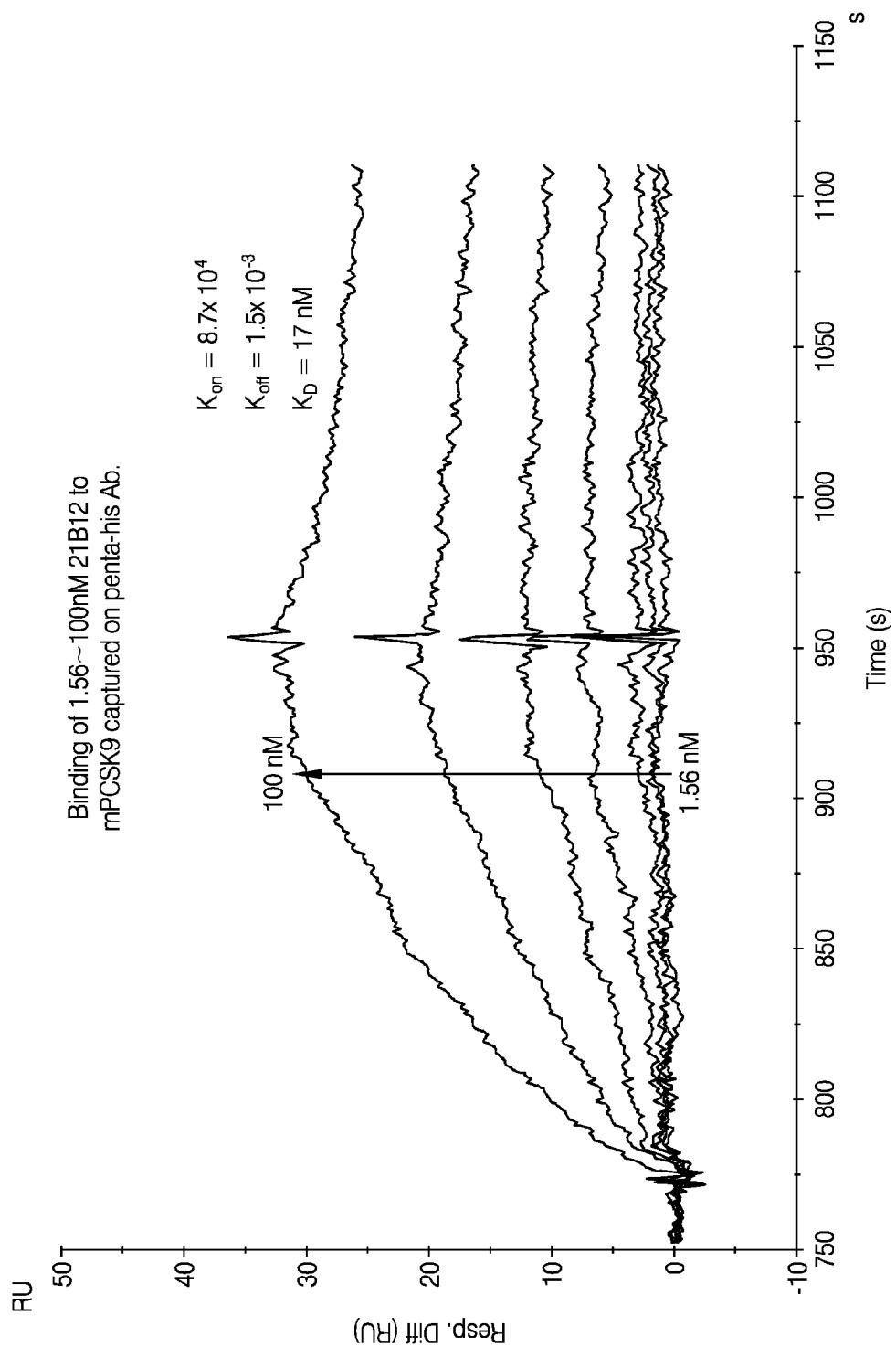


FIG. 5D

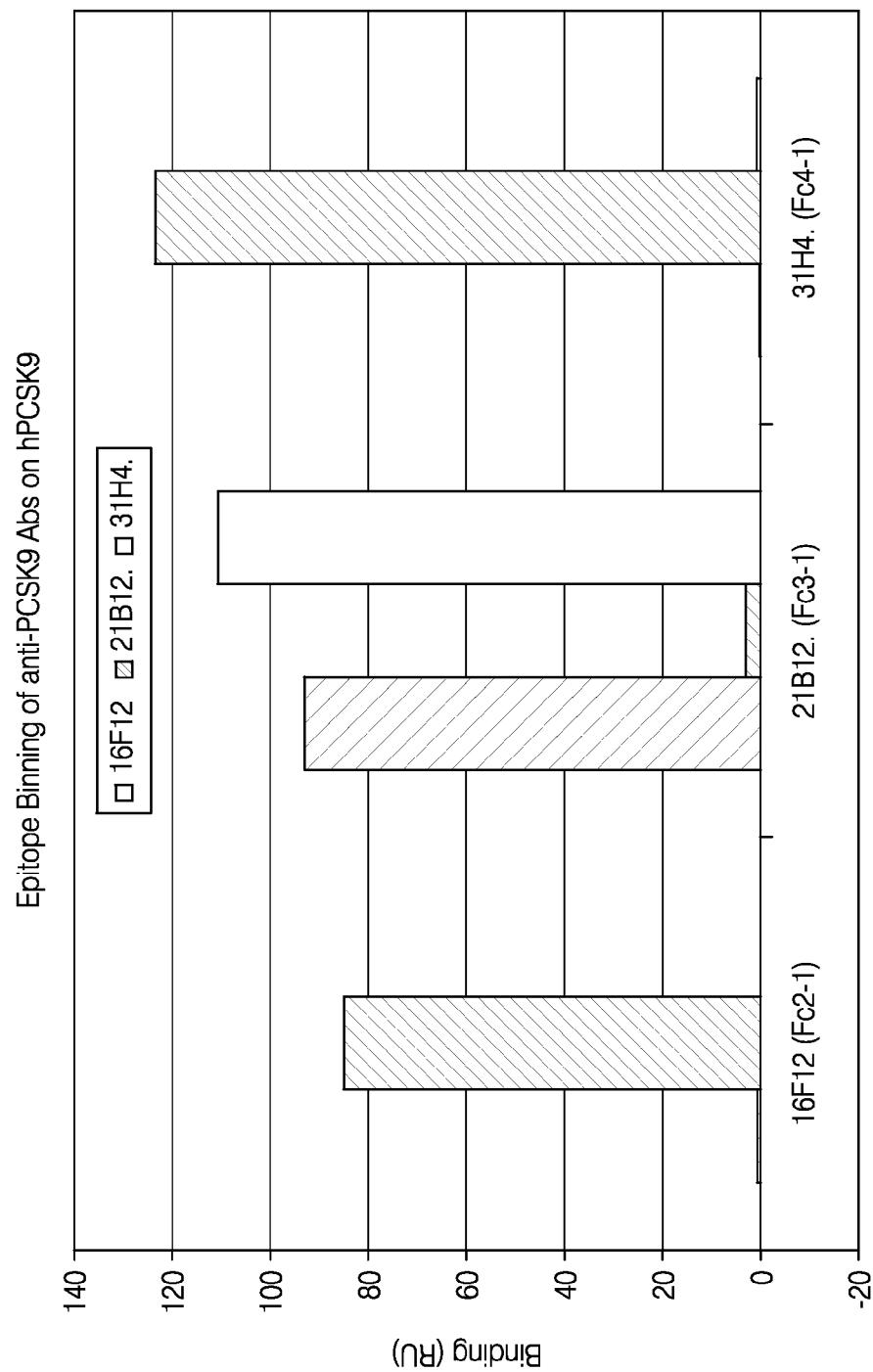


FIG. 5E

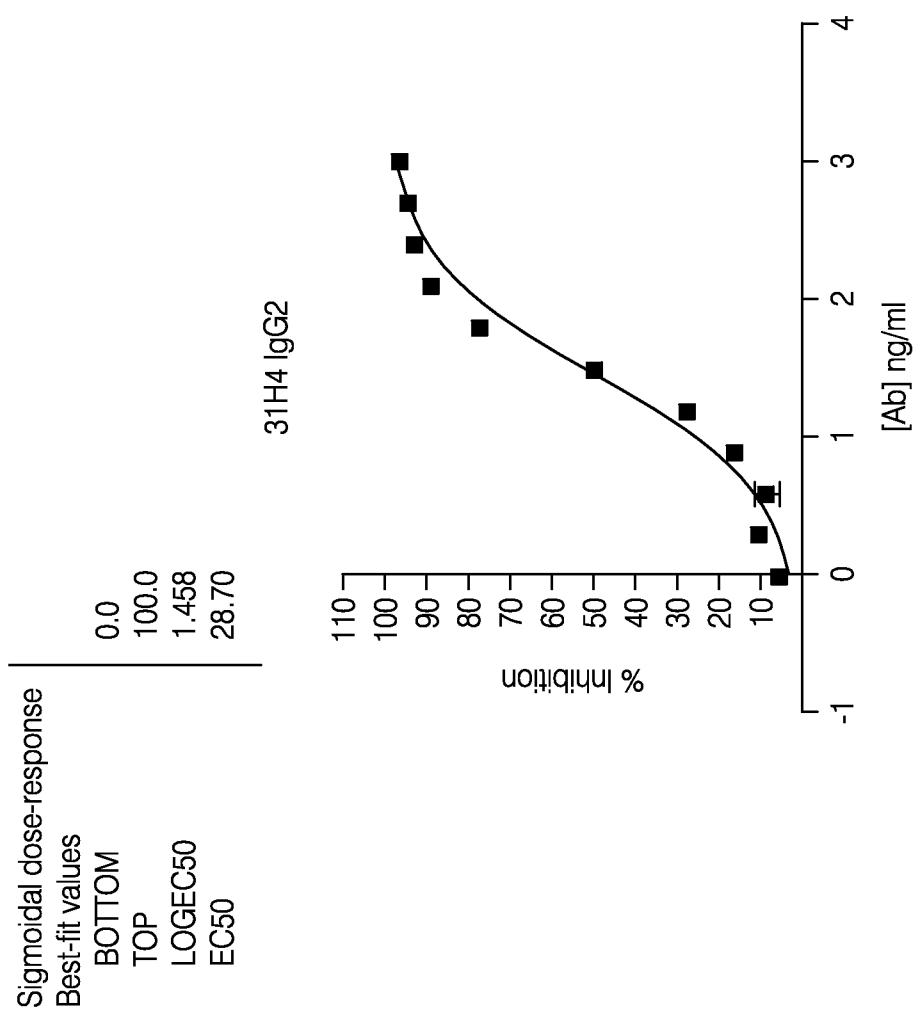


FIG. 6A

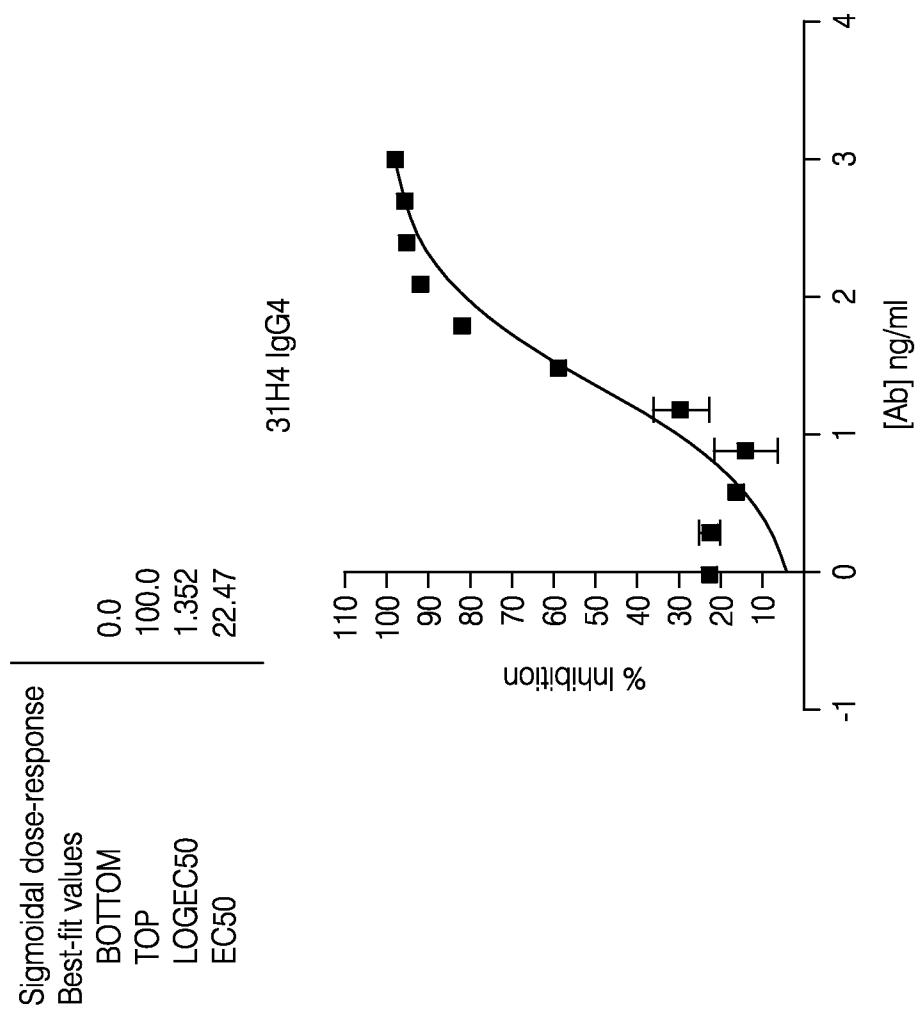


FIG. 6B

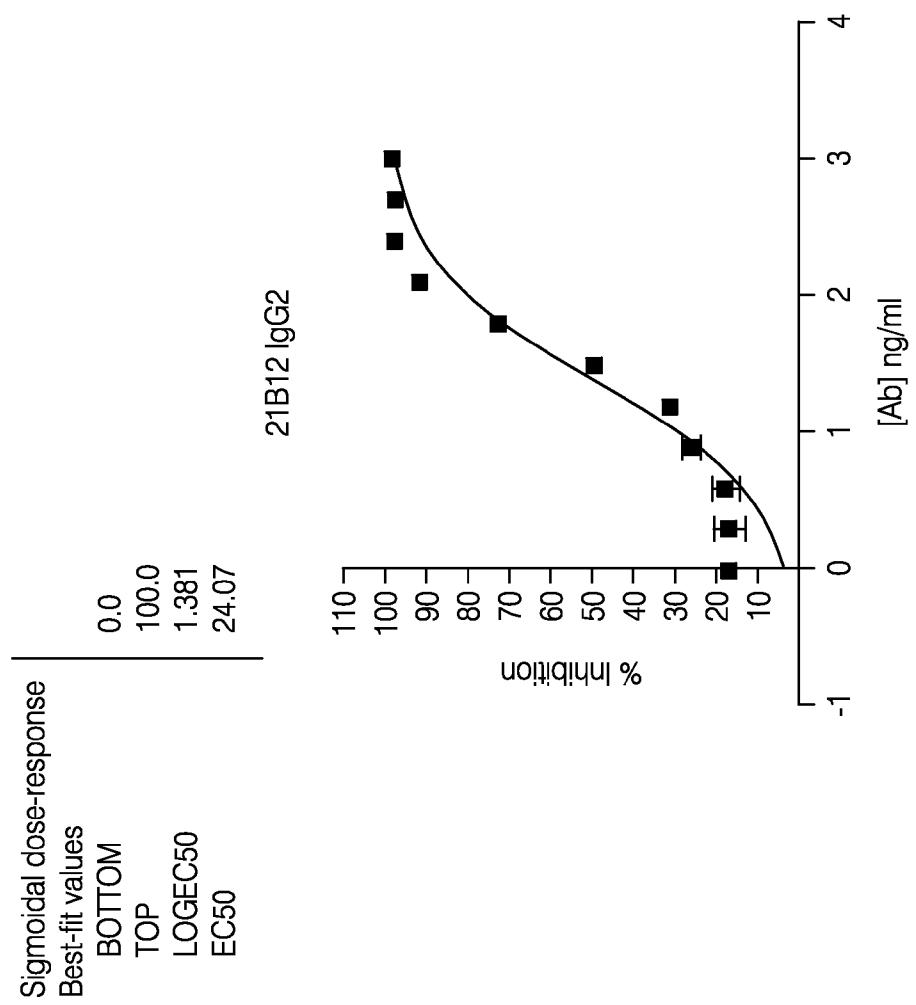


FIG. 6C

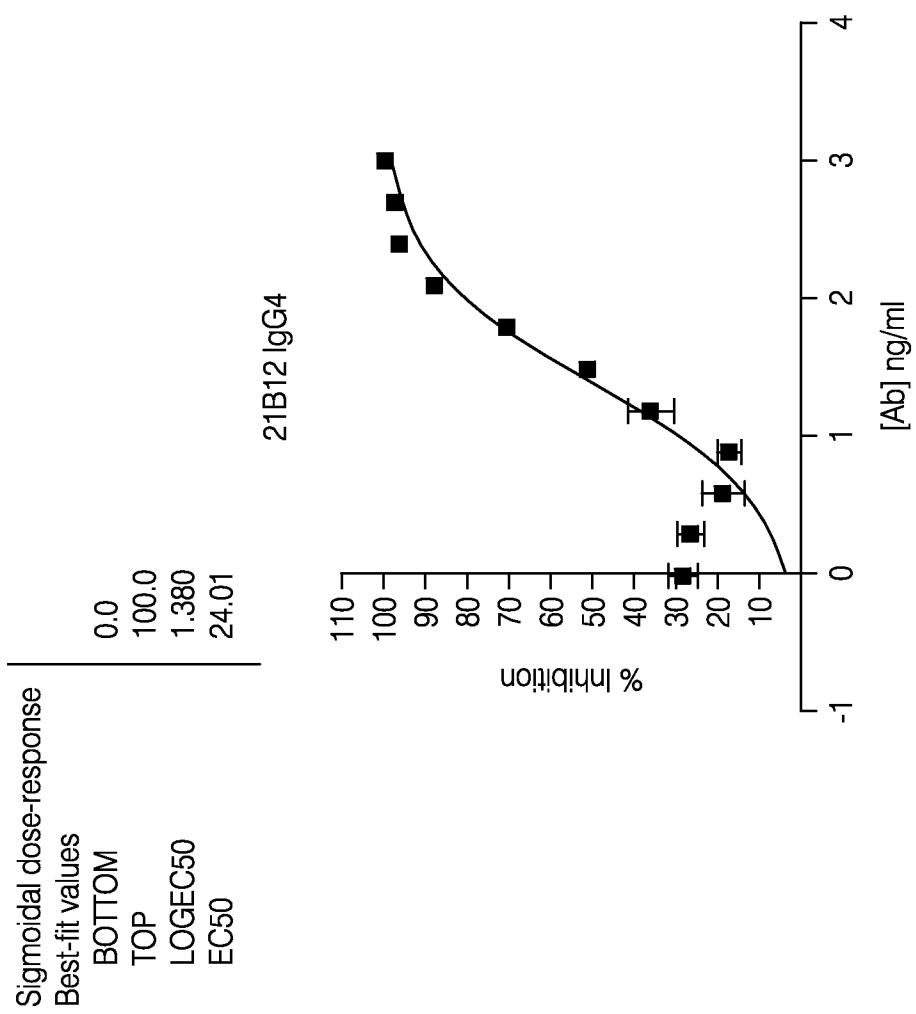


FIG. 6D

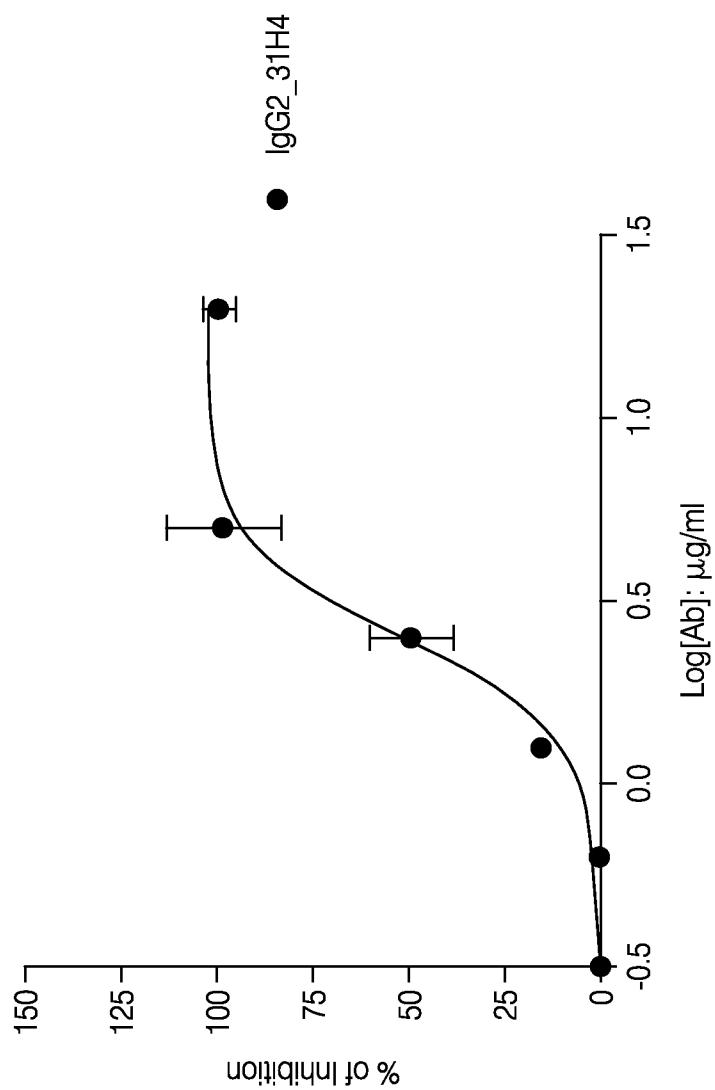


FIG. 7A

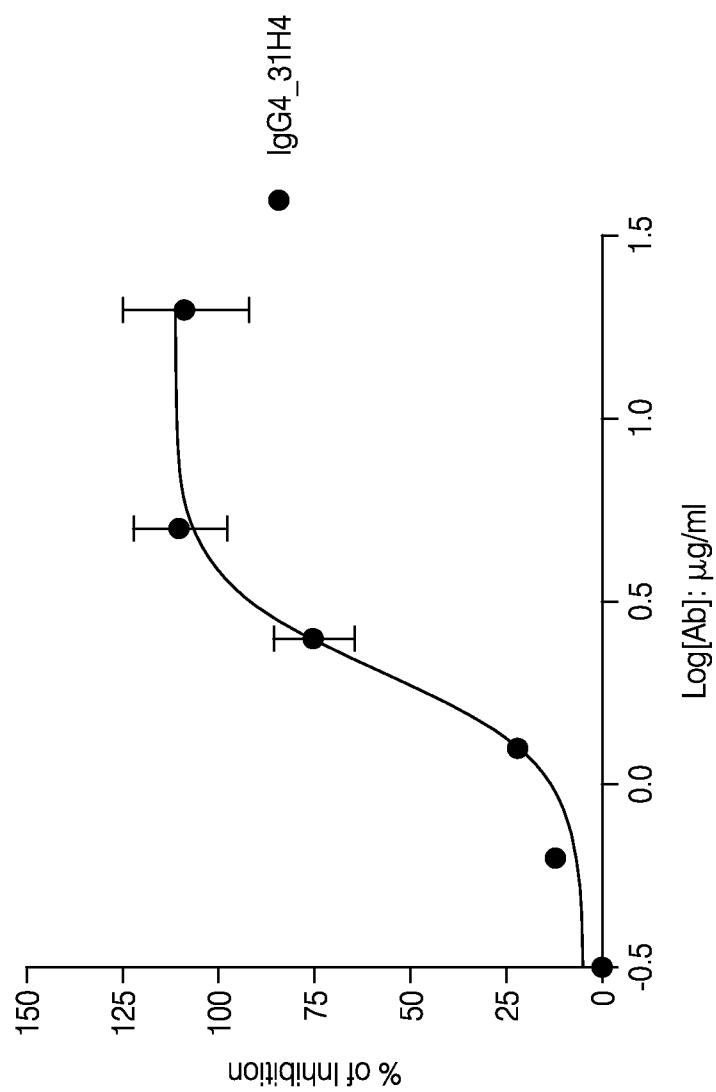


FIG. 7B

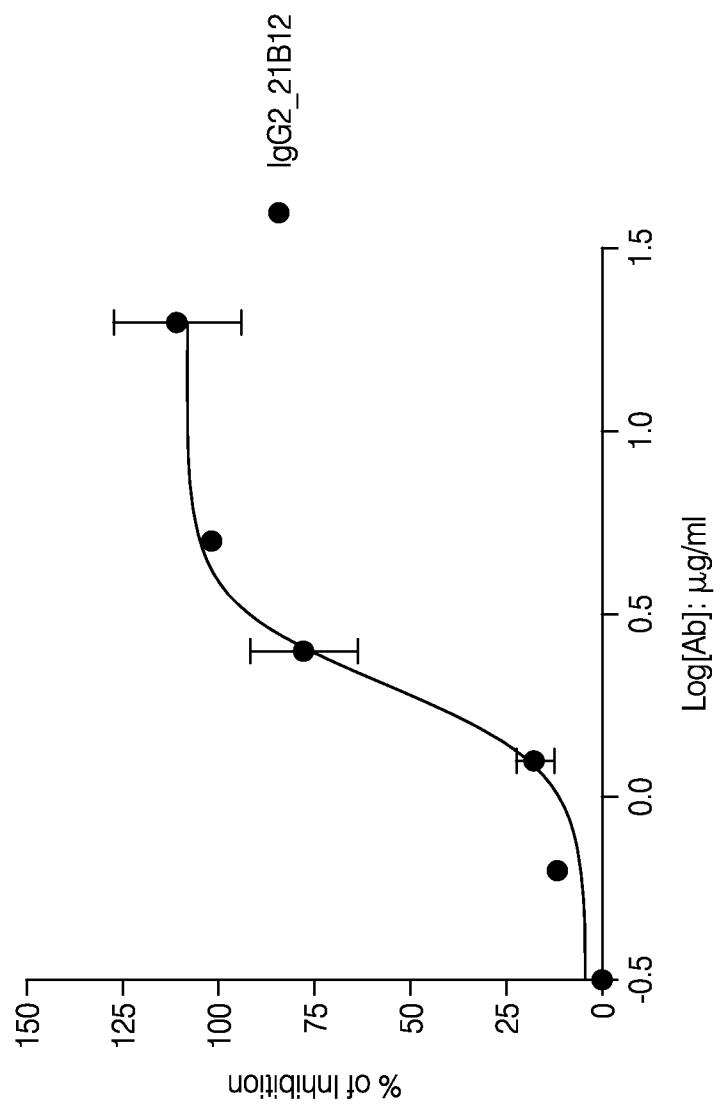


FIG. 7C

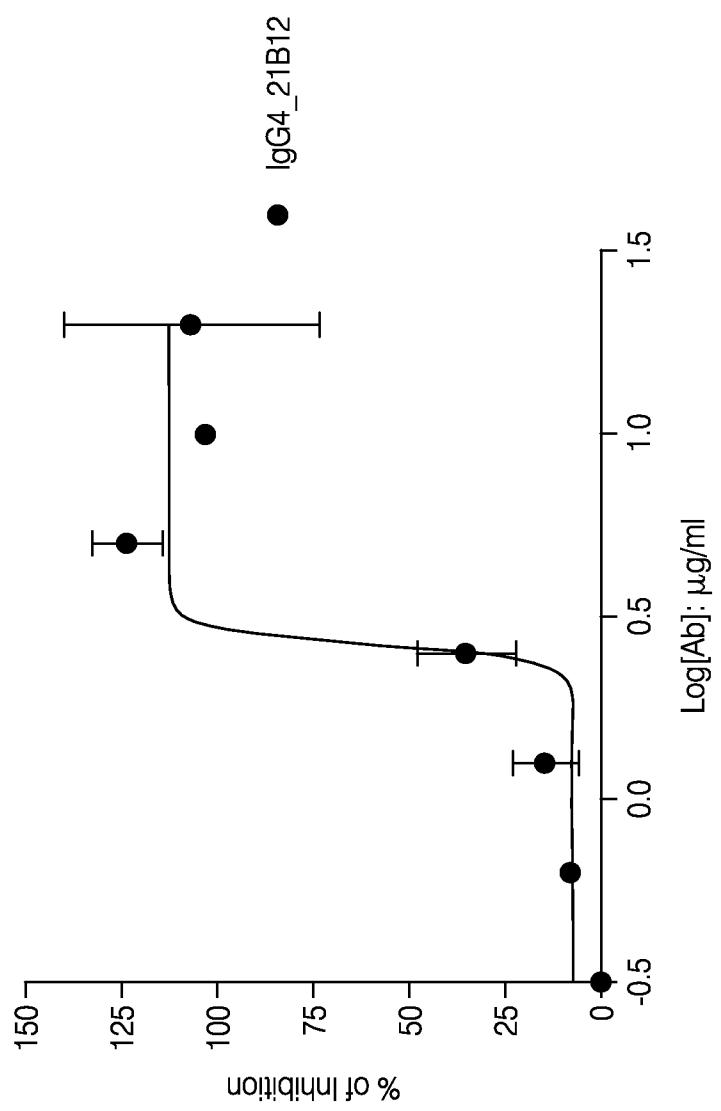


FIG. 7D

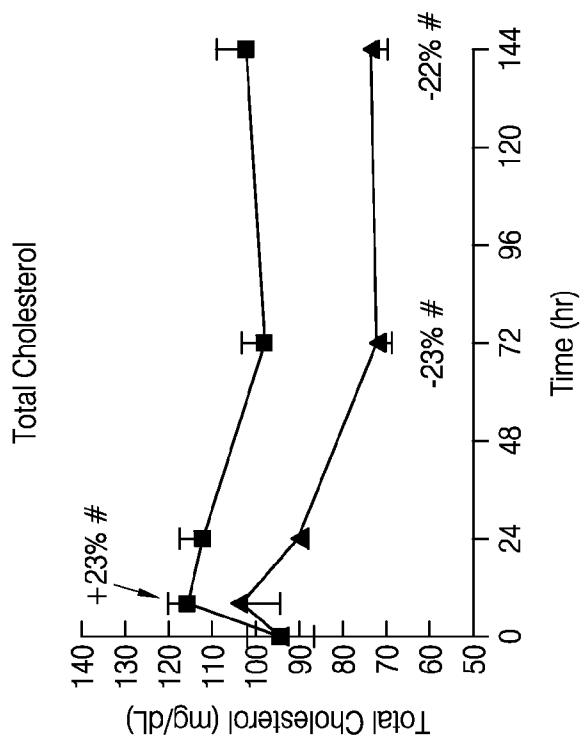


FIG. 8B

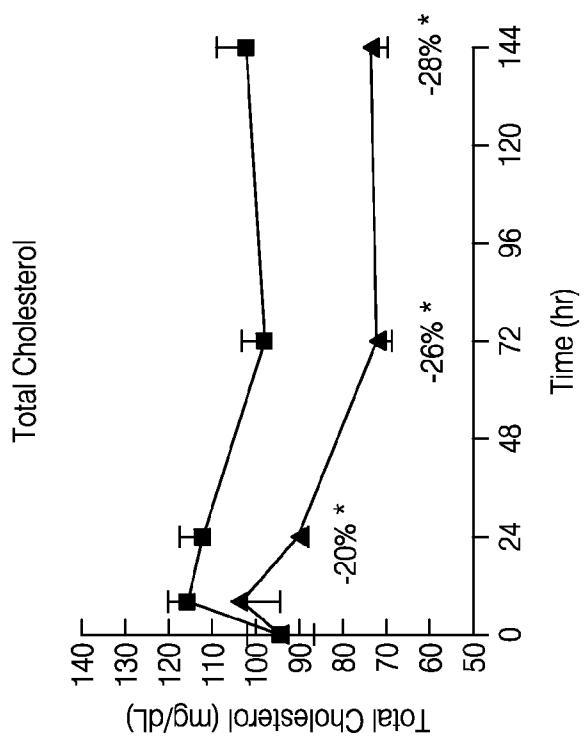


FIG. 8A

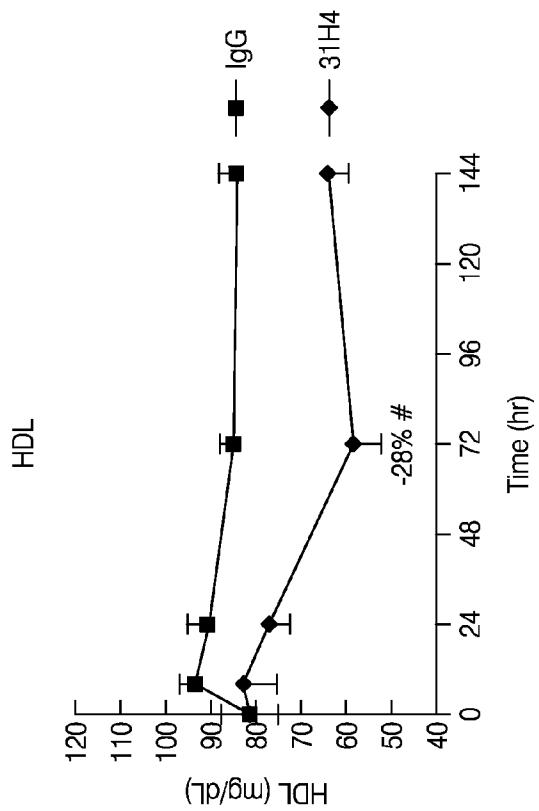


FIG. 8D

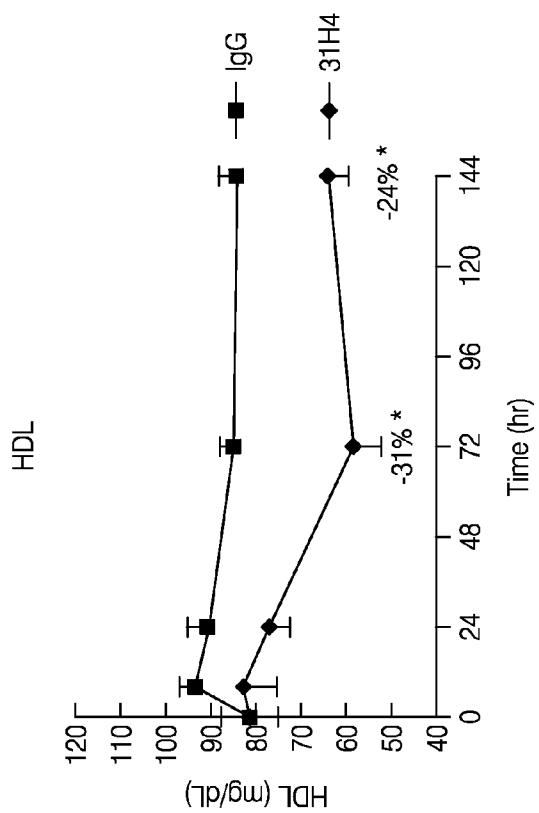


FIG. 8C

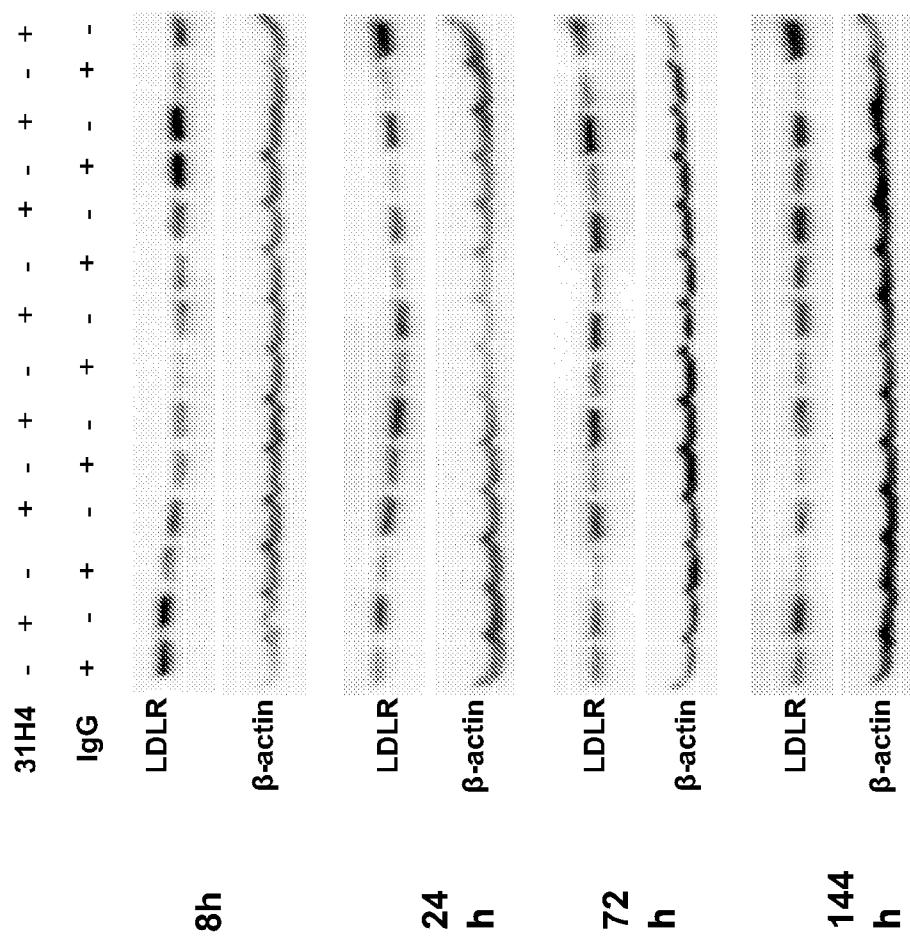


FIG. 9

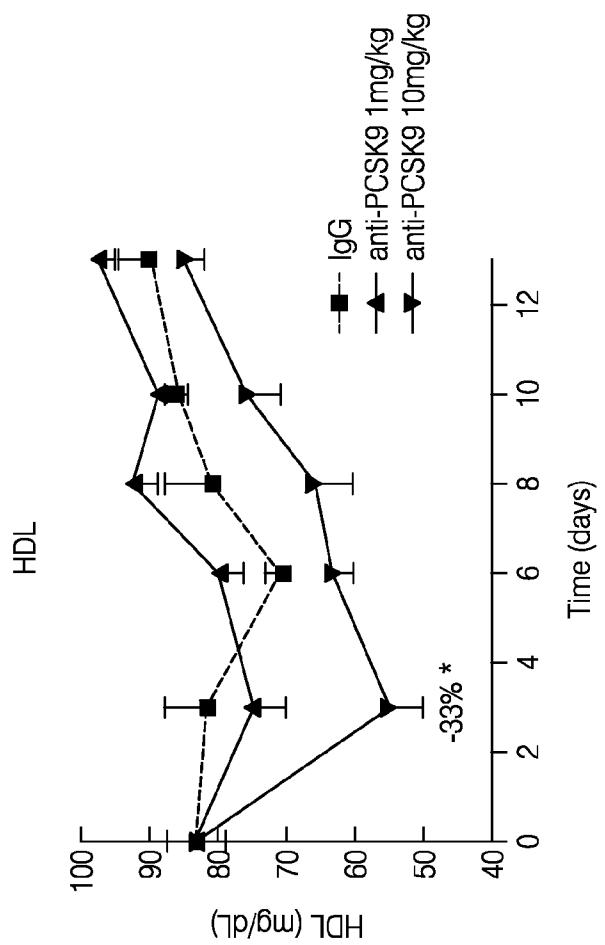


FIG. 10B

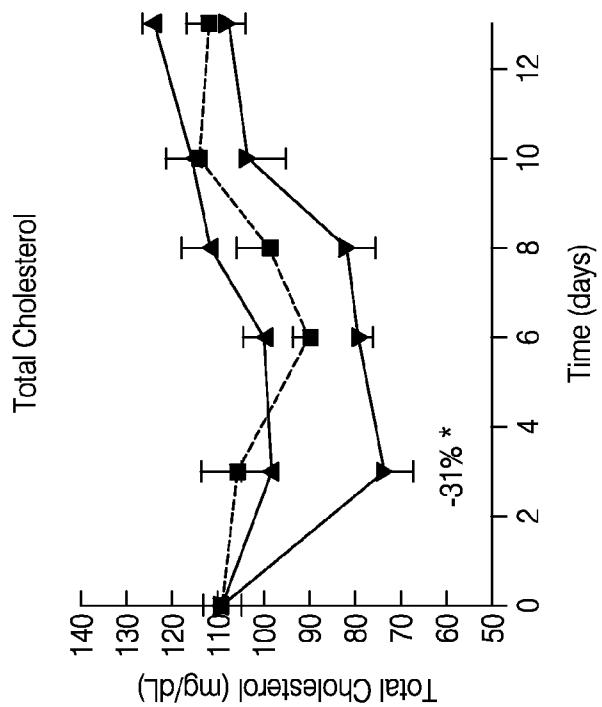


FIG. 10A

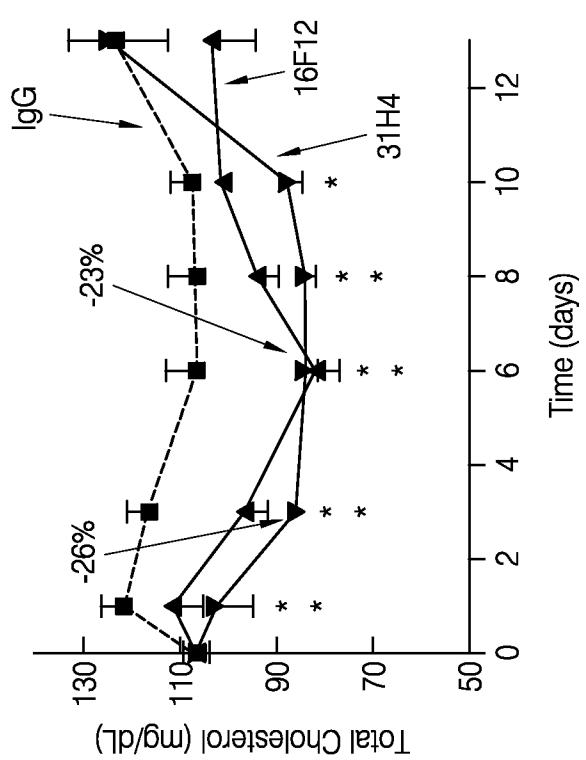


FIG. 10C

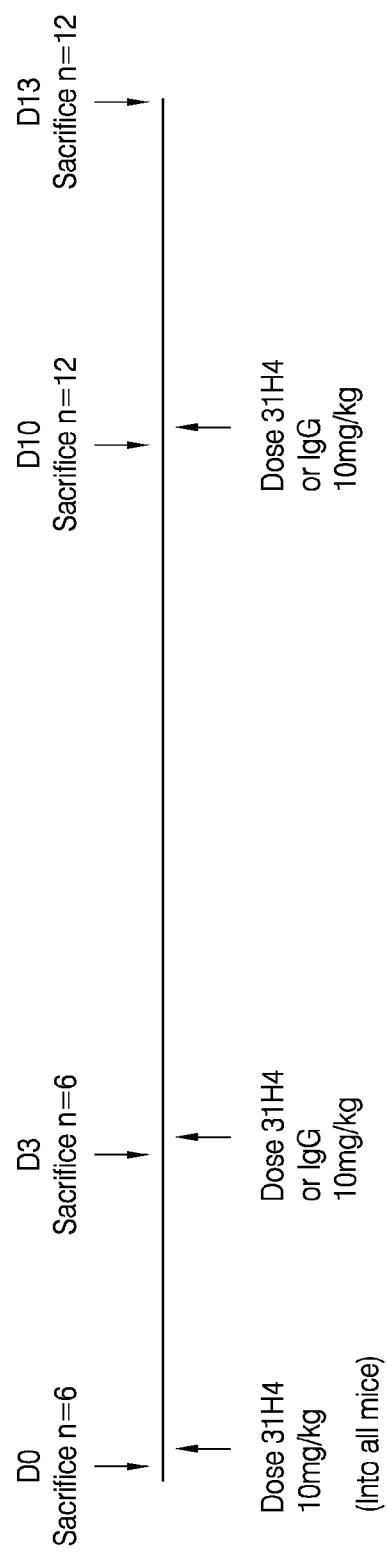


FIG. 11A

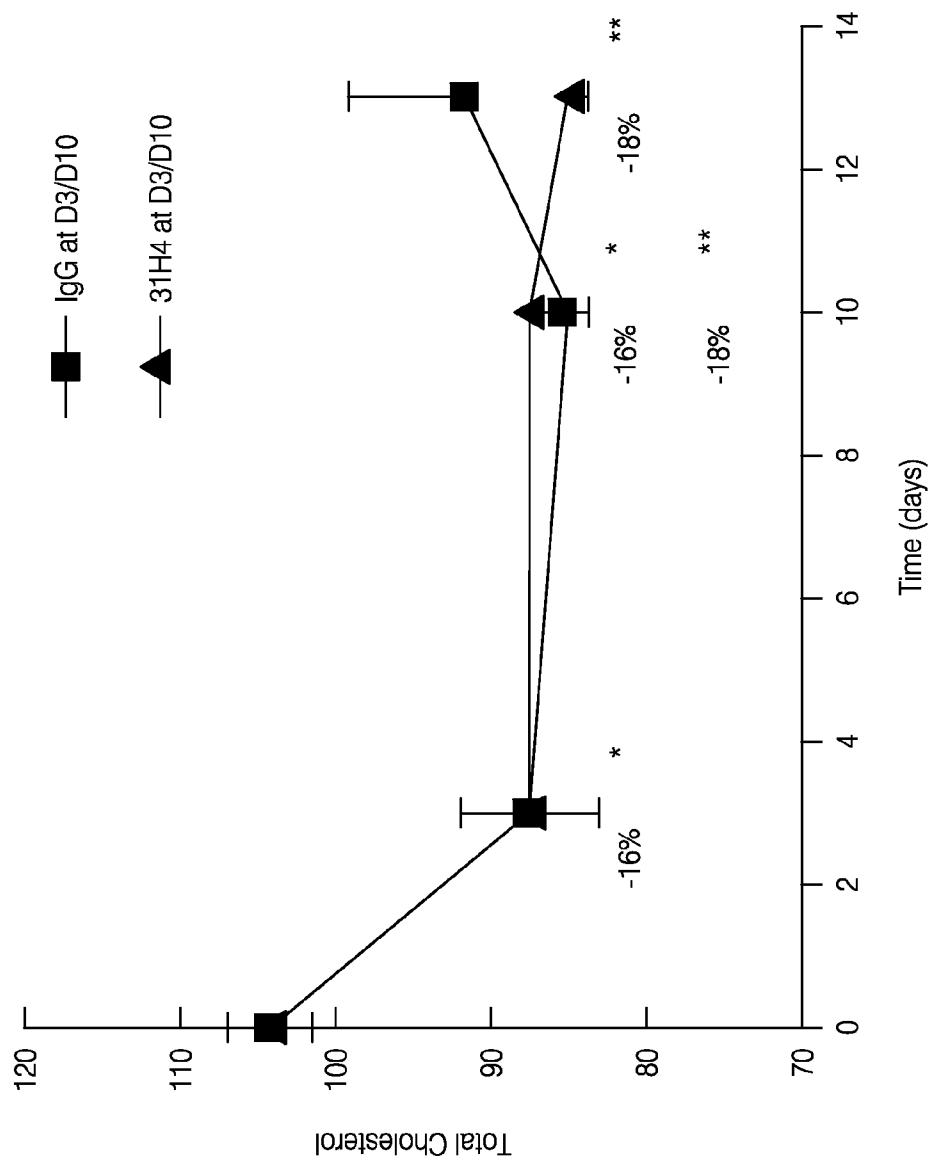


FIG. 11B

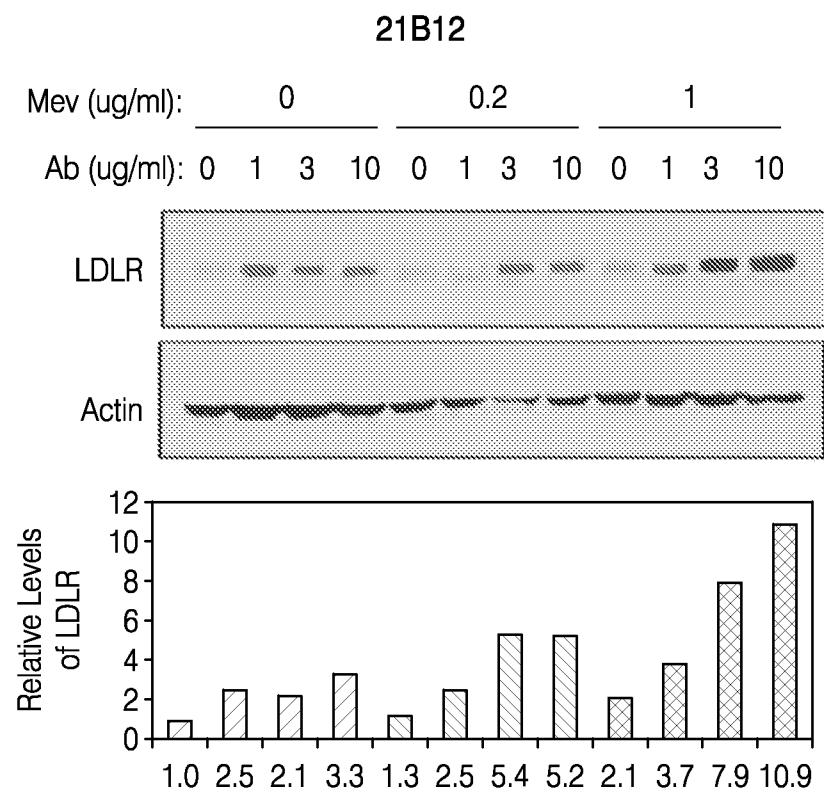


FIG. 12A

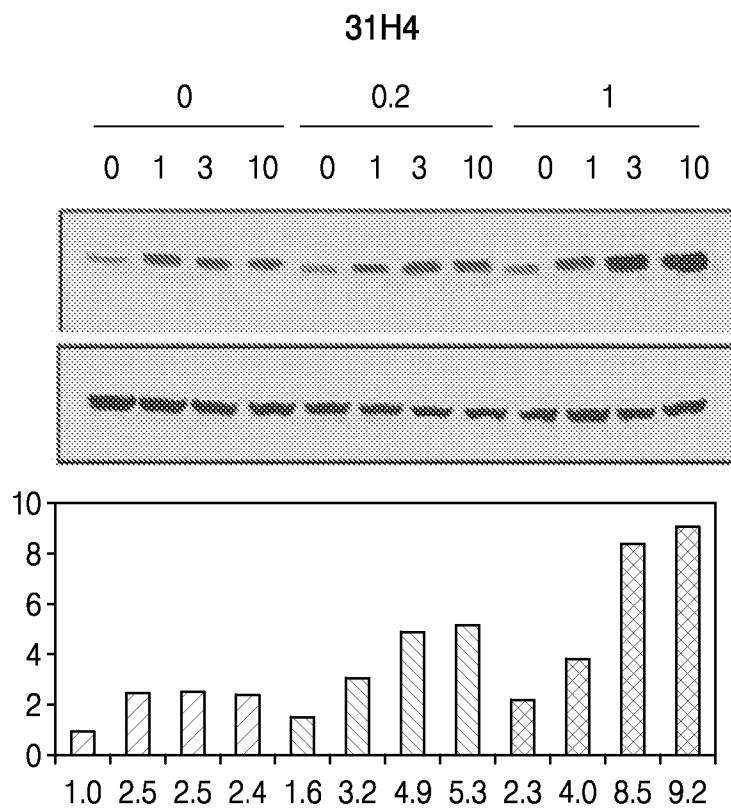


FIG. 12B

25A7.1

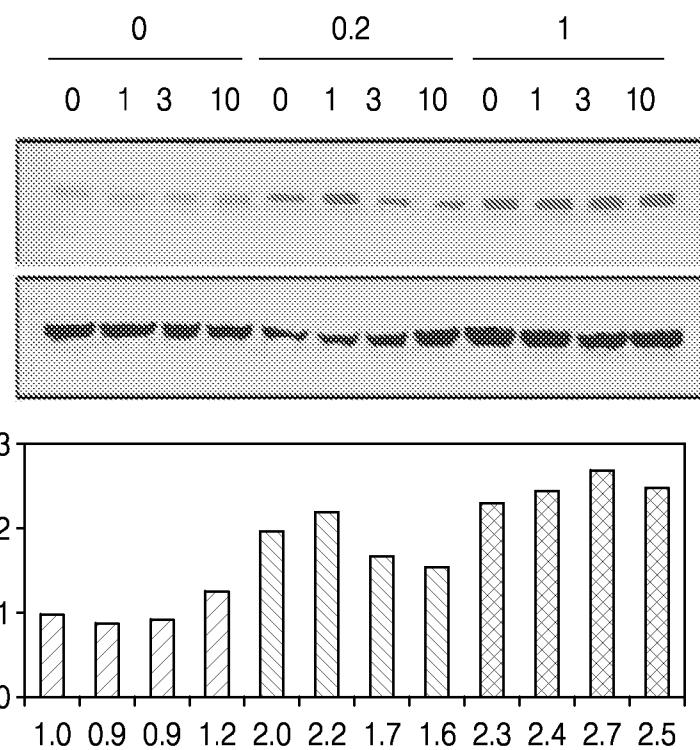
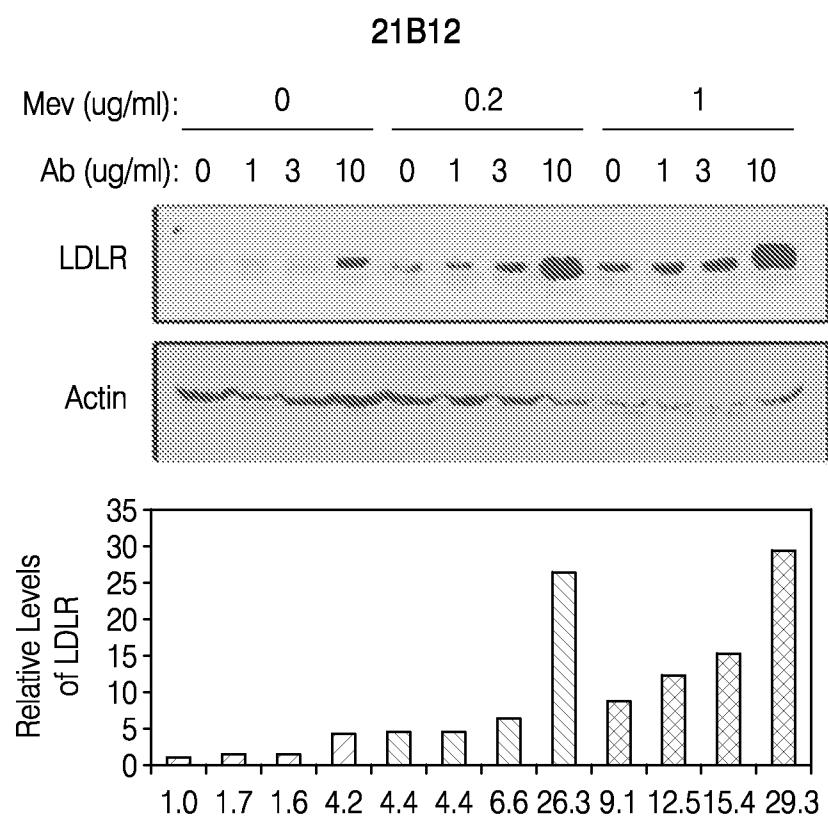


FIG. 12C

**FIG. 12D**

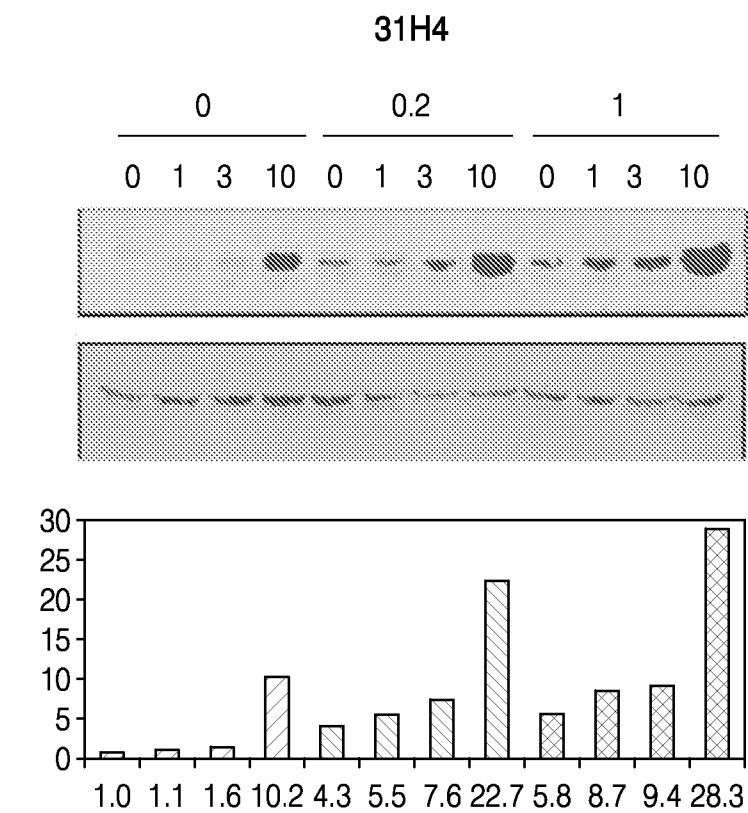


FIG. 12E

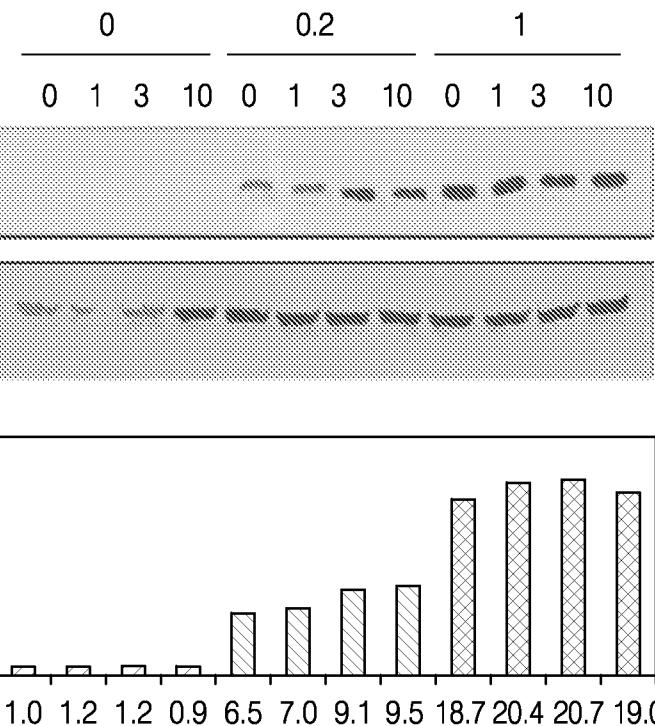
25A7.1**FIG. 12F**

FIG. 13A

23B5 Light_cdr (SEQ ID NO:209) RASOSI.....SITLN (SEQ ID NO:211) QSYSSSPIT~*~NNSNNNNNN~ (SEQ ID NO:213)
 25G4 Light_cdr (SEQ ID NO:308) RASOSI.....SITLN (SEQ ID NO:393) QSYSSAPIT~*~NNSNNNNNN~ (SEQ ID NO:394)
 3C4_Light_cdr (SEQ ID NO:219) RASOSI.....SITLN (SEQ ID NO:211) QSYSSPIT~*~NNSNNNNNN~ (SEQ ID NO:235)
 30A4_Light_cdr (SEQ ID NO:220) RASOSI.....SITLN (SEQ ID NO:227) QSYLQPTP~*~NNSNNNNNN~ (SEQ ID NO:236)
 21B12_Light_cdr (SEQ ID NO:158) EVSNRPS (SEQ ID NO:162) NSYSTSIVV~*~NNSNNNNNN~ (SEQ ID NO:395)
 23C1_Light_cdr (SEQ ID NO:158) EVTNRPS (SEQ ID NO:163) NSYSTSIVV~*~NNSNNNNNN~ (SEQ ID NO:395)
 20D10_Light_cdr (SEQ ID NO:159) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 26B3_Light_cdr (SEQ ID NO:158) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 31D1_Light_cdr (SEQ ID NO:158) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 27E7_Light_cdr (SEQ ID NO:158) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 27B5_Light_cdr (SEQ ID NO:158) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 30B9_Light_cdr (SEQ ID NO:158) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 19B9_Light_cdr (SEQ ID NO:369) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 17C2_Light_cdr (SEQ ID NO:390) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:164)
 25A7_Light_cdr (SEQ ID NO:391) EVSNRPS (SEQ ID NO:162) SSYSSTAVV~*~NNSNNNNNN~ (SEQ ID NO:396)
 13H1_Light_cdr (SEQ ID NO:221) EVSNRPS (SEQ ID NO:228) CSYAGSSILV~*~NNSNNNNNN~ (SEQ ID NO:237)
 31B4_Light_cdr (SEQ ID NO:222) GSNTKPS (SEQ ID NO:229) QSYDDESLGIV~*~NNSNNNNNN~ (SEQ ID NO:238)
 27B2_Light_cdr (SEQ ID NO:223) GSNTKPS (SEQ ID NO:230) QSYDDESLGIV~*~NNSNNNNNN~ (SEQ ID NO:239)
 9B6_Light_cdr (SEQ ID NO:197) SNTRKPS (SEQ ID NO:199) AANDDSIN~W~*~NNSNNNNNN~ (SEQ ID NO:397)
 1A12_Light_cdr (SEQ ID NO:199) SNTRKPS (SEQ ID NO:199) AANDDSIN~W~*~NNSNNNNNN~ (SEQ ID NO:397)
 9C9_Light_cdr (SEQ ID NO:495) RNWQRL (SEQ ID NO:592) AANDDSIN~W~*~NNSNNNNNN~ (SEQ ID NO:397)
 31A4_Light_cdr (SEQ ID NO:197) SNTRKPS (SEQ ID NO:231) AWDSDSLGIV~*~NNSNNNNNN~ (SEQ ID NO:240)
 22E2_Light_cdr (SEQ ID NO:182) DMTRKPS (SEQ ID NO:183) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:185)
 28B12_Light_cdr (SEQ ID NO:182) DMTRKPS (SEQ ID NO:183) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:185)
 28D5_Light_cdr (SEQ ID NO:182) DMTRKPS (SEQ ID NO:183) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:185)
 16F12_Light_cdr (SEQ ID NO:182) DMTRKPS (SEQ ID NO:183) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:185)
 27A6_Light_cdr (SEQ ID NO:182) DMTRKPS (SEQ ID NO:183) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:398)
 31G11_Light_cdr (SEQ ID NO:182) DMTRKPS (SEQ ID NO:184) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:399)
 13B5_Light_cdr (SEQ ID NO:224) DNTRKPS (SEQ ID NO:232) GMDSSSLGIV~*~NNSNNNNNN~ (SEQ ID NO:241)
 31B12_Light_cdr (SEQ ID NO:225) QNTTRKPL (SEQ ID NO:233) QANDSSSTVV~*~NNSNNNNNN~ (SEQ ID NO:242)
 386_Light_cdr (SEQ ID NO:226) VDTGCRV (SEQ ID NO:234) SDYNGCAGDSGSGSTNTVYV~*~NNSNNNNNN~ (SEQ ID NO:243)

Canabensis

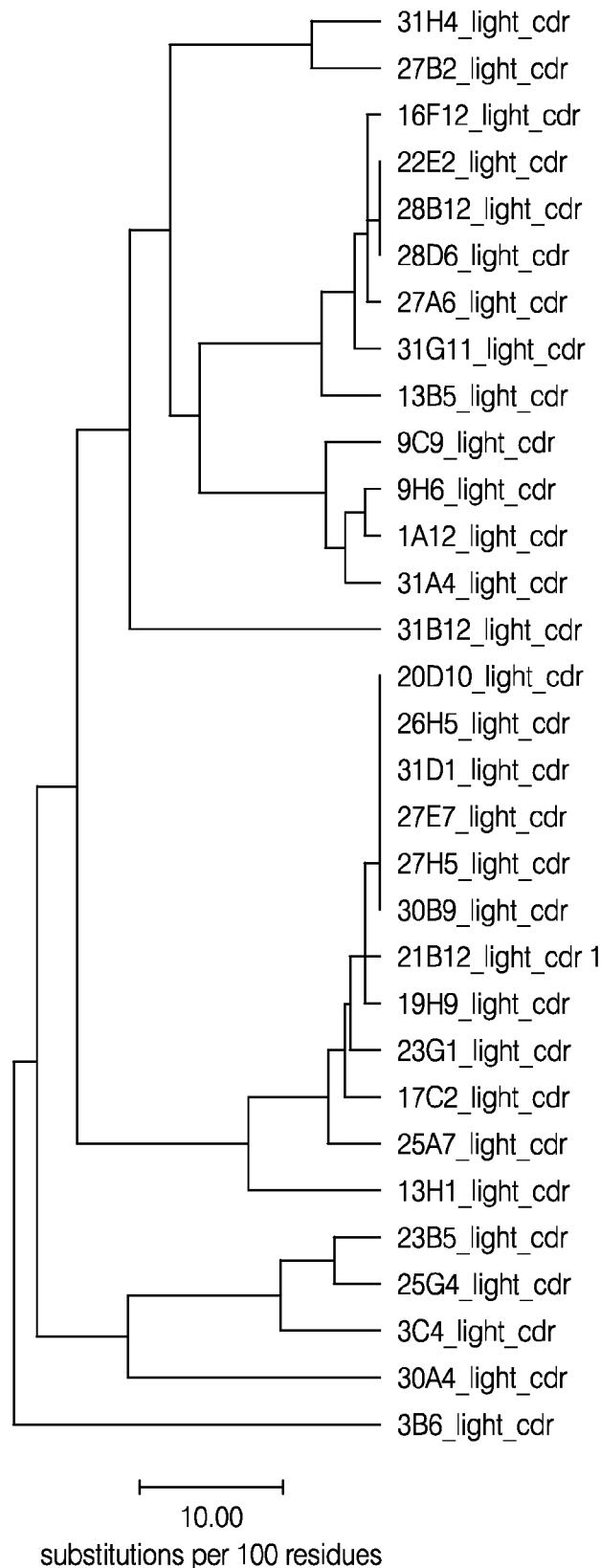


FIG. 13B

FIG. 13C

Heavy Chain:

20D10_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:168)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:174)	GYMDVY~~~~~(SEQ ID NO:180)
30B9_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:168)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:174)	GYMDVY~~~~~(SEQ ID NO:180)
27K7_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:366)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:174)	GYMDVY~~~~~(SEQ ID NO:180)
19H9_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:367)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:174)	GYMDVY~~~~~(SEQ ID NO:180)
21B12_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:368)	WISFYNG. NTNYAQKVQG	(SEQ ID NO:175)	GYMDVY~~~~~(SEQ ID NO:180)
23G1_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:368)	WISFYNG. NTNYAQKVQG	(SEQ ID NO:175)	GYMDVY~~~~~(SEQ ID NO:180)
26H5_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:368)	WISFYNG. NTNYAQKVQG	(SEQ ID NO:176)	GYMDVY~~~~~(SEQ ID NO:180)
31D1_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:368)	WISFYNG. NTNYAQKVQG	(SEQ ID NO:176)	GYMDVY~~~~~(SEQ ID NO:180)
27B5_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:368)	WISFYNG. NTNYAQKVQG	(SEQ ID NO:177)	GYMDVY~~~~~(SEQ ID NO:180)
17C2_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:369)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:178)	GYMDVY~~~~~(SEQ ID NO:180)
25A7_heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:370)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:179)	GYMDVY~~~~~(SEQ ID NO:180)
3B6_Heavy_cdr	~~GTTTTSYGSIS	(SEQ ID NO:244)	WISAYNG. NTNYAQKVQG	(SEQ ID NO:252)	GTTDDY~~~~~(SEQ ID NO:261)
9C9_heavy_cdr	~~GTTTSSYWS	(SEQ ID NO:371)	NIKODGS. EKYYDVSVEG	(SEQ ID NO:343)	E.... SWGKATI (SEQ ID NO:385)
9B6_heavy_cdr	~~GTTTSSYWS	(SEQ ID NO:372)	NIKEDGS. EKYYDVSVEG	(SEQ ID NO:347)	E.... SWGKATIY (SEQ ID NO:386)
1A12_heavy_cdr	~~GTTTSSNTWS	(SEQ ID NO:373)	NIKODGS. EKYYDVSVEG	(SEQ ID NO:343)	E.... SWGKATDI (SEQ ID NO:385)
23B5_heavy_cdr	~~GTTTSSYAMN	(SEQ ID NO:374)	TISGSD. NTNYADSVKG	(SEQ ID NO:365)	KFWLNTVYAMLDY~~~~(SEQ ID NO:218)
25G4_heavy_cdr	~~GTTTSSYAMN	(SEQ ID NO:374)	TISCGG. NTNYADSVKG	(SEQ ID NO:364)	KFWLNTVYAMLDY~~~~(SEQ ID NO:218)
13B5_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:245)	TISGGG. NTNYADSVKG	(SEQ ID NO:253)	E.... VSSPFDY~~~~(SEQ ID NO:262)
22E2_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:188)	LINWDSG. NKYYADSVKG	(SEQ ID NO:329)	AIAAL YYYGKMY (SEQ ID NO:195)
28B12_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:188)	LINWDSG. NKYYADSVKG	(SEQ ID NO:329)	AIAAL YYYGKMY (SEQ ID NO:195)
28D6_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:188)	LINWDSG. NKYYADSVKG	(SEQ ID NO:329)	AIAAL YYYGKMY (SEQ ID NO:195)
16T12_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:375)	LINWDSG. DEYYADSVKG	(SEQ ID NO:336)	AIAAL YYYGKMY (SEQ ID NO:195)
27A6_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:375)	LINWDSG. DKYYADSVKG	(SEQ ID NO:338)	AIAAL YYYGKMY (SEQ ID NO:195)
31G11_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:376)	LINWDSG. NTYYADSVKG	(SEQ ID NO:334)	GIAVA YYYGKMY (SEQ ID NO:196)
30A4_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:246)	VINYDGS. DKKYADSVKG	(SEQ ID NO:254)	ETCPKAKLYKYYGMY (SEQ ID NO:263)
31B12_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:246)	LINWDSG. NKYYADSVKG	(SEQ ID NO:255)	R. GCAAAKPGKMY (SEQ ID NO:264)
31H4_heavy_cdr	~~GTTTSSYAMS	(SEQ ID NO:247)	SISSSS. XISYADSVKG	(SEQ ID NO:256)	DYDEWSSAYDADYV (SEQ ID NO:265)
27B2_heavy_cdr	~~GTTTSSGTVWS	(SEQ ID NO:248)	YIYNESGTY. YNPESLRS	(SEQ ID NO:257)	ED TAWVY FDY~~~~(SEQ ID NO:266)
3C4_Heavy_cdr	~~GTTTSSDTWS	(SEQ ID NO:249)	YIYNESGTY. YNPESLRS	(SEQ ID NO:258)	GG VTTTIAAMDY~~~~(SEQ ID NO:267)
31A4_heavy_cdr	~~GTTTSSA. YIWN	(SEQ ID NO:250)	EINESGRD. YNPESLRS	(SEQ ID NO:259)	GQ IVPEDY~~~~~(SEQ ID NO:268)
13H1_heavy_cdr	~~GTTTSSGIAWN	(SEQ ID NO:251)	RTTYRSKKNYKNYSVVE	(SEQ ID NO:260)	GGPTMADY~~~~~(SEQ ID NO:269)

Consensus

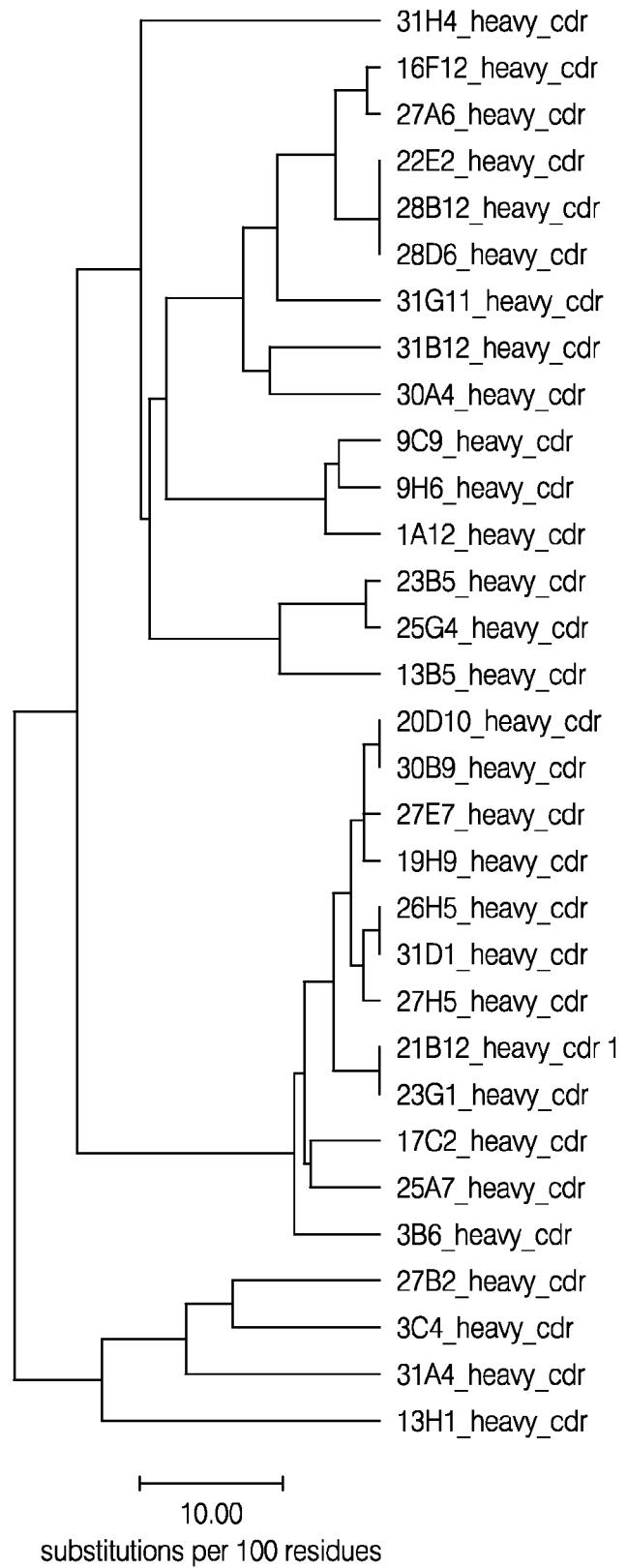


FIG. 13D

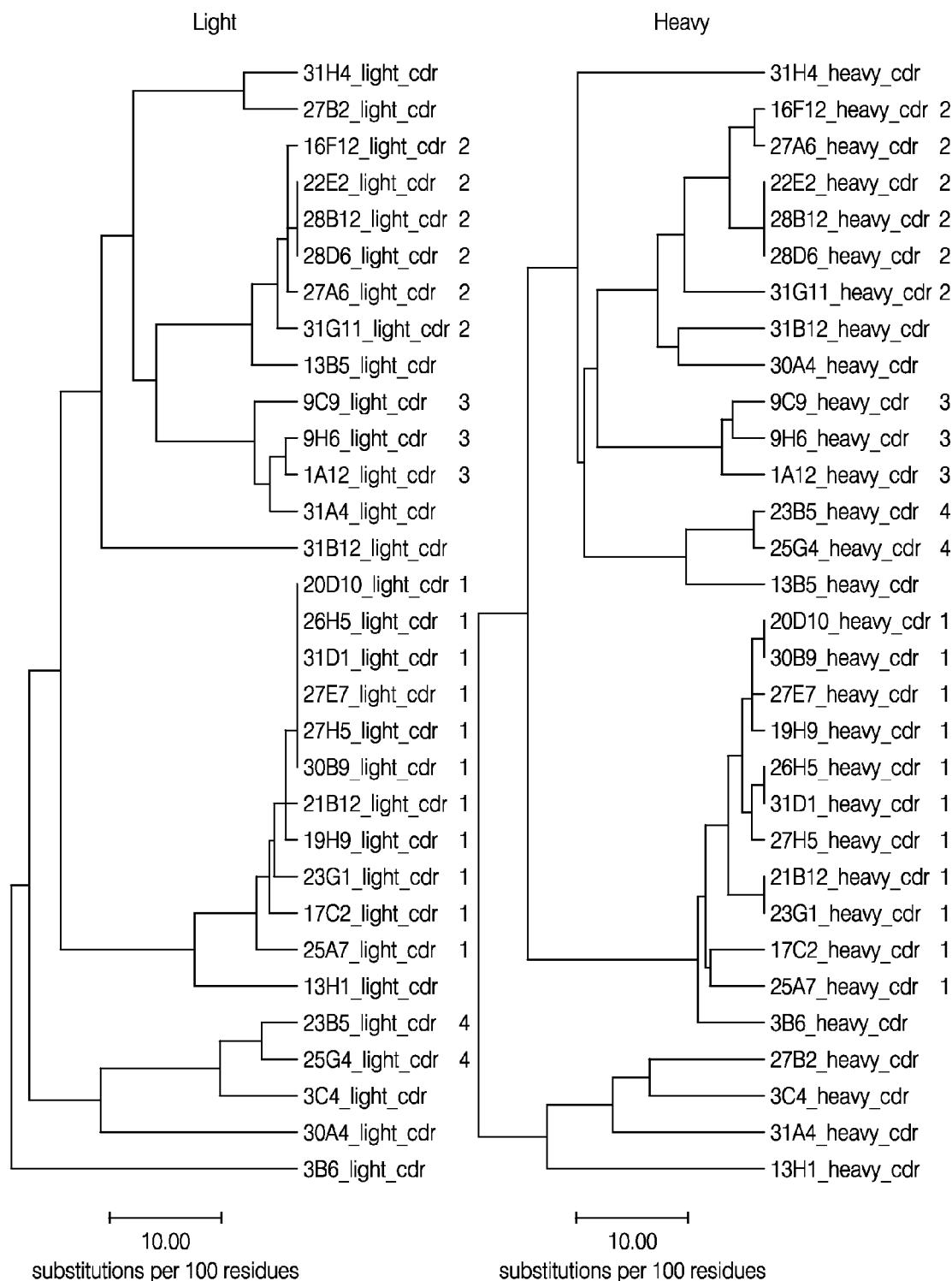


FIG. 13E

Consensus for Group 1:

Consensus for Group 2:

GPIHTSYGIG	(SEQ ID NO:168)	WISAYINGNNTYAQKVQG	(SEQ ID NO:174)	GYGMGV
PIL	(SEQ ID NO:168)	I A	Q V	(SEQ ID NO:174)
SLT	(SEQ ID NO:169)	I A	Q V	(SEQ ID NO:174)
SLT	(SEQ ID NO:170)	I A	Q V	(SEQ ID NO:174)
ALT	(SEQ ID NO:171)	N F E	Q H	(SEQ ID NO:175)
ALT	(SEQ ID NO:171)	N F E	Q H	(SEQ ID NO:175)
21B12	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:176)
21B12	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:176)
22G1	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:177)
22G1	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:177)
26H5	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:178)
31D1	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:178)
27H5	(SEQ ID NO:171)	I F E	Q V	(SEQ ID NO:179)
117C2	(SEQ ID NO:172)	I A	P H	(SEQ ID NO:181)
25A7	(SEQ ID NO:173)	T F P	*	(SEQ ID NO:181)

Consensus for Group 2:

22E2	light	heavy	cdr	(SEQ ID NO:188)	TWNDSNKYADSVKG	(SEQ ID NO:191)	ATAALYYYYGMDY	(SEQ ID NO:195)
28B12	light	heavy	cdr	(SEQ ID NO:188)	N NK	(SEQ ID NO:191)	A AL	(SEQ ID NO:195)
28D6	light	heavy	cdr	(SEQ ID NO:188)	N NK	(SEQ ID NO:191)	A AL	(SEQ ID NO:195)
16F12	light	heavy	cdr	(SEQ ID NO:189)	N DE	(SEQ ID NO:192)	A AL	(SEQ ID NO:195)
27A6	light	heavy	cdr	(SEQ ID NO:188)	S S	(SEQ ID NO:193)	A AL	(SEQ ID NO:195)
31G1	light	heavy	cdr	(SEQ ID NO:190)	H NH	(SEQ ID NO:194)	G VA	(SEQ ID NO:196)

EIC 13E

FIG. 13E

Consensus for Group 3:

9H6_light_heavy_cdr	S_GS_SS_NI_GS_NT_VN	(SEQ ID NO:197)	S_NN_RR_PS	(SEQ ID NO:199)	A_AW_DD_SL_NW_V	(SEQ ID NO:201)
1A12_light_heavy_cdr	K	(SEQ ID NO:198)	S R S	(SEQ ID NO:199)	[REDACTED]	
9C9_light_heavy_cdr	K	(SEQ ID NO:198)	R Q I	(SEQ ID NO:200)	[REDACTED]	

9H6_light_heavy_cdr	GFTFSSRYWMS	(SEQ ID NO:202)	N_IR_HD_GS_ER_YY_VD_SV_KG	(SEQ ID NO:205)	E_SN_WG_FA_FD_V	(SEQ ID NO:207)
1A12_light_heavy_cdr	E N_R	(SEQ ID NO:203)	Q	(SEQ ID NO:206)	I	(SEQ ID NO:208)
9C9_light_heavy_cdr	F S_V	(SEQ ID NO:204)	Q	(SEQ ID NO:206)	I	(SEQ ID NO:208)

Consensus for Group 4:

23B5_light_heavy_cdr	F_AS_QS_IS_SY_IN	(SEQ ID NO:209)	A_AS_IS_OS	(SEQ ID NO:211)	Q_QS_YS_SP_IT	(SEQ ID NO:213)
25G4_light_heavy_cdr	H	(SEQ ID NO:210)	A	(SEQ ID NO:212)	A	(SEQ ID NO:214)

23B5_light_heavy_cdr	GFTFSSYAMN	(SEQ ID NO:215)	T_IS_GS_GD_NT_YY_AD_SV_KG	(SEQ ID NO:216)	K_FV_LM_VA_MD_Y	(SEQ ID NO:218)
25G4_light_heavy_cdr	[REDACTED]		G	(SEQ ID NO:217)	[REDACTED]	

FIG. 13G

Group 1 (11 members)

LV_CDR1

LV_CDR1	SEQ_ID	LV_CDR2	SEQ_ID	LV_CDR3	SEQ_ID	H_CDR1	SEQ_ID	H_CDR2	SEQ_ID	H_CDR3	SEQ_ID
1	TGTSSDVGGYNSVS	305	EVSNRPS	306	SSYTSTSVM	307	SYGIS	308	WISAYNGNTNYAQKVQG	309	GYGMDV
CONSENSUS	R.....	311S.V.	313	317	308	314V...
25A7	A.....	316N..	312	319	308V	318V...
17C2	305T	321	N.....	319	308V.F	316F...
21B12	305	312	307	308V.F	320L...
23G1	N.....	322	312	307	308V.F	320L...
19H9	305	312	307	308V	323V...
27H5	305	312	307	308V	323V...
26H5	305	312	307	308F	324F...
31D1	305	312	307	308F	324F...
27E7	305	312	307	308	309
20D10	305	312	307	308	309
30B9	305	312	307	308	309

Group 2 (6 members)

chain:

<u>LV_CDR1</u>	<u>SEQ</u>	<u>LV_CDR2</u>	<u>SEQ</u>	<u>LV_CDR3</u>	<u>SEQ</u>
ID	ID	ID	ID	ID	ID
NO:	NO:	NO:	NO:	NO:	NO:
1	SGSSSNTGNFV S	32.5	DYNKRPS	326	GTWDDSSLGGYV
CONSENSUS	32.5	.S.....	331A..
31G11	32.5	326
28D6	32.5	326
28B12	32.5	326
22E2	32.5	326
1.6F12	32.5	326A..
27A6	32.5	326S..

FIG. 13H

Group 2, continued	Heavy chain:	H_CDR1	SEQ ID NO:	H_CDR2	SEQ ID NO:	H_CDR3	SEQ ID NO:
CONSENSUS	SFGMH	328	LIWNDGSNKKYADSVKG	329	AIAALYYYYGMDV	330	
31G11	.Y....	333	...H....T...V....	334	G...VA.....	335	
28D6	328	329	330	
28B12	328	329	330	
22E2	328	329	330	
16F12	328	...S...DE.....	336	330	
27A6	328	...S...D.....	338	330	

FIG. 13I

Group 3 (3 members)		LV_CDR1		LV_CDR2		LV_CDR3		H_CDR1		H_CDR2		H_CDR3	
		SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:
1													62
CONSENSUS	SGSSSNIGSKTVN	339	SNNRPPS	340	AAWDDSLINWV	341	YWMS	342	NIKQDGSEKYYDSVKG	343	ESNWGFAFDI	344	
9H6N...	345	340	341	R.....	346H.....	347V	348	
9C9	339	R...Q..L	349	341	S.....	350	343	344	
1A12	339	340	341	NF...	351	343	344	

Group 4 (2 members)		KV_CDR1		KV_CDR2		KV_CDR3		H_CDR2		H_CDR3		SEQ	
		SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:
1													
CONSENSUS	RASQTS YLN	352	AA SLQS	353	QQSYS PIT	354							
25G4I...	355	..A.....	356A...	357							
23B5S...	358	..S.....	359S...	360							

Group 5 (2 members)		H_CDR1		H_CDR2		H_CDR3		SEQ	
		SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:	SEQ ID	NO:
CONSENSUS	SYAMN	361	TISGSG NTYYADSVKG	362	KFTVLMVYAMLDY	363			
25G4	361G.....	364	363			
23B5	361D.....	365	363			

FIG. 13J

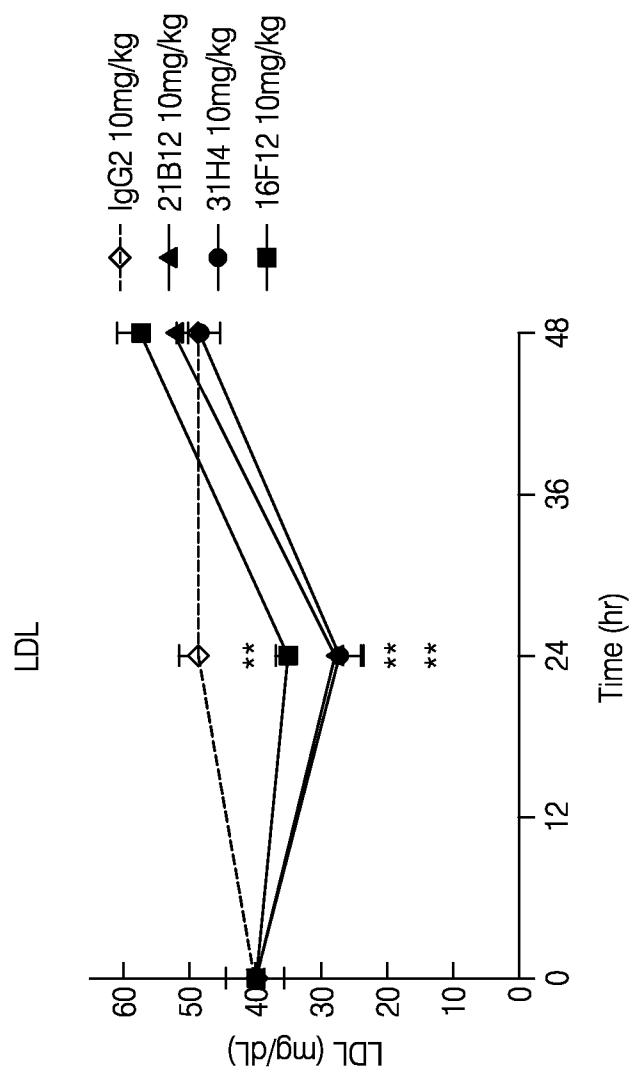


FIG. 14A

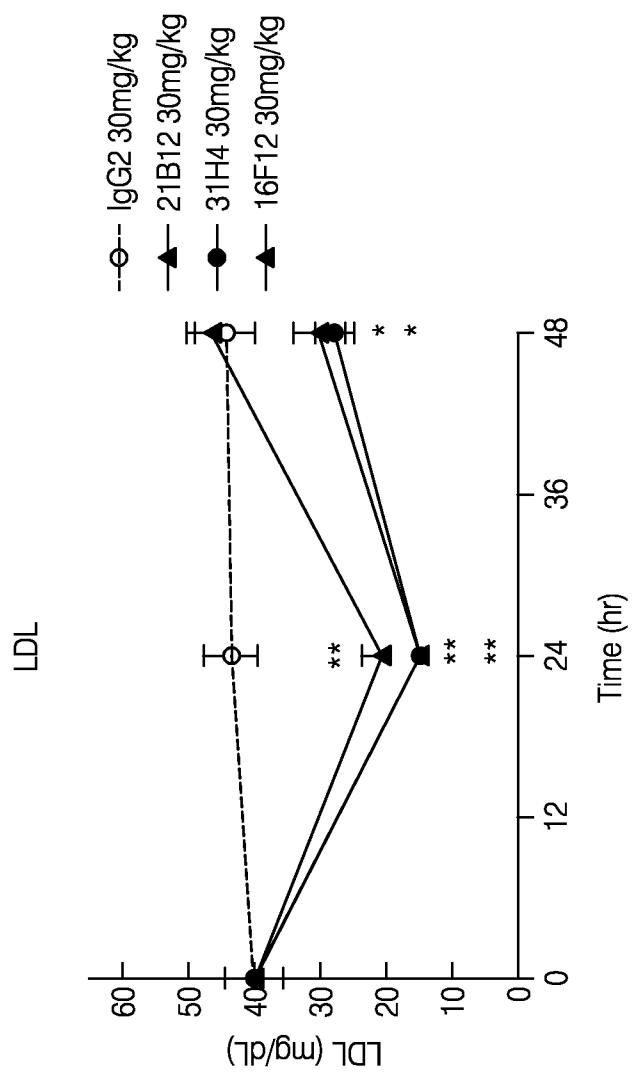


FIG. 14B

Chain Name	V	D	J	FR1	CDR1	FR2	SEQ ID NO:
Germline							
26E10.1	V1-4		JL2	QSLTQPASVSGSEFQSQITISC	TGTSSDVGGYYNVS	WYQQHPGKAPKLMIV	14
26E10	V1-4		JL2	-----	-----S--	-----	270
17C2.1	V1-4		JL2	-----F-----	-----S--	-----	23
17C2	V1-4		JL2	-----	-----A-S--	-----R---	271
				-----	-----A-S--	-----R---	24
Germline							
9C9.1	V1-16	JL3		QSVLTQPPSASGTPGQRTISC	SGSSSNIGSNTVYN	WYQQLPGTAPKLLIV	29
9C9.2	V1-16	JL3		-----P-----	-----	-----	272
				-----P-----	-----	-----	273
Germline							
31A4.2	V2-1	JL2		SYELTQPPSVSVSPGQTASITC	SGDKLGDKYAC	WYQQKGQSPVLIY	274
				-----R-----	-----	-----	275
Germline							
25A7.1	V2-1	JL2		SYELTQPPSVSVSPGQTASITC	SGDKLGDKYAC	WYQQKGQSPVLIY	276
				-----I-----	-----	-----R-----I-----	277

FIG. 15A

Chain Name	CDR2	FR3	CDR3	FR4	SEQ ID NO:
26E10.1	EVSNRPS	GVSNRFGSGSKSGNTASLTISGLOQAEDEADYYC --F-----	SYYTSSSS#V N----T-M-	FGGGTGTKLTIVL -----	14 270
26E10	-----	-----	N----T-M-	-----	23
17C2.1	-----	-----	-----TNM-	-----	271
17C2	-----	-----	-----TNM-	-----	24
9C9.1	SNNQRPS	GVPDRFSGSKSGTSASLAISGLOQSEDEADYYC ---R---	AAWDDSLN#V -----W-	FGGGTGTKLTIVL -----W-	29 272
9C9.2	-----R---	-----	-----W-	-----	273
31A4.2	QDSKRPS	GIPERFSGNSNSGNTATLTISGTQAMDEADYYC -NT-W-L -----K-----V	QAWDSSTVV -----	FGGGTGTKLTIVL -----	274 275
25A7.1	QDSKRPS	GIPERFSGNSNSGNTATLTISGTQAMDEADYYC ---T---	QAWDSSTAVV -----	FGGGTGTKLTIVL -----	276 277

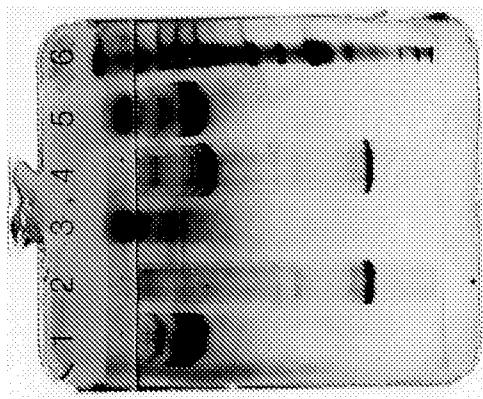
FIG. 15B

Chain Name	V	D	J	FR1	CDR1	FR2	SEQ ID NO:
26E10.1	VH1-18		JH6B	QVQLVQSGAEVKPGASVKVSCKAS	GYTFTSYGILS	WVRQAPGQGLEWMG	47
26E10	VH1-18		JH6B	-----	--L--	-----	49
17C2.1	VH1-18		JH6B	-----	--L--	-----	49
17C2	VH1-18		JH6B	-----	--S--	-----	57
				-----	--S--	-----	57
				-----	--S--	-----	
Germline							
9C9.1	VH3-7	D7- 27	JH3B	EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYWSMS	WVRQAPGKGLEWVA	63
9C9.2	VH3-7	D7- 27	JH3B	-----	--VV-	-----	64
				-----	--VV-	-----	401
				-----	--VV-	-----	
Germline							
25A7.1	VH4-59	D6- 19	JH4B	QVQLQESGPGLVKPSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG	400
				-----	--T--	-----	278
				-----	--T--	-----	

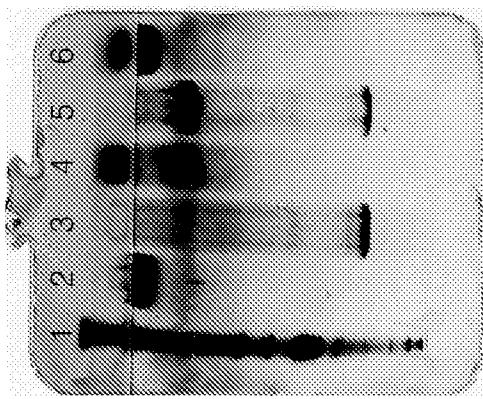
FIG. 15C

Chain Name	CDR2	FR3	CDR3	FR4	SEQ ID NO:
WISAYNGNTNYAQKLQG 26E10.1	-V-F-----	-G-----P-----	#YGMDV G-----	WGQGTTVTVSS -----	47 49
-V-F----- 26E10	-V-F-----	-G-----P-----	G-----	-----	49
-V-----F--- 17C2.1	-V-----F---	-----	G-V---	-----	57
-V-----F--- 17C2.2	-V-----F---	-----	G-V---	-----	57
NIKQDGSEKYYDSVKKG 9C9.1	-----	RFTISRDNAKNSLYLQMNSLRAEDDTAVYYCAR -----	#NWG#AFDI ES----F-----	WGQGTMVTVSS -----	63 64
----- 9C9.2	-----	-----	ES----F-----	-----	401
----- YIYSGSTNYPNSLKS 25A7.1	-----	RTVTISVDTTSKNQFSLKLSVTAADTAVYYCAR -----	#YSSGW##FDY GS----FE-----	WGQGTIVTVSS -----	400 278

FIG. 15D



1. 31H4
2. ProCat
3. VD
4. ProCat + 31H4
5. VD + 31H4
6. Std



1. Std
2. 21B12
3. ProCat
4. VD
5. ProCat + 21B12
6. VD + 21B12

FIG. 16B

FIG. 16A

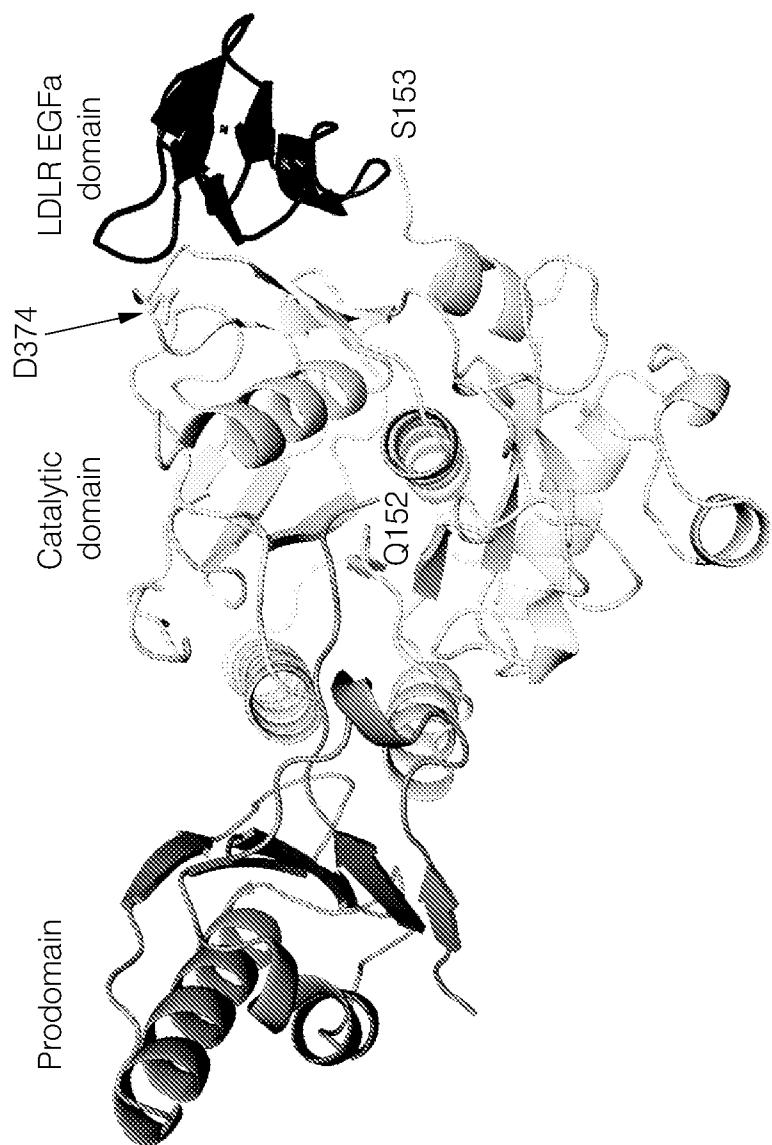


FIG. 17

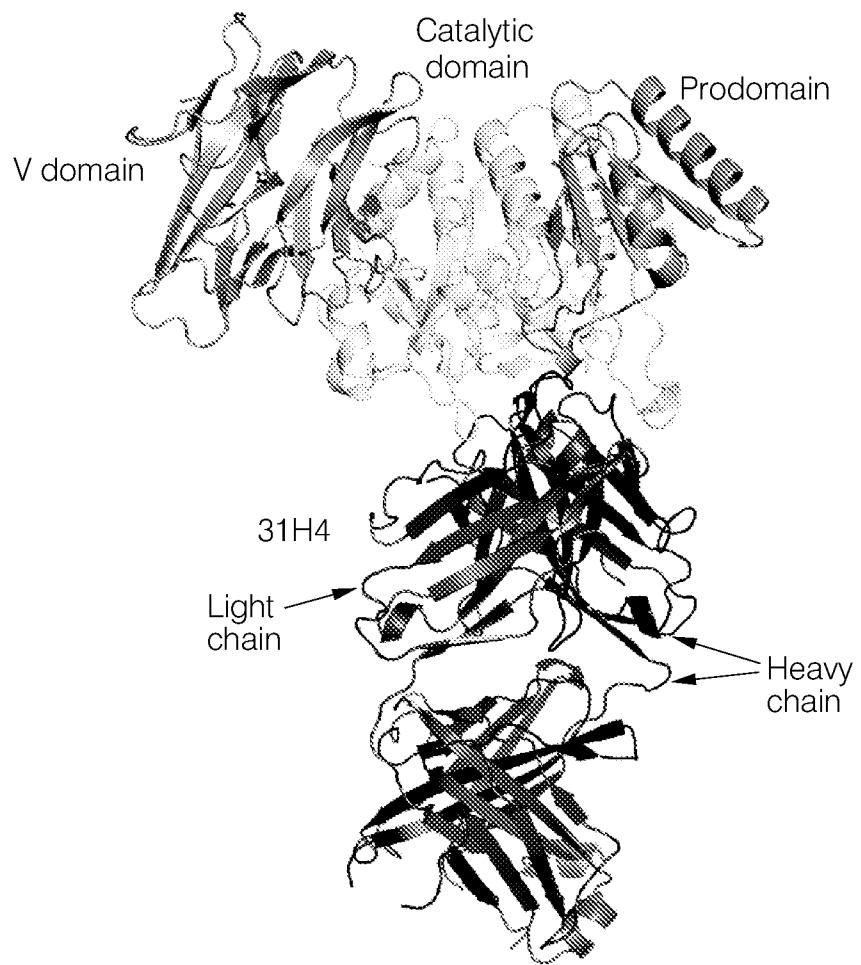


FIG. 18A



FIG. 18B

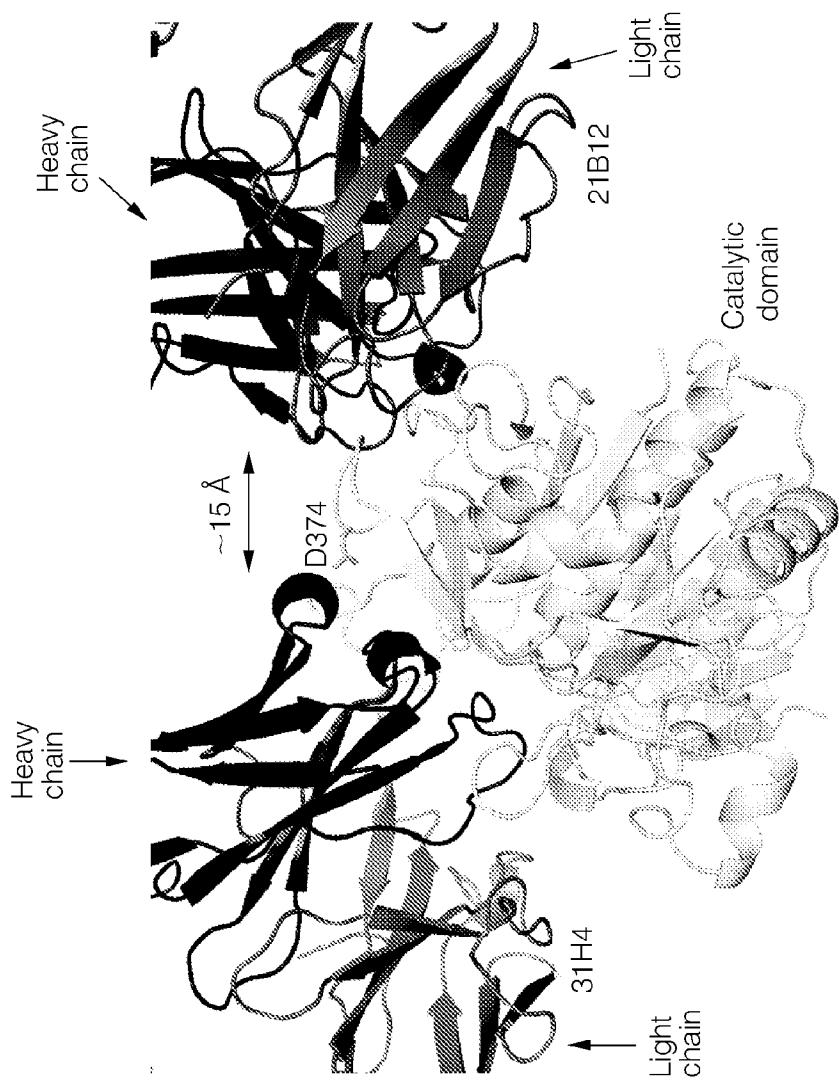


FIG. 19A



FIG. 19B

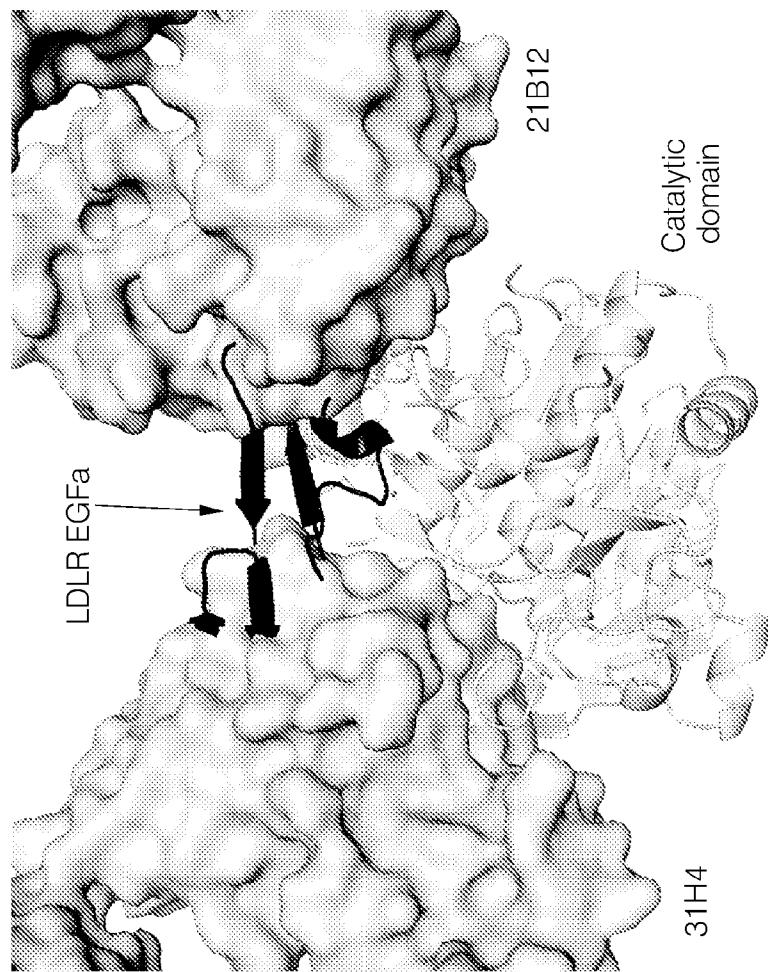


FIG. 20A

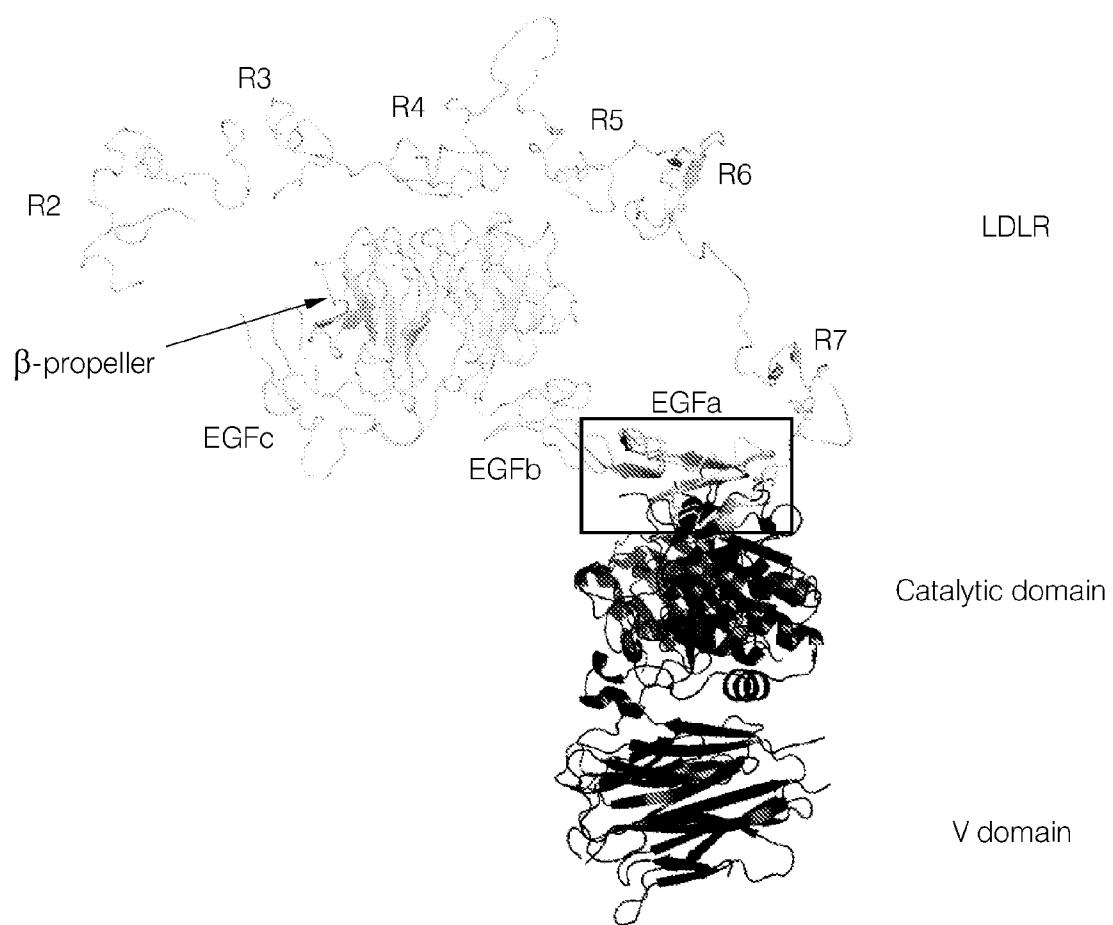


FIG. 20B

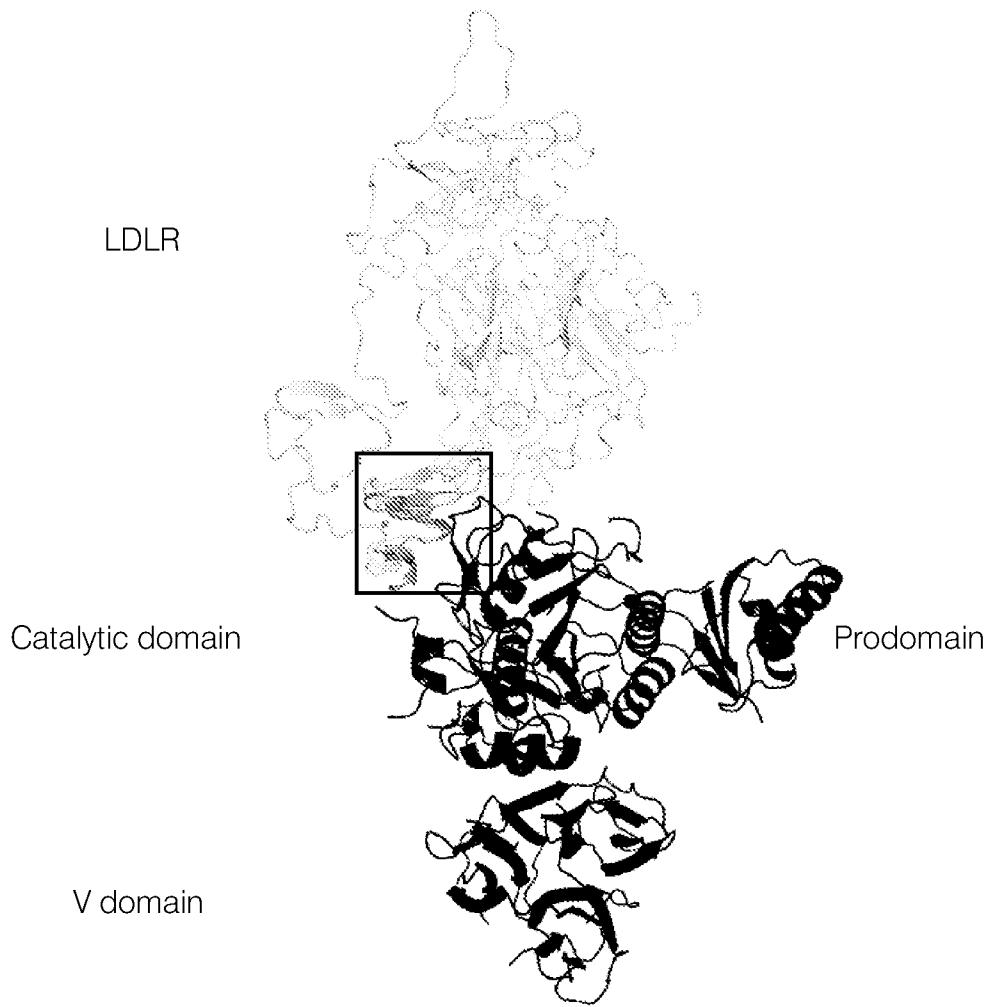


FIG. 20C

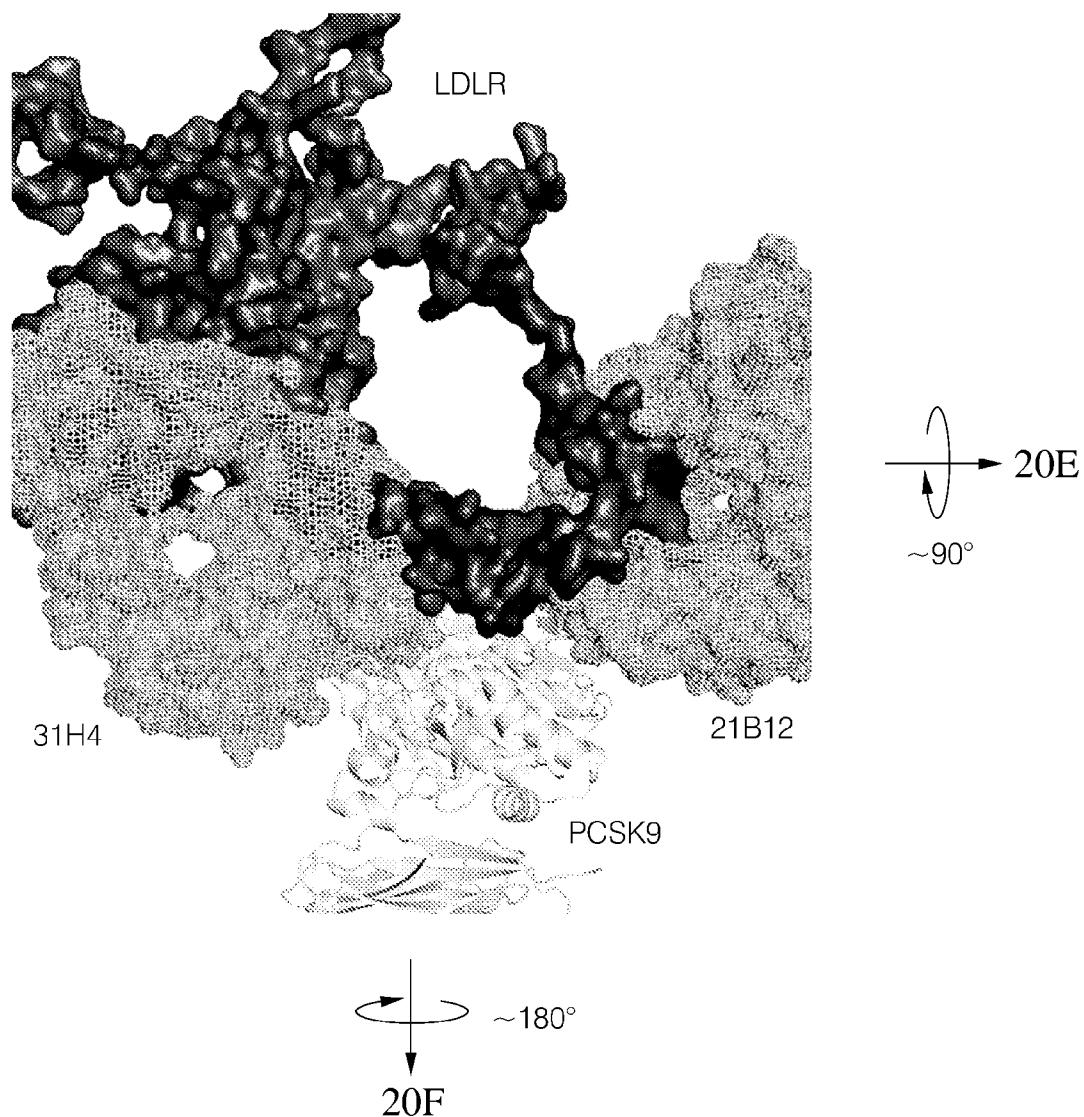


FIG. 20D

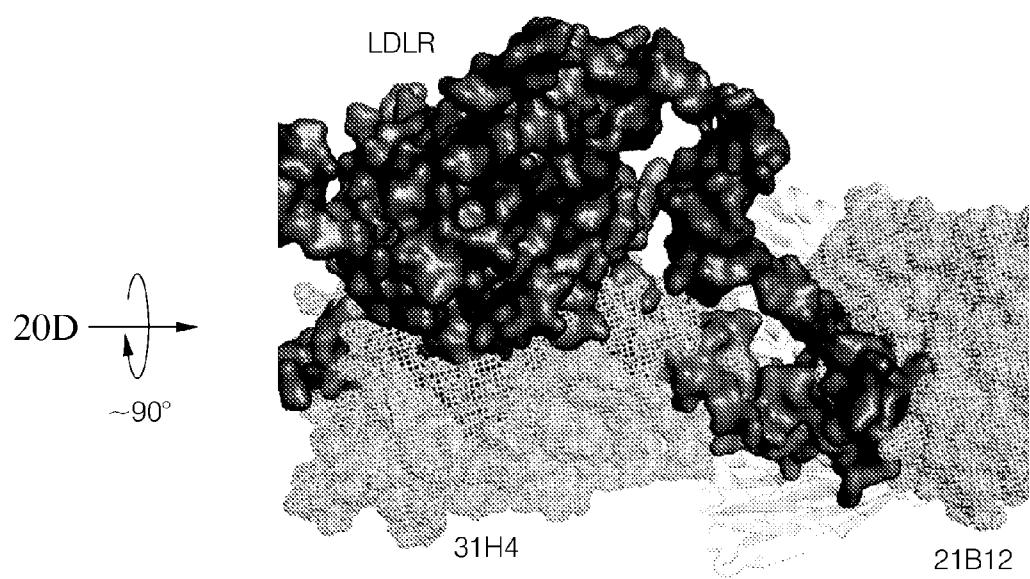


FIG. 20E

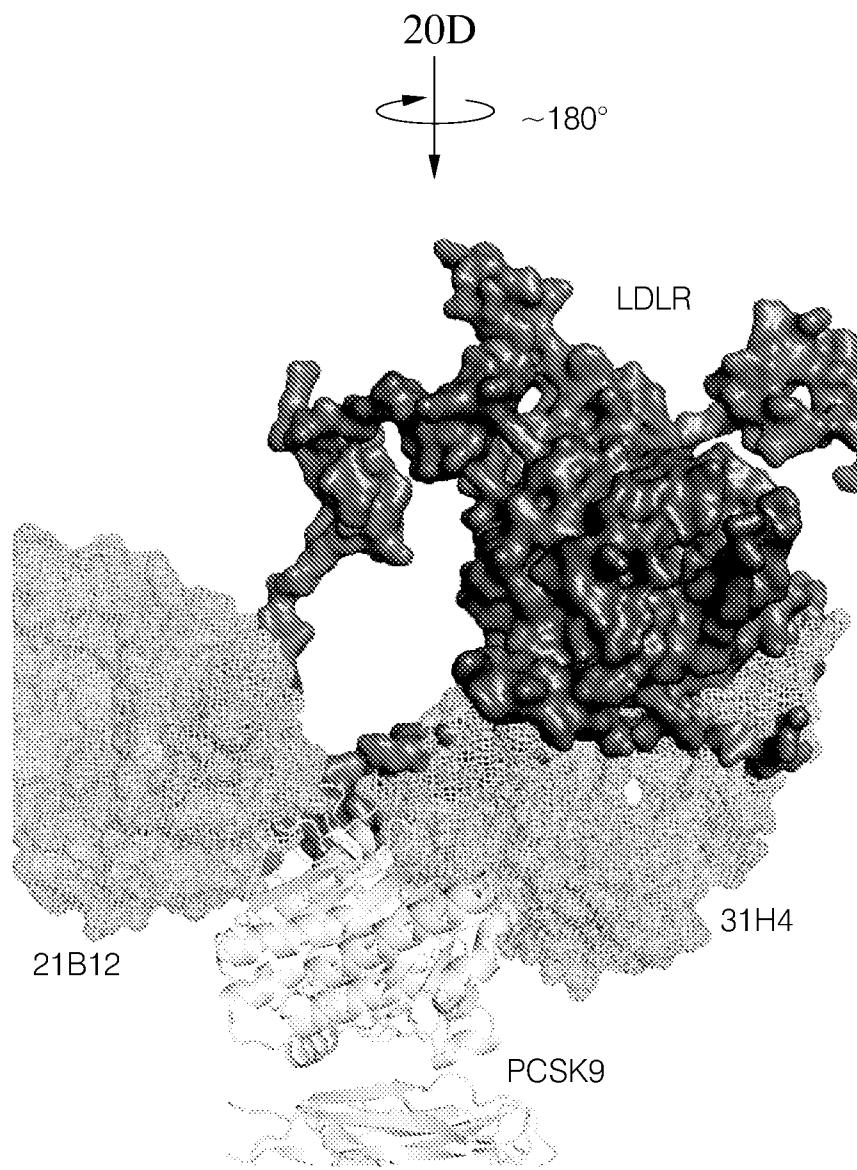


FIG. 20F

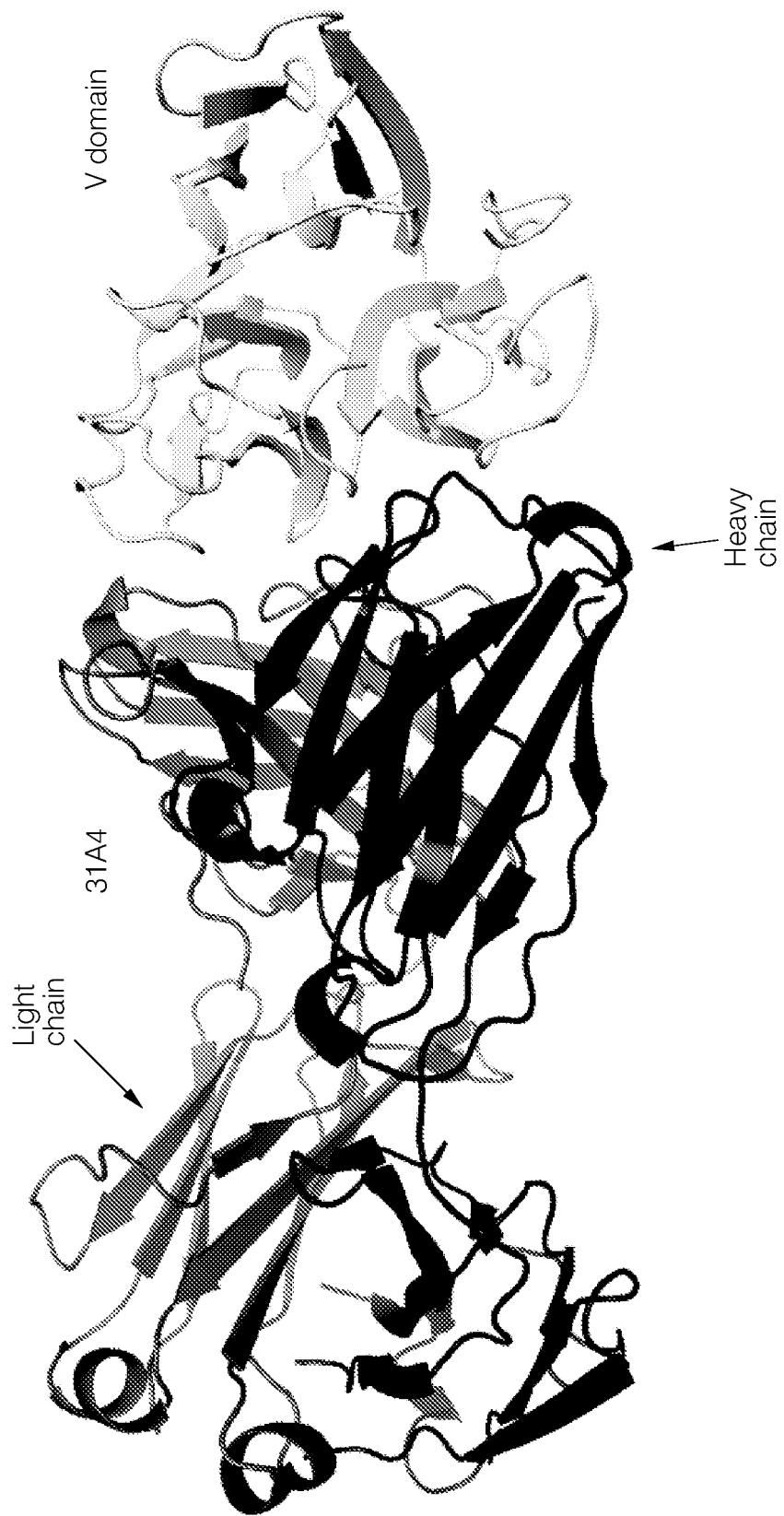


FIG. 21A

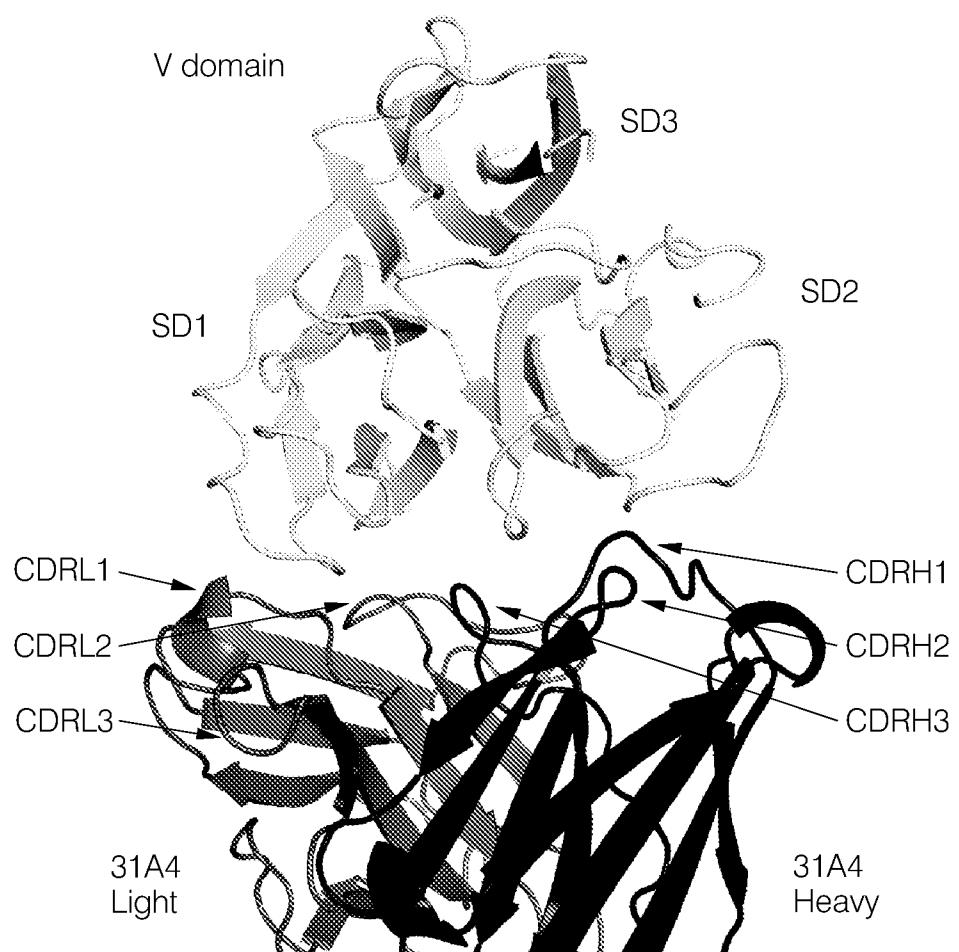


FIG. 21B

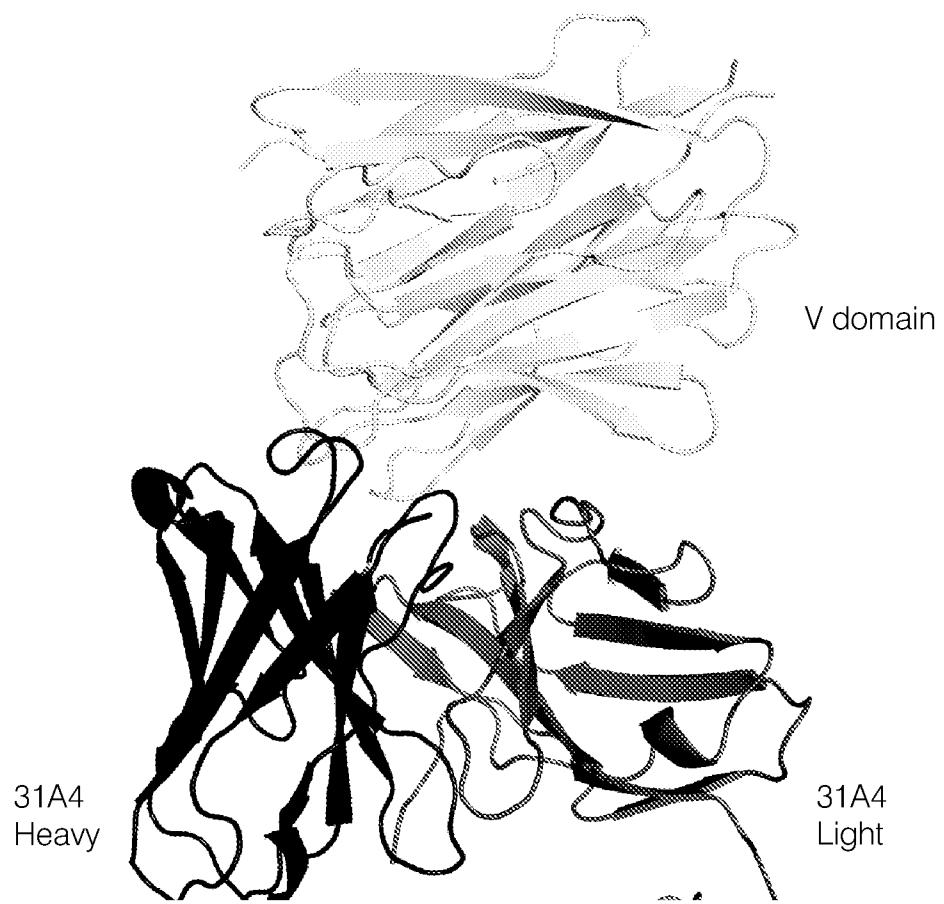


FIG. 21C

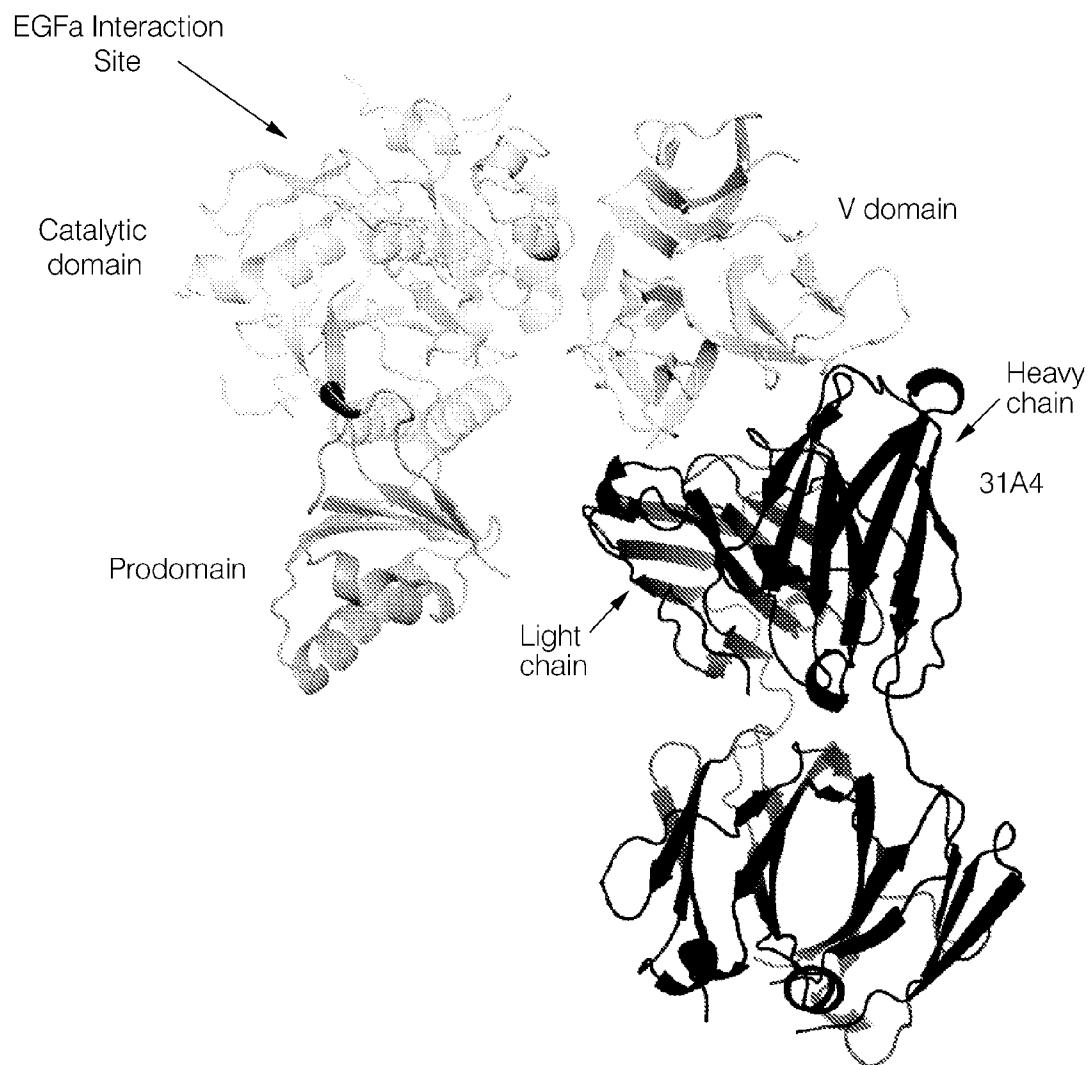


FIG. 21D

21B12Light Chain

ESALTQFASV SGSPGQSITI SCTCTSSDVG CYNCSVWYQQ HPGKAPKLMY YEVSNRPSGV SNRFSGSKSG NTASLTISCL QAEDEADYYC NSYTSTSMVF CGCTKLTVLG QPKAAPSVTI FPPSSEELQA NKATLVC LIS DFYPGAVTVA WKADSSPVKA GVEETTPSKQ SNNKYAASSY LSILTPEQWKS HRSYSCQVTH EGSTVEKTVA PTECS (SEQ ID NO:297)

Heavy Chain

EVQIVQSCAE VKKPGASVKV SCKASGYTLT SYCISWVRQA PGQGLEWMGW VSFYNGNTNY AQKLQGRGTM TTDPSTSTAY MEIRSLRSDD TAVYYCARGY GMDVWGQGTT VTSSASTKG PSVFLAPSS KSTSGGTAA L GCLVKDYFPE PVTVSWNSGA LTSGVHTFPV VLQSSGLYSL SSVVTPSSS LGTQTYICNVN HKPSNTKVD KVVEPKSCAAE DPKDHHHHHHH (SEQ ID NO:298)

31H4Light Chain

ESVLTQFFSV SGAPGQRVTI SCTGSSSNIG AGYDVHWYQQ LPGTAPKLLI SGNSNRPSGV PDRFSGSKSG TSASLAITCL QAEDEADYYC QSYDSSLGS VFGGGTKLTV LGQPKAAPS TLFPPSSEEL QANKATLVC ISDFYPGAVT VAWKADSSPV KAGVETTPS KQSNNKYAA SYLSLTPEQW KSHRSYSCQV THEGSTVEKT VAPTECS (SEQ ID NO:299)

Heavy Chain

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNVWRQA PGKGLEWVSS ISSSSSYISY ADSVKGRFTI SRDNNAKNSLY LQMNSLRAED TAVYFCARDY DFWSAYYDAF DVWGQGTMVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV TVSWNSGALT SCVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKVEPKSCAADE VDHHHHHHHH (SEQ ID NO:300)

31A4Light Chain

ALQSVLTQPP SASGTPGQRV TISCSGSSSN IGSNTVNWYQ QLPGTAPKLL IYSNNQRPSG VPDRFSGSKS GTSASLAISG LQSEDEADYY CAVWDDSLNG WVFGGGTKLT VLQPKAAPS VTLFPPSSEE LQANKATLVC LISDFYPGAV TVAWKADSSP VKAGVETTP SKQSNNKYAA SSYLSLTPEQ WKSHRSYSCQ VTHEGSTVEK TVAPTECS (SEQ ID NO:301)

Heavy Chain

QVQLQQWCAG LLKPSETLSL TCAVYGGFS AYYWNWIQRP PGKGLEWIGE INHSGRTDYN PSLKSRVTIS VDTSKKQFSL KLNSTVAAADT AVYYCARGQL VPFDYWQGQT LTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS HSSVVTVPSS SLGTQTYICN VHKPSNTKV DKKVEPKSCAADE VDHHHHHHHH (SEQ ID NO:302)

FIG. 22

FIG. 23A

		BIN 1													
bead	region	9	12	21	38	45	60	74	84		20	23	42	92	96
BIN 1	c5cne	01A12.2	03B6.1	09C9.1	17C2.1	21B2.2	23G1.1	25G4.1	26E1.0.1		11H4.1	11H8.1	19H9.2	26H5.1	27H7.1
	01A12.2	41	34	108	43	73	25	26	26		15	22	-1	40	-27
	03B6.1	60	69	107	44	76	49	53	49		60	69	6	41	17
	09C9.1	47	49	89	27	83	25	39	42		44	39	-18	22	1
	17C2.1	43	34	135	-2	58	14	47	12		53	75	-4	22	-28
	21B12.2	37	42	125	2	96	21	49	39		38	9	-19	50	-5
	23G1.1	29	41	114	-4	62	26	35	16		39	37	-13	34	-26
	25G1.1	16	59	91	-13	61	10	35	5		34	12	-17	28	-20
	26E1C.1	30	50	73	-5	61	-10	22	26		-5	17	-36	9	-33
	11H4.1	49	72	135	64	99	51	34	49		40	52	19	58	-3
	11H8.1	37	49	118	27	72	39	33	30		34	46	-27	41	4
	19H9.2	30	15	103	-53	39	-20	-23	-23		-5	-26	-51	-25	-33
	26H5.1	39	49	133	1	84	46	33	41		34	24	36	59	50
	27E7.1	19	25	92	-10	44	16	15	1		27	13	9	5	-115
	27H5.1	29	49	170	-12	159	11	49	73		69	-13	-26	68	-47
BIN 1.1	30B9.1	53	39	156	8	94	57	-06	53		72	35	-20	62	8
	02B5.1	42	67	130	61	126	85	33	83		47	62	15	80	23
	23B5.1	5	33	53	-29	11	-16	-16	-17		4	17	-55	-14	-15
	27B2.6	48	38	133	36	76	11	54	34		21	21	5	37	35
	09H6.1	59	110	118	120	289	289	73	289		75	63	-20	289	121
BIN 2	27B2.1	-62	161	258	-07	195		118	133		187	224	93	141	98
	27B2.5	-130	115	197	35	153	97	92	94		177	93	113	51	
	12H11.1	30	46	89	35	70	26	35	26		41	42	-4	57	-11
BIN 3	16F12.1														
	22B2.1														
	27A6.1														
	28B12.1														
	26D6.1														
	31G11.1														
	31H4.1														
	00A1.2														
BIN 3.1	08A3.1														
	11F1.1														
BIN 4 non-comp	11G1.5	1486	1738	1225	1229	2444	2215	2800	2493		2463	2243	2234	2232	2403
	03C4.1	1487	1739	1248	1239	2453	2234	2831	2493		2331	2048	2422	2884	2438
BIN 5	A30AA.1	45	62	125	60	107	39	48	42		40	59	-17	45	8
	B13B5.1	13103	1318	1392	1382	1612	1164	1318	1116		1303	1123	1381	1403	1312
	C13H1.1	13126	1328	1206	1203	1656	1393	2081	1832		2356	1223	2023	2030	1363
	D31A4.1	21438	2308	1460	1453	2443	1435	2422	1453		2384	1246	2354	1468	2403
	E31B12.1	21323	2362	1429	1430	2426	1434	2393	1430		2249	1208	2373	1413	2438
LOW SIGNAL	05H5	65	93	109	-02	135	107	57	14		66	87	69	110	43
	20A5	53	52	-20	32	67	32	49	58		61	77	4	52	-13
	20E5	56	54	129	44	63	19	39	24		71	64	-4	37	3
	22B11	43	56	127	41	49	20	49	34		51	41	20	20	12
	24D9	62	59	116	34	63	32	73	37		60	65	22	42	34
	24F7	72	80	127	81	106	59	38	62		70	71	17	81	20
	30P1	34	56	102	30	46	24	35	35		47	50	-6	45	-5
	hutTg3	91	155	163	-16	57	22	-5	18		31	87	-57	8	-71

FIG. 23B

BIN 1.1						BIN 2						BIN 3					
97	63	72	50	33	28	95	26	25	34	46	91	55	56	69	71		
705.1	3039.1	02B5.1	23B5.1	27B2.6	09B6.1	27B2.1	27B2.5	-12H-1.1	-16J-12.1	22J2.1	27A6.1	28J12.1	29D6.1	31G11.1	31H4.1	0	
-30	-18	62	4	-5	112	53	53	16	1833	1832	1833	1832	1832	1748	1834		
9	11	109	25	60	131	86	73	43	1830	1830	1830	1830	1830	1830	1830		
29	5	90	21	-6	123	79	50	47	1829	1829	1829	1829	1829	1829	1829		
-37	-9	122	33	22	174	63	42	32	1828	1828	1828	1828	1828	1828	1828		
-18	-18	72	5	31	190	69	76	46	1827	1827	1827	1827	1827	1827	1827		
4	31	42	21	-9	164	70	71	8	1826	1826	1826	1826	1826	1826	1826		
-2	-31	97	13	-1	153	45	51	41	1825	1825	1825	1825	1825	1825	1825		
-41	-71	61	-27	-20	122	44	61	23	1824	1824	1824	1824	1824	1824	1824		
						72	80	36	1823	1823	1823	1823	1823	1823	1823		
-22	9	59	34	-7	163	76	49	43	1822	1822	1822	1822	1822	1822	1822		
-34	-5	81	15	6	131	46	55	1	1821	1821	1821	1821	1821	1821	1821		
80	98	9	84	9	133	76	71	26	1820	1820	1820	1820	1820	1820	1820		
-62	-17	49	-14	8	163	69	26	-13	1819	1819	1819	1819	1819	1819	1819		
-30	-55	-14	-14	4	141	72	59	31	1818	1818	1818	1818	1818	1818	1818		
10	101	92	1	22	213	104	72	34	1817	1817	1817	1817	1817	1817	1817		
-30	-41	-16	12	43	176	99	75	37	1816	1816	1816	1816	1816	1816	1816		
23	1	88	22	32	164	24	17	5	1815	1815	1815	1815	1815	1815	1815		
82	74	30	-39	19	71	63	63	37	1814	1814	1814	1814	1814	1814	1814		
27	-11	72	-10	-21	183	132	-9	55	1813	1813	1813	1813	1813	1813	1813		
130	-12	113	50	79	151				1812	1812	1812	1812	1812	1812	1812		
						48	60	54	203	220	286	275	281	229	100		
78	57	256	77	126	334	39	34	42	165	159	182	181	176	192	85		
52	44	185	48	97	234	32	34	11	84	105	85	93	90	118	72		
-42	-24	75	18	25	96												
						-63	-74	-149	-162	-152	-132	-133	-126	-101	-189		
						91	88	-102	59	45	55	60	73	63	24		
						77	94	32	40	87	31	62	38	67	13		
						87	75	76	27	36	56	46	37	43	9		
						88	92	93	45	12	52	61	61	77	57		
						96	77	38	11	27	56	33	34	82	23		
						72	89	38	31	31	31	70	81	70	85	31	
						40	35	21	53	60	63	75	69	95	19		
						27	28	21	70	64	75	65	78	65	16		
						68	56	24	68	56	24	68	56	24	68	26	
						163	-51	333	893	863	783	773	873	753	733		
						-20	13	67	25	6	173	51	34	16	125	68	
						163	163	163	163	163	163	163	163	163	163	163	
						163	163	163	163	163	163	163	163	163	163	163	
						163	163	163	163	163	163	163	163	163	163	163	
						163	163	163	163	163	163	163	163	163	163	163	
						70	40	95	46	29	179	31	26	36	122	107	
						-7	6	92	27	31	175	16	13	7	83	87	
						-9	-1	107	7	-4	179	95	87	99	91	99	
						-13	-13	106	6	7	180	53	53	53	53	53	
						-58	-17	91	16	-3	175	163	163	163	163	163	
						12	15	119	25	47	232	163	163	163	163	163	
						-37	-8	83	23	21	171	163	163	163	163	163	
						-89	-102	154	12	-76	223	163	163	163	163	163	

FIG. 23C

BIN 3.1			BIN 4 non-comp			A			B			C			D			LOW SIGNAL																																																																					
76	77	78	18	16	61	30	32	64	66	3044.1	13P5.1	13A1.1	3' A4.1	31R'2.1	36	37	40	49	51	62	36	37	40	49	51	62																																																													
BA1.2	08A3.-	11F1.1	11G1.5	03C4.-	3CA4.1	13P5.1	13A1.1	3' A4.1	31R'2.1	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3815	8385	8385	8385	8385	1	603	1289	2075	372	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3816	8385	8385	8385	8385	26	794	1325	3076	545	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3817	8385	8385	8385	8385	17	625	1650	1972	390	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3818	8385	8385	8385	8385	87	1C29	1297	3741	808	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3819	8385	8385	8385	8385	49	957	1358	3740	990	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3820	8385	8385	8385	8385	35	1C03	1352	3554	903	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3821	8385	8385	8385	8385	10	883	1732	2492	504	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3822	8385	8385	8385	8385	70	1C75	1288	3742	944	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3823	8385	8385	8385	8385	17	763	1813	2205	419	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3824	8385	8385	8385	8385	19	749	1714	2292	421	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3825	8385	8385	8385	8385	31	1397	4385	834	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																													
3826	8385	8385	8385	8385	13	1480	4306	950	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																													
3827	8385	8385	8385	8385	99	1618	4092	894	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																													
3828	8385	8385	8385	8385	134	1718	4552	887	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																													
3829	8385	8385	8385	8385	113	1570	3684	1050	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																													
3830	8385	8385	8385	8385	34	750	1889	2458	517	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3831	8385	8385	8385	8385	-25	679	1440	2493	392	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3832	8385	8385	8385	8385	-11	608	1487	3325	605	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
3833	8385	8385	8385	8385	54	823	1889	2552	470	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
90	155	91	378	199	52	679	989	997	167	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
63	119	70	329	134	49	604	865	873	390	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
27	56	36	472	167	16	198	538	755	259	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
-136	-151	-154	141	141	141	365	1C08	2868	633	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
52	66	5	66	66	66	669	1671	3970	1033	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
65	85	20	85	85	85	665	1697	3825	1033	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
26	50	3	50	50	50	614	1645	3457	983	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
51	54	59	54	54	54	743	1828	4214	1055	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
61	62	40	62	62	62	624	1737	4100	1074	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
87	39	18	39	39	39	764	1800	4260	1142	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
36	41	42	817	635	12	256	757	512	238	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
29	36	29	882	639	19	271	779	514	230	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
24	32	27	797	528	16	228	654	486	219	36	37	40	49	51	62	36	37	40	49	51	62	36	37	40	49	51	62																																																												
298	3885	3885	3885	3885	102	344	291	1335	1886	1305	33	44	13	7	21	51	36	37	40	49	51	62	36	37	40	49	51	62																																																											
3886	3885	3885	3885	3885	60	572	793	1677	1091	24	51	11	17	1	46	36	37	40	49	51	62	36	37	40	49	51	62																																																												
34	50	44	314	314	0	181	1637	2706	511	5	14	12	1	1	32	36	37	40	49	51	62	36	37	40	49	51	62																																																												
270	320	320	314	314	362	1790	437	663	15	1C03	23	33	31	31	33	60	85	13	38	32	33	60	85	13	38	32	33																																																												
3887	3885	3885	3885	3885	314	188	1637	2706	511	616	2652	2073	2289	2232	2912	2169	78	61	56	52	53	53	78	61	56	52	53	53																																																											
3888	3885	3885	3885	3885	321	188	51	547	265	21	188	457	403	216	10	10	2	8	4	13	6	5	5	16	6	5	16																																																												
22	43	29	198	58	265	74	1	178	565	525	229	3	203	594	520	234	-3	4	3	3	-6	1	1	4	1	2	1																																																												
37	47	47	265	74	262	72	3	185	545	560	234	19	250	659	614	297	2	-2	-2	2	-1	8	2	-2	-2	2	-1	8																																																											
24	52	36	262	72	230	76	9	185	545	560	234	19	250	659	614	297	2	124	599	731	201	6	12	5	-4	2	27	31	58	38	230	76	222	94	2	150	514	527	227	-63	124	599	731	201	-2	-3	-3	-5	-1	4	6	-2	-3	-5	-1	4	6	40	73	53	222	94	225	83	423	128	-63	124	599	731	201	105	136	116	32	65	37	40	49	51	62	21	-49	28	34	-2	33
31	58	38	230	76	222	94	2	150	514	527	227	-63	124	599	731	201	-2	-3	-3	-5	-1	4	6	-2	-3	-5	-1	4	6																																																										
40	73	53	222	94	225	83	423	128	-63	124	599	731	201	105	136	116	32	65	37	40	49	51	62	21	-49	28	34	-2	33																																																										

	huIgG controls		
/3	17	98	54
30F'	hu ⁻ IgG	hu ⁺ IgG	hu ⁺ IgG
1	-81	-63	-1
14	55	4	37
17	-60	-7	-13
0	63	4	14
7	-17	-19	-3
19	-5	-8	-41
-2	-17	-20	2
-3	-45	-10	3
4	-23	-33	-52
3	21	27	2
-14	-111	-93	-2
3	36	19	51
-32	-30	-17	-109
-16	74	19	-17
3	27	1	51
11	24	-33	-61
-13	-34	-80	-4
2	-6	-1	24
34	21	38	17
14	-7	19	-56
0	97	49	-48
6	-52	-21	-40
-117	-264	-189	-248
15	1	-20	36
17	-78	-47	-5
18	-33	-55	-78
29	57	22	45
9	21	-1	50
25	25	23	2
3	-5	-13	21
6	-2	36	50
4	22	-21	55
12	-10	-29	7
12	40	34	35
3	13	-14	35
3	20	28	7
-4	-46	-45	-26
36	-7	30	-27
15	1	-31	-26
4	-4	-11	-8
2	33	17	3
-1	-75	-24	14
-5	-47	-14	-19
-3	-16	-5	25
0	-19	23	-48
-4	-42	-83	-20
30	39	-4	-38

FIG. 23D

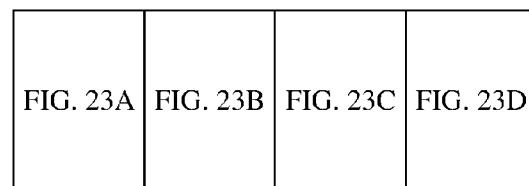


FIG. 23

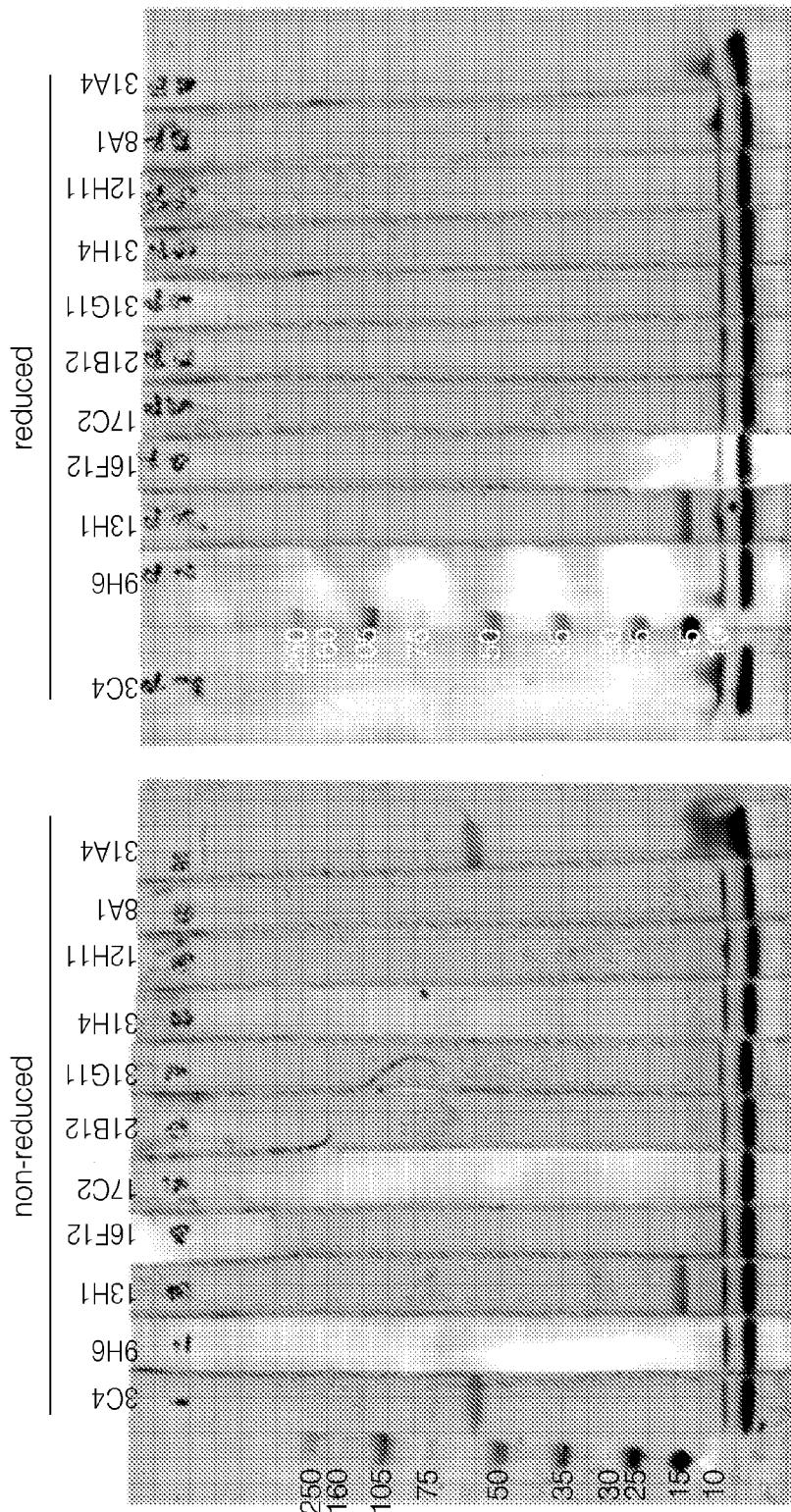


FIG. 24B

FIG. 24A

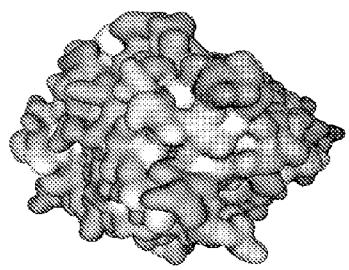


FIG. 25D

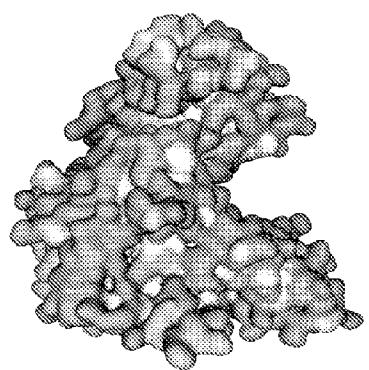


FIG. 25C

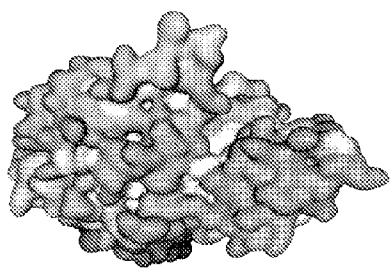


FIG. 25B

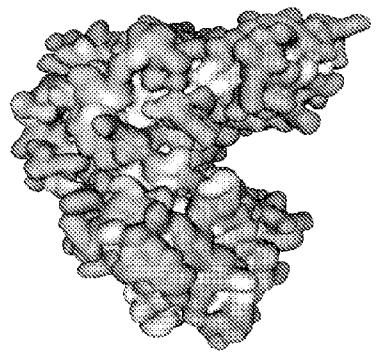


FIG. 25A

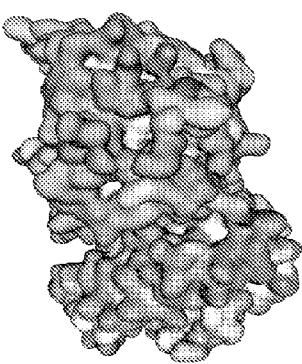


FIG. 25F

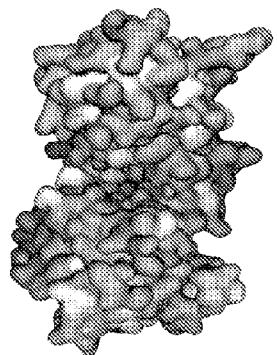


FIG. 25E

1-----50

PCSK9parent	(1) QEDEDGDYEELVLAIRSEEDGLAEAPEHGTITATEHRCAKDPWRIPGTYVV
PCSK9mutants	(1) RRRRRRRRRRRRLRRRRRRRRRRRHHRRRRRRRCRRRPWRRPGRYVV
	51--- pro domain -----100
PCSK9parent	(51) VLKEETHLQSERTARRLQQAARRGYITKILHVEHGLLPGFLVRMSGQL
PCSK9mutants	(51) VLRRRRRSRSRETAELQRRAEEGRRTKIRRERGLLPGFLVRMRRRL
	101----- -----150
PCSK9parent	(101) LELALKLPHVDYIEEDSSVFAQSIHWNLERITPPRYRADEYOPHDGGSIV
PCSK9mutants	(101) RRLARRPLPRVRYIEEDSSVERQIHWNRREIRPPRYRAARRRPHRGGRV
	151----- -----200
PCSK9parent	(151) EVYLLDTSTOSDHREIEGRVMVTDEFENVPEEDGTRFHQRQASKCDSHGTHL
PCSK9mutants	(151) EVYLLDTIRRRRHEEIIEGRVIRRERRRRRERRRRCDRRGTHL
	201----- -----250
PCSK9parent	(201) AGVVSGERAGVAKGASMRSLRVLNCGKGTVSGTLIGLEEIRKSOLVQHV
PCSK9mutants	(201) AGVVSGERAGVARARMRSLEVLNCRGRGRVSGTLIGLERIERRRRRRHR
	251----- catalytic domain -----300
PCSK9parent	(251) GPLVLLPLAGGYSRVLNAACQRALARAGVVLVTAAGNFDLDDACHYSPASA
PCSK9mutants	(251) GPLVLLPLAGNYSEVLNACRRLAENGVVLVTAAGNFDLDDACHYSPARA
	301----- -----350
PCSK9parent	(301) PEVITVGATNAQDOPVTIGTIGTNFGRCVDLFAPGEDIIGASSDCSTCFV
PCSK9mutants	(301) PEVITVGATNRRRPPVRRGRGTNFGRCVDLFAPGRRIIGASSRCSRGRH
	351----- -----400
PCSK9parent	(351) SQSGTSQAAAHVAGIAAMMLSAEHELTIAHLRQRLIHSAKDVINEAWFP
PCSK9mutants	(351) RRSGTSQAAAHVAGIAAMRLRRRHLRHLRQEIRRRSRRRFIRRRRFP
	401----- -----450
PCSK9parent	(401) EDQRVLTPNLVAALPPSTHAGGWQFCRTVWSAHSGPTRMATAIARCAHD
PCSK9mutants	(401) RRRERLTPRLVAVLPPIRRRRGRRLFCRTVWSRSGRERARAIACEAHR
	451----- -----500
PCSK9parent	(451) EELLSCSSFSRSRGKRGERMEAQGGKLVCRAHNAGCCEGVYAIARCCLLP
PCSK9mutants	(451) EELLSCSSFSRSRGKRGERMERQGGKLVCRAHNARHGRVYAIARCCLLP
	501----- v domain -----550
PCSK9parent	(501) QANCSVHITAPPAEASMGTRVHCHQGHVLTGCSHWEVEDIGTHKPFLR
PCSK9mutants	(501) QARCSVHAPPARRRGTEVRCRRGHVLTGCSHWRRRDRGTRKPHRLR
	551----- -----600
PCSK9parent	(551) PRGCPNQCVGHREASIHASCCCHAPGLECKVKEHGIPABGEQVTVACEEGW
PCSK9mutants	(551) PRGPRQCVGHREASIHASCCCHAPGLEGRRRRRIPAPRERVTVRGRGW
	601----- -----650
PCSK9parent	(601) TLTGCSALPGTSHVLGAYADNTCVRSRDVSTTGSTSEEAVTAICGR
PCSK9mutants	(601) TLTGCSALPGTSHVLGAYADNTCVRSRDRRRRRRRRERVTAVAIICGE
	651----- -----680
PCSK9parent	(651) SRHLAQASQELQGSSDYKDDDHHHHHHHHH (SEQ ID NO:303)
PCSK9mutants	(651) SEHLAQASQELQGSSDYKDDDHHHHHHHHH (SEQ ID NO:304)

FIG. 26

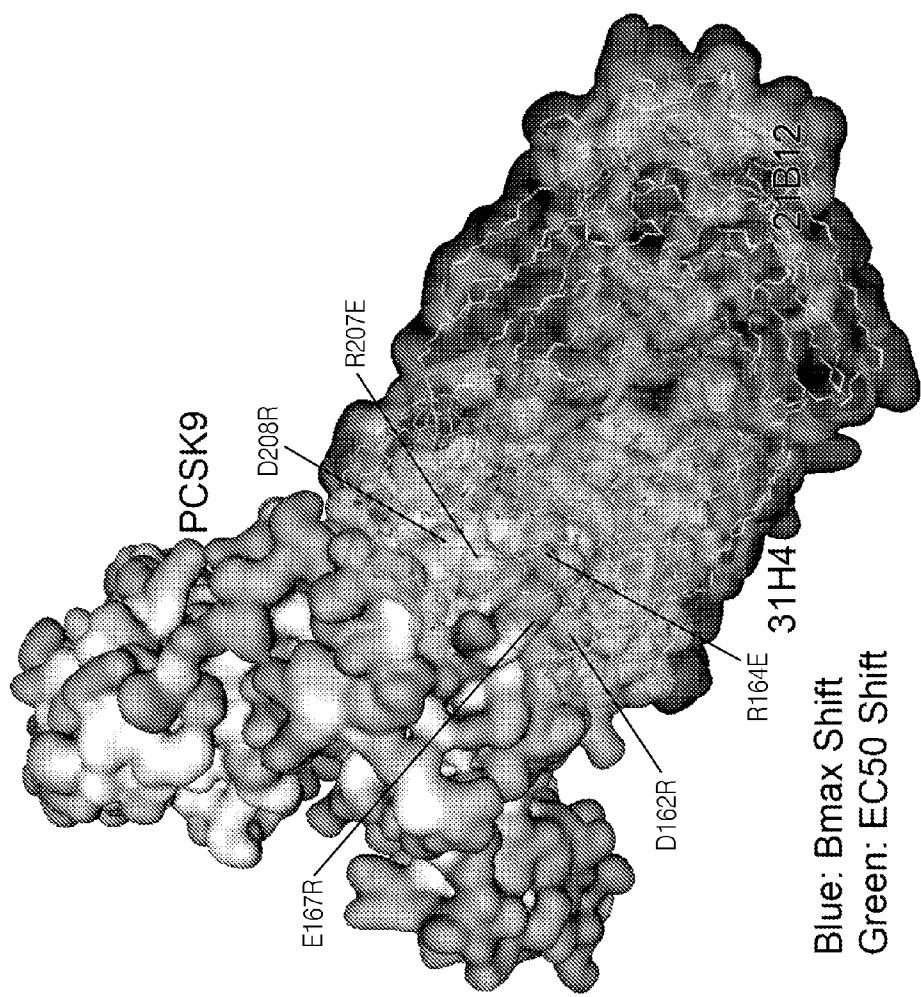


FIG. 27A

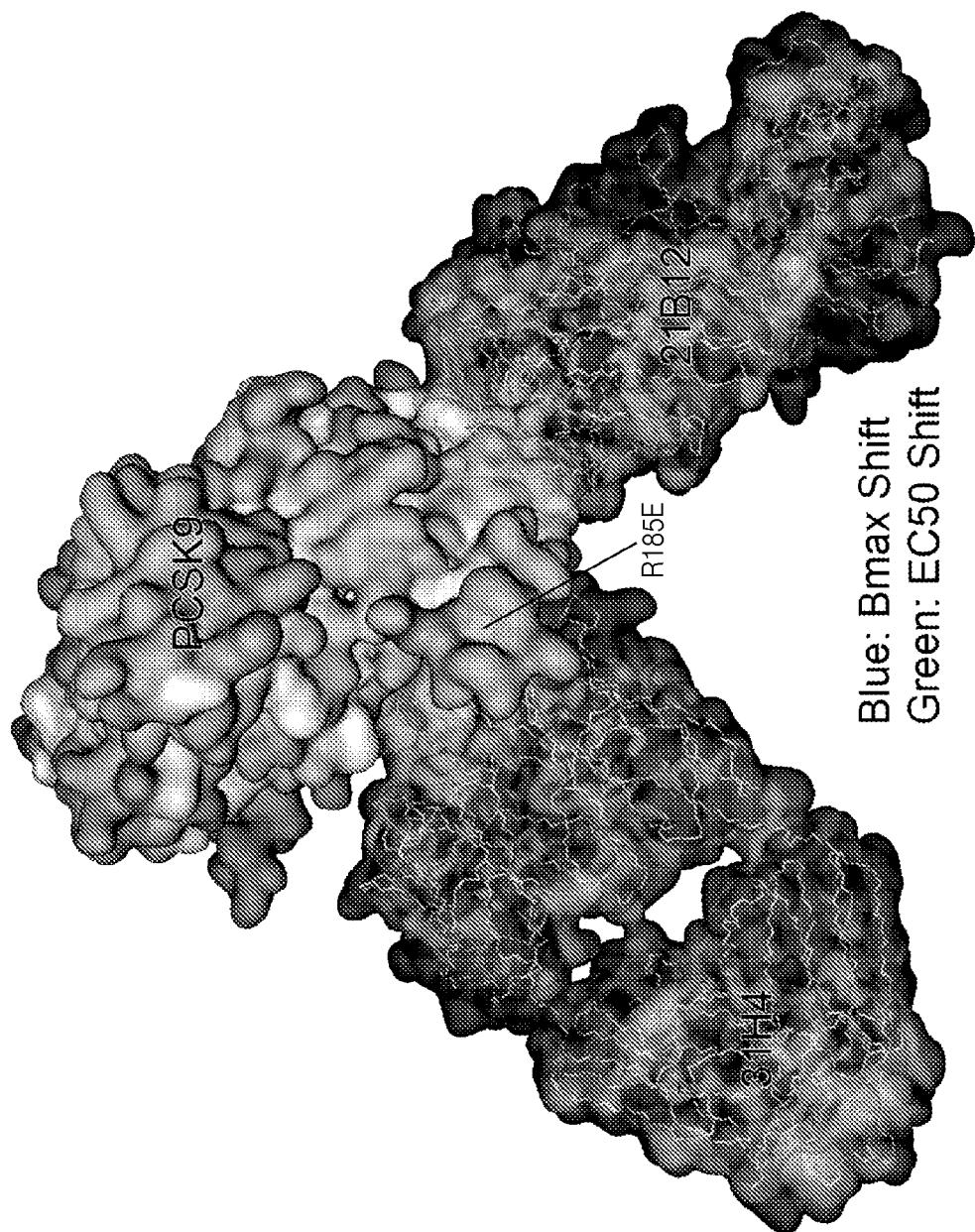


FIG. 27B

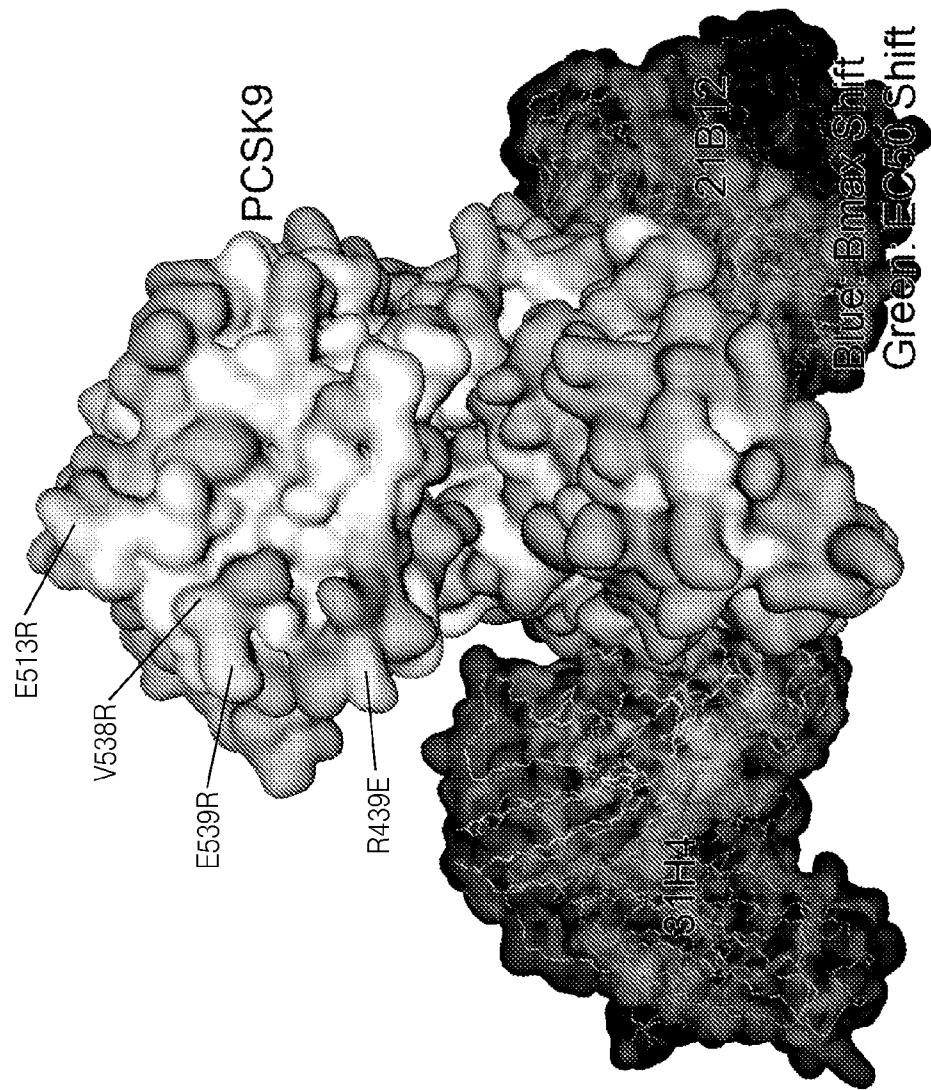
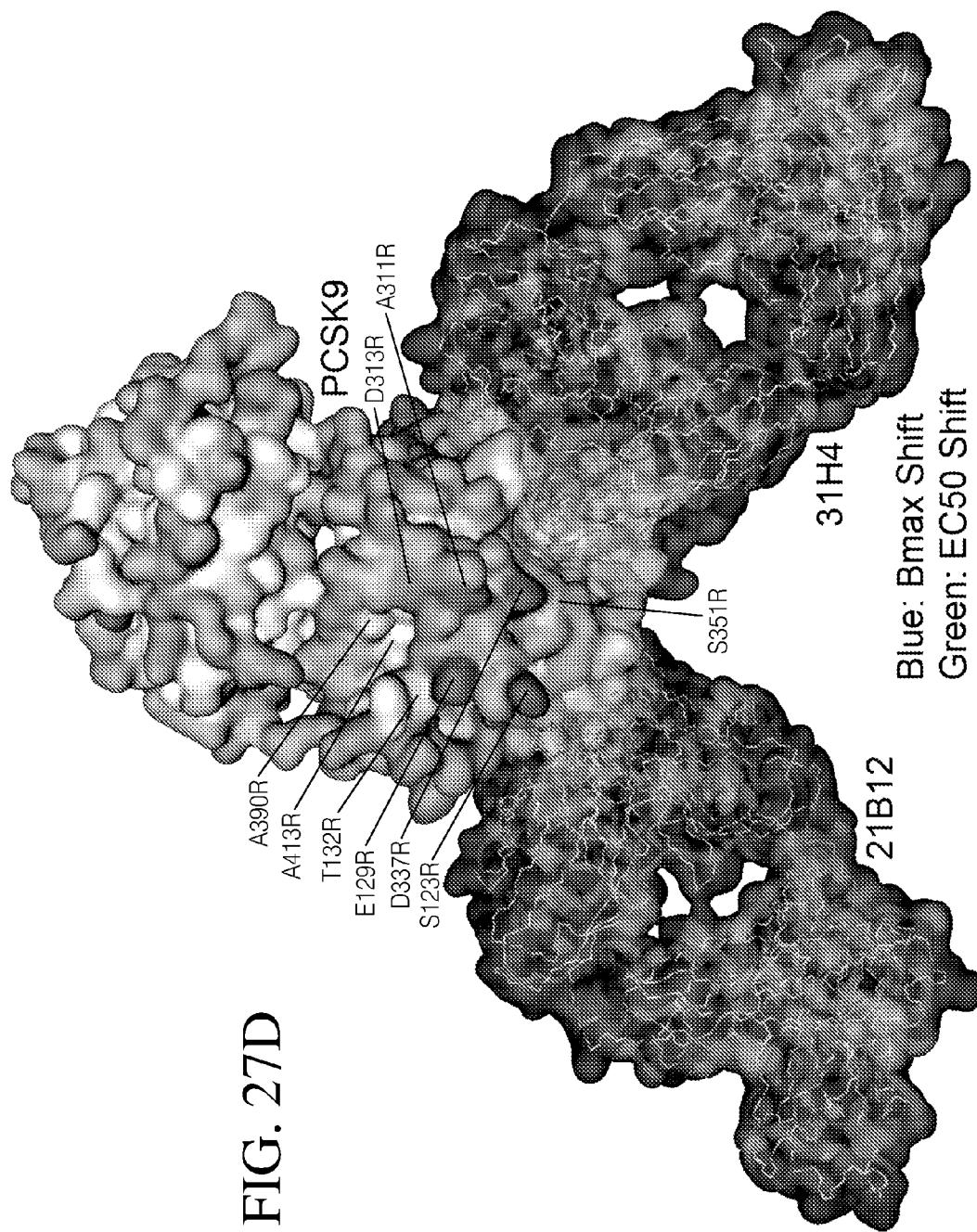


FIG. 27C



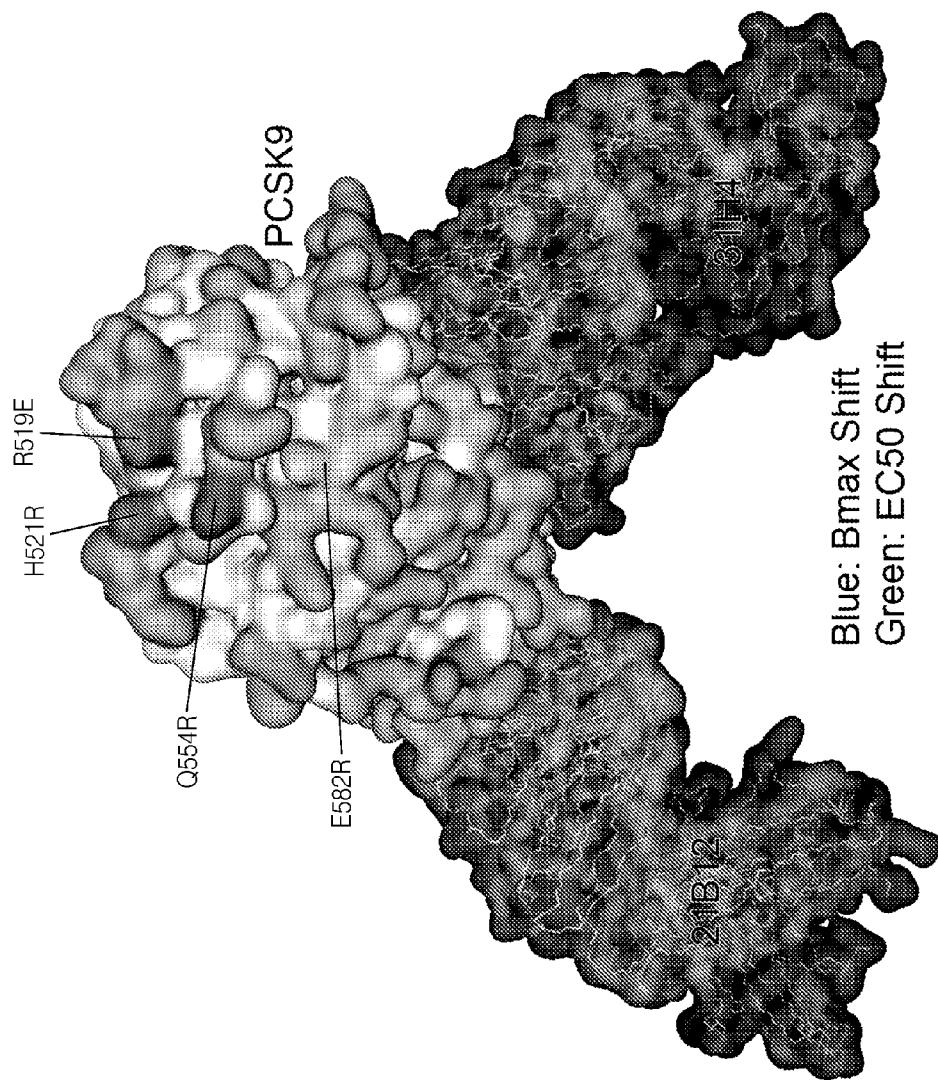


FIG. 27E

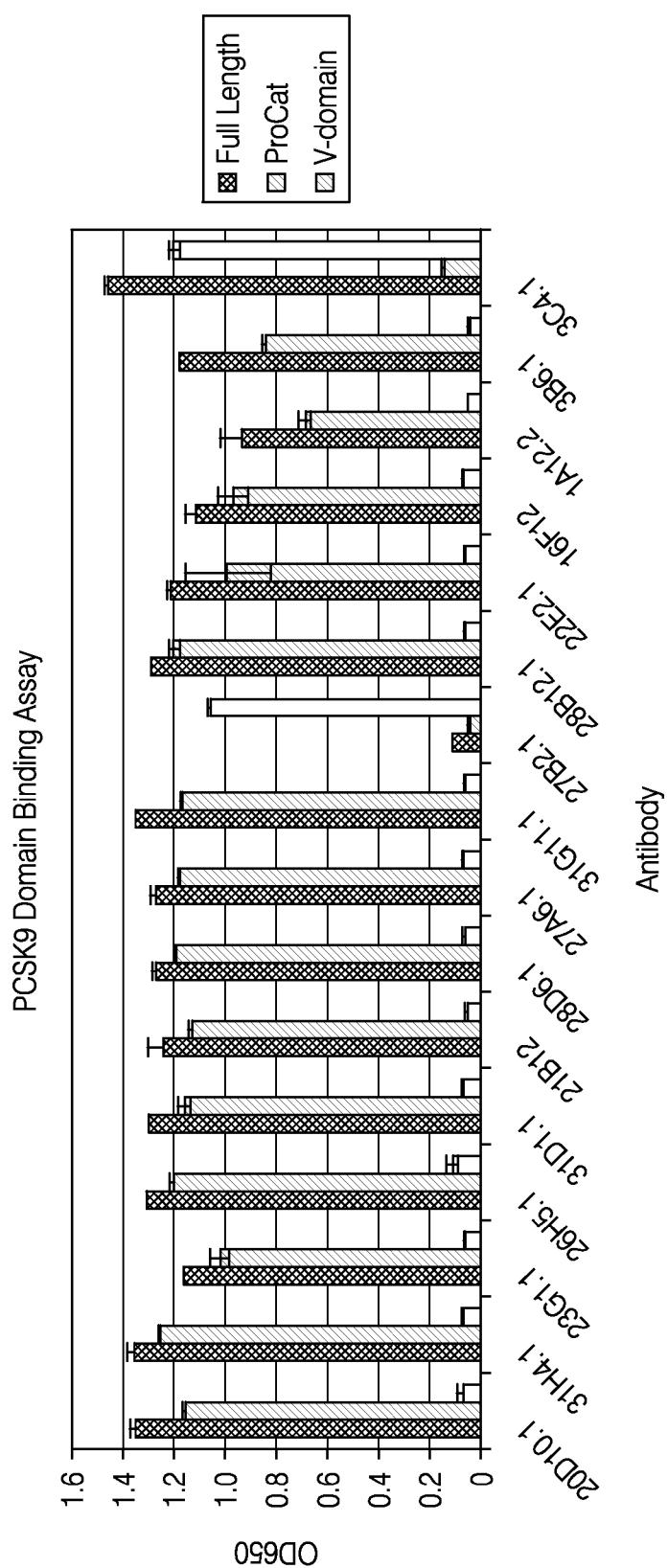


FIG. 28A

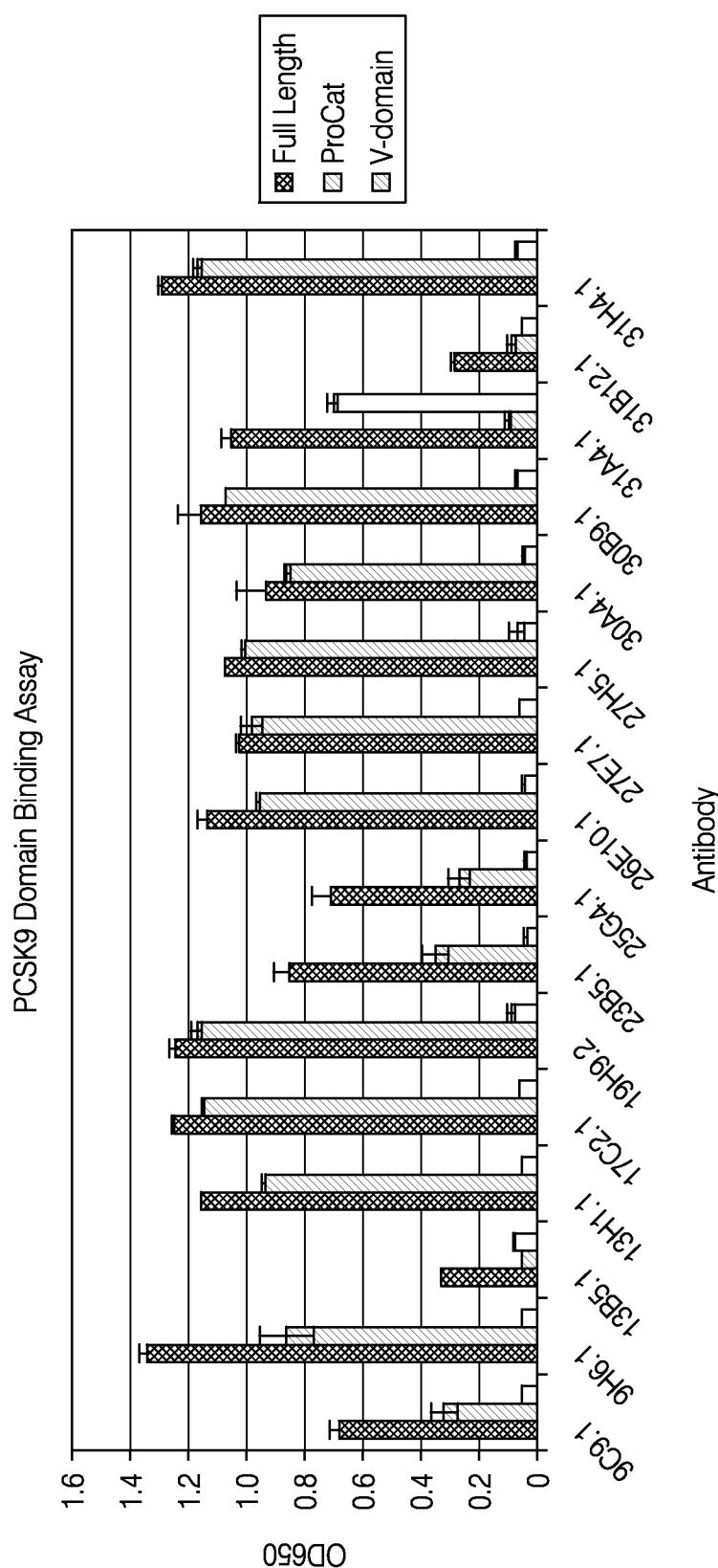


FIG. 28B

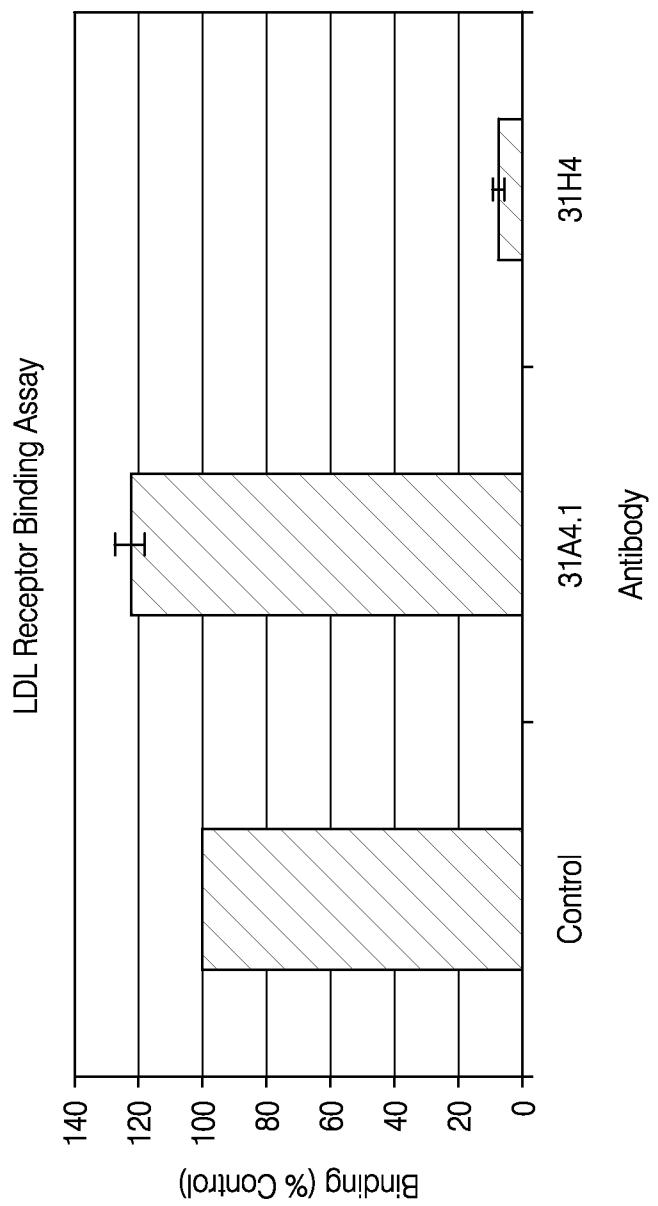


FIG. 28C

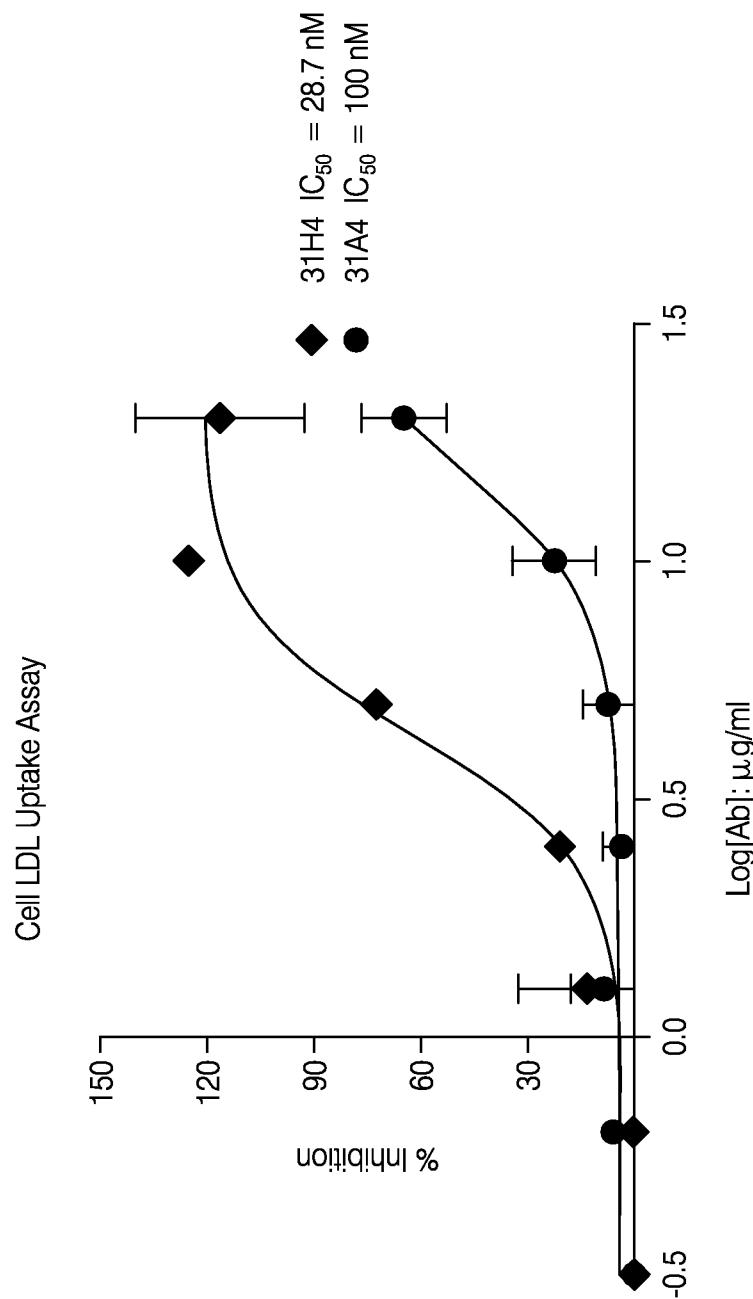


FIG. 28D

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**ANTIGEN BINDING PROTEINS TO
PROPROTEIN CONVERTASE SUBTILISIN
KEXIN TYPE 9 (PCSK9)**

RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 12/197,093, filed Aug. 22, 2008, now U.S. Pat. No. 8,030,457 which claims priority to U.S. Provisional Applications Ser. No. 61/086,133, filed Aug. 4, 2008, Ser. No. 60/957,668, filed Aug. 23, 2007, Ser. No. 61/008,965, filed Dec. 21, 2007, and Ser. No. 61/010,630, filed Jan. 9, 2008, each of which is hereby incorporated by reference in their entireties.

**SEQUENCE LISTING AND TABLES IN
ELECTRONIC FORMAT**

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled Seq_List_APMOL-003C1.txt, last saved May 26, 2009, created on May 22, 2009, which is 296,683 bytes in size, which was updated by a file entitled APMOL-00C1_Substitute.TXT, created Nov. 4, 2010, which is 297,145 bytes in size. The information in the electronic format of the Sequence Listing is incorporated herein by reference in its entirety. The present application is being filed along with a collection of Tables in electronic format. The collection of Tables is provided as a file entitled Table_35-1-4_APMOL-003C1.txt, created and last saved on May 22, 2009, which is 2,024,359 bytes in size. The information in the electronic format of the collection of Tables is incorporated herein by reference in its entirety.

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towski et al., 2006; Zhao et al., 2006). PCSK9 has been shown to directly interact with the LDLR protein, be endocytosed along with the LDLR, and co-immunofluoresce with the LDLR throughout the endosomal pathway (Lagace et al., 2006). Degradation of the LDLR by PCSK9 has not been observed and the mechanism through which it lowers extracellular LDLR protein levels is uncertain.

PCSK9 is a prohormone-proprotein convertase in the subtilisin (S8) family of serine proteases (Seidah et al., 2003). Humans have nine prohormone-protein convertases that can be divided between the S8A and S8B subfamilies (Rawlings et al., 2006). Furin, PC1/PC3, PC2, PACE4, PC4, PC5/PC6 and PC7/PC8/LPC/SPC7 are classified in subfamily S8B. Crystal and NMR structures of different domains from mouse furin and PC1 reveal subtilisin-like pro- and catalytic domains, and a P domain directly C-terminal to the catalytic domain (Henrich et al., 2003; Tangrea et al., 2002). Based on the amino acid sequence similarity within this subfamily, all seven members are predicted to have similar structures (Henrich et al., 2005). SKI-1/S1P and PCSK9 are classified in subfamily S8A. Sequence comparisons with these proteins also suggest the presence of subtilisin-like pro- and catalytic domains (Sakai et al., 1998; Seidah et al., 2003; Seidah et al., 1999). In these proteins the amino acid sequence C-terminal to the catalytic domain is more variable and does not suggest the presence of a P domain.

Prohormone-protein convertases are expressed as zymogens and they mature through a multi step process. The function of the pro-domain in this process is two-fold. The pro-domain first acts as a chaperone and is required for proper folding of the catalytic domain (Ikemura et al., 1987). Once

LENGTHY TABLES

The patent contains a lengthy table section. A copy of the table is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US08563698B2>). An electronic copy of the table will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

FIELD OF THE INVENTION

The present invention relates to antigen binding proteins that bind to proprotein convertase subtilisin kexin type 9 (PCSK9) and methods of using and making the antigen binding proteins.

BACKGROUND OF VARIOUS EMBODIMENTS

Proprotein convertase subtilisin kexin type 9 (PCSK9) is a serine protease involved in regulating the levels of the low density lipoprotein receptor (LDLR) protein (Horton et al., 2007; Seidah and Prat, 2007). In vitro experiments have shown that adding PCSK9 to HepG2 cells lowers the levels of cell surface LDLR (Benjannet et al., 2004; Lagace et al., 2006; Maxwell et al., 2005; Park et al., 2004). Experiments with mice have shown that increasing PCSK9 protein levels decreases levels of LDLR protein in the liver (Benjannet et al., 2004; Lagace et al., 2006; Maxwell et al., 2005; Park et al., 2004), while PCSK9 knockout mice have increased levels of LDLR in the liver (Rashid et al., 2005). Additionally, various human PCSK9 mutations that result in either increased or decreased levels of plasma LDL have been identified (Ko-

the catalytic domain is folded, autocatalysis occurs between the pro-domain and catalytic domain. Following this initial cleavage reaction, the pro-domain remains bound to the catalytic domain where it then acts as an inhibitor of catalytic activity (Fu et al., 2000). When conditions are correct, maturation proceeds with a second autocatalytic event at a site within the pro-domain (Anderson et al., 1997). After this second cleavage event occurs the pro-domain and catalytic domain dissociate, giving rise to an active protease.

Autocatalysis of the PCSK9 zymogen occurs between Gln152 and Ser153 (VFAQJSIP) (Naureckiene et al., 2003), and has been shown to be required for its secretion from cells (Seidah et al., 2003). A second autocatalytic event at a site within PCSK9's pro-domain has not been observed. Purified PCSK9 is made up of two species that can be separated by non-reducing SDS-PAGE; the pro-domain at 17 Kd, and the catalytic plus C-terminal domains at 65 Kd. PCSK9 has not been isolated without its inhibitory pro-domain, and measurements of PCSK9's catalytic activity have been variable (Naureckiene et al., 2003; Seidah et al., 2003).

SUMMARY OF VARIOUS EMBODIMENTS

In some embodiments, the invention comprises an antigen binding protein to PCSK9.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9 comprising: A) one or more heavy chain complementary determining regions (CDRHs) selected from the group consisting of: (i) a CDRH1 from a CDRH1 in a sequence selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; (ii) a CDRH2 from a CDRH2 in a sequence selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; (iii) a CDRH3 from a CDRH3 in a sequence selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; and (iv) a CDRH of (i), (ii), and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than 4 amino acids; B) one or more light chain complementary determining regions (CDRLs) selected from the group consisting of: (i) a CDRL1 from a CDRL1 in a sequence selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; (ii) a CDRL2 from a CDRL2 in a sequence selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; (iii) a CDRL3 from a CDRL3 in a sequence selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; and (iv) a CDRL of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than 4 amino acids; or C) one or more heavy chain CDRHs of A) and one or more light chain CDRLs of B). In some embodiments, the isolated antigen binding protein comprises at least one CDRH of A) and at least one CDRL of B). In some embodiments, the isolated antigen binding protein comprises at least two CDRH of A) and at least two CDRL of B). In some embodiments, the isolated antigen binding protein comprises said CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 and CDRL3. In some embodiments, the CDRH of A) is selected from at least one of the group consisting of: (i) a CDRH1 amino acid sequence selected from the CDRH1 in a sequence selected from the group consisting of SEQ ID NO: 67, 79, 89, and 49; (ii) a CDRH2 amino acid sequence selected from the CDRH2 in a sequence selected from the group consisting of SEQ ID NO: 67, 79, 89, and 49; (iii) a CDRH3 amino acid sequence selected from the CDRH3 in a sequence selected from the group consisting of SEQ ID NO: 67, 79, 89, and 49; and (iv) a CDRH of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than 2 amino acids. In addition, the CDRL of B) is selected from at least one of the group consisting of: (i) a CDRL1 amino acid sequence selected from the CDRL1 in a sequence selected from the group consisting of SEQ ID NO: 12, 35, 32, and 23; (ii) a CDRL2 amino acid sequence selected from the CDRL2 in a sequence selected from the group consisting of SEQ ID NO: 12, 35, 32, and 23; (iii) a CDRL3 amino acid sequence selected from the CDRL3 in a sequence selected from the group consisting of SEQ ID NO: 12, 35, 32, and 23; and (iv) a CDRL of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than 2 amino acids; or C) one or more heavy chain CDRHs of A) and one or more light chain CDRLs of B). In some embodiments, the CDRH of A) is selected from at least one of the group consisting of: (i) a CDRH1 amino acid sequence of the CDRH1 amino acid sequence in SEQ ID NO: 67; (ii) a CDRH2 amino acid sequence of the CDRH2 amino acid

sequence in SEQ ID NO: 67; (iii) a CDRH3 amino acid sequence of the CDRH3 amino acid sequence in SEQ ID NO: 67; and (iv) a CDRH of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than 2 amino acids; said CDRL of B) is selected from at least one of the group consisting of: (i) a CDRL1 amino acid sequence of the CDRL1 amino acid sequence in SEQ ID NO: 12; (ii) a CDRL2 amino acid sequence of the CDRL2 amino acid sequence in SEQ ID NO: 12; (iii) a CDRL3 amino acid sequence of the CDRL3 amino acid sequence in SEQ ID NO: 12; and (iv) a CDRL of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than 2 amino acids; or C) one or more heavy chain CDRHs of A) and one or more light chain CDRLs of B). In some embodiments, the antigen binding protein comprises A) a CDRH1 of the CDRH1 sequence in SEQ ID NO: 67, a CDRH2 of the CDRH2 sequence in SEQ ID NO: 67, and a CDRH3 of the CDRH3 sequence in SEQ ID NO: 67, and B) a CDRL1 of the CDRL1 sequence in SEQ ID NO: 12, a CDRL2 of the CDRL2 sequence in SEQ ID NO: 12, and a CDRL3 of the CDRL3 sequence in SEQ ID NO: 12. In some embodiments, the antigen binding protein comprises a heavy chain variable region (VH) having at least 80% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60, and/or a light chain variable region (VL) having at least 80% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46. In some embodiments, the VH has at least 90% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60, and/or the VL has at least 90% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46. In some embodiments, the VH is selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60, and/or the VL is selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46.

In some aspects, the invention comprises an isolated antigen binding protein that specifically binds to an epitope that is bound by any of the ABPs disclosed herein.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, wherein the antigen binding protein comprises: A) one or more heavy chain CDRs (CDRHs) selected from at least one of the group consisting of: (i) a CDRH1 with at least 80% sequence identity to a CDRH1 in one of the sequences selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; (ii) a CDRH2 with at least 80% sequence identity to a CDRH2 in one of the sequences selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; and (iii) a CDRH3 with at least 80% sequence identity to a CDRH3 in one of the sequences selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; B) one or more light chain CDRs (CDRLs) selected

from at least one of the group consisting of: (i) a CDRL1 with at least 80% sequence identity to a CDRL1 in one of the sequences selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; (ii) a CDRL2 with at least 80% sequence identity to a CDRL2 in one of the sequences selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; and (iii) a CDRL3 with at least 80% sequence identity to a CDRL3 in one of the sequences selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; or C) one or more heavy chain CDRHs of A) and one or more light chain CDRLs of B). In some embodiments, the antigen binding protein comprises: A) one or more CDRHs selected from at least one of the group consisting of: (i) a CDRH1 with at least 90% sequence identity to a CDRH1 in one of the sequences selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; (ii) a CDRH2 with at least 90% sequence identity to a CDRH2 in one of the sequences selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; and (iii) a CDRH3 with at least 90% sequence identity to a CDRH3 in one of the sequences selected from the group consisting of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60; B) one or more CDRLs selected from at least one of the group consisting of: (i) a CDRL1 with at least 90% sequence identity to a CDRL1 in one of the sequences selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; (ii) a CDRL2 with at least 90% sequence identity to a CDRL2 in one of the sequences selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; and (iii) a CDRL3 with at least 90% sequence identity to a CDRL3 in one of the sequences selected from the group consisting of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46; or C) one or more heavy chain CDRHs of A) and one or more light chain CDRLs of B).

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, the antigen binding protein comprises: A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of: (i) a CDRH3 selected from the CDRH3 within the sequences selected from the group consisting of SEQ ID NOs: 67, 79, and 49, (ii) a CDRH3 that differs in amino acid sequence from the CDRH3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO: 404), wherein X_1 is selected from the group consisting of D, A, R, and not amino acid, X_2 is selected from the group consisting of Y, I, G, and no amino acid, X_3 is selected from the group consisting of D, A, G, and no amino acid, X_4 is selected from the group consisting of F, A, L, and no amino acid, X_5 is selected from the group consisting of W, L, A, and no amino acid, X_6 is selected from the group consisting of S, Y, A, and no amino acid, X_7 is selected from the group consisting of A, Y, R, and no amino acid, X_8 is selected from the group consisting of Y, P, and no amino acid, X_9 is selected from the group consisting of Y, G, and no amino acid, X_{10} is

selected from the group consisting of D, G, and no amino acid, X_{11} is selected from the group consisting of A, M, and no amino acid, X_{12} is selected from the group consisting of F, D, and no amino acid, X_{13} is selected from the group consisting of D, V, and no amino acid, X_{14} is selected from the group consisting of V and no amino acid; B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of: (i) a CDRL3 selected from the CDRL3 within the sequences selected from the group consisting of SEQ ID NOs: 12, 35, and 23, (ii) a CDRL3 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL3 amino acid sequence selected from the group consisting of: $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}$ (SEQ ID NO: 405), wherein X_1 is selected from the group consisting of Q and G, X_2 is selected from the group consisting of S, T, A, and no amino acid, X_3 is selected from the group consisting of Y, no amino acid, and W, X_4 is selected from the group consisting of D and no amino acid, X_5 is selected from the group consisting of S and no amino acid, X_6 is selected from the group consisting of S and no amino acid, X_7 is selected from the group consisting of L, T, and no amino acid, X_8 is selected from the group consisting of no amino acid, A, and S, X_9 is selected from the group consisting of no amino acid, G, A, and V, X_{10} is selected from the group consisting of no amino acid, S, Y, and V, X_{11} is selected from the group consisting of no amino acid and V.

In some aspects, the invention comprises an isolated antigen binding protein comprising a light chain having the amino acid sequence selected from the group consisting of: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, 46, and some combination thereof.

In some embodiments, the antigen binding protein specifically binds to an epitope that is bound by at least one of the antigen binding proteins disclosed herein. In some embodiments, the isolated antigen binding protein further comprises a heavy chain having the amino acid sequence selected from the group consisting of: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, 60, and some combination thereof. In some embodiments, the amino acid sequence of the ABP is selected from the group consisting of SEQ ID NO: 12, 35, 23, and some combination thereof. In some embodiments, the heavy chain of the ABP comprises a CDRH3 of SEQ ID NO: 67, a CDRH2 of SEQ ID NO: 67, and a CDRH1 of SEQ ID NO: 67, and said light chain comprises a CDRL3 of SEQ ID NO: 12, a CDRL2 of SEQ ID NO: 12, and a CDRL1 of SEQ ID NO: 12. In some embodiments, the isolated antigen binding protein is a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof. In some embodiments, the isolated antigen binding protein is a Fab fragment, a Fab' fragment, a F(ab')₂ fragment, a Fv fragment, a diabody, or a single chain antibody molecule. In some embodiments, the isolated antigen binding protein is a human antibody. In some embodiments, the isolated antigen binding protein is a monoclonal antibody. In some embodiments, the isolated antigen binding protein is of the IgG1-, IgG2- IgG3- or IgG4-type. In some embodiments, the isolated antigen binding protein is of the IgG4- or IgG2-type. In some embodiments, the isolated antigen binding protein is coupled to a labeling group. In some embodiments, the isolated antigen binding protein competes for binding to PCSK9 with an antigen binding protein described herein. In some embodiments, the isolated antigen binding protein is a

monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof. In some embodiments, the isolated antigen binding protein is a Fab fragment, a Fab' fragment, a F(ab')₂ fragment, a Fv fragment, a diabody, or a single chain antibody molecule. In some embodiments, the isolated antigen binding protein is coupled to a labeling group. In some embodiments, the isolated antigen binding protein reduces binding of PCSK9 to LDLR. In some embodiments, the isolated antigen binding protein decreases an amount of LDL present in a subject when administered to the subject. In some embodiments, the isolated antigen binding protein decreases an amount of serum cholesterol present in a subject when administered to the subject. In some embodiments, the isolated antigen binding protein increases an amount of LDLR present in a subject when administered to the subject.

In some aspects, the invention comprises a vector comprising a nucleic acid molecule as described herein. In some embodiments, the invention comprises a host cell comprising a nucleic acid molecule as described herein.

In some aspects, the invention comprises an isolated antigen binding protein that competes for binding to PCSK9 with an antigen binding protein disclosed herein.

In some aspects, the invention comprises a nucleic acid molecule encoding the antigen binding protein according disclosed herein.

In some aspects, the invention comprises a pharmaceutical composition comprising at least one antigen binding protein described herein.

In some aspects, the invention comprises a method for treating or preventing a condition associated with elevated serum cholesterol levels in a patient, comprising administering to a patient in need thereof an effective amount of at least one isolated antigen binding protein disclosed herein.

In some aspects, the invention comprises a method of inhibiting binding of PCSK9 to LDLR in a subject comprising administering an effective amount of at least one antigen binding protein disclosed herein.

In some aspects, the invention comprises an antigen binding protein that selectively binds to PCSK9, wherein the antigen binding protein binds to PCSK9 with a K_d that is smaller than 100 pM.

In some aspects, the invention comprises a method for treating or preventing a condition associated with elevated serum cholesterol levels in a subject, the method comprising administering to a subject in need thereof an effective amount of at least one isolated antigen binding protein disclosed herein simultaneously or sequentially with an agent that elevates the availability of LDLR protein.

In some aspects, the invention comprises a method of lowering serum cholesterol level in a subject, the method comprising administering to a subject an effective amount of at least one isolated antigen binding protein as disclosed herein.

In some aspects, the invention comprises a method of lowering serum cholesterol level in a subject, the method comprising administering to a subject an effective amount of at least one isolated antigen binding protein as disclosed herein, simultaneously or sequentially with an agent that elevates the availability of LDLR protein.

In some aspects, the invention comprises a method of increasing LDLR protein level in a subject, the method comprising administering to a subject an effective amount of at least one isolated antigen binding protein as disclosed herein.

In some aspects, the invention comprises a method of increasing LDLR protein levels in a subject, the method com-

prising administering to a subject an effective amount of at least one isolated antigen binding protein as disclosed herein simultaneously or sequentially with an agent that elevates the availability of LDLR protein.

5 In some aspects, the invention comprises a pharmaceutical composition comprising an ABP as disclosed herein and an agent that elevates the availability of LDLR protein levels. In some embodiments, the agent that elevates the availability of LDLR protein comprises a statin. In some embodiments, the 10 statin is selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, simvastatin, and some combination thereof.

15 In some aspect, the invention comprises a method of making the antigen binding protein as described herein, comprising the step of preparing said antigen binding protein from a host cell that secretes said antigen binding protein.

20 In some aspect, the invention comprises a pharmaceutical composition comprising at least one antigen binding protein as described herein and a pharmaceutically acceptable excipient. In some embodiments, the pharmaceutical composition further comprises an additional active agent. In some embodiments, said additional active agent is selected from the group consisting of a radioisotope, radionuclide, a toxin, or a therapeutic and a chemotherapeutic group.

25 In some aspects, the invention comprises a method for treating or preventing a condition associated with an elevated serum cholesterol level in a patient. The method comprises administering to a patient in need thereof an effective amount of at least one isolated antigen binding protein as disclosed herein. In some embodiments, the condition is hypercholesterolemia.

30 In some aspects, the invention comprises a method of inhibiting binding of PCSK9 to LDLR in a patient comprising administering an effective amount of at least one antigen binding protein according as described herein.

35 In some aspect, the invention comprises an antigen binding protein that binds to PCSK9 with a K_d that is smaller than 100 μM . In some embodiments, the antigen binding protein binds with a K_d that is smaller than 10 μM . In some embodiments, the antigen binding protein binds with a K_d that is less than 5 μM .

40 In some aspects, the invention comprises a method for treating or preventing a condition associated with elevated serum cholesterol levels in a subject, said method comprising administering to a subject in need thereof an effective amount of at least one isolated antigen binding protein described herein simultaneously or sequentially with an agent that elevates the availability of LDLR protein. In some embodiments, the agent that elevates the availability of LDLR protein comprises a statin. In some embodiments, the statin is selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, simvastatin, and some combination thereof.

45 In some aspects, the invention comprises a method of lowering the serum cholesterol level in a subject. The method comprises administering to a subject an effective amount of at least one isolated antigen binding protein as described herein.

50 In some aspects, the invention comprises a method of lowering serum cholesterol levels in a subject comprising administering to a subject an effective amount of at least one isolated antigen binding protein, as described herein, simultaneously or sequentially with an agent that elevates the availability of LDLR protein. In some embodiments, the agent that elevates the availability of LDLR protein comprises a statin. In some embodiments, the statin is selected from the group consisting of atorvastatin, cerivastatin, fluv-

astatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, simvastatin, and some combination thereof.

In some aspects, the invention comprises a method of increasing LDLR protein levels in a subject by administering to a subject an effective amount of at least one isolated antigen binding protein as provided herein.

In some aspects, the invention comprises a method of increasing LDLR protein levels in a subject by administering to a subject an effective amount of at least one isolated antigen binding protein, as described herein, simultaneously or sequentially with an agent that elevates the availability of LDLR protein. In some embodiments, the agent that elevates the availability of LDLR protein levels comprises a statin. In some embodiments, the statin is selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, simvastatin, and some combination thereof.

In some aspects, the invention comprises a neutralizing antibody that binds to PCSK9 and reduces a low density lipoprotein receptor (LDLR) lowering effect of PCSK9 on LDLR. In some embodiments, the antibody specifically binds to PCSK9. In some embodiments, the antibody binds to the catalytic domain of PCSK9. In some embodiments, the antibody binds to an epitope within residues 31-447 of SEQ ID NO: 3. In some embodiments, the antibody binds to PCSK9 having an amino acid sequence that is at least 90% identical to SEQ ID NO: 3.

In some aspects, the invention comprises a neutralizing antigen binding protein that binds to PCSK9, wherein the antigen binding protein binds to PCSK9 at a location within residues 31-447 of SEQ ID NO: 3. In some embodiments, when the antigen binding protein is bound to PCSK9, the antibody is positioned 8 angstroms or less from at least one of the following residues of PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, Q382, W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, G384, K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, Q387, S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, F379, I154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, or C378.

In some embodiments, the antibody is positioned 8 angstroms or less from at least one of the following residues of PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, or Q382. In some embodiments, the antibody is positioned 5 angstroms or less from at least one of the following residues of PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, or S381. In some embodiments, the antibody is positioned 5 angstroms or less from at least two of the following residues of PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, or S381. In some embodiments, the antibody is 5 angstroms or less from at least four of the following residues of PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, or S381. In some embodiments, the antibody is positioned 8 angstroms or less from at least one of

the following residues of PCSK9: W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, G384, K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, or Q387. In some embodiments, the antibody is positioned 5 angstroms or less from at least one of the following residues of PCSK9: W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, or G384. In some embodiments, the antibody is positioned 5 angstroms or less from at least two of the following residues of PCSK9: W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, or G384. In some embodiments, the antibody is positioned 5 angstroms or less from at least four of the following residues of PCSK9: W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, or G384. In some embodiments, the antibody is positioned 8 angstroms or less from at least one of the following residues of PCSK9: S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, F379, I154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, or C378. In some embodiments, the antibody is positioned 5 angstroms or less from at least one of the following residues of PCSK9: S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, or F379. In some embodiments, the antibody is positioned 5 angstroms or less from at least two of the following residues of PCSK9: S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, or F379. In some embodiments, the antibody is positioned 5 angstroms or less from at least four of the following residues of PCSK9: S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, or F379. In some embodiments, the antibody is positioned 5 angstroms or less from at least one of the following residues of PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, Q382, W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, G384, K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, Q387, S153, S188, I189, Q190, S191, D192,

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R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, F379, I154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, or C378.

In some embodiments, an isolated antibody or antigen binding molecule that blocks an antibody to PCSK9 from binding within 8 angstroms of a residue of PCSK9 is provided. In some embodiments the residue of PCSK9 is selected from at least one of the following PCSK9 residues: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, Q382, W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, G384, K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, Q387, S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, F379, I154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, or C378.

In some embodiments, an isolated antibody or antigen binding molecule that binds to PCSK9 at a location that overlaps with a location that LDLR binds to PCSK9 is provided. In some embodiments, the location that LDLR binds to PCSK9 includes at least one amino acid residue selected from the group consisting of: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, and S381.

In some embodiments, an isolated antibody or antigen binding molecule that binds to PCSK9 is provided. In some embodiments, the antibody or antigen binding molecule reduces the likelihood that EGFa will bind to PCSK9 within 8 angstroms of at least one of the following residues on PCSK9: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, or Q382.

In some embodiments, an antibody, antigen binding protein, or antigen binding molecule that binds to a surface of PCSK9 that overlaps with a surface that EGFa binds, Ab 21B12 binds, and/or 31H4 binds is provided. In some embodiments, an antibody, antigen binding protein, or antigen binding molecule that binds to PCSK9 in a manner that is similar to that depicted in the figures is provided.

In some embodiments, the above embodiments are neutralizing antibodies or antigen binding proteins. In some embodiments, the antigen binding protein is not LDLR or a fragment thereof (such as EGFa).

In some aspects, the invention comprises an isolated neutralizing antibody, wherein when the antibody is bound to PCSK9, the antibody is positioned 8 angstroms or less from at least one of the following residues of PCSK9: T468, R469, M470, A471, T472, R496, R499, E501, A502, Q503, R510, H512, F515, P540, P541, A542, E543, H565, W566, E567, V568, E569, R592, E593, S465, G466, P467, A473, I474, R476, G497, E498, M500, G504, K506, L507, V508, A511, N513, A514, G516, V536, T538, A539, A544, T548, D570, L571, H591, A594, S595, and H597 of SEQ ID NO: 3. In some embodiments, the antibody is positioned 5 angstroms or less from at least one of the following residues of PCSK9: T468, R469, M470, A471, T472, R496, R499, E501, A502,

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Q503, R510, H512, F515, P540, P541, A542, E543, H565, W566, E567, V568, E569, R592, and E593 of SEQ ID NO: 3.

In some aspects, the invention comprises an isolated antigen binding protein. The antigen binding protein comprises:

- 5 A) a CDRH1 of the CDRH1 sequence in SEQ ID NO: 89, a CDRH2 of the CDRH2 sequence in SEQ ID NO: 89, and a CDRH3 of the CDRH3 sequence in SEQ ID NO: 89, and B) a CDRL1 of the CDRL1 sequence in SEQ ID NO:32, a CDRL2 of the CDRL2 sequence in SEQ ID NO:32, and a CDRL3 of the CDRL3 sequence in SEQ ID NO:32.
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In some aspects, the invention comprises an isolated antigen binding protein that binds to a PCSK9 protein of SEQ ID NO: 1 where the binding between said isolated antigen binding protein and a variant PCSK9 protein is less than 50% of the binding between the isolated antigen binding protein and the PCSK9 protein of SEQ ID NO: 1 and/or SEQ ID NO: 303. In some embodiments, the variant PCSK9 protein comprises at least one mutation of a residue at a position selected from the group consisting of or comprising 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554, as shown in SEQ ID NO: 1. In some embodiments, the at least one mutation selected from the group comprising or consisting of R207E, D208R, E181R, R185E, R439E, E513R, V538R, E539R, T132R, S351R, A390R, A413R, and E582R. In some embodiments, the at least one mutation is selected from the group consisting of D162R, R164E, E167R, S123R, E129R, A311R, D313R, D337R, R519E, H521R, and Q554R.

In some aspects, the invention comprises an antigen binding protein that binds to a PCSK-9 protein of SEQ ID NO: 303 in a first manner and binds to a variant of PCSK9 in a second manner. The PCSK9 variant has at least one point mutation at a position selected from the group comprising or consisting of: 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554 of SEQ ID NO: 303 and/or SEQ ID NO: 1. In some embodiments, the first manner comprises a first EC50, a first Bmax, or a first EC50 and a first Bmax. In some embodiments, the second manner comprises a second EC50, a second Bmax, or a second EC50 and a second Bmax. The value for the first manner is different from the value for the second manner. In some embodiments, the first manner comprises a first EC50, wherein the second manner involves a second EC50, and wherein the point mutation is selected from the group consisting of or comprising: R207E, D208R, E181R, R185E, R439E, E513R, V538R, E539R, T132R, S351R, A390R, A413R, and E582R. In some embodiments, the first EC50 is at least 20% different from the second EC50. In some embodiments, the first EC50 is at least 50% different from the second EC50. In some embodiments, the second EC50 is a larger numerical value than the first EC50. In some embodiments, the first EC50 is determined by a multiplex bead binding assay. In some embodiments, the second EC50 is greater than 1 um. In some embodiments, the antigen binding

55 protein is a neutralizing antigen binding protein. In some embodiments, the neutralizing antigen binding protein is a competitive neutralizing antigen binding protein. In some embodiments, the neutralizing antigen binding protein is a non-competitive neutralizing antigen binding protein. In some embodiments, the first manner comprises a first Bmax and the second manner comprises a second Bmax that is different from the first Bmax. The PCSK9 variant has at least one point mutation selected from the group consisting of or comprising: D162R, R164E, E167R, S123R, E129R, A311R, D313R, D337R, R519E, H521R, and Q554R. In some embodiments, the second Bmax is about 10% of the first Bmax. In some embodiments, the first Bmax is at least 20%

different from the second Bmax. In some embodiments, the first Bmax is at least 50% different from the second Bmax.

In some aspects, the invention comprises an isolated antigen binding protein that binds to a PCSK9 protein of SEQ ID NO: 3, wherein the epitope of the antigen binding protein includes at least one of the following amino acids of SEQ ID NO: 1: 207, 208, 181, 185, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554.

In some aspects, the invention comprises an isolated neutralizing antigen binding protein that binds to a PCSK9 protein comprising the amino acid sequence of SEQ ID NO: 1, wherein the neutralizing antigen binding protein decreases the LDLR lowering effect of PCSK9 on LDLR. In some embodiments, the antigen binding protein is a LDLR non-competitive neutralizing antigen binding protein. In some embodiments, the antigen binding protein is a LDLR competitive neutralizing antigen binding protein.

In some aspects, the invention comprises an isolated antigen binding protein, wherein said antigen binding protein comprises: A) a CDRH1 of the CDRH1 sequence in SEQ ID NO: 49, a CDRH2 of the CDRH2 sequence in SEQ ID NO: 49, and a CDRH3 of the CDRH3 sequence in SEQ ID NO: 49; and B) a CDRL1 of the CDRL1 sequence in SEQ ID NO: 23, a CDRL2 of the CDRL2 sequence in SEQ ID NO: 23, and a CDRL3 of the CDRL3 sequence in SEQ ID NO: 23.

In some aspects, the invention comprises a composition comprising a crystallized PCSK9 protein and an antigen binding protein that binds to PCSK9. The composition comprises the crystallized PCSK9 protein is such that the three dimensional structure of the PCSK9 protein can be determined to a resolution of about 2.2 angstroms or better. In some embodiments, the antigen binding protein is an antibody or a fragment thereof.

In some aspects, the invention comprises a crystallized PCSK9 protein and at least an EGFa section of a LDLR protein, wherein the EGFa section of the LDLR protein is bound by a PCSK9 protein, wherein said crystallized PCSK9 protein is such that the three dimensional structure of the PCSK9 protein can be determined to a resolution of about 2.2 angstroms or better. In some embodiments, the molecular model is on a computer readable medium.

In some aspects, the invention comprises the use of an antigen binding protein as described herein, in the preparation of a medicament for the lowering of serum cholesterol.

In some aspects, the invention comprises the use of an antigen binding protein as described herein, in the preparation of a medicament for treating or preventing a condition associated with elevated serum cholesterol levels in a subject.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, the antigen binding protein comprising: A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of: (i) a CDRH1 selected from the CDRH1 within the sequences selected from the group consisting of SEQ ID NOs: 67, 79, 89, and 49, (ii) a CDRH1 that differs in amino acid sequence from the CDRH1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH1 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ (SEQ ID NO: 406), wherein X_1 is selected from the group consisting of G, X_2 is selected from the group consisting of Y, F, and G, X_3 is selected from the group consisting of T and S, X_4 is selected from the group consisting of L and F, X_5 is selected from the group consisting of T, S, and N, X_6 is selected from the group consisting of S and A, X_7 is selected from the group consisting of Y and F, X_8 is selected from the group consisting

of G, S, and Y, X_9 is selected from the group consisting of I, M, and W, X_{10} is selected from the group consisting of S, N and H, B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of: (i) a CDRL1 selected from the CDRL1 within the sequences selected from the group consisting of SEQ ID NOs: 12, 32, 35, and 23, (ii) a CDRL1 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL1 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO: 407), wherein X_1 is selected from the group consisting of T and no amino acid, X_2 is selected from the group consisting of G and S, X_3 is selected from the group consisting of S, T, and G, X_4 is selected from the group consisting of S, X_5 is selected from the group consisting of S, X_6 is selected from the group consisting of N, D, and S, X_7 is selected from the group consisting of I, V, and N, X_8 is selected from the group consisting of G and I, X_9 is selected from the group consisting of A and G, X_{10} is selected from the group consisting of G, Y, S, and N, X_{11} is selected from the group consisting of Y and N, X_{12} is selected from the group consisting of D, S, T, and F, X_{13} is selected from the group consisting of V, X_{14} is selected from the group consisting of S, N, and H. One of skill in the art will appreciate that a single ABP or antibody can meet one or more of the above options and still fall within the described invention for this embodiment.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, the antigen binding protein comprising: A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of the following: (i) a CDRH2 selected from the CDRH2 within the sequences selected from the group consisting of SEQ ID NOs: 67, 79, 89, and 49, (ii) a CDRH2 that differs in amino acid sequence from the CDRH2 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH2 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 408), wherein X_1 is selected from the group consisting of W, S, L and no amino acid, X_2 is selected from the group consisting of V, I, and E, X_3 is selected from the group consisting of S, W, and I, X_4 is selected from the group consisting of F, S, and N, X_5 is selected from the group consisting of Y, S, D, and H, X_6 is selected from the group consisting of N, S, and G, X_7 is selected from the group consisting of S and G, X_8 is selected from the group consisting of N, Y, D, and R, X_9 is selected from the group consisting of T, I, and E, X_{10} is selected from the group consisting of N, S, Y, and D, X_{11} is selected from the group consisting of Y, X_{12} is selected from the group consisting of A and N, X_{13} is selected from the group consisting of Q, D, and P, X_{14} is selected from the group consisting of K and S, X_{15} is selected from the group consisting of L, and V, X_{16} is selected from the group consisting of Q and K, X_{17} is selected from the group consisting of G and S, B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of the following: (i) a CDRL2 selected from the CDRL2 within the sequences selected from the group consisting of SEQ ID NOs: 12, 32, 35, and 23, (ii) a CDRL2 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL2 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7$ (SEQ ID NO: 409), wherein X_1 is selected from the group consisting of G, E, S, and D, X_2 is selected from the group consisting of N, V, and Y, X_3 is selected from the group consisting of N, V, and Y, X_4 is selected from the group

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consisting of S and N, X₄ is selected from the group consisting of N, Q, and K, X₅ is selected from the group consisting of R, X₆ is selected from the group consisting of P, X₇ is selected from the group consisting of S.

In some aspects, the invention comprises An isolated antigen binding protein that binds PCSK9, the antigen binding protein comprising: A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of the following: (i) a CDRH3 selected from the CDRH3 within the sequences selected from the group consisting of SEQ ID NOs: 67, 79, 89, and 49, (ii) a CDRH3 that differs in amino acid sequence from the CDRH3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH3 amino acid sequence selected from the group consisting of X₁X₂X₃X₄X₅X₆X₇X₈X₉X₁₀X₁₁X₁₂X₁₃X₁₄ (SEQ ID NO: 410), wherein X₁ is selected from the group consisting of D, and no amino acid, X₂ is selected from the group consisting of Y, A, and no amino acid, X₃ is selected from the group consisting of D, I, and no amino acid, X₄ is selected from the group consisting of F, A, and no amino acid, X₅ is selected from the group consisting of W, A, and no amino acid, X₆ is selected from the group consisting of S, L, and no amino acid, X₇ is selected from the group consisting of A, Y, G, and no amino acid, X₈ is selected from the group consisting of Y, Q, and no amino acid, X₉ is selected from the group consisting of G, Y, and L, X₁₀ is selected from the group consisting of Y, D, and V, X₁₁ is selected from the group consisting of G, A, and P, X₁₂ is selected from the group consisting of M and F, X₁₃ is selected from the group consisting of D, X₁₄ is selected from the group consisting of V and Y, and B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of the following: (i) a CDRL3 selected from the CDRL3 within the sequences selected from the group consisting of SEQ ID NOs: 12, 32, 35, and 23, (ii) a CDRL3 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL3 amino acid sequence selected from the group consisting of X₁X₂X₃X₄X₅X₆X₇X₈X₉X₁₀X₁₁ (SEQ ID NO: 411), wherein X₁ is selected from the group consisting of Q, A, G, and no amino acid, X₂ is selected from the group consisting of S, V, T, and no amino acid, X₃ is selected from the group consisting of Y, N, and W, X₄ is selected from the group consisting of S and D, X₅ is selected from the group consisting of S, Y, and D, X₆ is selected from the group consisting of S and T, X₇ is selected from the group consisting of L and S, X₈ is selected from the group consisting of S, T, and N, X₉ is selected from the group consisting of G, S, and A, X₁₀ is selected from the group consisting of S, M, W, and Y, and X₁₁ is selected from the group consisting of V. In some embodiments, any of the above amino acids can be replaced by a conservative amino acid substitution.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, the antigen binding protein comprises A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of (i) a CDRH1 selected from the CDRH1 within the sequences selected from the group consisting of SEQ ID NOs: 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and 58, (ii) a CDRH1 that differs in amino acid sequence from the CDRH1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH1 amino acid sequence selected from the group consisting of X₁X₂X₃X₄X₅X₆X₇X₈X₉X₁₀ (SEQ ID NO: 412), wherein X₁ is selected from the group consisting of G, P, and A, X₂ is selected from the group consisting of Y, W, F, T, and S, X₃ is

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selected from the group consisting of T, P, S and A, C, V, L, and I, X₄ is selected from the group consisting of L, F, I, V, M, A, and Y, X₅ is selected from the group consisting of T, P, S, and A, X₆ is selected from the group consisting of S, T, A, and C, X₇ is selected from the group consisting of Y, W, F, T, and S, X₈ is selected from the group consisting of G, P, and A, X₉ is selected from the group consisting of I, L, V, M, A, and F, X₁₀ is selected from the group consisting of S, T, A, and C, B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of: (i) a CDRL1 selected from the CDRL1 within the sequences selected from the group consisting of SEQ ID NOs: 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, and 24, (ii) a CDRL1 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL1 amino acid sequence selected from the group consisting of X₁X₂X₃X₄X₅X₆X₇X₈X₉X₁₀X₁₁X₁₂X₁₃X₁₄ (SEQ ID NO: 413), wherein, X₁ is selected from the group consisting of T and S, X₂ is selected from the group consisting of G, P, and A, X₃ is selected from the group consisting of T, and S, X₄ is selected from the group consisting of S, N, T, A, C, and Q, X₅ is selected from the group consisting of S, T, A, and C, X₆ is selected from the group consisting of D, and E, X₇ is selected from the group consisting of V, I, M, L, F, and A, X₈ is selected from the group consisting of G, P, and A, X₉ is selected from the group consisting of G, A, R, P, V, L, I, K, Q, and N, X₁₀ is selected from the group consisting of Y, W, F, T, and S, X₁₁ is selected from the group consisting of N, and Q, X₁₂ is selected from the group consisting of Y, S, W, F, T, A, and C, X₁₃ is selected from the group consisting of V, I, M, L, F, and A, X₁₄ is selected from the group consisting of S, T, A, and C.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, the antigen binding protein comprising: A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of: (i) a CDRH2 selected from the CDRH2 within the sequences selected from the group consisting of SEQ ID NOs: 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and 58, (ii) a CDRH2 that differs in amino acid sequence from the CDRH2 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH2 amino acid sequence selected from the group consisting of X₁X₂X₃X₄X₅X₆X₇X₈X₉X₁₀X₁₁X₁₂X₁₃X₁₄X₁₅X₁₆X₁₇, (SEQ ID NO: 414), wherein X₁ is selected from the group consisting of W, Y, and F, X₂ is selected from the group consisting of V, I, M, L, F, and A, X₃ is selected from the group consisting of S, T, A, and C, X₄ is selected from the group consisting of A, F, V, L, I, Y, and M, X₅ is selected from the group consisting of Y, W, F, T, and S, X₆ is selected from the group consisting of N and Q, X₇ is selected from the group consisting of G, P, and A, X₈ is selected from the group consisting of N, and Q, X₉ is selected from the group consisting of T, and S, X₁₀ is selected from the group consisting of N, and Q, X₁₁ is selected from the group consisting of Y, W, F, T, and S, X₁₂ is selected from the group consisting of A, V, L, and I, X₁₃ is selected from the group consisting of Q, E, N, and D, X₁₄ is selected from the group consisting of K, R, Q, and N, X₁₅ is selected from the group consisting of L, F, V, I, M, A, and Y, X₁₆ is selected from the group consisting of Q, and N, X₁₇ is selected from the group consisting of G, P, and A, B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of: (i) a CDRL2 selected from the CDRL3 within the sequences selected from the group consisting of SEQ ID NOs: 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, and 24, (ii) a CDRL2 that differs in amino acid sequence from the CDRL3 of (i) by an amino

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acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL2 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7$ (SEQ ID NO: 415), wherein X_1 is selected from the group consisting of E, and D, X_2 is selected from the group consisting of V, I, M, L, F, and A, X_3 is selected from the group consisting of S, T, A, and C, X_4 is selected from the group consisting of N, and Q, X_5 is selected from the group consisting of R, K, Q, and N, X_6 is selected from the group consisting of P, and A, X_7 is selected from the group consisting of S, T, A, and C.

In some aspects, the invention comprises an isolated antigen binding protein that binds PCSK9, the antigen binding protein comprising: A) a heavy chain complementary determining region (CDRH) selected from at least one of the group consisting of (i) a CDRH3 selected from the CDRH3 within the sequences selected from the group consisting of SEQ ID NOS: 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and 58, (ii) a CDRH3 that differs in amino acid sequence from the CDRH3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH3 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6$ (SEQ ID NO: 416), wherein X_1 is selected from the group consisting of G, P, A and no amino acid, X_2 is selected from the group consisting of Y, W, F, T, and S, X_3 is selected from the group consisting of G, V, P, A, I, M, L, and F, X_4 is selected from the group consisting of M, L, F, and I, X_5 is selected from the group consisting of D, and E, X_6 is selected from the group consisting of V, I, M, L, F, and A, B) a light chain complementary determining region (CDRL) selected from at least one of the group consisting of: (i) a CDRL3 selected from the CDRL3 within the sequences selected from the group consisting of SEQ ID NOS: 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, and 24, (ii) a CDRL3 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL3 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7X_8X_9$ (SEQ ID NO: 417), wherein X_1 is selected from the group consisting of S, N, T, A, C, and Q, X_2 is selected from the group consisting of S, T, A, and C, X_3 is selected from the group consisting of Y, W, F, T, and S, X_4 is selected from the group consisting of T, and S, X_5 is selected from the group consisting of S, T, A, and C, X_6 is selected from the group consisting of S, T, A, and C, X_7 is selected from the group consisting of N, S, Q, T, A, and C, X_8 is selected from the group consisting of M, V, L, F, I, and A, X_9 is selected from the group consisting of V, I, M, L, F, and A.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1A depicts an amino acid sequence of the mature form of the PCSK9 with the pro-domain underlined.

FIGS. 1B₁-1B₄ depict amino acid and nucleic acid sequences of PCSK9 with the pro-domain underlined and the signal sequence in bold.

FIGS. 2A-2D are sequence comparison tables of various light chains of various antigen binding proteins. FIG. 2C continues the sequence started in FIG. 2A. FIG. 2D continues the sequence started on FIG. 2B.

FIGS. 3A-3D are sequence comparison tables of various heavy chains of various antigen binding proteins. FIG. 3C continues the sequence started in FIG. 3A. FIG. 3D continues the sequence started on FIG. 3B.

FIGS. 3E-3JJ depict the amino acid and nucleic acid sequences for the variable domains of some embodiments of the antigen binding proteins.

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FIG. 3KK depicts the amino acid sequences for various constant domains.

FIGS. 3LL-3BBB depict the amino acid and nucleic acid sequences for the variable domains of some embodiments of the antigen binding proteins.

FIGS. 3CCC-3JJJ are sequence comparison tables of various heavy and light chains of some embodiments of the antigen binding proteins.

FIG. 4A is a binding curve of an antigen binding protein to human PCSK9.

FIG. 4B is a binding curve of an antigen binding protein to human PCSK9.

FIG. 4C is a binding curve of an antigen binding protein to cynomolgus PCSK9.

FIG. 4D is a binding curve of an antigen binding protein to cynomolgus PCSK9.

FIG. 4E is a binding curve of an antigen binding protein to mouse PCSK9.

FIG. 4F is a binding curve of an antigen binding protein to mouse PCSK9.

FIG. 5A depicts the results of an SDS PAGE experiment involving PCSK9 and various antigen binding proteins demonstrating the relative purity and concentration of the proteins.

FIGS. 5B and 5C depict graphs from biacore solution equilibrium assays for 21B12.

FIG. 5D depicts the graph of the kinetics from a biacore capture assay.

FIG. 5E depicts a bar graph depicting binning results for three ABPs.

FIG. 6A is an inhibition curve of antigen binding protein 31H4 IgG2 to PCSK9 in an in vitro PCSK9:LDLR binding assay

FIG. 6B is an inhibition curve of antigen binding protein 31H4 IgG4 to PCSK9 in an in vitro PCSK9:LDLR binding assay.

FIG. 6C is an inhibition curve of antigen binding protein 21B12 IgG2 to PCSK9 in an in vitro PCSK9:LDLR binding assay.

FIG. 6D is an inhibition curve of antigen binding protein 21B12 IgG4 to PCSK9 in an in vitro PCSK9:LDLR binding assay.

FIG. 7A is an inhibition curve of antigen binding protein 31H4 IgG2 in the cell LDL uptake assay showing the effect of the ABP to reduce the LDL uptake blocking effects of PCSK9

FIG. 7B is an inhibition curve of antigen binding protein 31H4 IgG4 in the cell LDL uptake assay showing the effect of the ABP to reduce the LDL uptake blocking effects of PCSK9

FIG. 7C is an inhibition curve of antigen binding protein 21B12 IgG2 in the cell LDL uptake assay showing the effect of the ABP to reduce the LDL uptake blocking effects of PCSK9

FIG. 7D is an inhibition curve of antigen binding protein 21B12 IgG4 in the cell LDL uptake assay showing the effect of the ABP to reduce the LDL uptake blocking effects of PCSK9

FIG. 8A is a graph depicting the serum cholesterol lowering ability in mice of ABP 31H4, changes relative to the IgG control treated mice (* p<0.01).

FIG. 8B is a graph depicting the serum cholesterol lowering ability in mice of ABP 31H4, changes relative to time=zero hours (# p, 0.05).

FIG. 8C is a graph depicting the effect of ABP 31H4 on HDL cholesterol levels in C57B1/6 mice (* p<0.01).

FIG. 8D is a graph depicting the effect of ABP 31H4 on HDL cholesterol levels in C57B1/6 mice (# p<0.05).

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FIG. 9 depicts a western blot analysis of the ability of ABP 31H4 to enhance the amount of liver LDLR protein present after various time points.

FIG. 10A is a graph depicting the ability of an antigen binding protein 31H4 to lower total serum cholesterol in wild type mice, relative.

FIG. 10B is a graph depicting the ability of an antigen binding protein 31H4 to lower HDL in wild type mice.

FIG. 10C is a graph depicting the serum cholesterol lowering ability of various antigen binding proteins 31H4 and 16F12.

FIG. 11A depicts an injection protocol for testing the duration and ability of antigen binding proteins to lower serum cholesterol.

FIG. 11B is a graph depicting the results of the protocol in FIG. 11A.

FIG. 12A depicts LDLR levels in response to the combination of a statin and ABP 21B12 in HepG2 cells.

FIG. 12B depicts LDLR levels in response to the combination of a statin and ABP 31H4 in HepG2 cells.

FIG. 12C depicts LDLR levels in response to the combination of a statin and ABP 25A7.1, a normeutralizing antibody, (in contrast the "25A7" a neutralizing antibody) in HepG2 cells.

FIG. 12D depicts LDLR levels in response to the combination of a statin and ABP 21B12 in HepG2 cells overexpressing PCSK9.

FIG. 12E depicts LDLR levels in response to the combination of a statin and ABP 31H4 in HepG2 cells overexpressing PCSK9.

FIG. 12F depicts LDLR levels in response to the combination of a statin and ABP 25A7.1, a normeutralizing antibody, (in contrast the "25A7" a neutralizing antibody) in HepG2 cells overexpressing PCSK9.

FIG. 13A depicts the various light chain amino acid sequences of various ABPs to PCSK9. The dots (.) indicate no amino acid.

FIG. 13B depicts a light chain cladogram for various ABPs to PCSK9.

FIG. 13C depicts the various heavy chain amino acid sequences of various ABPs to PCSK9. The dots (.) indicate no amino acid.

FIG. 13D depicts a heavy chain dendrogram for various ABPs to PCSK9.

FIG. 13E depicts a comparison of light and heavy CDRs and designation of groups from which to derive consensus.

FIG. 13F depicts the consensus sequences for Groups 1 and 2.

FIG. 13G depicts the consensus sequences for Groups 3 and 4.

FIG. 13H depicts the consensus sequences for Groups 1 and 2. The dots (.) indicated identical residues.

FIG. 13I depicts the consensus sequences for Group 2. The dots (.) indicated identical residues.

FIG. 13J depicts the consensus sequences for Groups 3 and 4. The dots (.) indicated identical residues.

FIG. 14A is a graph depicting in vivo LDL lowering ability of various ABPs (at 10 mg/kg).

FIG. 14B is a graph depicting in vivo LDL lowering ability of various ABPs (at 30 mg/kg).

FIG. 15A and FIG. 15B are sequence comparison tables of various light chains of various embodiments of antigen binding proteins. FIG. 15B continues the sequence started in FIG. 15A.

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FIG. 15C and FIG. 15D are sequence comparison tables of various light chains of various embodiments of antigen binding proteins. FIG. 15D continues the sequence started in FIG. 15C.

5 FIG. 16A is a depiction of a gel used to test the ability of Ab 21B12 to bind to the ProCat or VD sections of PCSK9.

FIG. 16B is a depiction of a gel used to test the ability of Ab 31H4 to bind to the ProCat or VD sections of PCSK9.

FIG. 17 is a depiction of the structure of PCSK9 and the 10 EGFa section of LDLR.

FIG. 18A is a depiction of the structure of PCSK9 and the 31H4 Ab.

FIG. 18B is a depiction of the structure of PCSK9 and the 31H4 Ab.

15 FIG. 19A is a depiction of the structure of PCSK9, the 31H4 Ab, and the 21B12 Ab.

FIG. 19B is a depiction of the structure of PCSK9 and the 21B12 Ab.

FIG. 20A is a depiction of the structure of PCSK9 and 20 EGFa from the LDLR superimposed with the structure of antibodies 31H4 and 21B12 bound to PCSK9.

FIG. 20B is a depiction of the structural model of PCSK9 and LDLR.

FIG. 20C is a depiction of the structural model of PCSK9 25 and LDLR from an alternative perspective.

FIG. 20D is a depiction of the structural model of PCSK9 and LDLR with structural representations of 31H4 and 21B12 included.

FIG. 20E is a depiction of the structural model in FIG. 20D, 30 rotated 90 degrees about the noted axis.

FIG. 20F is a depiction of the structural model in FIG. 20D rotated 180 degrees about the noted axis.

FIG. 21A is a depiction of the structure of PCSK9 and 31A4.

FIG. 21B is a depiction of the structure of PCSK9 and 31A4.

FIG. 21C is a depiction of the structure of PCSK9 and 31A4.

FIG. 21D is a depiction of the structural model of full 35 length PCSK9 and 31A4.

FIG. 22 is a set of ABP sequences identifying various differences between the human ABP sequences and the ABP sequences that were raised in *E. coli* and used for the crystal structures.

FIG. 23 is a table depicting the various binning results.

FIG. 23A is a first part of a table depicting the various binning results.

FIG. 23B is a second part of a table depicting the various binning results.

50 FIG. 23C is a third part of a table depicting the various binning results.

FIG. 23D is a fourth part of a table depicting the various binning results.

FIG. 24A is a depiction of a western blot under non-reduced conditions.

55 FIG. 24B is a depiction of a western blot under reduced conditions.

FIG. 25A is a depiction of the surface coverage of PCSK9.

FIG. 25B is a depiction of the surface coverage of PCSK9.

FIG. 25C is a depiction of the surface coverage of PCSK9.

FIG. 25D is a depiction of the surface coverage of PCSK9.

FIG. 25E is a depiction of the surface coverage of PCSK9.

FIG. 25F is a depiction of the surface coverage of PCSK9.

60 FIG. 26 is a sequence comparison of the PCSK9 amino acid sequence and all of the residues that were mutated in PCSK9 variants to examine the epitopes of the various antibodies.

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FIG. 27A depicts the 21B12 epitope hits, as mapped onto a crystal structure of PCSK9 with the 21B12.

FIG. 27B depicts the 31H4 epitope hits, as mapped onto a crystal structure of PCSK9 with 31H4 and 21B1.

FIG. 27C depicts the 31A4 epitope hits, as mapped onto a crystal structure of PCSK9 with 31H4 and 21B12.

FIG. 27D depicts the 12H11 epitope hits, as mapped onto the crystal structure of PCSK9 with 31H4 and 21B12.

FIG. 27E depicts the 3C4 epitope hits, as mapped onto the crystal structure of PCSK9 with 31H4 and 21B12.

FIG. 28A is a graph demonstrating the binding ability of the various ABPs to various parts of PCSK9.

FIG. 28B is a graph demonstrating the binding ability of the various ABPs to various parts of PCSK9.

FIG. 28C is a graph comparing the LDLR binding ability of two ABPs.

FIG. 28D is a graph comparing the cell LDL uptake activity of two ABPs.

DETAILED DESCRIPTION OF CERTAIN EXEMPLARY EMBODIMENTS

Antigen binding proteins (such as antibodies and functional binding fragments thereof) that bind to PCSK9 are disclosed herein. In some embodiments, the antigen binding proteins bind to PCSK9 and prevent PCSK9 from functioning in various ways. In some embodiments, the antigen binding proteins block or reduce the ability of PCSK9 to interact with other substances. For example, in some embodiments, the antigen binding protein binds to PCSK9 in a manner that prevents or reduces the likelihood that PCSK9 will bind to LDLR. In other embodiments, antigen binding proteins bind to PCSK9 but do not block PCSK9's ability to interact with LDLR. In some embodiments, the antigen binding proteins are human monoclonal antibodies.

As will be appreciated by one of skill in the art, in light of the present disclosure, altering the interactions between PCSK9 and LDLR can increase the amount of LDLR available for binding to LDL, which in turn decreases the amount of serum LDL in a subject, resulting in a reduction in the subject's serum cholesterol level. As such, antigen binding proteins to PCSK9 can be used in various methods and compositions for treating subjects with elevated serum cholesterol levels, at risk of elevated serum cholesterol levels, or which could benefit from a reduction in their serum cholesterol levels. Thus, various methods and techniques for lowering, maintaining, or preventing an increase in serum cholesterol are also described herein. In some embodiments, the antigen binding protein allows for binding between PCSK9 and LDLR, but the antigen binding protein prevents or reduces the adverse activity of PCSK9 on LDLR. In some embodiments, the antigen binding protein prevents or reduces the binding of PCSK9 to LDLR.

For convenience, the following sections generally outline the various meanings of the terms used herein. Following this discussion, general aspects regarding antigen binding proteins are discussed, followed by specific examples demonstrating the properties of various embodiments of the antigen binding proteins and how they can be employed.

Definitions and Embodiments

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention as claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise. In this application, the use of "or" means "and/or" unless stated otherwise. Furthermore, the use of the term "including", as

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well as other forms, such as "includes" and "included", is not limiting. Also, terms such as "element" or "component" encompass both elements and components comprising one unit and elements and components that comprise more than one subunit unless specifically stated otherwise. Also, the use of the term "portion" can include part of a moiety or the entire moiety.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including but not limited to 10 patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference in their entirety for any purpose. As utilized in accordance with the present disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings:

The term "proprotein convertase subtilisin kexin type 9" or "PCSK9" refers to a polypeptide as set forth in SEQ ID NO: 1 and/or 3 or fragments thereof, as well as related polypeptides, which include, but are not limited to, allelic variants, splice variants, derivative variants, substitution variants, deletion variants, and/or insertion variants including the addition of an N-terminal methionine, fusion polypeptides, and interspecies homologs. In certain embodiments, a PCSK9 polypeptide includes terminal residues, such as, but not limited to, leader sequence residues, targeting residues, amino terminal methionine residues, lysine residues, tag residues and/or fusion protein residues. "PCSK9" has also been referred to as FH3, NARC1, HCHOLA3, proprotein convertase subtilisin/kexin type 9, and neural apoptosis regulated convertase 1. The PCSK9 gene encodes a proprotein convertase protein that belongs to the proteinase K subfamily of the secretory subtilase family. The term "PCSK9" denotes both the proprotein and the product generated following autocatalysis of the proprotein. When only the autocatalyzed product is being referred to (such as for an antigen binding protein that selectively binds to the cleaved PCSK9), the protein can be referred to as the "mature," "cleaved," "processed" or "active" PCSK9. When only the inactive form is being referred to, the protein can be referred to as the "inactive," "pro-form", or "unprocessed" form of PCSK9. The term PCSK9 as used herein also includes naturally occurring alleles, such as the mutations D374Y, S127R and F216L. The term PCSK9 also encompasses PCSK9 molecules incorporating post-translational modifications of the PCSK9 amino acid sequence, such as PCSK9 sequences that have been glycosylated, PEGylated, PCSK9 sequences from which its signal sequence has been cleaved, PCSK9 sequence from which its pro domain has been cleaved from the catalytic domain but not separated from the catalytic domain (e.g., FIGS. 1A and 1B).

The term "PCSK9 activity" includes any biological effect of PCSK9. In certain embodiments, PCSK9 activity includes the ability of PCSK9 to interact or bind to a substrate or receptor. In some embodiments, PCSK9 activity is represented by the ability of PCSK9 to bind to a LDL receptor (LDLR). In some embodiments, PCSK9 binds to and catalyzes a reaction involving LDLR. In some embodiments, PCSK9 activity includes the ability of PCSK9 to alter (e.g., 55 reduce) the availability of LDLR. In some embodiments, PCSK9 activity includes the ability of PCSK9 to increase the amount of LDL in a subject. In some embodiments, PCSK9 activity includes the ability of PCSK9 to decrease the amount of LDLR that is available to bind to LDL. In some embodiments, "PCSK9 activity" includes any biological activity resulting from PCSK9 signaling. Exemplary activities include, but are not limited to, PCSK9 binding to LDLR,

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PCSK9 enzyme activity that cleaves LDLR or other proteins, PCSK9 binding to proteins other than LDLR that facilitate PCSK9 action, PCSK9 altering APOB secretion (Sun X-M et al., "Evidence for effect of mutant PCSK9 on apolipoprotein B secretion as the cause of unusually severe dominant hypercholesterolemia, Human Molecular Genetics 14: 1161-1169, 2005 and Ouguerram K et al., "Apolipoprotein B100 metabolism in autosomal-dominant hypercholesterolemia related to mutations in PCSK9, Arterioscler thromb Vasc Biol. 24: 1448-1453, 2004), PCSK9's role in liver regeneration and neuronal cell differentiation (Seidah NG et al., "The secretory proprotein convertase neural apoptosis-regulated convertase 1 (NARC-1): Liver regeneration and neuronal differentiation" PNAS 100: 928-933, 2003), and PCSK9's role in hepatic glucose metabolism (Costet et al., "Hepatic PCSK9 expression is regulated by nutritional status via insulin and sterol regulatory element-binding protein 1c" J. Biol. Chem. 281 (10):6211-18, 2006).

The term "hypercholesterolemia," as used herein, refers to a condition in which cholesterol levels are elevated above a desired level. In some embodiments, this denotes that serum cholesterol levels are elevated. In some embodiments, the desired level takes into account various "risk factors" that are known to one of skill in the art (and are described or referenced herein).

The term "polynucleotide" or "nucleic acid" includes both single-stranded and double-stranded nucleotide polymers. The nucleotides comprising the polynucleotide can be ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide. Said modifications include base modifications such as bromouridine and inosine derivatives, ribose modifications such as 2',3'-dideoxyribose, and inter-nucleotide linkage modifications such as phosphorothioate, phosphorodithioate, phosphoresenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoranylilate and phosphoroamidate.

The term "oligonucleotide" means a polynucleotide comprising 200 or fewer nucleotides. In some embodiments, oligonucleotides are 10 to 60 bases in length. In other embodiments, oligonucleotides are 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 nucleotides in length. Oligonucleotides can be single stranded or double stranded, e.g., for use in the construction of a mutant gene. Oligonucleotides can be sense or antisense oligonucleotides. An oligonucleotide can include a label, including a radiolabel, a fluorescent label, a hapten or an antigenic label, for detection assays. Oligonucleotides can be used, for example, as PCR primers, cloning primers or hybridization probes.

An "isolated nucleic acid molecule" means a DNA or RNA of genomic, mRNA, cDNA, or synthetic origin or some combination thereof which is not associated with all or a portion of a polynucleotide in which the isolated polynucleotide is found in nature, or is linked to a polynucleotide to which it is not linked in nature. For purposes of this disclosure, it should be understood that "a nucleic acid molecule comprising" a particular nucleotide sequence does not encompass intact chromosomes. Isolated nucleic acid molecules "comprising" specified nucleic acid sequences can include, in addition to the specified sequences, coding sequences for up to ten or even up to twenty other proteins or portions thereof, or can include operably linked regulatory sequences that control expression of the coding region of the recited nucleic acid sequences, and/or can include vector sequences.

Unless specified otherwise, the left-hand end of any single-stranded polynucleotide sequence discussed herein is the 5' end; the left-hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction

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of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA transcript that are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences;" sequence regions on the DNA strand having the same sequence as the RNA transcript that are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences."

The term "control sequence" refers to a polynucleotide sequence that can affect the expression and processing of coding sequences to which it is ligated. The nature of such control sequences can depend upon the host organism. In particular embodiments, control sequences for prokaryotes can include a promoter, a ribosomal binding site, and a transcription termination sequence. For example, control sequences for eukaryotes can include promoters comprising one or a plurality of recognition sites for transcription factors, transcription enhancer sequences, and transcription termination sequence. "Control sequences" can include leader sequences and/or fusion partner sequences.

The term "vector" means any molecule or entity (e.g., nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell.

The term "expression vector" or "expression construct" refers to a vector that is suitable for transformation of a host cell and contains nucleic acid sequences that direct and/or control (in conjunction with the host cell) expression of one or more heterologous coding regions operatively linked thereto. An expression construct can include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto.

As used herein, "operably linked" means that the components to which the term is applied are in a relationship that allows them to carry out their inherent functions under suitable conditions. For example, a control sequence in a vector that is "operably linked" to a protein coding sequence is ligated thereto so that expression of the protein coding sequence is achieved under conditions compatible with the transcriptional activity of the control sequences.

The term "host cell" means a cell that has been transformed, or is capable of being transformed, with a nucleic acid sequence and thereby expresses a gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present.

The term "transfection" means the uptake of foreign or exogenous DNA by a cell, and a cell has been "transfected" when the exogenous DNA has been introduced inside the cell membrane. A number of transfection techniques are well known in the art and are disclosed herein. See, e.g., Graham et al., 1973, *Virology* 52:456; Sambrook et al., 2001, *Molecular Cloning: A Laboratory Manual*, supra; Davis et al., 1986, *Basic Methods in Molecular Biology*, Elsevier; Chu et al., 1981, *Gene* 13:197. Such techniques can be used to introduce one or more exogenous DNA moieties into suitable host cells.

The term "transformation" refers to a change in a cell's genetic characteristics, and a cell has been transformed when it has been modified to contain new DNA or RNA. For example, a cell is transformed where it is genetically modified from its native state by introducing new genetic material via transfection, transduction, or other techniques. Following transfection or transduction, the transforming DNA can recombine with that of the cell by physically integrating into a chromosome of the cell, or can be maintained transiently as an episomal element without being replicated, or can repli-

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cate independently as a plasmid. A cell is considered to have been "stably transformed" when the transforming DNA is replicated with the division of the cell.

The terms "polypeptide" or "protein" means a macromolecule having the amino acid sequence of a native protein, that is, a protein produced by a naturally-occurring and non-recombinant cell; or it is produced by a genetically-engineered or recombinant cell, and comprise molecules having the amino acid sequence of the native protein, or molecules having deletions from, additions to, and/or substitutions of one or more amino acids of the native sequence. The term also includes amino acid polymers in which one or more amino acids are chemical analogs of a corresponding naturally-occurring amino acid and polymers. The terms "polypeptide" and "protein" specifically encompass PCSK9 antigen binding proteins, antibodies, or sequences that have deletions from, additions to, and/or substitutions of one or more amino acid of antigen-binding protein. The term "polypeptide fragment" refers to a polypeptide that has an amino-terminal deletion, a carboxyl-terminal deletion, and/or an internal deletion as compared with the full-length native protein. Such fragments can also contain modified amino acids as compared with the native protein. In certain embodiments, fragments are about five to 500 amino acids long. For example, fragments can be at least 5, 6, 8, 10, 14, 20, 50, 70, 100, 110, 150, 200, 250, 300, 350, 400, or 450 amino acids long. Useful polypeptide fragments include immunologically functional fragments of antibodies, including binding domains. In the case of a PCSK9-binding antibody, useful fragments include but are not limited to a CDR region, a variable domain of a heavy and/or light chain, a portion of an antibody chain or just its variable region including two CDRs, and the like.

The term "isolated protein" referred means that a subject protein (1) is free of at least some other proteins with which it would normally be found, (2) is essentially free of other proteins from the same source, e.g., from the same species, (3) is expressed by a cell from a different species, (4) has been separated from at least about 50 percent of polynucleotides, lipids, carbohydrates, or other materials with which it is associated in nature, (5) is operably associated (by covalent or noncovalent interaction) with a polypeptide with which it is not associated in nature, or (6) does not occur in nature. Typically, an "isolated protein" constitutes at least about 5%, at least about 10%, at least about 25%, or at least about 50% of a given sample. Genomic DNA, cDNA, mRNA or other RNA, of synthetic origin, or any combination thereof can encode such an isolated protein. Preferably, the isolated protein is substantially free from proteins or polypeptides or other contaminants that are found in its natural environment that would interfere with its therapeutic, diagnostic, prophylactic, research or other use.

The term "amino acid" includes its normal meaning in the art.

A "variant" of a polypeptide (e.g., an antigen binding protein, or an antibody) comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to another polypeptide sequence. Variants include fusion proteins.

The term "identity" refers to a relationship between the sequences of two or more polypeptide molecules or two or more nucleic acid molecules, as determined by aligning and comparing the sequences. "Percent identity" means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) are preferably

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addressed by a particular mathematical model or computer program (i.e., an "algorithm"). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in *Computational Molecular Biology*, (Lesk, A. M., ed.), 1988, New York: Oxford University Press; Biocomputing Informatics and Genome Projects, (Smith, D. W., ed.), 1993, New York: Academic Press; Computer Analysis of Sequence Data, Part I, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von

Heinje, G., 1987, Sequence Analysis in Molecular Biology, New York: Academic Press; Sequence Analysis Primer, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press; and Carillo et al., 1988, *SIAM J. Applied Math.* 48:1073.

In calculating percent identity, the sequences being compared are typically aligned in a way that gives the largest match between the sequences. One example of a computer program that can be used to determine percent identity is the GCG program package, which includes GAP (Devereux et al., 1984, *Nucl. Acid Res.* 12:387; Genetics Computer Group, University of Wisconsin, Madison, Wis.). The computer algorithm GAP is used to align the two polypeptides or polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the "matched span", as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the "average diagonal" is the average of the diagonal of the comparison matrix being used; the "diagonal" is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually $\frac{1}{10}$ times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., 1978, *Atlas of Protein Sequence and Structure* 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., 1992, *Proc. Natl. Acad. Sci. U.S.A.* 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

Examples of parameters that can be employed in determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

Algorithm: Needleman et al., 1970, *J. Mol. Biol.* 48:443-453

Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra

Gap Penalty: 12 (but with no penalty for end gaps)

Gap Length Penalty: 4

Threshold of Similarity: 0

Certain alignment schemes for aligning two amino acid sequences may result in matching of only a short region of the two sequences, and this small aligned region may have very high sequence identity even though there is no significant relationship between the two full-length sequences. Accordingly; the selected alignment method (GAP program) can be adjusted if so desired to result in an alignment that spans at least 50 or other number of contiguous amino acids of the target polypeptide.

As used herein, the twenty conventional (e.g., naturally occurring) amino acids and their abbreviations follow conventional usage. See *Immunology—A Synthesis* (2nd Edition, E. S. Golub and D. R. Gren, Eds., Sinauer Associates, Sunderland, Mass. (1991)), which is incorporated herein by reference for any purpose. Stereoisomers (e.g., D-amino acids) of the twenty conventional amino acids, unnatural amino acids such as α,α -disubstituted amino acids, N-alkyl amino acids, lactic acid, and other unconventional amino acids can

also be suitable components for polypeptides of the present invention. Examples of unconventional amino acids include: 4-hydroxyproline, γ -carboxyglutamate, ϵ -N,N,N-trimethyllysine, ϵ -N-acetylysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, σ -N-methylarginine, and other similar amino acids and imino acids (e.g., 4-hydroxyproline). In the polypeptide notation used herein, the left-hand direction is the amino terminal direction and the right-hand direction is the carboxy-terminal direction, in accordance with standard usage and convention.

Similarly, unless specified otherwise, the left-hand end of single-stranded polynucleotide sequences is the 5' end; the left-hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences."

Conservative amino acid substitutions can encompass non-naturally occurring amino acid residues, which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics and other reversed or inverted forms of amino acid moieties.

Naturally occurring residues can be divided into classes based on common side chain properties:

- 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- 2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;
- 3) acidic: Asp, Glu;
- 4) basic: His, Lys, Arg;
- 5) residues that influence chain orientation: Gly, Pro; and
- 6) aromatic: Trp, Tyr, Phe.

For example, non-conservative substitutions can involve the exchange of a member of one of these classes for a member from another class. Such substituted residues can be introduced, for example, into regions of a human antibody that are homologous with non-human antibodies, or into the non-homologous regions of the molecule.

In making changes to the antigen binding protein or the PCSK9 protein, according to certain embodiments, the hydrodynamic index of amino acids can be considered. Each amino acid has been assigned a hydrodynamic index on the basis of its hydrophobicity and charge characteristics. They are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

The importance of the hydrodynamic amino acid index in conferring interactive biological function on a protein is understood in the art. Kyte et al., J. Mol. Biol., 157:105-131 (1982). It is known that certain amino acids can be substituted for other amino acids having a similar hydrodynamic index or score and still retain a similar biological activity. In making changes based upon the hydrodynamic index, in certain embodiments, the substitution of amino acids whose hydrodynamic indices are within ± 2 is included. In certain embodiments, those which are within ± 1 are included, and in certain embodiments, those within ± 0.5 are included.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functional protein or peptide thereby created is intended for use in immu-

nological embodiments, as in the present case. In certain embodiments, the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, i.e., with a biological property of the protein.

The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0±1); glutamate (+3.0±1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5±1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5) and tryptophan (-3.4). In making changes based upon similar hydrophilicity values, in certain embodiments, the substitution of amino acids whose hydrophilicity values are within ± 2 is included, in certain embodiments, those which are within ± 1 are included, and in certain embodiments, those within ± 0.5 are included. One can also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

Exemplary amino acid substitutions are set forth in Table 1.

TABLE 1

Amino Acid Substitutions			
	Original Residues	Exemplary Substitutions	Preferred Substitutions
	Ala	Val, Leu, Ile	Val
	Arg	Lys, Gln, Asn	Lys
30	Asn	Gln	Gln
	Asp	Glu	Glu
	Cys	Ser, Ala	Ser
	Gln	Asn	Asn
	Glu	Asp	Asp
	Gly	Pro, Ala	Ala
35	His	Asn, Gln, Lys, Arg	Arg
	Ile	Leu, Val, Met, Ala, Phe, Norleucine	Leu
	Leu	Norleucine, Ile, Val, Met, Ala, Phe	Ile
	Lys	Arg, 1,4 Diamino-butyric Acid, Gln, Asn	Arg
40	Met	Leu, Phe, Ile	Leu
	Phe	Leu, Val, Ile, Ala, Tyr	Leu
	Pro	Ala	Gly
	Ser	Thr, Ala, Cys	Thr
	Thr	Ser	Ser
45	Trp	Tyr, Phe	Tyr
	Tyr	Trp, Phe, Thr, Ser	Phe
	Val	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

The term "derivative" refers to a molecule that includes a chemical modification other than an insertion, deletion, or substitution of amino acids (or nucleic acids). In certain embodiments, derivatives comprise covalent modifications, including, but not limited to, chemical bonding with polymers, lipids, or other organic or inorganic moieties. In certain embodiments, a chemically modified antigen binding protein can have a greater circulating half-life than an antigen binding protein that is not chemically modified. In certain embodiments, a chemically modified antigen binding protein can have improved targeting capacity for desired cells, tissues, and/or organs. In some embodiments, a derivative antigen binding protein is covalently modified to include one or more water soluble polymer attachments, including, but not limited to, polyethylene glycol, polyoxyethylene glycol, or polypropylene glycol. See, e.g., U.S. Pat. Nos. 4,640,835, 4,496,689, 4,301,144, 4,670,417, 4,791,192 and 4,179,337. In certain embodiments, a derivative antigen binding protein comprises

one or more polymer, including, but not limited to, monomethoxy-polyethylene glycol, dextran, cellulose, or other carbohydrate based polymers, poly-(N-vinyl pyrrolidone)-polyethylene glycol, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polyoxyethylated polyols (e.g., glycerol) and polyvinyl alcohol, as well as mixtures of such polymers.

In certain embodiments, a derivative is covalently modified with polyethylene glycol (PEG) subunits. In certain embodiments, one or more water-soluble polymer is bonded at one or more specific position, for example at the amino terminus, of a derivative. In certain embodiments, one or more water-soluble polymer is randomly attached to one or more side chains of a derivative. In certain embodiments, PEG is used to improve the therapeutic capacity for an antigen binding protein. In certain embodiments, PEG is used to improve the therapeutic capacity for a humanized antibody. Certain such methods are discussed, for example, in U.S. Pat. No. 6,133,426, which is hereby incorporated by reference for any purpose.

Peptide analogs are commonly used in the pharmaceutical industry as non-peptide drugs with properties analogous to those of the template peptide. These types of non-peptide compound are termed "peptide mimetics" or "peptidomimetics." Fauchere, J., *Adv. Drug Res.*, 15:29 (1986); Veber & Freidinger, TINS, p. 392 (1985); and Evans et al., *J. Med. Chem.*, 30:1229 (1987), which are incorporated herein by reference for any purpose. Such compounds are often developed with the aid of computerized molecular modeling. Peptide mimetics that are structurally similar to therapeutically useful peptides can be used to produce a similar therapeutic or prophylactic effect. Generally, peptidomimetics are structurally similar to a paradigm polypeptide (i.e., a polypeptide that has a biochemical property or pharmacological activity), such as human antibody, but have one or more peptide linkages optionally replaced by a linkage selected from: —CH₂NH—, —CH₂S—, —CH₂—CH₂—, —CH=CH-(cis and trans), —COCH₂—, —CH(OH)CH₂—, and —CH₂SO—, by methods well known in the art. Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (e.g., D-lysine in place of L-lysine) can be used in certain embodiments to generate more stable peptides. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus sequence variation can be generated by methods known in the art (Rizo and Giersch, *Ann. Rev. Biochem.*, 61:387 (1992), incorporated herein by reference for any purpose); for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

The term "naturally occurring" as used throughout the specification in connection with biological materials such as polypeptides, nucleic acids, host cells, and the like, refers to materials which are found in nature or a form of the materials that is found in nature.

An "antigen binding protein" ("ABP") as used herein means any protein that binds a specified target antigen. In the instant application, the specified target antigen is the PCSK9 protein or fragment thereof. "Antigen binding protein" includes but is not limited to antibodies and binding parts thereof, such as immunologically functional fragments. Peptides are another example of antigen binding proteins. The term "immunologically functional fragment" (or simply "fragment") of an antibody or immunoglobulin chain (heavy or light chain) antigen binding protein, as used herein, is a species of antigen binding protein comprising a portion (regardless of how that portion is obtained or synthesized) of an antibody that lacks at least some of the amino acids present in

a full-length chain but which is still capable of specifically binding to an antigen. Such fragments are biologically active in that they bind to the target antigen and can compete with other antigen binding proteins, including intact antibodies, for binding to a given epitope. In some embodiments, the fragments are neutralizing fragments. In some embodiments, the fragments can block or reduce the likelihood of the interaction between LDLR and PCSK9. In one aspect, such a fragment will retain at least one CDR present in the full-length light or heavy chain, and in some embodiments will comprise a single heavy chain and/or light chain or portion thereof. These biologically active fragments can be produced by recombinant DNA techniques, or can be produced by enzymatic or chemical cleavage of antigen binding proteins, including intact antibodies. Immunologically functional immunoglobulin fragments include, but are not limited to, Fab, a diabody (heavy chain variable domain on the same polypeptide as a light chain variable domain, connected via a short peptide linker that is too short to permit pairing between the two domains on the same chain), Fab', F(ab')₂, Fv, domain antibodies and single-chain antibodies, and can be derived from any mammalian source, including but not limited to human, mouse, rat, camelid or rabbit. It is further contemplated that a functional portion of the antigen binding proteins disclosed herein, for example, one or more CDRs, could be covalently bound to a second protein or to a small molecule to create a therapeutic agent directed to a particular target in the body, possessing bifunctional therapeutic properties, or having a prolonged serum half-life. As will be appreciated by one of skill in the art, an antigen binding protein can include nonprotein components. In some sections of the present disclosure, examples of ABPs are described herein in terms of "number/letter/number" (e.g., 25A7). In these cases, the exact name denotes a specific antibody. That is, an ABP named 25A7 is not necessarily the same as an antibody named 25A7.1, (unless they are explicitly taught as the same in the specification, e.g., 25A7 and 25A7.3). As will be appreciated by one of skill in the art, in some embodiments LDLR is not an antigen binding protein. In some embodiments, binding subsections of LDLR are not antigen binding proteins, e.g., EGFa. In some embodiments, other molecules through which PCSK9 signals in vivo are not antigen binding proteins. Such embodiments will be explicitly identified as such.

Certain antigen binding proteins described herein are antibodies or are derived from antibodies. In certain embodiments, the polypeptide structure of the antigen binding proteins is based on antibodies, including, but not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions (sometimes referred to herein as "antibody conjugates"), and fragments thereof, respectively. In some embodiments, the ABP comprises or consists of avimers (tightly binding peptide). These various antigen binding proteins are further described herein.

An "Fc" region comprises two heavy chain fragments comprising the C_H1 and C_H2 domains of an antibody. The two heavy chain fragments are held together by two or more disulfide bonds and by hydrophobic interactions of the C_H3 domains.

A "Fab fragment" comprises one light chain and the C_H1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

A "Fab' fragment" comprises one light chain and a portion of one heavy chain that contains the VH domain and the C_H1

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domain and also the region between the C_{H1} and C_{H2} domains, such that an interchain disulfide bond can be formed between the two heavy chains of two Fab' fragments to form an $F(ab')_2$ molecule.

A “ $F(ab')_2$ fragment” contains two light chains and two heavy chains containing a portion of the constant region between the C_{H1} and C_{H2} domains, such that an interchain disulfide bond is formed between the two heavy chains. A $F(ab')_2$ fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains.

The “Fv region” comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

“Single-chain antibodies” are Fv molecules in which the heavy and light chain variable regions have been connected by a flexible linker to form a single polypeptide chain, which forms an antigen binding region. Single chain antibodies are discussed in detail in International Patent Application Publication No. WO 88/01649 and U.S. Pat. Nos. 4,946,778 and No. 5,260,203, the disclosures of which are incorporated by reference.

A “domain antibody” is an immunologically functional immunoglobulin fragment containing only the variable region of a heavy chain or the variable region of a light chain. In some instances, two or more V_H regions are covalently joined with a peptide linker to create a bivalent domain antibody. The two V_H regions of a bivalent domain antibody can target the same or different antigens.

A “bivalent antigen binding protein” or “bivalent antibody” comprises two antigen binding sites. In some instances, the two binding sites have the same antigen specificities. Bivalent antigen binding proteins and bivalent antibodies can be bispecific, see, infra. A bivalent antibody other than a “multispecific” or “multifunctional” antibody, in certain embodiments, typically is understood to have each of its binding sites identical.

A “multispecific antigen binding protein” or “multispecific antibody” is one that targets more than one antigen or epitope.

A “bispecific,” “dual-specific” or “bifunctional” antigen binding protein or antibody is a hybrid antigen binding protein or antibody, respectively, having two different antigen binding sites. Bispecific antigen binding proteins and antibodies are a species of multispecific antigen binding protein antibody and can be produced by a variety of methods including, but not limited to, fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsvilai and Lachmann, 1990, *Clin. Exp. Immunol.* 79:315-321; Kostelny et al., 1992, *J. Immunol.* 148:1547-1553. The two binding sites of a bispecific antigen binding protein or antibody will bind to two different epitopes, which can reside on the same or different protein targets.

An antigen binding protein is said to “specifically bind” its target antigen when the dissociation constant (K_d) is $\leq 10^{-7}$ M. The ABP specifically binds antigen with “high affinity” when the K_d is $\leq 5 \times 10^{-9}$ M, and with “very high affinity” when the K_d is $\leq 5 \times 10^{-10}$ M. In one embodiment, the ABP has a K_d of $\leq 10^{-9}$ M. In one embodiment, the off-rate is $\leq 1 \times 10^{-5}$. In other embodiments, the ABPs will bind to human PCSK9 with a K_d of between about 10^{-9} M and 10^{-13} M, and in yet another embodiment the ABPs will bind with a $K_d \leq 5 \times 10^{-10}$. As will be appreciated by one of skill in the art, in some embodiments, any or all of the antigen binding fragments can specifically bind to PCSK9.

An antigen binding protein is “selective” when it binds to one target more tightly than it binds to a second target.

“Antigen binding region” means a protein, or a portion of a protein, that specifically binds a specified antigen (e.g., a

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paratope). For example, that portion of an antigen binding protein that contains the amino acid residues that interact with an antigen and confer on the antigen binding protein its specificity and affinity for the antigen is referred to as “antigen binding region.” An antigen binding region typically includes one or more “complementary binding regions” (“CDRs”). Certain antigen binding regions also include one or more “framework” regions. A “CDR” is an amino acid sequence that contributes to antigen binding specificity and affinity.

“Framework” regions can aid in maintaining the proper conformation of the CDRs to promote binding between the antigen binding region and an antigen. Structurally, framework regions can be located in antibodies between CDRs. Examples of framework and CDR regions are shown in FIGS. 2A-3D, 3CCC-3JJ, and 15A-15D. In some embodiments, the sequences for CDRs for the light chain of antibody 3B6 are as follows: CDR1 TLSSGYSSYEV (SEQ ID NO: 279); CDR2 VDTGGIVGSKGE (SEQ ID NO: 280); CDR3 GADHGSGTNFVVV (SEQ ID NO: 281), and the FRs are as follows: FR1 QPVLTQPLFEASASLGASVTLTC (SEQ ID NO: 282); FR2 WYQQRPGKGPRFVMR (SEQ ID NO: 283); FR3 GIPDRFSVLGSGLNRYLTIKNIQEEDESDYHC (SEQ ID NO: 284); and FR4 FGGGTKLTVL (SEQ ID NO: 285).

In certain aspects, recombinant antigen binding proteins that bind PCSK9, for example human PCSK9, are provided. In this context, a “recombinant antigen binding protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as described herein. Methods and techniques for the production of recombinant proteins are well known in the art.

The term “antibody” refers to an intact immunoglobulin of any isotype, or a fragment thereof that can compete with the intact antibody for specific binding to the target antigen, and includes, for instance, chimeric, humanized, fully human, and bispecific antibodies. An “antibody” is a species of an antigen binding protein. An intact antibody will generally comprise at least two full-length heavy chains and two full-length light chains, but in some instances can include fewer chains such as antibodies naturally occurring in camelids which can comprise only heavy chains. Antibodies can be derived solely from a single source, or can be “chimeric,” that is, different portions of the antibody can be derived from two different antibodies as described further below. The antigen binding proteins, antibodies, or binding fragments can be produced in hybridomas, by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact antibodies. Unless otherwise indicated, the term “antibody” includes, in addition to antibodies comprising two full-length heavy chains and two full-length light chains, derivatives, variants, fragments, and muteins thereof, examples of which are described below. Furthermore, unless explicitly excluded, antibodies include monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as “antibody mimetics”), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions (sometimes referred to herein as “antibody conjugates”), and fragments thereof, respectively. In some embodiments, the term also encompasses peptibodies.

Naturally occurring antibody structural units typically comprise a tetramer. Each such tetramer typically is composed of two identical pairs of polypeptide chains, each pair having one full-length “light” (in certain embodiments, about 25 kDa) and one full-length “heavy” chain (in certain embodiments, about 50-70 kDa). The amino-terminal portion of each chain typically includes a variable region of about 100 to 10 or more amino acids that typically is responsible for

antigen recognition. The carboxy-terminal portion of each chain typically defines a constant region that can be responsible for effector function. Human light chains are typically classified as kappa and lambda light chains. Heavy chains are typically classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subclasses, including, but not limited to, IgG1, IgG2, IgG3, and IgG4. IgM has subclasses including, but not limited to, IgM1 and IgM2. IgA is similarly subdivided into subclasses including, but not limited to, IgA1 and IgA2. Within full-length light and heavy chains, typically, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. See, e.g., *Fundamental Immunology*, Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)) (incorporated by reference in its entirety for all purposes). The variable regions of each light/heavy chain pair typically form the antigen binding site.

The variable regions typically exhibit the same general structure of relatively conserved framework regions (FR) joined by three hyper variable regions, also called complementarity determining regions or CDRs. The CDRs from the two chains of each pair typically are aligned by the framework regions, which can enable binding to a specific epitope. From N-terminal to C-terminal, both light and heavy chain variable regions typically comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain is typically in accordance with the definitions of Kabat Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)), or Chothia & Lesk, *J. Mol. Biol.*, 196:901-917 (1987); Chothia et al., *Nature*, 342:878-883 (1989).

In certain embodiments, an antibody heavy chain binds to an antigen in the absence of an antibody light chain. In certain embodiments, an antibody light chain binds to an antigen in the absence of an antibody heavy chain. In certain embodiments, an antibody binding region binds to an antigen in the absence of an antibody light chain. In certain embodiments, an antibody binding region binds to an antigen in the absence of an antibody heavy chain. In certain embodiments, an individual variable region specifically binds to an antigen in the absence of other variable regions.

In certain embodiments, definitive delineation of a CDR and identification of residues comprising the binding site of an antibody is accomplished by solving the structure of the antibody and/or solving the structure of the antibody-ligand complex. In certain embodiments, that can be accomplished by any of a variety of techniques known to those skilled in the art, such as X-ray crystallography. In certain embodiments, various methods of analysis can be employed to identify or approximate the CDR regions. Examples of such methods include, but are not limited to, the Kabat definition, the Chothia definition, the AbM definition and the contact definition.

The Kabat definition is a standard for numbering the residues in an antibody and is typically used to identify CDR regions. See, e.g., Johnson & Wu, *Nucleic Acids Res.*, 28: 214-8 (2000). The Chothia definition is similar to the Kabat definition, but the Chothia definition takes into account positions of certain structural loop regions. See, e.g., Chothia et al., *J. Mol. Biol.*, 196: 901-17 (1986); Chothia et al., *Nature*, 342: 877-83 (1989). The AbM definition uses an integrated suite of computer programs produced by Oxford Molecular Group that model antibody structure. See, e.g., Martin et al., *Proc Natl Acad Sci (USA)*, 86:9268-9272 (1989); "AbM™, A Computer Program for Modeling Variable Regions of Anti-

bodies," Oxford, UK; Oxford Molecular, Ltd. The AbM definition models the tertiary structure of an antibody from primary sequence using a combination of knowledge databases and ab initio methods, such as those described by Samudrala et al., "Ab Initio Protein Structure Prediction Using a Combined Hierarchical Approach," in *PROTEINS, Structure, Function and Genetics Suppl.*, 3:194-198 (1999). The contact definition is based on an analysis of the available complex crystal structures. See, e.g., MacCallum et al., *J. Mol. Biol.*, 5:732-45 (1996).

By convention, the CDR regions in the heavy chain are typically referred to as H1, H2, and H3 and are numbered sequentially in the direction from the amino terminus to the carboxy terminus. The CDR regions in the light chain are typically referred to as L1, L2, and L3 and are numbered sequentially in the direction from the amino terminus to the carboxy terminus.

The term "light chain" includes a full-length light chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length light chain includes a variable region domain, V_L , and a constant region domain, C_L . The variable region domain of the light chain is at the amino-terminus of the polypeptide. Light chains include kappa chains and lambda chains.

The term "heavy chain" includes a full-length heavy chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length heavy chain includes a variable region domain, V_H , and three constant region domains, C_{H1} , C_{H2} , and C_{H3} . The V_H domain is at the amino-terminus of the polypeptide, and the C_H domains are at the carboxyl-terminus, with the C_{H3} being closest to the carboxy-terminus of the polypeptide. Heavy chains can be of any isotype, including IgG (including IgG1, IgG2, IgG3 and IgG4 subtypes), IgA (including IgA1 and IgA2 subtypes), IgM and IgE.

A bispecific or bifunctional antibody typically is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies can be produced by a variety of methods including, but not limited to, fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai et al., *Clin. Exp. Immunol.*, 79: 315-321 (1990); Kostelnik et al., *J. Immunol.*, 148:1547-1553 (1992).

Some species of mammals also produce antibodies having only a single heavy chain.

Each individual immunoglobulin chain is typically composed of several "immunoglobulin domains," each consisting of roughly 90 to 110 amino acids and having a characteristic folding pattern. These domains are the basic units of which antibody polypeptides are composed. In humans, the IgA and IgD isotypes contain four heavy chains and four light chains; the IgG and IgE isotypes contain two heavy chains and two light chains; and the IgM isotype contains five heavy chains and five light chains. The heavy chain C region typically comprises one or more domains that can be responsible for effector function. The number of heavy chain constant region domains will depend on the isotype. IgG heavy chains, for example, contain three C region domains known as C_{H1} , C_{H2} and C_{H3} . The antibodies that are provided can have any of these isotypes and subtypes. In certain embodiments of the present invention, an anti-PCSK9 antibody is of the IgG2 or IgG4 subtype.

The term "variable region" or "variable domain" refers to a portion of the light and/or heavy chains of an antibody, typically including approximately the amino-terminal 120 to 130 amino acids in the heavy chain and about 100 to 110 amino terminal amino acids in the light chain. In certain embodiments, variable regions of different antibodies differ exten-

sively in amino acid sequence even among antibodies of the same species. The variable region of an antibody typically determines specificity of a particular antibody for its target

The term "neutralizing antigen binding protein" or "neutralizing antibody" refers to an antigen binding protein or antibody, respectively, that binds to a ligand and prevents or reduces the biological effect of that ligand. This can be done, for example, by directly blocking a binding site on the ligand or by binding to the ligand and altering the ligand's ability to bind through indirect means (such as structural or energetic alterations in the ligand). In some embodiments, the term can also denote an antigen binding protein that prevents the protein to which it is bound from performing a biological function. In assessing the binding and/or specificity of an antigen binding protein, e.g., an antibody or immunologically functional fragment thereof, an antibody or fragment can substantially inhibit binding of a ligand to its binding partner when an excess of antibody reduces the quantity of binding partner bound to the ligand by at least about 1-20, 20-30%, 30-40%, 40-50%, 50-60%, 60-70%, 70-80%, 80-85%, 85-90%, 90-95%, 95-97%, 97-98%, 98-99% or more (as measured in an *in vitro* competitive binding assay). In some embodiments, in the case of PCSK9 antigen binding proteins, such a neutralizing molecule can diminish the ability of PCSK9 to bind the LDLR. In some embodiments, the neutralizing ability is characterized and/or described via a competition assay. In some embodiments, the neutralizing ability is described in terms of an IC_{50} or EC_{50} value. In some embodiments, ABPs 27B2, 13H1, 13B5 and 3C4 are non-neutralizing ABPs, 3B6, 9C9 and 31A4 are weak neutralizers, and the remaining ABPs in Table 2 are strong neutralizers. In some embodiments, the antibodies or antigen binding proteins neutralize by binding to PCSK9 and preventing PCSK9 from binding to LDLR (or reducing the ability of PCSK9 to bind to LDLR). In some embodiments, the antibodies or ABPs neutralize by binding to PCSK9, and while still allowing PCSK9 to bind to LDLR, preventing or reducing the PCSK9 mediated degradation of LDLR. Thus, in some embodiments, a neutralizing ABP or antibody can still permit PCSK9/LDLR binding, but will prevent (or reduce) subsequent PCSK9 involved degradation of LDLR.

The term "target" refers to a molecule or a portion of a molecule capable of being bound by an antigen binding protein. In certain embodiments, a target can have one or more epitopes. In certain embodiments, a target is an antigen. The use of "antigen" in the phrase "antigen binding protein" simply denotes that the protein sequence that comprises the antigen can be bound by an antibody. In this context, it does not require that the protein be foreign or that it be capable of inducing an immune response.

The term "compete" when used in the context of antigen binding proteins (e.g., neutralizing antigen binding proteins or neutralizing antibodies) that compete for the same epitope means competition between antigen binding proteins as determined by an assay in which the antigen binding protein (e.g., antibody or immunologically functional fragment thereof) being tested prevents or inhibits (e.g., reduces) specific binding of a reference antigen binding protein (e.g., a ligand, or a reference antibody) to a common antigen (e.g., PCSK9 or a fragment thereof). Numerous types of competitive binding assays can be used to determine if one antigen binding protein competes with another, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al., 1983, *Methods in Enzymology* 9:242-253); solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., 1986, *J. Immunol.* 137:3614-3619)

solid phase direct labeled assay, solid phase direct labeled sandwich assay (see, e.g., Harlow and Lane, 1988, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (see, e.g., Morel et al., 1988, *Molec. Immunol.* 25:7-15); solid phase direct biotin-avidin EIA (see, e.g., Cheung, et al., 1990, *Virology* 176:546-552); and direct labeled RIA (Moldenhauer et al., 1990, *Scand. J. Immunol.* 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabelled test antigen binding protein and a labeled reference antigen binding protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antigen binding protein. Usually the test antigen binding protein is present in excess. Antigen binding proteins identified by competition assay (competing antigen binding proteins) include antigen binding proteins binding to the same epitope as the reference antigen binding proteins and antigen binding proteins binding to an adjacent epitope sufficiently proximal to the epitope bound by the reference antigen binding protein for steric hindrance to occur. Additional details regarding methods for determining competitive binding are provided in the examples herein. Usually, when a competing antigen binding protein is present in excess, it will inhibit (e.g., reduce) specific binding of a reference antigen binding protein to a common antigen by at least 40-45%, 45-50%, 50-55%, 55-60%, 60-65%, 65-70%, 70-75% or 75% or more. In some instances, binding is inhibited by at least 80-85%, 85-90%, 90-95%, 95-97%, or 97% or more.

The term "antigen" refers to a molecule or a portion of a molecule capable of being bound by a selective binding agent, such as an antigen binding protein (including, e.g., an antibody or immunological functional fragment thereof). In some embodiments, the antigen is capable of being used in an animal to produce antibodies capable of binding to that antigen. An antigen can possess one or more epitopes that are capable of interacting with different antigen binding proteins, e.g., antibodies.

The term "epitope" includes any determinant capable of being bound by an antigen binding protein, such as an antibody or to a T-cell receptor. An epitope is a region of an antigen that is bound by an antigen binding protein that targets that antigen, and when the antigen is a protein, includes specific amino acids that directly contact the antigen binding protein. Most often, epitopes reside on proteins, but in some instances can reside on other kinds of molecules, such as nucleic acids. Epitope determinants can include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and can have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antibodies specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules.

As used herein, "substantially pure" means that the described species of molecule is the predominant species present, that is, on a molar basis it is more abundant than any other individual species in the same mixture. In certain embodiments, a substantially pure molecule is a composition wherein the object species comprises at least 50% (on a molar basis) of all macromolecular species present. In other embodiments, a substantially pure composition will comprise at least 80%, 85%, 90%, 95%, or 99% of all macromolecular species present in the composition. In other embodiments, the object species is purified to essential homogeneity wherein contaminating species cannot be detected in the composition

by conventional detection methods and thus the composition consists of a single detectable macromolecular species.

The term "agent" is used herein to denote a chemical compound, a mixture of chemical compounds, a biological macromolecule, or an extract made from biological materials.

As used herein, the terms "label" or "labeled" refers to incorporation of a detectable marker, e.g., by incorporation of a radiolabeled amino acid or attachment to a polypeptide of biotin moieties that can be detected by marked avidin (e.g., streptavidin containing a fluorescent marker or enzymatic activity that can be detected by optical or colorimetric methods). In certain embodiments, the label or marker can also be therapeutic. Various methods of labeling polypeptides and glycoproteins are known in the art and can be used. Examples of labels for polypeptides include, but are not limited to, the following: radioisotopes or radionuclides (e.g., ³H, ¹⁴C, ¹⁵N, ³⁵S, ⁹⁰Y, ⁹⁹Tc, ¹¹¹In, ¹²⁵I, ¹³¹I), fluorescent labels (e.g., FITC, rhodamine, lanthanide phosphors), enzymatic labels (e.g., horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase), chemiluminescent, biotinyl groups, predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In certain embodiments, labels are attached by spacer arms of various lengths to reduce potential steric hindrance.

The term "biological sample", as used herein, includes, but is not limited to, any quantity of a substance from a living thing or formerly living thing. Such living things include, but are not limited to, humans, mice, monkeys, rats, rabbits, and other animals. Such substances include, but are not limited to, blood, serum, urine, cells, organs, tissues, bone, bone marrow, lymph nodes, and skin.

The term "pharmaceutical agent composition" (or agent or drug) as used herein refers to a chemical compound, composition, agent or drug capable of inducing a desired therapeutic effect when properly administered to a patient. It does not necessarily require more than one type of ingredient.

The term "therapeutically effective amount" refers to the amount of a PCSK9 antigen binding protein determined to produce a therapeutic response in a mammal. Such therapeutically effective amounts are readily ascertained by one of ordinary skill in the art.

The term "modulator," as used herein, is a compound that changes or alters the activity or function of a molecule. For example, a modulator can cause an increase or decrease in the magnitude of a certain activity or function of a molecule compared to the magnitude of the activity or function observed in the absence of the modulator. In certain embodiments, a modulator is an inhibitor, which decreases the magnitude of at least one activity or function of a molecule. Certain exemplary activities and functions of a molecule include, but are not limited to, binding affinity, enzymatic activity, and signal transduction. Certain exemplary inhibitors include, but are not limited to, proteins, peptides, antibodies, peptibodies, carbohydrates or small organic molecules. Peptibodies are described in, e.g., U.S. Pat. No. 6,660,843 (corresponding to PCT Application No. WO 01/83525).

The terms "patient" and "subject" are used interchangeably and include human and non-human animal subjects as well as those with formally diagnosed disorders, those without formally recognized disorders, those receiving medical attention, those at risk of developing the disorders, etc.

The term "treat" and "treatment" includes therapeutic treatments, prophylactic treatments, and applications in which one reduces the risk that a subject will develop a disorder or other risk factor. Treatment does not require the

complete curing of a disorder and encompasses embodiments in which one reduces symptoms or underlying risk factors.

The term "prevent" does not require the 100% elimination of the possibility of an event. Rather, it denotes that the likelihood of the occurrence of the event has been reduced in the presence of the compound or method.

Standard techniques can be used for recombinant DNA, oligonucleotide synthesis, and tissue culture and transformation (e.g., electroporation, lipofection). Enzymatic reactions and purification techniques can be performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein. The foregoing techniques and procedures can be generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)), which is incorporated herein by reference for any purpose. Unless specific definitions are provided, the nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

Antigen Binding Proteins to PCSK9

Proprotein convertase subtilisin kexin type 9 (PCSK9) is a serine protease involved in regulating the levels of the low density lipoprotein receptor (LDLR) protein (Horton et al., 2007; Seidah and Prat, 2007). PCSK9 is a prohormone-protein convertase in the subtilisin (S8) family of serine proteases (Seidah et al., 2003). An exemplary human PCSK9 amino acid sequence is presented as SEQ ID NOs: 1 and 3. in FIG. 1A (depicting the "pro" domain of the protein as underlined) and FIG. 1B (depicting the signal sequence in bold and the pro domain underlined). An exemplary human PCSK9 coding sequence is presented as SEQ ID NO: 2 (FIG. 1B). As described herein, PCSK9 proteins can also include fragments of the full length PCSK9 protein. The structure of the PCSK9 protein has recently been solved by two groups (Cunningham et al., *Nature Structural & Molecular Biology*, 2007, and Piper et al., *Structure*, 15:1-8, 2007), the entireties of both of which are herein incorporated by reference. PCSK9 includes a signal sequence, a N-terminal prodomain, a subtilisin-like catalytic domain and a C-terminal domain.

Antigen binding proteins (ABPs) that bind PCSK9, including human PCSK9, are provided herein. In some embodiments, the antigen binding proteins provided are polypeptides which comprise one or more complementary determining regions (CDRs), as described herein. In some antigen binding proteins, the CDRs are embedded into a "framework" region, which orients the CDR(s) such that the proper antigen binding properties of the CDR(s) is achieved. In some embodiments, antigen binding proteins provided herein can interfere with, block, reduce or modulate the interaction between PCSK9 and LDLR. Such antigen binding proteins are denoted as "neutralizing." In some embodiments, binding between PCSK9 and LDLR can still occur, even though the antigen binding protein is neutralizing and bound to PCSK9. For example, in some embodiments, the ABP prevents or reduces the adverse influence of PCSK9 on LDLR without blocking the LDLR binding site on PCSK9. Thus, in some embodiments, the ABP modulates or alters PCSK9's ability to result in the degradation of LDLR, without having to pre-

vent the binding interaction between PCSK9 and LDLR. Such ABPs can be specifically described as “non-competitively neutralizing” ABPs. In some embodiments, the neutralizing ABP binds to PCSK9 in a location and/or manner that prevents PCSK9 from binding to LDLR. Such ABPs can be specifically described as “competitively neutralizing” ABPs. Both of the above neutralizers can result in a greater amount of free LDLR being present in a subject, which results in more LDLR binding to LDL (thereby reducing the amount of LDL in the subject). In turn, this results in a reduction in the amount of serum cholesterol present in a subject.

In some embodiments, the antigen binding proteins provided herein are capable of inhibiting PCSK9-mediated activity (including binding). In some embodiments, antigen binding proteins binding to these epitopes inhibit, *inter alia*, interactions between PCSK9 and LDLR and other physiological effects mediated by PCSK9. In some embodiments, the antigen binding proteins are human, such as fully human antibodies to PCSK9.

In some embodiments, the ABP binds to the catalytic domain of PCSK9. In some embodiments, the ABP binds to the mature form of PCSK9. In some embodiments the ABP binds in the prodomain of PCSK9. In some embodiments, the ABP selectively binds to the mature form of PCSK9. In some embodiments, the ABP binds to the catalytic domain in a manner such that PCSK9 cannot bind or bind as efficiently to LDLR. In some embodiments, the antigen binding protein does not bind to the c-terminus of the catalytic domain. In some embodiments, the antigen binding protein does not bind to the n-terminus of the catalytic domain. In some embodiments, the ABP does not bind to the n- or c-terminus of the PCSK9 protein. In some embodiments, the ABP binds to any one of the epitopes bound by the antibodies discussed herein. In some embodiments, this can be determined by competition assays between the antibodies disclosed herein and other antibodies. In some embodiments, the ABP binds to an epitope bound by one of the antibodies described in Table 2. In some embodiments, the antigen binding proteins bind to a specific conformational state of PCSK9 so as to prevent PCSK9 from interacting with LDLR. In some embodiments, the ABP binds to the V domain of PCSK9. In some embodiments, the ABP binds to the V domain of PCSK9 and prevents (or reduces) PCSK9 from binding to LDLR. In some embodiments, the ABP binds to the V domain of PCSK9, and while it does not prevent (or reduce) the binding of PCSK9 to LDLR, the ABP prevents or reduces the adverse activities mediated through PCSK9 on LDLR.

The antigen binding proteins that are disclosed herein have a variety of utilities. Some of the antigen binding proteins, for instance, are useful in specific binding assays, affinity purification of PCSK9, in particular human PCSK9 or its ligands and in screening assays to identify other antagonists of PCSK9 activity. Some of the antigen binding proteins are useful for inhibiting binding of PCSK9 to LDLR, or inhibiting PCSK9-mediated activities.

The antigen binding proteins can be used in a variety of therapeutic applications, as explained herein. For example, in some embodiments the PCSK9 antigen binding proteins are useful for treating conditions associated with PCSK9, such as cholesterol related disorders (or “serum cholesterol related disorders”) such as hypercholesterolemia, as further described herein. Other uses for the antigen binding proteins include, for example, diagnosis of PCSK9-associated diseases or conditions and screening assays to determine the presence or absence of PCSK9. Some of the antigen binding

proteins described herein are useful in treating consequences, symptoms, and/or the pathology associated with PCSK9 activity.

In some embodiments, the antigen binding proteins that are provided comprise one or more CDRs (e.g., 1, 2, 3, 4, 5 or 6 CDRs). In some embodiments, the antigen binding protein comprises (a) a polypeptide structure and (b) one or more CDRs that are inserted into and/or joined to the polypeptide structure. The polypeptide structure can take a variety of different forms. For example, it can be, or comprise, the framework of a naturally occurring antibody, or fragment or variant thereof, or can be completely synthetic in nature. Examples of various polypeptide structures are further described below.

5 In certain embodiments, the polypeptide structure of the antigen binding proteins is an antibody or is derived from an antibody, including, but not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as “antibody mimetics”), chimeric antibodies, humanized antibodies, antibody fusions (sometimes referred to as “antibody conjugates”), and portions or fragments of each, respectively. In some instances, the antigen binding protein is an immunological fragment of an antibody (e.g., a Fab, a Fab', a F(ab')₂, or a scFv). The various structures are further described and defined herein.

10 Certain of the antigen binding proteins as provided herein specifically and/or selectively bind to human PCSK9. In some embodiments, the antigen binding protein specifically and/or selectively binds to human PCSK9 protein having and/or consisting of residues 153-692 of SEQ ID NO: 3. In some embodiments the ABP specifically and/or selectively binds to human PCSK9 having and/or consisting of residues 31-152 of SEQ ID NO: 3. In some embodiments, the ABP 15 selectively binds to a human PCSK9 protein as depicted in FIG. 1A (SEQ ID NO: 1). In some embodiments, the antigen binding protein specifically binds to at least a fragment of the PCSK9 protein and/or a full length PCSK9 protein, with or without a signal sequence.

15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810

In embodiments where the antigen binding protein is used for therapeutic applications, an antigen binding protein can inhibit, interfere with or modulate one or more biological activities of PCSK9. In one embodiment, an antigen binding protein binds specifically to human PCSK9 and/or substantially inhibits binding of human PCSK9 to LDLR by at least about 20%-40%, 40-60%, 60-80%, 80-85%, or more (for example, by measuring binding in an *in vitro* competitive binding assay). Some of the antigen binding proteins that are provided herein are antibodies. In some embodiments, the ABP has a K_d of less (binding more tightly) than 10^{-7} , 10^{-8} , 10^{-9} , 10^{-10} , 10^{-11} , 10^{-12} , 10^{-13} M. In some embodiments, the ABP has an IC_{50} for blocking the binding of LDLR to PCSK9 (D374Y, high affinity variant) of less than 1 microM, 1000 nM to 100 nM, 100mM to 10 nM, 1 nM to 1 pM, 1000 pM to 500 pM, 500 pM to 200 pM, less than 200 pM, 200 pM to 150 pM, 200 pM to 100 pM, 100 pM to 10 pM, 10 pM to 1 pM.

60 One example of an IgG2 heavy chain constant domain of an anti-PCSK9 antibody of the present invention has the amino acid sequence as shown in SEQ ID NO: 154, FIG. 3KK.

65 One example of an IgG4 heavy chain constant domain of an anti-PCSK9 antibody of the present invention has the amino acid sequence as shown in SEQ ID NO: 155, FIG. 3KK.

70 One example of a kappa light chain constant domain of an anti-PCSK9 antibody has the amino acid sequence as shown in SEQ ID NO: 157, FIG. 3KK.

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One example of a lambda light chain constant domain of an anti-PCSK9 antibody has the amino acid sequence as shown in SEQ ID NO: 156, FIG. 3KK.

Variable regions of immunoglobulin chains generally exhibit the same overall structure, comprising relatively conserved framework regions (FR) joined by three hypervariable regions, more often called "complementarity determining regions" or CDRs. The CDRs from the two chains of each heavy chain/light chain pair mentioned above typically are aligned by the framework regions to form a structure that binds specifically with a specific epitope on the target protein (e.g., PCSK9). From N-terminal to C-terminal, naturally-occurring light and heavy chain variable regions both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, Md.), or Chothia & Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia et al., 1989, *Nature* 342:878-883.

Various heavy chain and light chain variable regions are provided herein and are depicted in FIGS. 2A-3JJ and 3LL-3BBB. In some embodiments, each of these variable regions can be attached to the above heavy and light chain constant regions to form a complete antibody heavy and light chain, respectively. Further, each of the so generated heavy and light chain sequences can be combined to form a complete antibody structure.

Specific examples of some of the variable regions of the light and heavy chains of the antibodies that are provided and their corresponding amino acid sequences are summarized in TABLE 2.

TABLE 2

Exemplary Heavy and Light Chain Variable Regions	
Antibody	Light/Heavy SEQ ID NO
30A4	5/74
3C4	7/85
23B5	9/71
25G4	10/72
31H4	12/67
27B2	13/87
25A7	15/58
27H5	16/52
26H5	17/51
31D1	18/53
20D10	19/48
27E7	20/54
30B9	21/55
19H9	22/56
26E10	23/49
21B12	23/49
17C2	24/57
23G1	26/50
13H1	28/91
9C9	30/64
9H6	31/62
31A4	32/89
1A12	33/65
16F12	35/79
22E2	36/80
27A6	37/76
28B12	38/77
28D6	39/78
31G11	40/83
13B5	42/69
31B12	44/81
3B6	46/60

42

Again, each of the exemplary variable heavy chains listed in Table 2 can be combined with any of the exemplary variable light chains shown in Table 2 to form an antibody. Table 2 shows exemplary light and heavy chain pairings found in several of the antibodies disclosed herein. In some instances, the antibodies include at least one variable heavy chain and one variable light chain from those listed in Table 2. In other instances, the antibodies contain two identical light chains and two identical heavy chains. As an example, an antibody or antigen binding protein can include a heavy chain and a light chain, two heavy chains, or two light chains. In some embodiments the antigen binding protein comprises (and/or consists) of 1, 2, and/or 3 heavy and/or light CDRs from at least one of the sequences listed in Table 2 (CDRs for the sequences are outlined in FIGS. 2A-3D, and other embodiments in FIGS. 3CCC-3JJ and 15A-15D). In some embodiments, all 6 CDRs (CDR1-3 from the light (CDRL1, CDRL2, CDRL3) and CDR1-3 from the heavy (CDRH1, CDRH2, and CDRH3)) are part of the ABP. In some embodiments, 1, 2, 3, 4, 5, or more CDRs are included in the ABP. In some embodiments, one heavy and one light CDR from the CDRs in the sequences in Table 2 is included in the ABP (CDRs for the sequences in table 2 are outlined in FIGS. 2A-3D). In some embodiments, additional sections (e.g., as depicted in FIG. 2A-2D, 3A-3D, and other embodiments in 3CCC-3JJ and 15A-15D) are also included in the ABP. Examples of CDRs and FRs for the heavy and light chains noted in Table 2 are outlined in FIGS. 2A-3D (and other embodiments in FIGS. 3CCC-3JJ and 15A-15D). Optional light chain variable sequences (including CDR1, CDR2, CDR3, FR1, FR2, FR3, and FR4) can be selected from the following: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46. Optional heavy chain variable sequences (including CDR1, CDR2, CDR3, FR1, FR2, FR3, and FR4) can be selected from the following: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60. In some of the entries in FIG. 2A-3D, variations of the sequences or alternative boundaries of the CDRs and FRs are identified. These alternatives are identified with a "v1" following the ABP name. As most of these alternatives are minor in nature, only sections with differences are displayed in the table. It is understood that the remaining section of the light or heavy chain is the same as shown for the base ABP in the other panels. Thus, for example, 19H9v1 in FIG. 2C has the same FR1, CDR1, and FR2 as 19H9 in FIG. 2A as the only difference is noted in FIG. 2C. For three of the nucleic acid sequences (ABPs 26E10, 30B9, and 31B12), additional alternative nucleic acid sequences are provided in the figures. As will be appreciated by one of skill in the art, no more than one such sequence need actually be used in the creation of an antibody or ABP. Indeed, in some embodiments, only one or neither of the specific heavy or light chain nucleic acids need be present. In some embodiments, the ABP is encoded by a nucleic acid sequence that can encode any of the protein sequences in Table 2. In some embodiments, the ABP binds selectively to the form of PCSK9 that binds to LDLR (e.g., the autocatalyzed form of the molecule). In some embodiments, the antigen binding protein does not bind to the c-terminus of the catalytic domain (e.g., the 5. 5-10, 10-15, 15-20, 20-25, 25-30, 30-40 most amino acids in the c-terminus). In some embodiments, the antigen binding protein does not bind to the n-terminus of the catalytic domain (e.g., the 5. 5-10, 10-15, 15-20, 20-25, 25-30, 30-40 most amino acids in the n-terminus). In some embodiments, the ABP binds to amino acids within

amino acids 1-100 of the mature form of PCSK9. In some embodiments, the ABP binds to amino acids within (and/or amino acid sequences consisting of) amino acids 31-100, 100-200, 31-152, 153-692, 200-300, 300-400, 452-683, 400-500, 500-600, 31-692, 31-449, and/or 600-692. In some embodiments, the ABP binds to the catalytic domain. In some embodiments, the neutralizing and/or non-neutralizing ABP binds to the prodomain. In some embodiments, the ABP binds to both the catalytic and pro domains. In some embodiments, the ABP binds to the catalytic domain so as to obstruct an area on the catalytic domain that interacts with the pro domain. In some embodiments, the ABP binds to the catalytic domain at a location or surface that the pro-domain interacts with as outlined in Piper et al. (Structure 15:1-8 (2007), the entirety of which is hereby incorporated by reference, including the structural representations therein). In some embodiments, the ABP binds to the catalytic domain and restricts the mobility of the prodomain. In some embodiments, the ABP binds to the catalytic domain without binding to the pro-domain. In some embodiments, the ABP binds to the catalytic domain, without binding to the pro-domain, while preventing the pro-domain from reorienting to allow PCSK9 to bind to LDLR. In some embodiments, the ABP binds in the same epitope as those surrounding residues 149-152 of the pro-domain in Piper et al. In some embodiments, the ABPs bind to the groove (as outlined in Piper et al.) on the V domain. In some embodiments, the ABPs bind to the histidine-rich patch proximal to the groove on the V domain. In some embodiments, such antibodies (that bind to the V domain) are not neutralizing. In some embodiments, antibodies that bind to the V domain are neutralizing. In some embodiments, the neutralizing ABPs prevent the binding of PCSK9 to LDLR. In some embodiments, the neutralizing ABPs, while preventing the PCSK9 degradation of LDLR, do not prevent the binding of PCSK9 to LDLR (for example ABP 31A4). In some embodiments, the ABP binds to or blocks at least one of the histidines depicted in FIG. 4 of the Piper et al. paper. In some embodiments, the ABP blocks the catalytic triad in PCSK9.

In some embodiments, the antibody binds selectively to variant PCSK9 proteins, e.g., D374Y over wild type PCSK9. In some embodiments, these antibodies bind to the variant at least twice as strongly as the wild type, and preferably 2-5, 5-10, 10-100, 100-1000, 1000-10,000 fold or more to the mutant than the wild type (as measured via a K_d). In some embodiments, the antibody selectively inhibits variant D374Y PCSK9 from interacting with LDLR over wild type PCSK9's ability to interact with LDLR. In some embodiments, these antibodies block the variant's ability to bind to LDLR more strongly than the wild type's ability, e.g., at least twice as strongly as the wild type, and preferably 2-5, 5-10, 10-100, 100-1000 fold or more to the mutant than the wild type (as measured via an IC_{50}). In some embodiments, the antibody binds to and neutralizes both wild type PCSK9 and variant forms of PCSK9, such as D374Y at similar levels. In some embodiments, the antibody binds to PCSK9 to prevent variants of LDLR from binding to PCSK9. In some embodiments, the variants of LDLR are at least 50% identical to human LDLR. It is noted that variants of LDLR are known to those of skill in the art (e.g., Brown M S et al, "Calcium cages, acid baths and recycling receptors" Nature 388: 629-630, 1997). In some embodiments, the ABP can raise the level of effective LDLR in heterozygote familial hypercholesterolemia (where a loss-of function variant of LDLR is present).

In some embodiments, the ABP binds to (but does not block) variants of PCSK9 that are at least 50%, 50-60, 60-70, 70-80, 80-90, 90-95, 95-99, or greater percent identity to the form of PCSK9 depicted in FIG. 1A and/or FIG. 1B. In some

embodiments, the ABP binds to (but does not block) variants of PCSK9 that are at least 50%, 50-60, 60-70, 70-80, 80-90, 90-95, 95-99, or greater percent identity to the mature form of PCSK9 depicted in FIG. 1A and/or FIG. 1B. In some embodiments, the ABP binds to and prevents variants of PCSK9 that are at least 50%, 50-60, 60-70, 70-80, 80-90, 90-95, 95-99, or greater percent identity to the form of PCSK9 depicted in FIG. 1A and/or FIG. 1B from interacting with LDLR. In some embodiments, the ABP binds to and prevents variants of PCSK9 that are at least 50, 50-60, 60-70, 70-80, 80-90, 90-95, 95-99, or greater percent identity to the mature form of PCSK9 depicted in FIG. 1B from interacting with LDLR. In some embodiments, the variant of PCSK9 is a human variant, such as variants at position 474, E620G, and/or E670G. In some embodiments, the amino acid at position 474 is valine (as in other humans) or threonine (as in cyno and mouse). Given the cross-reactivity data presented herein, it is believed that the present antibodies will readily bind to the above variants.

In some embodiments, the ABP binds to an epitope bound by one of the antibodies described in Table 2. In some embodiments, the antigen binding proteins bind to a specific conformational state of PCSK9 so as to prevent PCSK9 from interacting with LDLR.

Humanized Antigen Binding Proteins (e.g. Antibodies)

As described herein, an antigen binding protein to PCSK9 can comprise a humanized antibody and/or part thereof. An important practical application of such a strategy is the "humanization" of the mouse humoral immune system.

In certain embodiments, a humanized antibody is substantially non-immunogenic in humans. In certain embodiments, a humanized antibody has substantially the same affinity for a target as an antibody from another species from which the humanized antibody is derived. See, e.g., U.S. Pat. Nos. 5,530,101, 5,693,761; 5,693,762; 5,585,089.

In certain embodiments, amino acids of an antibody variable domain that can be modified without diminishing the native affinity of the antigen binding domain while reducing its immunogenicity are identified. See, e.g., U.S. Pat. Nos. 5,766,886 and 5,869,619.

In certain embodiments, modification of an antibody by methods known in the art is typically designed to achieve increased binding affinity for a target and/or to reduce immunogenicity of the antibody in the recipient. In certain embodiments, humanized antibodies are modified to eliminate glycosylation sites in order to increase affinity of the antibody for its cognate antigen. See, e.g., Co et al., Mol. Immunol., 30:1361-1367 (1993). In certain embodiments, techniques such as "reshaping," "hyperchimerization," or "veeneering/resurfacing" are used to produce humanized antibodies. See, e.g., Vaswami et al., Annals of Allergy, Asthma, & Immunol. 81:105 (1998); Roguska et al., Prot. Engineer., 9:895-904 (1996); and U.S. Pat. No. 6,072,035. In certain such embodiments, such techniques typically reduce antibody immunogenicity by reducing the number of foreign residues, but do not prevent anti-idiotypic and anti-allotypic responses following repeated administration of the antibodies. Certain other methods for reducing immunogenicity are described, e.g., in Gilliland et al., J. Immunol., 62(6): 3663-71 (1999).

In certain instances, humanizing antibodies results in a loss of antigen binding capacity. In certain embodiments, humanized antibodies are "back mutated." In certain such embodiments, the humanized antibody is mutated to include one or more of the amino acid residues found in the donor antibody. See, e.g., Saldanha et al., Mol Immunol 36:709-19 (1999).

In certain embodiments the complementarity determining regions (CDRs) of the light and heavy chain variable regions

of an antibody to PCSK9 can be grafted to framework regions (FRs) from the same, or another, species. In certain embodiments, the CDRs of the light and heavy chain variable regions of an antibody to PCSK9 can be grafted to consensus human FRs. To create consensus human FRs, in certain embodiments, FRs from several human heavy chain or light chain amino acid sequences are aligned to identify a consensus amino acid sequence. In certain embodiments, the FRs of an antibody to PCSK9 heavy chain or light chain are replaced with the FRs from a different heavy chain or light chain. In certain embodiments, rare amino acids in the FRs of the heavy and light chains of an antibody to PCSK9 are not replaced, while the rest of the FR amino acids are replaced. Rare amino acids are specific amino acids that are in positions in which they are not usually found in FRs. In certain embodiments, the grafted variable regions from an antibody to PCSK9 can be used with a constant region that is different from the constant region of an antibody to PCSK9. In certain embodiments, the grafted variable regions are part of a single chain Fv antibody. CDR grafting is described, e.g., in U.S. Pat. Nos. 6,180,370, 6,054,297, 5,693,762, 5,859,205, 5,693,761, 5,565,332, 5,585,089, and 5,530,101, and in Jones et al., *Nature*, 321: 522-525 (1986); Riechmann et al., *Nature*, 332: 323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988), Winter, *FEBS Letts.*, 430:92-94 (1998), which are hereby incorporated by reference for any purpose.

Human Antigen Binding Proteins (e.g., Antibodies)

As described herein, an antigen binding protein that binds to PCSK9 can comprise a human (i.e., fully human) antibody and/or part thereof. In certain embodiments, nucleotide sequences encoding, and amino acid sequences comprising, heavy and light chain immunoglobulin molecules, particularly sequences corresponding to the variable regions are provided. In certain embodiments, sequences corresponding to complementarity determining regions (CDR's), specifically from CDR1 through CDR3, are provided. According to certain embodiments, a hybridoma cell line expressing such an immunoglobulin molecule is provided. According to certain embodiments, a hybridoma cell line expressing such a monoclonal antibody is provided. In certain embodiments a hybridoma cell line is selected from at least one of the cell lines described in Table 2, e.g., 21B12, 16F12 and 31H4. In certain embodiments, a purified human monoclonal antibody to human PCSK9 is provided.

One can engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce human antibodies in the absence of mouse antibodies. Large human Ig fragments can preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains can yield high affinity fully human antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human MAbs with the desired specificity can be produced and selected. Certain exemplary methods are described in WO 98/24893, U.S. Pat. No. 5,545,807, EP 546073, and EP 546073.

In certain embodiments, one can use constant regions from species other than human along with the human variable region(s).

The ability to clone and reconstruct megabase sized human loci in yeast artificial chromosomes (YACs) and to introduce them into the mouse germline provides an approach to elucidating the functional components of very large or crudely

mapped loci as well as generating useful models of human disease. Furthermore, the utilization of such technology for substitution of mouse loci with their human equivalents could provide insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

Human antibodies avoid some of the problems associated with antibodies that possess murine or rat variable and/or constant regions. The presence of such murine or rat derived proteins can lead to the rapid clearance of the antibodies or can lead to the generation of an immune response against the antibody by a patient. In order to avoid the utilization of murine or rat derived antibodies, fully human antibodies can be generated through the introduction of functional human antibody loci into a rodent, other mammal or animal so that the rodent, other mammal or animal produces fully human antibodies.

Humanized antibodies are those antibodies that, while initially starting off containing antibody amino acid sequences that are not human, have had at least some of these nonhuman antibody amino acid sequences replaced with human antibody sequences. This is in contrast with human antibodies, in which the antibody is encoded (or capable of being encoded) by genes possessed a human.

Antigen Binding Protein Variants

Other antibodies that are provided are variants of the ABPs listed above formed by combination or subparts of the variable heavy and variable light chains shown in Table 2 and comprise variable light and/or variable heavy chains that each have at least 50%, 50-60, 60-70, 70-80%, 80-85%, 85-90%, 90-95%, 95-97%, 97-99%, or above 99% identity to the amino acid sequences of the sequences in Table 2 (either the entire sequence or a subpart of the sequence, e.g., one or more CDR). In some instances, such antibodies include at least one heavy chain and one light chain, whereas in other instances the variant forms contain two identical light chains and two identical heavy chains (or subparts thereof). In some embodiments, the sequence comparison in FIG. 2A-3D (and 13A-13J and other embodiments in 15A-15D) can be used in order to identify sections of the antibodies that can be modified by observing those variations that impact binding and those variations that do not appear to impact binding. For example, by comparing similar sequences, one can identify those sections (e.g., particular amino acids) that can be modified and how they can be modified while still retaining (or improving) the functionality of the ABP. In some embodiments, variants of ABPs include those consensus groups and sequences depicted in FIGS. 13A, 13C, 13F, 13G, 13H, 13I and/or 13J and variations are allowed in the positions identified as variable in the figures. The CDRs shown in FIGS. 13A, 13C, 13F, and 13G were defined based upon a hybrid combination of the Chothia method (based on the location of the structural loop regions, see, e.g., "Standard conformations for the canonical structures of immunoglobulins," Bissan Al-Lazikani, Arthur M. Lesk and Cyrus Chothia, *Journal of Molecular Biology*, 273(4): 927-948, 7 November (1997)) and the Kabat method (based on sequence variability, see, e.g., *Sequences of Proteins of Immunological Interest*, Fifth Edition. NIH Publication No. 91-3242, Kabat et al., (1991)). Each residue determined by either method, was included in the final list of CDR residues (and is presented in FIGS. 13A, 13C, 13F, and 13G). The CDRs in FIGS. 13H, 13I, and 13J were obtained by the Kabat method alone. Unless specified otherwise, the defined consensus sequences, CDRs, and FRs in FIGS. 13H-13J will define and control the noted CDRs and FRs for the referenced ABPs in FIG. 13.

In certain embodiments, an antigen binding protein comprises a heavy chain comprising a variable region comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from at least one of the sequences of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60. In certain embodiments, an antigen binding protein comprises a heavy chain comprising a variable region comprising an amino acid sequence at least 95% identical to an amino acid sequence selected from at least one of the sequences of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60. In certain embodiments, an antigen binding protein comprises a heavy chain comprising a variable region comprising an amino acid sequence at least 99% identical to an amino acid sequence selected from at least one of the sequences of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60.

In some embodiments, the antigen binding protein comprises a sequence that is at least 90%, 90-95%, and/or 95-99% identical to one or more CDRs from the CDRs in at least one of sequences of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60. In some embodiments, 1, 2, 3, 4, 5, or 6 CDR (each being at least 90%, 90-95%, and/or 95-99% identical to the above sequences) is present.

In some embodiments, the antigen binding protein comprises a sequence that is at least 90%, 90-95%, and/or 95-99% identical to one or more FRs from the FRs in at least one of sequences of SEQ ID NO: 74, 85, 71, 72, 67, 87, 58, 52, 51, 53, 48, 54, 55, 56, 49, 57, 50, 91, 64, 62, 89, 65, 79, 80, 76, 77, 78, 83, 69, 81, and 60. In some embodiments, 1, 2, 3, or 4 FR (each being at least 90%, 90-95%, and/or 95-99% identical to the above sequences) is present.

In certain embodiments, an antigen binding protein comprises a light chain comprising a variable region comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from at least one of the sequences of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46. In certain embodiments, an antigen binding protein comprises a light chain comprising a variable region comprising an amino acid sequence at least 95% identical to an amino acid sequence selected from at least one of the sequences of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46. In certain embodiments, an antigen binding protein comprises a light chain comprising a variable region comprising an amino acid sequence at least 99% identical to an amino acid sequence selected from at least one of the sequences of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46.

In some embodiments, the antigen binding protein comprises a sequence that is at least 90%, 90-95%, and/or 95-99% identical to one or more CDRs from the CDRs in at least one of sequences of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 42, 44, and 46. In some embodiments, 1, 2, 3, 4, 5, or 6 CDR (each being at least 90%, 90-95%, and/or 95-99% identical to the above sequences) is present.

In some embodiments, the antigen binding protein comprises a sequence that is at least 90%, 90-95%, and/or 95-99% identical to one or more FRs from the FRs in at least one of sequences of SEQ ID NO: 5, 7, 9, 10, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 28, 30, 31, 32, 33, 35, 36, 37, 38, 39,

40, 42, 44, and 46. In some embodiments, 1, 2, 3, or 4 FR (each being at least 90%, 90-95%, and/or 95-99% identical to the above sequences) is present.

In light of the present disclosure, a skilled artisan will be able to determine suitable variants of the ABPs as set forth herein using well-known techniques. In certain embodiments, one skilled in the art can identify suitable areas of the molecule that may be changed without destroying activity by targeting regions not believed to be important for activity. In certain embodiments, one can identify residues and portions of the molecules that are conserved among similar polypeptides. In certain embodiments, even areas that can be important for biological activity or for structure can be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the polypeptide structure.

Additionally, one skilled in the art can review structure-function studies identifying residues in similar polypeptides that are important for activity or structure. In view of such a comparison, one can predict the importance of amino acid residues in a protein that correspond to amino acid residues which are important for activity or structure in similar proteins. One skilled in the art can opt for chemically similar amino acid substitutions for such predicted important amino acid residues.

One skilled in the art can also analyze the three-dimensional structure and amino acid sequence in relation to that structure in similar ABPs. In view of such information, one skilled in the art can predict the alignment of amino acid residues of an antibody with respect to its three dimensional structure. In certain embodiments, one skilled in the art can choose not to make radical changes to amino acid residues predicted to be on the surface of the protein, since such residues can be involved in important interactions with other molecules. Moreover, one skilled in the art can generate test variants containing a single amino acid substitution at each desired amino acid residue. The variants can then be screened using activity assays known to those skilled in the art. Such variants can be used to gather information about suitable variants. For example, if one discovered that a change to a particular amino acid residue resulted in destroyed, undesirably reduced, or unsuitable activity, variants with such a change can be avoided. In other words, based on information gathered from such routine experiments, one skilled in the art can readily determine the amino acids where further substitutions should be avoided either alone or in combination with other mutations.

A number of scientific publications have been devoted to the prediction of secondary structure. See Moult J., *Curr. Op. in Biotech.*, 7(4):422-427 (1996), Chou et al., *Biochemistry*, 13(2):222-245 (1974); Chou et al., *Biochemistry*, 113(2): 211-222 (1974); Chou et al., *Adv. Enzymol. Relat. Areas Mol. Biol.*, 47:45-148 (1978); Chou et al., *Ann. Rev. Biochem.*, 47:251-276 and Chou et al., *Biophys. J.*, 26:367-384 (1979). Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins which have a sequence identity of greater than 30%, or similarity greater than 40% often have similar structural topologies. The recent growth of the protein structural database (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. See Holm et al., *Nucl. Acid. Res.*, 27(1):244-247 (1999). It has been suggested (Brenner et al., *Curr. Op. Struct. Biol.*, 7(3):369-376 (1997)) that there are a limited number of folds in a given polypeptide or protein and that once a critical

number of structures have been resolved, structural prediction will become dramatically more accurate.

Additional methods of predicting secondary structure include "threading" (Jones, D., *Curr. Opin. Struct. Biol.*, 7(3): 377-87 (1997); Sippl et al., *Structure*, 4(1):15-19 (1996)), "profile analysis" (Bowie et al., *Science*, 253:164-170 (1991); Gribskov et al., *Meth. Enzym.*, 183:146-159 (1990); Gribskov et al., *Proc. Natl. Acad. Sci. USA*, 84(13):4355-4358 (1987)), and "evolutionary linkage" (See Holm, *supra* (1999), and Brenner, *supra* (1997)).

In certain embodiments, antigen binding protein variants include glycosylation variants wherein the number and/or type of glycosylation site has been altered compared to the amino acid sequences of a parent polypeptide. In certain embodiments, protein variants comprise a greater or a lesser number of N-linked glycosylation sites than the native protein. An N-linked glycosylation site is characterized by the sequence: Asn-X-Ser or Asn-X-Thr, wherein the amino acid residue designated as X can be any amino acid residue except proline. The substitution of amino acid residues to create this sequence provides a potential new site for the addition of an N-linked carbohydrate chain. Alternatively, substitutions which eliminate this sequence will remove an existing N-linked carbohydrate chain. Also provided is a rearrangement of N-linked carbohydrate chains wherein one or more N-linked glycosylation sites (typically those that are naturally occurring) are eliminated and one or more new N-linked sites are created. Additional preferred antibody variants include cysteine variants wherein one or more cysteine residues are deleted from or substituted for another amino acid (e.g., serine) as compared to the parent amino acid sequence. Cysteine variants can be useful when antibodies must be refolded into a biologically active conformation such as after the isolation of insoluble inclusion bodies. Cysteine variants generally have fewer cysteine residues than the native protein, and typically have an even number to minimize interactions resulting from unpaired cysteines.

According to certain embodiments, amino acid substitutions are those which: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter binding affinities, and/or (4) confer or modify other physicochemical or functional properties on such polypeptides. According to certain embodiments, single or multiple amino acid substitutions (in certain embodiments, conservative amino acid substitutions) can be made in the naturally-occurring sequence (in certain embodiments, in the portion of the polypeptide outside the domain(s) forming intermolecular contacts). In certain embodiments, a conservative amino acid substitution typically may not substantially change the structural characteristics of the parent sequence (e.g., a replacement amino acid should not tend to break a helix that occurs in the parent sequence, or disrupt other types of secondary structure that characterizes the parent sequence). Examples of art-recognized polypeptide secondary and tertiary structures are described in *Proteins, Structures and Molecular Principles* (Creighton, Ed., W. H. Freeman and Company, New York (1984)); *Introduction to Protein Structure* (C. Branden & J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton et al., *Nature*, 354:105 (1991), which are each incorporated herein by reference.

In some embodiments, the variants are variants of the nucleic acid sequences of the ABPs disclosed herein. One of skill in the art will appreciate that the above discussion can be used for identifying, evaluating, and/creating ABP protein variants and also for nucleic acid sequences that can encode for those protein variants. Thus, nucleic acid sequences

encoding for those protein variants (as well as nucleic acid sequences that encode for the ABPs in Table 2, but are different from those explicitly disclosed herein) are contemplated. For example, an ABP variant can have at least 80, 80-85, 85-90, 90-95, 95-97, 97-99 or greater identity to at least one nucleic acid sequence described in SEQ ID NOs: 152, 153, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151 or at least one to six (and various combinations thereof) of the CDR(s) encoded by the nucleic acid sequences in SEQ ID NOs: 152, 153, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, and 151.

In some embodiments, the antibody (or nucleic acid sequence encoding it) is a variant if the nucleic acid sequence that encodes the particular ABP (or the nucleic acid sequence itself) can selectively hybridize to any of the nucleic acid sequences that encode the proteins in Table 2 (such as, but not limited to SEQ ID NO: 152, 153, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, and 151). In some embodiments, the antibody (or nucleic acid sequence encoding it) is a variant if the nucleic acid sequence that encodes the particular ABP (or the nucleic acid sequence itself) can selectively hybridize to any of the nucleic acid sequences that encode the proteins in Table 2 (such as, but not limited to SEQ ID NO: 152, 153, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, and 151) under stringent conditions. In one embodiment, suitable moderately stringent conditions include prewashing in a solution of 5×SSC; 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50° C., -65° C., 5×SSC, overnight or, in the event of cross-species homology, at 45° C. with 0.5×SSC; followed by washing twice at 65° C. for 20 minutes with each of 2×, 0.5× and 0.2×SSC containing 0.1% SDS. Such hybridizing DNA sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode an antibody polypeptide that is encoded by a hybridizing DNA sequence and the amino acid sequences that are encoded by these nucleic acid sequences. In some embodiments, variants of CDRs include nucleic acid sequences and the amino acid sequences encoded by those sequences, that hybridize to one or more of the CDRs within the sequences noted above (individual CDRs can readily be determined in light of FIGS. 2A-3D, and other embodiments in FIGS. 3CCC-3JJJ and 15A-15D). The phrase "selectively hybridize" referred to in this context means to detectably and selectively bind. Polynucleotides, oligonucleotides and fragments thereof in accordance with the invention selectively hybridize to nucleic acid strands under hybridization and wash conditions that minimize appreciable amounts of detectable binding to nonspecific nucleic acids. High stringency conditions can be used to achieve selective hybridization conditions as known in the art and discussed herein. Generally, the nucleic acid sequence homology between the polynucleotides, oligonucleotides, and fragments of the invention and a nucleic acid sequence of interest will be at least 80%, and more typically with preferably increasing homologies of at least 85%, 90%, 95%, 99%, and 100%. Two amino acid sequences are homologous if there is a partial or complete identity between their sequences. For example, 85% homology means that 85% of the amino acids are identical when the two sequences are aligned for maximum matching. Gaps (in either of the two sequences being matched) are allowed in maximizing matching; gap lengths of 5 or less are preferred with 2 or less being more preferred. Alternatively and preferably, two protein sequences (or

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polypeptide sequences derived from them of at least 30 amino acids in length) are homologous, as this term is used herein, if they have an alignment score of at more than 5 (in standard deviation units) using the program ALIGN with the mutation data matrix and a gap penalty of 6 or greater. See Dayhoff, M. O., in *Atlas of Protein Sequence and Structure*, pp. 101-110 (Volume 5, National Biomedical Research Foundation (1972)) and Supplement 2 to this volume, pp. 1-10. The two sequences or parts thereof are more preferably homologous if their amino acids are greater than or equal to 50% identical when optimally aligned using the ALIGN program. The term "corresponds to" is used herein to mean that a polynucleotide sequence is homologous (i.e., is identical, not strictly evolutionarily related) to all or a portion of a reference polynucleotide sequence, or that a polypeptide sequence is identical to a reference polypeptide sequence. In contradistinction, the term "complementary to" is used herein to mean that the complementary sequence is homologous to all or a portion of a reference polynucleotide sequence. For illustration, the nucleotide sequence "TATAC" corresponds to a reference sequence "TATAC" and is complementary to a reference sequence "GTATA".

Preparation of Antigen Binding Proteins (e.g., Antibodies)

In certain embodiments, antigen binding proteins (such as antibodies) are produced by immunization with an antigen (e.g., PCSK9). In certain embodiments, antibodies can be produced by immunization with full-length PCSK9, a soluble form of PCSK9, the catalytic domain alone, the mature form of PCSK9 shown in FIG. 1A, a splice variant form of PCSK9, or a fragment thereof. In certain embodiments, the antibodies of the invention can be polyclonal or monoclonal, and/or can be recombinant antibodies. In certain embodiments, antibodies of the invention are human antibodies prepared, for example, by immunization of transgenic animals capable of producing human antibodies (see, for example, PCT Published Application No. WO 93/12227).

In certain embodiments, certain strategies can be employed to manipulate inherent properties of an antibody, such as the affinity of an antibody for its target. Such strategies include, but are not limited to, the use of site-specific or random mutagenesis of the polynucleotide molecule encoding an antibody to generate an antibody variant. In certain embodiments, such generation is followed by screening for antibody variants that exhibit the desired change, e.g. increased or decreased affinity.

In certain embodiments, the amino acid residues targeted in mutagenic strategies are those in the CDRs. In certain embodiments, amino acids in the framework regions of the variable domains are targeted. In certain embodiments, such framework regions have been shown to contribute to the target binding properties of certain antibodies. See, e.g., Hudson, *Curr. Opin. Biotech.*, 9:395-402 (1999) and references therein.

In certain embodiments, smaller and more effectively screened libraries of antibody variants are produced by restricting random or site-directed mutagenesis to hyper-mutation sites in the CDRs, which are sites that correspond to areas prone to mutation during the somatic affinity maturation process. See, e.g., Chowdhury & Pastan, *Nature Biotech.*, 17: 568-572 (1999) and references therein. In certain embodiments, certain types of DNA elements can be used to identify hyper-mutation sites including, but not limited to, certain direct and inverted repeats, certain consensus sequences, certain secondary structures, and certain palindromes. For example, such DNA elements that can be used to identify hyper-mutation sites include, but are not limited to, a tetra-base sequence comprising a purine (A or G), followed by

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guanine (G), followed by a pyrimidine (C or T), followed by either adenine or thymidine (A or T) (i.e., A/G-G-C/T-A/T). Another example of a DNA element that can be used to identify hyper-mutation sites is the serine codon, A-G-C/T. Preparation of Fully Human Abps (e.g., Antibodies)

In certain embodiments, a phage display technique is used to generate monoclonal antibodies. In certain embodiments, such techniques produce fully human monoclonal antibodies. In certain embodiments, a polynucleotide encoding a single Fab or Fv antibody fragment is expressed on the surface of a phage particle. See, e.g., Hoogenboom et al., *J. Mol. Biol.*, 227: 381 (1991); Marks et al., *J Mol Biol* 222: 581 (1991); U.S. Pat. No. 5,885,793. In certain embodiments, phage are "screened" to identify those antibody fragments having affinity for target. Thus, certain such processes mimic immune selection through the display of antibody fragment repertoires on the surface of filamentous bacteriophage, and subsequent selection of phage by their binding to target. In certain such procedures, high affinity functional neutralizing antibody fragments are isolated. In certain such embodiments (discussed in more detail below), a complete repertoire of human antibody genes is created by cloning naturally rearranged human V genes from peripheral blood lymphocytes. See, e.g., Mullinax et al., *Proc Natl Acad Sci (USA)*, 87: 8095-8099 (1990).

According to certain embodiments, antibodies of the invention are prepared through the utilization of a transgenic mouse that has a substantial portion of the human antibody producing genome inserted but that is rendered deficient in the production of endogenous, murine antibodies. Such mice, then, are capable of producing human immunoglobulin molecules and antibodies and are deficient in the production of murine immunoglobulin molecules and antibodies. Technologies utilized for achieving this result are disclosed in the patents, applications and references disclosed in the specification, herein. In certain embodiments, one can employ methods such as those disclosed in PCT Published Application No. WO 98/24893 or in Mendez et al., *Nature Genetics*, 15:146-156 (1997), which are hereby incorporated by reference for any purpose.

Generally, fully human monoclonal ABPs (e.g., antibodies) specific for PCSK9 can be produced as follows. Transgenic mice containing human immunoglobulin genes are immunized with the antigen of interest, e.g. PCSK9, lymphatic cells (such as B-cells) from the mice that express antibodies are obtained. Such recovered cells are fused with a myeloid-type cell line to prepare immortal hybridoma cell lines, and such hybridoma cell lines are screened and selected to identify hybridoma cell lines that produce antibodies specific to the antigen of interest. In certain embodiments, the production of a hybridoma cell line that produces antibodies specific to PCSK9 is provided.

In certain embodiments, fully human antibodies are produced by exposing human splenocytes (B or T cells) to an antigen in vitro, and then reconstituting the exposed cells in an immunocompromised mouse, e.g. SCID or nod/SCID. See, e.g., Brams et al., *J. Immunol.* 160: 2051-2058 (1998); Carballido et al., *Nat. Med.*, 6: 103-106 (2000). In certain such approaches, engraftment of human fetal tissue into SCID mice (SCID-hu) results in long-term hematopoiesis and human T-cell development. See, e.g., McCune et al., *Science*, 241:1532-1639 (1988); Ifversen et al., *Sem. Immunol.*, 8:243-248 (1996). In certain instances, humoral immune response in such chimeric mice is dependent on co-development of human T-cells in the animals. See, e.g., Martensson et al., *Immunol.*, 83:1271-179 (1994). In certain approaches, human peripheral blood lymphocytes are transplanted into

SCID mice. See, e.g., Mosier et al., *Nature*, 335:256-259 (1988). In certain such embodiments, when such transplanted cells are treated either with a priming agent, such as Staphylococcal Enterotoxin A (SEA), or with anti-human CD40 monoclonal antibodies, higher levels of B cell production is detected. See, e.g., Martensson et al., *Immunol.*, 84: 224-230 (1995); Murphy et al., *Blood*, 86:1946-1953 (1995).

Thus, in certain embodiments, fully human antibodies can be produced by the expression of recombinant DNA in host cells or by expression in hybridoma cells. In other embodiments, antibodies can be produced using the phage display techniques described herein.

The antibodies described herein were prepared through the utilization of the XenoMouse® technology, as described herein. Such mice, then, are capable of producing human immunoglobulin molecules and antibodies and are deficient in the production of murine immunoglobulin molecules and antibodies. Technologies utilized for achieving the same are disclosed in the patents, applications, and references disclosed in the background section herein. In particular, however, a preferred embodiment of transgenic production of mice and antibodies therefrom is disclosed in U.S. patent application Ser. No. 08/759,620, filed Dec. 3, 1996 and International Patent Application Nos. WO 98/24893, published Jun. 11, 1998 and WO 00/76310, published Dec. 21, 2000, the disclosures of which are hereby incorporated by reference. See also Mendez et al., *Nature Genetics*, 15:146-156 (1997), the disclosure of which is hereby incorporated by reference.

Through the use of such technology, fully human monoclonal antibodies to a variety of antigens have been produced. Essentially, XenoMouse® lines of mice are immunized with an antigen of interest (e.g. PCSK9), lymphatic cells (such as B-cells) are recovered from the hyper-immunized mice, and the recovered lymphocytes are fused with a myeloid-type cell line to prepare immortal hybridoma cell lines. These hybridoma cell lines are screened and selected to identify hybridoma cell lines that produced antibodies specific to the antigen of interest. Provided herein are methods for the production of multiple hybridoma cell lines that produce antibodies specific to PCSK9. Further, provided herein are characterization of the antibodies produced by such cell lines, including nucleotide and amino acid sequence analyses of the heavy and light chains of such antibodies.

The production of the XenoMouse® strains of mice is further discussed and delineated in U.S. patent application Ser. Nos. 07/466,008, filed Jan. 12, 1990, 07/610,515, filed Nov. 8, 1990, 07/919,297, filed Jul. 24, 1992, 07/922,649, filed Jul. 30, 1992, 08/031,801, filed Mar. 15, 1993, 08/112,848, filed Aug. 27, 1993, 08/234,145, filed Apr. 28, 1994, 08/376,279, filed Jan. 20, 1995, 08/430,938, filed Apr. 27, 1995, 08/464,584, filed Jun. 5, 1995, 08/464,582, filed Jun. 5, 1995, 08/463,191, filed Jun. 5, 1995, 08/462,837, filed Jun. 5, 1995, 08/486,853, filed Jun. 5, 1995, 08/486,857, filed Jun. 5, 1995, 08/486,859, filed Jun. 5, 1995, 08/462,513, filed Jun. 5, 1995, 08/724,752, filed Oct. 2, 1996, 08/759,620, filed Dec. 3, 1996, U.S. Publication 2003/0093820, filed Nov. 30, 2001 and U.S. Pat. Nos. 6,162,963, 6,150,584, 6,114,598, 6,075, 181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also European Patent No., EP 0 463 151 B1, grant published Jun. 12, 1996, International Patent Application No., WO 94/02602, published Feb. 3, 1994, International Patent Application No., WO 96/34096, published Oct. 31, 1996, WO 98/24893, published Jun. 11, 1998, WO 00/76310, published Dec. 21, 2000. The disclosures of each of the above-cited patents, applications, and references are hereby incorporated by reference in their entirety.

In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more V_H genes, one or more DH genes, one or more JH genes, a mu constant region, and usually a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani et al. and U.S. Pat. Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877,397, 5,874,299, and 6,255,458 each to Lonberg & Kay, U.S. Pat. Nos. 5,591,669 and 6,023,010 to Krimpenfort & Berns, U.S. Pat. Nos. 5,612,205, 5,721,367, and 5,789,215 to Bems et al., and U.S. Pat. No. 5,643,763 to Choi & Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, filed Aug. 29, 1990, 07/575,962, filed Aug. 31, 1990, 07/810,279, filed Dec. 17, 1991, 07/853,408, filed Mar. 18, 1992, 07/904,068, filed Jun. 23, 1992, 07/990,860, filed Dec. 16, 1992, 08/053,131, filed Apr. 26, 1993, 08/096,762, filed Jul. 22, 1993, 08/155,301, filed Nov. 18, 1993, 08/161,739, filed Dec. 3, 1993, 08/165,699, filed Dec. 10, 1993, 08/209,741, filed Mar. 9, 1994, the disclosures of which are hereby incorporated by reference. See also European Patent No. 0 546 073 B1, International Patent Application Nos. WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175, the disclosures of which are hereby incorporated by reference in their entirety. See further Taylor et al., 1992, Chen et al., 1993, Tuailion et al., 1993, Choi et al., 1993, Lonberg et al., (1994), Taylor et al., (1994), and Tuailion et al., (1995), Fishwild et al., (1996), the disclosures of which are hereby incorporated by reference in their entirety.

Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961, the disclosures of which are hereby incorporated by reference. Additionally, KM™ mice, which are the result of cross-breeding of Kirin's Tc mice with Medarex's minilocus (Humab) mice have been generated. These mice possess the human IgH transchromosome of the Kirin mice and the kappa chain transgene of the Genpharm mice (Ishida et al., Cloning Stem Cells, (2002) 4:91-102).

Human antibodies can also be derived by in vitro methods. Suitable examples include but are not limited to phage display (CAT, Morphosys, Dyax, Biosite/Medarex, Xoma, Sympogen, Alexion (formerly Proliferon), Affimed) ribosome display (CAT), yeast display, and the like.

In some embodiments, the antibodies described herein possess human IgG4 heavy chains as well as IgG2 heavy chains. Antibodies can also be of other human isotypes, including IgG1. The antibodies possessed high affinities, typically possessing a K_d of from about 10^{-6} through about 10^{-13} M or below, when measured by various techniques.

As will be appreciated, antibodies can be expressed in cell lines other than hybridoma cell lines. Sequences encoding particular antibodies can be used to transform a suitable mammalian host cell. Transformation can be by any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in a virus (or into a viral vector) and transducing a host cell with the virus (or vector) or by transfection procedures known in the art, as exemplified by U.S. Pat. Nos. 4,399,216, 4,912,040, 4,740,461, and 4,959,455 (which patents are hereby incorporated herein by reference). The transformation proce-

dure used depends upon the host to be transformed. Methods for introducing heterologous polynucleotides into mammalian cells are well known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are well known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), human epithelial kidney 293 cells, and a number of other cell lines. Cell lines of particular preference are selected through determining which cell lines have high expression levels and produce antibodies with constitutive PCSK9 binding properties.

In certain embodiments, antibodies and/or ABP are produced by at least one of the following hybridomas: 21B12, 31H4, 16F12, any other hybridomas listed in Table 2 or disclosed in the examples. In certain embodiments, antigen binding proteins bind to PCSK9 with a dissociation constant (K_D) of less than approximately 1 nM, e.g., 1000 pM to 100 pM, 100 pM to 10 pM, 10 pM to 1 pM, and/or 1 pM to 0.1 pM or less.

In certain embodiments, antigen binding proteins comprise an immunoglobulin molecule of at least one of the IgG1, IgG2, IgG3, IgG4, IgE, IgA, IgD, and IgM isotype. In certain embodiments, antigen binding proteins comprise a human kappa light chain and/or a human heavy chain. In certain embodiments, the heavy chain is of the IgG1, IgG2, IgG3, IgG4, IgE, IgA, IgD, or IgM isotype. In certain embodiments, antigen binding proteins have been cloned for expression in mammalian cells. In certain embodiments, antigen binding proteins comprise a constant region other than any of the constant regions of the IgG1, IgG2, IgG3, IgG4, IgE, IgA, IgD, and IgM isotype.

In certain embodiments, antigen binding proteins comprise a human lambda light chain and a human IgG2 heavy chain. In certain embodiments, antigen binding proteins comprise a human lambda light chain and a human IgG4 heavy chain. In certain embodiments, antigen binding proteins comprise a human lambda light chain and a human IgG1, IgG3, IgE, IgA, IgD or IgM heavy chain. In other embodiments, antigen binding proteins comprise a human kappa light chain and a human IgG2 heavy chain. In certain embodiments, antigen binding proteins comprise a human kappa light chain and a human IgG4 heavy chain. In certain embodiments, antigen binding proteins comprise a human kappa light chain and a human IgG1, IgG3, IgE, IgA, IgD or IgM heavy chain. In certain embodiments, antigen binding proteins comprise variable regions of antibodies ligated to a constant region that is neither the constant region for the IgG2 isotype, nor the constant region for the IgG4 isotype. In certain embodiments, antigen binding proteins have been cloned for expression in mammalian cells.

In certain embodiments, conservative modifications to the heavy and light chains of antibodies from at least one of the hybridoma lines: 21B12, 31H4 and 16F12 (and corresponding modifications to the encoding nucleotides) will produce antibodies to PCSK9 having functional and chemical characteristics similar to those of the antibodies from the hybridoma lines: 21B12, 31H4 and 16F12. In contrast, in certain embodiments, substantial modifications in the functional and/or chemical characteristics of antibodies to PCSK9 can be accomplished by selecting substitutions in the amino acid

sequence of the heavy and light chains that differ significantly in their effect on maintaining (a) the structure of the molecular backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

For example, a "conservative amino acid substitution" can involve a substitution of a native amino acid residue with a normative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide can also be substituted with alanine, as has been previously described for "alanine scanning mutagenesis."

Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. In certain embodiments, amino acid substitutions can be used to identify important residues of antibodies to PCSK9, or to increase or decrease the affinity of the antibodies to PCSK9 as described herein.

In certain embodiments, antibodies of the present invention can be expressed in cell lines other than hybridoma cell lines. In certain embodiments, sequences encoding particular antibodies can be used for transformation of a suitable mammalian host cell. According to certain embodiments, transformation can be by any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in a virus (or into a viral vector) and transducing a host cell with the virus (or vector) or by transfection procedures known in the art, as exemplified by U.S. Pat. Nos. 4,399,216, 4,912,040, 4,740,461, and 4,959,455 (which patents are hereby incorporated herein by reference for any purpose). In certain embodiments, the transformation procedure used can depend upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are well known in the art and include, but are not limited to, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines. In certain embodiments, cell lines can be selected through determining which cell lines have high expression levels and produce antibodies with constitutive HGF binding properties. Appropriate expression vectors for mammalian host cells are well known.

In certain embodiments, antigen binding proteins comprise one or more polypeptides. In certain embodiments, any of a variety of expression vector/host systems can be utilized to express polynucleotide molecules encoding polypeptides comprising one or more ABP components or the ABP itself. Such systems include, but are not limited to, microorganisms, such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transfected with virus expression vectors (e.g., cauliflower mosaic virus, CaMV, tobacco mosaic virus, TMV) or transformed with bacterial expression vectors (e.g., Ti or pBR322 plasmid); or animal cell systems.

In certain embodiments, a polypeptide comprising one or more ABP components or the ABP itself is recombinantly expressed in yeast. Certain such embodiments use commercially available expression systems, e.g., the *Pichia* Expression System (Invitrogen, San Diego, Calif.), following the manufacturer's instructions. In certain embodiments, such a system relies on the pre-pro-alpha sequence to direct secretion. In certain embodiments, transcription of the insert is driven by the alcohol oxidase (AOX1) promoter upon induction by methanol.

In certain embodiments, a secreted polypeptide comprising one or more ABP components or the ABP itself is purified from yeast growth medium. In certain embodiments, the methods used to purify a polypeptide from yeast growth medium is the same as those used to purify the polypeptide from bacterial and mammalian cell supernatants.

In certain embodiments, a nucleic acid encoding a polypeptide comprising one or more ABP components or the ABP itself is cloned into a baculovirus expression vector, such as pVL1393 (PharMingen, San Diego, Calif.). In certain embodiments, such a vector can be used according to the manufacturer's directions (PharMingen) to infect *Spodoptera frugiperda* cells in SF9 protein-free media and to produce recombinant polypeptide. In certain embodiments, a polypeptide is purified and concentrated from such media using a heparin-Sepharose column (Pharmacia).

In certain embodiments, a polypeptide comprising one or more ABP components or the ABP itself is expressed in an insect system. Certain insect systems for polypeptide expression are well known to those of skill in the art. In one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia larvae*. In certain embodiments, a nucleic acid molecule encoding a polypeptide can be inserted into a nonessential gene of the virus, for example, within the polyhedrin gene, and placed under control of the promoter for that gene. In certain embodiments, successful insertion of a nucleic acid molecule will render the nonessential gene inactive. In certain embodiments, that inactivation results in a detectable characteristic. For example, inactivation of the polyhedrin gene results in the production of virus lacking coat protein.

In certain embodiments, recombinant viruses can be used to infect *S. frugiperda* cells or *Trichoplusia larvae*. See, e.g., Smith et al., J. Virol., 46: 584 (1983); Engelhard et al., Proc. Nat. Acad. Sci. (USA), 91: 3224-7 (1994).

In certain embodiments, polypeptides comprising one or more ABP components or the ABP itself made in bacterial cells are produced as insoluble inclusion bodies in the bacteria. In certain embodiments, host cells comprising such inclusion bodies are collected by centrifugation; washed in 0.15 M NaCl, 10 mM Tris, pH 8, 1 mM EDTA; and treated with 0.1 mg/ml lysozyme (Sigma, St. Louis, Mo.) for 15 minutes at room temperature. In certain embodiments, the lysate is cleared by sonication, and cell debris is pelleted by centrifugation for 10 minutes at 12,000×g. In certain embodiments, the polypeptide-containing pellet is resuspended in 50 mM Tris, pH 8, and 10 mM EDTA; layered over 50% glycerol; and centrifuged for 30 minutes at 6000×g. In certain embodiments, that pellet can be resuspended in standard phosphate buffered saline solution (PBS) free of Mg⁺⁺ and Ca⁺⁺. In certain embodiments, the polypeptide is further purified by fractionating the resuspended pellet in a denaturing SDS polyacrylamide gel (See, e.g., Sambrook et al., supra). In certain embodiments, such a gel can be soaked in 0.4 M KCl to visualize the protein, which can be excised and electroeluted in gel-running buffer lacking SDS. According to cer-

tain embodiments, a Glutathione-S-Transferase (GST) fusion protein is produced in bacteria as a soluble protein. In certain embodiments, such GST fusion protein is purified using a GST Purification Module (Pharmacia).

In certain embodiments, it is desirable to "refold" certain polypeptides, e.g., polypeptides comprising one or more ABP components or the ABP itself. In certain embodiments, such polypeptides are produced using certain recombinant systems discussed herein. In certain embodiments, polypeptides are 10 "refolded" and/or oxidized to form desired tertiary structure and/or to generate disulfide linkages. In certain embodiments, such structure and/or linkages are related to certain biological activity of a polypeptide. In certain embodiments, refolding is accomplished using any of a number of procedures known in the art. Exemplary methods include, but are not limited to, exposing the solubilized polypeptide agent to a pH typically above 7 in the presence of a chaotropic agent. An exemplary chaotropic agent is guanidine. In certain embodiments, the refolding/oxidation solution also contains a reducing agent 15 and the oxidized form of that reducing agent. In certain embodiments, the reducing agent and its oxidized form are present in a ratio that will generate a particular redox potential that allows disulfide shuffling to occur. In certain embodiments, such shuffling allows the formation of cysteine bridges. Exemplary redox couples include, but are not limited to, cysteine/cystamine, glutathione/dithiobisGSH, cupric chloride, dithiothreitol DTT/dithiane DTT, and 2-mercaptoethanol (bME)/dithio-bME. In certain embodiments, a co-solvent is used to increase the efficiency of refolding. Exemplary cosolvents include, but are not limited to, glycerol, polyethylene glycol of various molecular weights, and arginine.

In certain embodiments, one substantially purifies a polypeptide comprising one or more ABP components or the ABP itself. Certain protein purification techniques are known to those of skill in the art. In certain embodiments, protein purification involves crude fractionation of polypeptide fractions from non-polypeptide fractions. In certain embodiments, polypeptides are purified using chromatographic and/or electrophoretic techniques. Exemplary purification methods include, but are not limited to, precipitation with ammonium sulphate; precipitation with PEG; immunoprecipitation; heat denaturation followed by centrifugation; chromatography, including, but not limited to, affinity chromatography (e.g., Protein-A-Sepharose), ion exchange chromatography, exclusion chromatography, and reverse phase chromatography; gel filtration; hydroxyapatite chromatography; isoelectric focusing; polyacrylamide gel electrophoresis; and combinations of such and other techniques. In certain embodiments, a polypeptide is purified by fast protein liquid chromatography or by high pressure liquid chromatography (HPLC). In certain embodiments, purification steps can be changed or certain steps can be omitted, and still result in a suitable method for the preparation of a substantially purified polypeptide.

In certain embodiments, one quantitates the degree of purification of a polypeptide preparation. Certain methods for quantifying the degree of purification are known to those of skill in the art. Certain exemplary methods include, but are not limited to, determining the specific binding activity of the preparation and assessing the amount of a polypeptide within a preparation by SDS/PAGE analysis. Certain exemplary methods for assessing the amount of purification of a polypeptide preparation comprise calculating the binding activity of a preparation and comparing it to the binding activity of an initial extract. In certain embodiments, the results of such a calculation are expressed as "fold purifica-

tion." The units used to represent the amount of binding activity depend upon the particular assay performed.

In certain embodiments, a polypeptide comprising one or more ABP components or the ABP itself is partially purified. In certain embodiments, partial purification can be accomplished by using fewer purification steps or by utilizing different forms of the same general purification scheme. For example, in certain embodiments, cation-exchange column chromatography performed utilizing an HPLC apparatus will generally result in a greater "fold purification" than the same technique utilizing a low-pressure chromatography system. In certain embodiments, methods resulting in a lower degree of purification can have advantages in total recovery of polypeptide, or in maintaining binding activity of a polypeptide.

In certain instances, the electrophoretic migration of a polypeptide can vary, sometimes significantly, with different conditions of SDS/PAGE. See, e.g., Capaldi et al, *Biochem. Biophys. Res. Comm.*, 76: 425 (1977). It will be appreciated that under different electrophoresis conditions, the apparent molecular weights of purified or partially purified polypeptide can be different.

Exemplary Epitopes

Epitopes to which anti-PCSK9 antibodies bind are provided. In some embodiments, epitopes that are bound by the presently disclosed antibodies are particularly useful. In some embodiments, antigen binding proteins that bind to any of the epitopes that are bound by the antibodies described herein are useful. In some embodiments, the epitopes bound by any of the antibodies listed in Table 2 and FIGS. 2 and 3 are especially useful. In some embodiments, the epitope is on the catalytic domain PCSK9.

In certain embodiments, a PCSK9 epitope can be utilized to prevent (e.g., reduce) binding of an anti-PCSK9 antibody or antigen binding protein to PCSK9. In certain embodiments, a PCSK9 epitope can be utilized to decrease binding of an anti-PCSK9 antibody or antigen binding protein to PCSK9. In certain embodiments, a PCSK9 epitope can be utilized to substantially inhibit binding of an anti-PCSK9 antibody or antigen binding protein to PCSK9.

In certain embodiments, a PCSK9 epitope can be utilized to isolate antibodies or antigen binding proteins that bind to PCSK9. In certain embodiments, a PCSK9 epitope can be utilized to generate antibodies or antigen binding proteins which bind to PCSK9. In certain embodiments, a PCSK9 epitope or a sequence comprising a PCSK9 epitope can be utilized as an immunogen to generate antibodies or antigen binding proteins that bind to PCSK9. In certain embodiments, a PCSK9 epitope can be administered to an animal, and antibodies that bind to PCSK9 can subsequently be obtained from the animal. In certain embodiments, a PCSK9 epitope or a sequence comprising a PCSK9 epitope can be utilized to interfere with normal PCSK9-mediated activity, such as association of PCSK9 with the LDLR.

In some embodiments, antigen binding proteins disclosed herein bind specifically to N-terminal prodomain, a subtilisin-like catalytic domain and/or a C-terminal domain. In some embodiments, the antigen binding protein binds to the substrate-binding groove of PCSK-9 (described in Cunningham et al., incorporated herein in its entirety by reference).

In some embodiments, the domain(s)/region(s) containing residues that are in contact with or are buried by an antibody can be identified by mutating specific residues in PCSK9 (e.g., a wild-type antigen) and determining whether the antigen binding protein can bind the mutated or variant PCSK9 protein. By making a number of individual mutations, residues that play a direct role in binding or that are in sufficiently

close proximity to the antibody such that a mutation can affect binding between the antigen binding protein and antigen can be identified. From a knowledge of these amino acids, the domain(s) or region(s) of the antigen that contain residues in contact with the antigen binding protein or covered by the antibody can be elucidated. Such a domain can include the binding epitope of an antigen binding protein. One specific example of this general approach utilizes an arginine/glutamic acid scanning protocol (see, e.g., Nanovicz, T., et al., 1995, *J. Biol. Chem.*, 270:37, 21619-21625 and Zupnick, A., et al., 2006, *J. Biol. Chem.*, 281:29, 20464-20473). In general, arginine and glutamic acids are substituted (typically individually) for an amino acid in the wild-type polypeptide because these amino acids are charged and bulky and thus have the potential to disrupt binding between an antigen binding protein and an antigen in the region of the antigen where the mutation is introduced. Arginines that exist in the wild-type antigen are replaced with glutamic acid. A variety of such individual mutants are obtained and the collected binding results analyzed to determine what residues affect binding.

Example 39 describes one such arginine/glutamic acid scanning of PCSK9 for PCSK9 antigen binding proteins provided herein. A series of mutant PCSK9 antigens were created, with each mutant antigen having a single mutation. Binding of each mutant PCSK9 antigen with various PCSK9 ABPs was measured and compared to the ability of the selected ABPs to bind wild-type PCSK9 (SEQ ID NO: 303).

An alteration (for example a reduction or increase) in binding between an antigen binding protein and a variant PCSK9 as used herein means that there is a change in binding affinity (e.g., as measured by known methods such as Biacore testing or the bead based assay described below in the examples), EC₅₀, and/or a change (for example a reduction) in the total binding capacity of the antigen binding protein (for example, as evidenced by a decrease in Bmax in a plot of antigen binding protein concentration versus antigen concentration). A significant alteration in binding indicates that the mutated residue is directly involved in binding to the antigen binding protein or is in close proximity to the binding protein when the binding protein is bound to antigen.

In some embodiments, a significant reduction in binding means that the binding affinity, EC₅₀, and/or capacity between an antigen binding protein and a mutant PCSK9 antigen is reduced by greater than 10%, greater than 20%, greater than 40%, greater than 50%, greater than 55%, greater than 60%, greater than 65%, greater than 70%, greater than 75%, greater than 80%, greater than 85%, greater than 90% or greater than 95% relative to binding between the antigen binding protein and a wild type PCSK9 (e.g., shown in SEQ ID NO: 1 and/or SEQ ID NO: (303)). In certain embodiments, binding is reduced below detectable limits. In some embodiments, a significant reduction in binding is evidenced when binding of an antigen binding protein to a variant PCSK9 protein is less than 50% (for example, less than 40%, 35%, 30%, 25%, 20%, 15% or 10%) of the binding observed between the antigen binding protein and a wild-type PCSK9 protein (for example, the protein of SEQ ID NO: 1 and/or SEQ ID NO: (303)). Such binding measurements can be made using a variety of binding assays known in the art. A specific example of one such assay is described in Example 39.

In some embodiments, antigen binding proteins are provided that exhibit significantly lower binding for a variant PCSK9 protein in which a residue in a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303) is substituted with arginine or glutamic acid. In some embodiments, binding of an antigen binding protein is significantly reduced or

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increased for a variant PCSK9 protein having any one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 244) of the following mutations: R207E, D208R, R185E, R439E, E513R, V538R, E539R, T132R, S351R, A390R, A413R, E582R, D162R, R164E, E167R, S123R, E129R, A311R, D313R, D337R, R519E, H521R, and Q554R as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303). In the shorthand notation used here, the format is: Wild type residue: Position in polypeptide: Mutant residue, with the numbering of the residues as indicated in SEQ ID NO: 1 or SEQ ID NO: 303.

In some embodiments, binding of an antigen binding protein is significantly reduced or increased for a mutant PCSK9 protein having one or more (e.g., 1, 2, 3, 4, 5, or more) mutations at the following positions: 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554, as shown in SEQ ID NO: 1 as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303). In some embodiments, binding of an antigen binding protein is reduced or increased for a mutant PCSK9 protein having one or more (e.g., 1, 2, 3, 4, 5, or more) mutations at the following positions: 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554, as shown in SEQ ID NO: 1 as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303). In some embodiments, binding of an antigen binding protein is substantially reduced or increased for a mutant PCSK9 protein having one or more (e.g., 1, 2, 3, 4, 5, or more) mutations at the following positions: 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554, within SEQ ID NO: 1 as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303).

In some embodiments, binding of an ABP is significantly reduced or increased for a mutant PCSK9 protein having one or more (e.g., 1, 2, 3, 4, 5, etc.) of the following mutations: R207E, D208R, R185E, R439E, E513R, V538R, E539R, T132R, S351R, A390R, A413R, E582R, D162R, R164E, E167R, S123R, E129R, A311R, D313R, D337R, R519E, H521R, and Q554R within SEQ ID NO: 1 or SEQ ID NO: 303, as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303).

In some embodiments, binding of an ABP is significantly reduced or increased for a mutant PCSK9 protein having one or more (e.g., 1, 2, 3, 4, 5, etc.) of the following mutations: R207E, D208R, R185E, R439E, E513R, V538R, E539R, T132R, S351R, A390R, A413R, and E582R within SEQ ID NO: 1 or SEQ ID NO: 303, as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303). In some embodiments, the binding is reduced. In some embodiments, the reduction in binding is observed as a change in EC50. In some embodiments, the change in EC50 is an increase in the numerical value of the EC50 (and thus is a decrease in binding).

In some embodiments, binding of an ABP is significantly reduced or increased for a mutant PCSK9 protein having one or more (e.g., 1, 2, 3, 4, 5, etc.) of the following mutations: D162R, R164E, E167R, S123R, E129R, A311R, D313R, D337R, R519E, H521R, and Q554R within SEQ ID NO: 1, as compared to a wild-type PCSK9 protein (e.g., SEQ ID NO: 1 or SEQ ID NO: 303). In some embodiments, the binding is reduced. In some embodiments, the reduction in binding is observed as a change in Bmax. In some embodiments, the shift in Bmax is a reduction of the maximum signal generated by the ABP. In some embodiments, for an amino acid to be part of an epitope, the Bmax is reduced by at least 10%, for example, reductions of at least any of the following amounts:

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20, 30, 40, 50, 60, 70, 80, 90, 95, 98, 99, or 100 percent can, in some embodiments, indicate that the residue is part of the epitope.

Although the variant forms just listed are referenced with respect to the wild-type sequence shown in SEQ ID NO: 1 or SEQ ID NO: 303, it will be appreciated that in an allelic variant of PCSK9 the amino acid at the indicated position could differ. Antigen binding proteins showing significantly lower binding for such allelic forms of PCSK9 are also contemplated. Accordingly, in some embodiments, any of the above embodiments can be compared to an allelic sequence, rather than purely the wild-type sequence shown in FIG. 1A

In some embodiments, binding of an antigen binding protein is significantly reduced for a variant PCSK9 protein in which the residue at a selected position in the wild-type PCSK9 protein is mutated to any other residue. In some embodiments, the herein described arginine/glutamic acid replacements are used for the identified positions. In some embodiments, alanine is used for the identified positions.

As noted above, residues directly involved in binding or covered by an antigen binding protein can be identified from scanning results. These residues can thus provide an indication of the domains or regions of SEQ ID NO: 1 (or SEQ ID NO: 303 or SEQ ID NO: 3) that contain the binding region(s) to which antigen binding proteins bind. As can be seen from the results summarized in Example 39, in some embodiments an antigen binding protein binds to a domain containing at least one of amino acids: 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554 of SEQ ID NO: 1 or SEQ ID NO: 303. In some embodiments, the antigen binding protein binds to a region containing at least one of amino acids 207, 208, 185, 181, 439, 513, 538, 539, 132, 351, 390, 413, 582, 162, 164, 167, 123, 129, 311, 313, 337, 519, 521, and 554 of SEQ ID NO: 1 or SEQ ID NO: 303.

In some embodiments, the antigen binding protein binds to a region containing at least one of amino acids 162, 164, 167, 207 and/or 208 of SEQ ID NO: 1 or SEQ ID NO: 303. In some embodiments, more than one (e.g., 2, 3, 4, or 5) of the identified residues are part of the region that is bound by the ABP. In some embodiments, the ABP competes with ABP 21B12.

In some embodiments, the antigen binding protein binds to a region containing at least one of amino acid 185 of SEQ ID NO: 1 or SEQ ID NO: 303. In some embodiments, the ABP competes with ABP 31H4.

In some embodiments, the antigen binding protein binds to a region containing at least one of amino acids 439, 513, 538, and/or 539 of SEQ ID NO: 1 or SEQ ID NO: 303. In some embodiments, more than one (e.g., 2, 3, or 4) of the identified residues are part of the region that is bound by the ABP. In some embodiments, the ABP competes with ABP 31A4.

In some embodiments, the antigen binding protein binds to a region containing at least one of amino acids 123, 129, 311, 313, 337, 132, 351, 390, and/or 413 of SEQ ID NO: 1 or SEQ ID NO: 303. In some embodiments, more than one (e.g., 2, 3, 4, 5, 6, 7, 8, or 9) of the identified residues are part of the region that is bound by the ABP. In some embodiments, the ABP competes with ABP 12H11.

In some embodiments, the antigen binding protein binds to a region containing at least one of amino acid 582, 519, 521, and/or 554 of SEQ ID NO: 1 or SEQ ID NO: 303. In some embodiments, more than one (e.g., 2, 3, or 4) of the identified residues are part of the region that is bound by the ABP. In some embodiments, the ABP competes with ABP 3C4.

In some embodiments, the antigen binding proteins binds to the foregoing regions within a fragment or the full length sequence of SEQ ID NO: 1 or SEQ ID NO: 303. In other

embodiments, antigen binding proteins bind to polypeptides consisting of these regions. The reference to “SEQ ID NO: 1 or SEQ ID NO: 303” denotes that one or both of these sequences can be employed or relevant. The phrase does not denote that only one should be employed.

As noted above, the above description references specific amino acid positions with reference to SEQ ID NO: 1. However, throughout the specification generally, reference is made to a Pro/Cat domain that commences at position 31, which is provided in SEQ ID NO: 3. As noted below, SEQ ID NO: 1 and SEQ ID NO: 303 lack the signal sequence of PCSK9. As such, any comparison between these various disclosures should take this difference in numbering into account. In particular, any amino acid position in SEQ ID NO: 1, will correspond to an amino acid position 30 amino acids further into the protein in SEQ ID NO: 3. For example, position 207 of SEQ ID NO: 1, corresponds to position 237 of SEQ ID NO: 3 (the full length sequence, and the numbering system used in the present specification generally). Table 39.6 outlines how the above noted positions, which reference SEQ ID NO: 1 (and/or SEQ ID NO: 303) correspond to SEQ ID NO: 3 (which includes the signal sequence). Thus, any of the above noted embodiments that are described in regard to SEQ ID NO: 1 (and/or SEQ ID NO: 303), are described in reference to SEQ ID NO: 3, by the noted corresponding positions.

In some embodiments, ABP 21B12 binds to an epitope including residues 162-167 (e.g., residues D162-E167 of SEQ ID NO: 1). In some embodiments, ABP 12H11 binds to an epitope that includes residues 123-132 (e.g., S123-T132 of SEQ ID NO: 1). In some embodiments, ABP 12H11 binds to an epitope that includes residues 311-313 (e.g., A311-D313 of SEQ ID NO: 1). In some embodiments, ABPs can bind to an epitope that includes any one of these strands of sequences.

Competing Antigen Binding Proteins

In another aspect, antigen binding proteins are provided that compete with one of the exemplified antibodies or functional fragments binding to the epitope described herein for specific binding to PCSK9. Such antigen binding proteins can also bind to the same epitope as one of the herein exemplified antigen binding proteins, or an overlapping epitope. Antigen binding proteins and fragments that compete with or bind to the same epitope as the exemplified antigen binding proteins are expected to show similar functional properties. The exemplified antigen binding proteins and fragments include those described above, including those with the heavy and light chains, variable region domains and CDRs included in TABLE 2 And/or FIGS. 2-3 and 15. Thus, as a specific example, the antigen binding proteins that are provided include those that compete with an antibody or antigen binding protein having:

- (a) all 6 of the CDRs listed for an antibody listed in FIGS. 2-3 and 15;
- (b) a VH and a VL listed for an antibody listed in Table 2; or
- (c) two light chains and two heavy chains as specified for an antibody listed in Table 2.

Certain Therapeutic Uses and Pharmaceutical Compositions

In certain instances, PCSK9 activity correlates with a number of human disease states. For example, in certain instances, too much or too little PCSK9 activity correlates with certain conditions, such as hypercholesterolemia. Therefore, in certain instances, modulating PCSK9 activity can be therapeutically useful. In certain embodiments, a neutralizing antigen binding protein to PCSK9 is used to modulate at least one PCSK9 activity (e.g., binding to LDLR). Such methods can treat and/or prevent and/or reduce the risk of disorders that

relate to elevated serum cholesterol levels or in which elevated cholesterol levels are relevant.

As will be appreciated by one of skill in the art, in light of the present disclosure, disorders that relate to, involve, or can be influenced by varied cholesterol, LDL, or LDLR levels can be addressed by various embodiments of the antigen binding proteins. In some embodiments, a “cholesterol related disorder” (which includes “serum cholesterol related disorders”) includes any one or more of the following: hypercholesterolemia, heart disease, metabolic syndrome, diabetes, coronary heart disease, stroke, cardiovascular diseases, Alzheimers disease and generally dyslipidemias, which can be manifested, for example, by an elevated total serum cholesterol, elevated LDL, elevated triglycerides, elevated VLDL, and/or low HDL. Some non-limiting examples of primary and secondary dyslipidemias that can be treated using an ABP, either alone, or in combination with one or more other agents include the metabolic syndrome, diabetes mellitus, familial combined hyperlipidemia, familial hypertriglyceridemia, familial hypercholesterolemias, including heterozygous hypercholesterolemia, homozygous hypercholesterolemia, familial defective apolipoprotein B-100; polygenic hypercholesterolemia; remnant removal disease, hepatic lipase deficiency; dyslipidemia secondary to any of the following: dietary indiscretion, hypothyroidism, drugs including estrogen and progestin therapy, beta-blockers, and thiazide diuretics; nephrotic syndrome, chronic renal failure, Cushing’s syndrome, primary biliary cirrhosis, glycogen storage diseases, hepatoma, cholestasis, acromegaly, insulinoma, isolated growth hormone deficiency, and alcohol-induced hypertriglyceridemia. ABP can also be useful in preventing or treating atherosclerotic diseases, such as, for example, coronary heart disease, coronary artery disease, peripheral arterial disease, stroke (ischaemic and hemorrhagic), angina pectoris, or cerebrovascular disease and acute coronary syndrome, myocardial infarction. In some embodiments, the ABP is useful in reducing the risk of: nonfatal heart attacks, fatal and non-fatal strokes, certain types of heart surgery, hospitalization for heart failure, chest pain in patients with heart disease, and/or cardiovascular events because of established heart disease such as prior heart attack, prior heart surgery, and/or chest pain with evidence of clogged arteries. In some embodiments, the ABP and methods can be used to reduce the risk of recurrent cardiovascular events.

As will be appreciated by one of skill in the art, diseases or disorders that are generally addressable (either treatable or preventable) through the use of statins can also benefit from the application of the instant antigen binding proteins. In addition, in some embodiments, disorders or disease that can benefit from the prevention of cholesterol synthesis or increased LDLR expression can also be treated by various embodiments of the antigen binding proteins. In addition, as will be appreciated by one of skill in the art, the use of the anti-PCSK9 antibodies can be especially useful in the treatment of Diabetes. Not only is Diabetes a risk factor for coronary heart disease, but insulin increases the expression of PCSK9. That is, people with Diabetes have elevated plasma lipid levels (which can be related to high PCSK9 levels) and can benefit from lowering those levels. This is generally discussed in more detail in Costet et al. (“Hepatic PCSK9 Expression is Regulated by Nutritional Status via Insulin and Sterol Regulatory Element-binding Protein 1C”, J. Biol. Chem., 281: 6211-6218, 2006), the entirety of which is incorporated herein by reference.

In some embodiments, the antigen binding protein is administered to those who have diabetes mellitus, abdominal aortic aneurysm, atherosclerosis and/or peripheral vascular

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disease in order to decrease their serum cholesterol levels to a safer range. In some embodiments, the antigen binding protein is administered to patients at risk of developing any of the herein described disorders. In some embodiments, the ABPs are administered to subjects that smoke, have hypertension or a familial history of early heart attacks.

In some embodiments, a subject is administered an ABP if they are at a moderate risk or higher on the 2004 NCEP treatment goals. In some embodiments, the ABP is administered to a subject if the subject's LDL cholesterol level is greater than 160 mg/dL. In some embodiments, the ABP is administered if the subjects LDL cholesterol level is greater than 130 (and they have a moderate or moderately high risk according to the 2004 NCEP treatment goals). In some embodiments, the ABP is administered if the subjects LDL cholesterol level is greater than 100 (and they have a high or very high risk according to the 2004 NCEP treatment goals).

A physician will be able to select an appropriate treatment indications and target lipid levels depending on the individual profile of a particular patient. One well-accepted standard for guiding treatment of hyperlipidemia is the Third Report of the National Cholesterol Education Program (NCEP) Expert Panel on Detection, Evaluation, and Treatment of the High Blood Cholesterol in Adults (Adult Treatment Panel III) Final Report, National Institutes of Health, NIH Publication No. 02-5215 (2002), the printed publication of which is hereby incorporated by reference in its entirety.

In some embodiments, antigen binding proteins to PCSK9 are used to decrease the amount of PCSK9 activity from an abnormally high level or even a normal level. In some embodiments, antigen binding proteins to PCSK9 are used to treat or prevent hypercholesterolemia and/or in the preparation of medicaments therefore and/or for other cholesterol related disorders (such as those noted herein). In certain embodiments, an antigen binding protein to PCSK9 is used to treat or prevent conditions such as hypercholesterolemia in which PCSK9 activity is normal. In such conditions, for example, reduction of PCSK9 activity to below normal can provide a therapeutic effect.

In some embodiments, more than one antigen binding protein to PCSK9 is used to modulate PCSK9 activity.

In certain embodiments, methods are provided of treating a cholesterol related disorder, such as hypercholesterolemia comprising administering a therapeutically effective amount of one or more antigen binding proteins to PCSK9 and another therapeutic agent.

In certain embodiments, an antigen binding protein to PCSK9 is administered alone. In certain embodiments, an antigen binding protein to PCSK9 is administered prior to the administration of at least one other therapeutic agent. In certain embodiments, an antigen binding protein to PCSK9 is administered concurrent with the administration of at least one other therapeutic agent. In certain embodiments, an antigen binding protein to PCSK9 is administered subsequent to the administration of at least one other therapeutic agent. In other embodiments, an antigen binding protein to PCSK9 is administered prior to the administration of at least one other therapeutic agent. Therapeutic agents (apart from the antigen binding protein), include, but are not limited to, at least one other cholesterol-lowering (serum and/or total body cholesterol) agent or an agent. In some embodiments, the agent increases the expression of LDLR, have been observed to increase serum HDL levels, lower LDL levels or lower triglyceride levels. Exemplary agents include, but are not limited to, statins (atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, simvastatin), Nicotinic acid (Niacin) (NIACOR, NIASPAN (slow

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release niacin), SLO-NIACIN (slow release niacin)), Fibric acid (LOPID (Gemfibrozil), TRICOR (fenofibrate), Bile acid sequestrants (QUESTRAN (cholestyramine), colestevam (WELCHOL), COLESTID (colestipol)), Cholesterol absorption inhibitors (ZETIA (ezetimibe)), Combining nicotinic acid with statin (ADVICOR (LOVASTATIN and NIASPAN), Combining a statin with an absorption inhibitor (VYTORIN (ZOCOR and ZETIA) and/or lipid modifying agents. In some embodiments, the ABP is combined with PPAR gamma agonists, PPAR alpha/gamma agonists, squalene synthase inhibitors, CETP inhibitors, anti-hypertensives, anti-diabetic agents (such as sulphonyl ureas, insulin, GLP-1 analogs, DDPIV inhibitors), ApoB modulators, MTP inhibitoris and/or arteriosclerosis obliterans treatments. In some embodiments, the ABP is combined with an agent that increases the level of LDLR protein in a subject, such as statins, certain cytokines like oncostatin M, estrogen, and/or certain herbal ingredients such as berberine. In some embodiments, the ABP is combined with an agent that increases serum cholesterol levels in a subject (such as certain anti-psycotic agents, certain HIV protease inhibitors, dietary factors such as high fructose, sucrose, cholesterol or certain fatty acids and certain nuclear receptor agonists and antagonists for RXR, RAR, LXR, FXR). In some embodiments, the ABP is combined with an agent that increases the level of PCSK9 in a subject, such as statins and/or insulin. The combination of the two can allow for the undesirable side-effects of other agents to be mitigated by the ABP. As will be appreciated by one of skill in the art, in some embodiments, the ABP is combined with the other agent/compound. In some embodiments, the ABP and other agent are administered concurrently. In some embodiments, the ABP and other agent are not administered simultaneously, with the ABP being administered before or after the agent is administered. In some embodiments, the subject receives both the ABP and the other agent (that increases the level of LDLR) during a same period of prevention, occurrence of a disorder, and/or period of treatment.

Pharmaceutical compositions of the invention can be administered in combination therapy, i.e., combined with other agents. In certain embodiments, the combination therapy comprises an antigen binding protein capable of binding PCSK9, in combination with at least one anti-cholesterol agent. Agents include, but are not limited to, in vitro synthetically prepared chemical compositions, antibodies, antigen binding regions, and combinations and conjugates thereof. In certain embodiments, an agent can act as an agonist, antagonist, allosteric modulator, or toxin. In certain embodiments, an agent can act to inhibit or stimulate its target (e.g., receptor or enzyme activation or inhibition), and thereby promote increased expression of LDLR or decrease serum cholesterol levels.

In certain embodiments, an antigen binding protein to PCSK9 can be administered prior to, concurrent with, and subsequent to treatment with a cholesterol-lowering (serum and/or total cholesterol) agent. In certain embodiments, an antigen binding protein to PCSK9 can be administered prophylactically to prevent or mitigate the onset of hypercholesterolemia, heart disease, diabetes, and/or any of the cholesterol related disorder. In certain embodiments, an antigen binding protein to PCSK9 can be administered for the treatment of an existing hypercholesterolemia condition. In some embodiments, the ABP delays the onset of the disorder and/or symptoms associated with the disorder. In some embodiments, the ABP is provided to a subject lacking any symptoms of any one of the cholesterol related disorders or a subset thereof.

In certain embodiments, an antigen binding protein to PCSK9 is used with particular therapeutic agents to treat various cholesterol related disorders, such as hypercholesterolemia. In certain embodiments, in view of the condition and the desired level of treatment, two, three, or more agents can be administered. In certain embodiments, such agents can be provided together by inclusion in the same formulation. In certain embodiments, such agent(s) and an antigen binding protein to PCSK9 can be provided together by inclusion in the same formulation. In certain embodiments, such agents can be formulated separately and provided together by inclusion in a treatment kit. In certain embodiments, such agents and an antigen binding protein to PCSK9 can be formulated separately and provided together by inclusion in a treatment kit. In certain embodiments, such agents can be provided separately. In certain embodiments, when administered by gene therapy, the genes encoding protein agents and/or an antigen binding protein to PCSK9 can be included in the same vector. In certain embodiments, the genes encoding protein agents and/or an antigen binding protein to PCSK9 can be under the control of the same promoter region. In certain embodiments, the genes encoding protein agents and/or an antigen binding protein to PCSK9 can be in separate vectors.

In certain embodiments, the invention provides for pharmaceutical compositions comprising an antigen binding protein to PCSK9 together with a pharmaceutically acceptable diluent, carrier, solubilizer, emulsifier, preservative and/or adjuvant.

In certain embodiments, the invention provides for pharmaceutical compositions comprising an antigen binding protein to PCSK9 and a therapeutically effective amount of at least one additional therapeutic agent, together with a pharmaceutically acceptable diluent, carrier, solubilizer, emulsifier, preservative and/or adjuvant.

In certain embodiments, an antigen binding protein to PCSK9 can be used with at least one therapeutic agent for inflammation. In certain embodiments, an antigen binding protein to PCSK9 can be used with at least one therapeutic agent for an immune disorder. Exemplary therapeutic agents for inflammation and immune disorders include, but are not limited to cyclooxygenase type 1 (COX-1) and cyclooxygenase type 2 (COX-2) inhibitors small molecule modulators of 38 kDa mitogen-activated protein kinase (p38-MAPK); small molecule modulators of intracellular molecules involved in inflammation pathways, wherein such intracellular molecules include, but are not limited to, jnk, IKK, NF- κ B, ZAP70, and lck. Certain exemplary therapeutic agents for inflammation are described, e.g., in C. A. Dinarello & L. L. Moldawer *Proinflammatory and Anti-Inflammatory Cytokines in Rheumatoid Arthritis: A Primer for Clinicians* Third Edition (2001) Amgen Inc. Thousand Oaks, Calif.

In certain embodiments, pharmaceutical compositions will include more than one different antigen binding protein to PCSK9. In certain embodiments, pharmaceutical compositions will include more than one antigen binding protein to PCSK9 wherein the antigen binding proteins to PCSK9 bind more than one epitope. In some embodiments, the various antigen binding proteins will not compete with one another for binding to PCSK9. In some embodiments, any of the antigen binding proteins depicted in Table 2 and FIGS. 2 and/or 3 can be combined together in a pharmaceutical composition.

In certain embodiments, acceptable formulation materials preferably are nontoxic to recipients at the dosages and concentrations employed. In some embodiments, the formulation material(s) are for s.c. and/or I.V. administration. In certain embodiments, the pharmaceutical composition can contain

formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In certain embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate 80, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. (*Remington's Pharmaceutical Sciences*, 18th Edition, A. R. Gennaro, ed., Mack Publishing Company (1995). In some embodiments, the formulation comprises PBS; 20 mM NaOAC, pH 5.2, 50 mM NaCl; and/or 10 mM NAOAC, pH 5.2, 9% Sucrose.

In certain embodiments, an antigen binding protein to PCSK9 and/or a therapeutic molecule is linked to a half-life extending vehicle known in the art. Such vehicles include, but are not limited to, polyethylene glycol, glycogen (e.g., glycosylation of the ABP), and dextran. Such vehicles are described, e.g., in U.S. application Ser. No. 09/428,082, now U.S. Pat. No. 6,660,843 and published PCT Application No. WO 99/25044, which are hereby incorporated by reference for any purpose.

In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, *Remington's Pharmaceutical Sciences*, supra. In certain embodiments, such compositions may influence the physical state, stability, rate of in vivo release and rate of in vivo clearance of the antibodies of the invention.

In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition can be either aqueous or non-aqueous in nature. For example, in certain embodiments, a suitable vehicle or carrier can be water for injection, physiological saline solution or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. In some embodiments, the saline comprises isotonic phosphate-buffered saline. In certain embodiments, neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. In certain embodiments, pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, which can further include sorbitol or a suitable sub-

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stitute therefore. In certain embodiments, a composition comprising an antigen binding protein to PCSK9, with or without at least one additional therapeutic agents, can be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (*Remington's Pharmaceutical Sciences*, supra) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, a composition comprising an antigen binding protein to PCSK9, with or without at least one additional therapeutic agents, can be formulated as a lyophilizate using appropriate excipients such as sucrose.

In certain embodiments, the pharmaceutical composition can be selected for parenteral delivery. In certain embodiments, the compositions can be selected for inhalation or for delivery through the digestive tract, such as orally. The preparation of such pharmaceutically acceptable compositions is within the ability of one skilled in the art.

In certain embodiments, the formulation components are present in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

In certain embodiments, when parenteral administration is contemplated, a therapeutic composition can be in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising a desired antigen binding protein to PCSK9, with or without additional therapeutic agents, in a pharmaceutically acceptable vehicle. In certain embodiments, a vehicle for parenteral injection is sterile distilled water in which an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that can provide for the controlled or sustained release of the product which can then be delivered via a depot injection. In certain embodiments, hyaluronic acid can also be used, and can have the effect of promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices can be used to introduce the desired molecule.

In certain embodiments, a pharmaceutical composition can be formulated for inhalation. In certain embodiments, an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, can be formulated as a dry powder for inhalation. In certain embodiments, an inhalation solution comprising an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, can be formulated with a propellant for aerosol delivery. In certain embodiments, solutions can be nebulized. Pulmonary administration is further described in PCT application no. PCT/US94/001875, which describes pulmonary delivery of chemically modified proteins.

In certain embodiments, it is contemplated that formulations can be administered orally. In certain embodiments, an antigen binding protein to PCSK9, with or without at least one additional therapeutic agents, that is administered in this fashion can be formulated with or without those carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. In certain embodiments, a capsule can be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. In certain embodiments, at least one additional agent can be included to facilitate absorption of an antigen

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binding protein to PCSK9 and/or any additional therapeutic agents. In certain embodiments, diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders can also be employed.

In certain embodiments, a pharmaceutical composition can involve an effective quantity of an antigen binding protein to PCSK9, with or without at least one additional therapeutic agents, in a mixture with non-toxic excipients which are suitable for the manufacture of tablets. In certain embodiments, by dissolving the tablets in sterile water, or another appropriate vehicle, solutions can be prepared in unit-dose form. In certain embodiments, suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving antigen binding proteins to PCSK9, with or without at least one additional therapeutic agent(s), in sustained- or controlled-delivery formulations. In certain embodiments, techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See for example, PCT Application No. PCT/US93/00829 which describes the controlled release of porous polymeric microparticles for the delivery of pharmaceutical compositions. In certain embodiments, sustained-release preparations can include semipermeable polymer matrices in the form of shaped articles, e.g. films, or microcapsules. Sustained release matrices can include polyesters, hydrogels, polylactides (U.S. Pat. No. 3,773,919 and EP 058,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et al., *Biopolymers*, 22:547-556 (1983)), poly (2-hydroxyethyl-methacrylate) (Langer et al., *J. Biomed. Mater. Res.*, 15:167-277 (1981) and Langer, *Chem. Tech.*, 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., supra) or poly-D(-)-3-hydroxybutyric acid (EP 133,988). In certain embodiments, sustained release compositions can also include liposomes, which can be prepared by any of several methods known in the art. See, e.g., Eppstein et al., *Proc. Natl. Acad. Sci. USA*, 82:3688-3692 (1985); EP 036,676; EP 088,046 and EP 143,949.

The pharmaceutical composition to be used for in vivo administration typically is sterile. In certain embodiments, this can be accomplished by filtration through sterile filtration membranes. In certain embodiments, where the composition is lyophilized, sterilization using this method can be conducted either prior to or following lyophilization and reconstitution. In certain embodiments, the composition for parenteral administration can be stored in lyophilized form or in a solution. In certain embodiments, parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

In certain embodiments, once the pharmaceutical composition has been formulated, it can be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or as a dehydrated or lyophilized powder. In certain embodiments, such formulations can be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration.

In certain embodiments, kits are provided for producing a single-dose administration unit. In certain embodiments, the kit can contain both a first container having a dried protein

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and a second container having an aqueous formulation. In certain embodiments, kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosynges) are included.

In certain embodiments, the effective amount of a pharmaceutical composition comprising an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, to be employed therapeutically will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment, according to certain embodiments, will thus vary depending, in part, upon the molecule delivered, the indication for which an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician can titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. In certain embodiments, a typical dosage can range from about 0.1 µg/kg up to about 100 mg/kg or more, depending on the factors mentioned above. In certain embodiments, the dosage can range from 0.1 µg/kg up to about 100 mg/kg; or 1 µg/kg up to about 100 mg/kg; or 5 µg/kg up to about 100 mg/kg.

In certain embodiments, the frequency of dosing will take into account the pharmacokinetic parameters of an antigen binding protein to PCSK9 and/or any additional therapeutic agents in the formulation used. In certain embodiments, a clinician will administer the composition until a dosage is reached that achieves the desired effect. In certain embodiments, the composition can therefore be administered as a single dose, or as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion via an implantation device or catheter. Further refinement of the appropriate dosage is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. In certain embodiments, appropriate dosages can be ascertained through use of appropriate dose-response data. In some embodiments, the amount and frequency of administration can take into account the desired cholesterol level (serum and/or total) to be obtained and the subject's present cholesterol level, LDL level, and/or LDLR levels, all of which can be obtained by methods that are well known to those of skill in the art.

In certain embodiments, the route of administration of the pharmaceutical composition is in accord with known methods, e.g. orally, through injection by intravenous, intraperitoneal, intracerebral (intra-parenchymal), intracerebroventricular, intramuscular, subcutaneously, intra-ocular, intraarterial, intraportal, or intralesional routes; by sustained release systems or by implantation devices. In certain embodiments, the compositions can be administered by bolus injection or continuously by infusion, or by implantation device.

In certain embodiments, the composition can be administered locally via implantation of a membrane, sponge or another appropriate material onto which the desired molecule has been absorbed or encapsulated. In certain embodiments, where an implantation device is used, the device can be implanted into any suitable tissue or organ, and delivery of the desired molecule can be via diffusion, timed-release bolus, or continuous administration.

In certain embodiments, it can be desirable to use a pharmaceutical composition comprising an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, in an ex vivo manner. In such instances, cells,

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tissues and/or organs that have been removed from the patient are exposed to a pharmaceutical composition comprising an antigen binding protein to PCSK9, with or without at least one additional therapeutic agent, after which the cells, tissues and/or organs are subsequently implanted back into the patient.

In certain embodiments, an antigen binding protein to PCSK9 and/or any additional therapeutic agents can be delivered by implanting certain cells that have been genetically engineered, using methods such as those described herein, to express and secrete the polypeptides. In certain embodiments, such cells can be animal or human cells, and can be autologous, heterologous, or xenogeneic. In certain embodiments, the cells can be immortalized. In certain embodiments, in order to decrease the chance of an immunological response, the cells can be encapsulated to avoid infiltration of surrounding tissues. In certain embodiments, the encapsulation materials are typically biocompatible, semi-permeable polymeric enclosures or membranes that allow the release of the protein product(s) but prevent the destruction of the cells by the patient's immune system or by other detrimental factors from the surrounding tissues.

Based on the ability of ABPs to significantly neutralize PCSK9 activity (as demonstrated in the Examples below), these ABPs will have therapeutic effects in treating and preventing symptoms and conditions resulting from PCSK9-mediated activity, such as hypercholesterolemia.

Diagnostic Applications

In some embodiments, the ABP is used as a diagnostic tool. The ABP can be used to assay the amount of PCSK9 present in a sample and/or subject. As will be appreciated by one of skill in the art, such ABPs need not be neutralizing ABPs. In some embodiments, the diagnostic ABP is not a neutralizing ABP. In some embodiments, the diagnostic ABP binds to a different epitope than the neutralizing ABP binds to. In some embodiments, the two ABPs do not compete with one another.

In some embodiments, the ABPs disclosed herein are used or provided in an assay kit and/or method for the detection of PCSK9 in mammalian tissues or cells in order to screen/diagnose for a disease or disorder associated with changes in levels of PCSK9. The kit comprises an ABP that binds

PCSK9 and means for indicating the binding of the ABP with PCSK9, if present, and optionally PCSK9 protein levels. Various means for indicating the presence of an ABP can be used. For example, fluorophores, other molecular probes, or enzymes can be linked to the ABP and the presence of the ABP can be observed in a variety of ways. The method for screening for such disorders can involve the use of the kit, or simply the use of one of the disclosed ABPs and the determination of whether the ABP binds to PCSK9 in a sample. As will be appreciated by one of skill in the art, high or elevated

levels of PCSK9 will result in larger amounts of the ABP binding to PCSK9 in the sample. Thus, degree of ABP binding can be used to determine how much PCSK9 is in a sample. Subjects or samples with an amount of PCSK9 that is greater than a predetermined amount (e.g., an amount or range that a person without a PCSK9 related disorder would have) can be characterized as having a PCSK9 mediated disorder. In some embodiments, the ABP is administered to a subject taking a statin, in order to determine if the statin has increased the amount of PCSK9 in the subject.

In some embodiments, the ABP is a non-neutralizing ABP and is used to determine the amount of PCSK9 in a subject receiving an ABP and/or statin treatment.

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EXAMPLES

The following examples, including the experiments conducted and results achieved, are provided for illustrative purposes only and are not to be construed as limiting the present invention.

Example 1

Immunization and Titering

Generation of Anti-PCSK9 Antibodies and Hybridomas

Antibodies to the mature form of PCSK9 (depicted as the sequence in FIG. 1A, with the pro-domain underlined), were raised in XenoMouse® mice (Abgenix, Fremont, Calif.), which are mice containing human immunoglobulin genes. Two groups of XenoMouse® mice, group 1 and 2, were used to produce antibodies to PCSK9. Group 1 included mice of the XenoMouse® strain XMG2-KL, which produces fully human IgG2K and IgG2L antibodies. Group 1 mice were immunized with human PCSK9. PCSK9 was prepared using standard recombinant techniques using the GenBank sequence as reference (NM_174936). Group 2 involved mice of the XenoMouse® strain XMG4-KL, which produce fully human IgG4K and IgG4L antibodies. Group 2 mice were also immunized with human PCSK9.

The mice of both groups were injected with antigen eleven times, according to the schedule in Table 3. In the initial immunizations, each mouse was injected with a total of 10 µg of antigen delivered intraperitoneally into the abdomen. Subsequent boosts are 5 µg doses and injection method is staggered between intraperitoneal injections into the abdomen and sub-cutaneous injections at the base of the tail. For intraperitoneal injections antigen is prepared as an emulsion with TiterMax® Gold (Sigma, Cat # T2684) and for subcutaneous injections antigen is mixed with Alum (aluminum phosphate) and CpG oligos. In injections 2 through 8 and 10, each mouse was injected with a total of 5 µg of antigen in the adjuvant alum gel. A final injection of 5 µg of antigen per mouse is delivered in Phospho buffered saline and delivered into 2 sites 50% IP into the abdomen and 50% SQ at the base of tail. The immunization programs are summarized in Table 3, shown below.

TABLE 3

mouse strain	XMG2/kl	XMG4/kl
# of animals	10	10
immunogen	PCSK9-V5/His	PCSK9-V5/His
1st boost	IP injection 10 ug each Titermax Gold	IP injection 10 ug each Titermax Gold
2nd boost	tail injection 5 ug each Alum/CpG ODN	tail injection 5 ug each Alum/CpG ODN
3rd boost	IP injection 5 ug each Titermax Gold	IP injection 5 ug each Titermax Gold
4th boost	tail injection 5 ug each Alum/CpG ODN	tail injection 5 ug each Alum/CpG ODN
5th boost	IP injection 5 ug each Titermax Gold	IP injection 5 ug each Titermax Gold
6th boost	tail injection 5 ug each Alum/CpG ODN	tail injection 5 ug each Alum/CpG ODN
7th boost	IP injection 5 ug each Titermax Gold	IP injection 5 ug each Titermax Gold

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TABLE 3-continued

8th boost	tail injection 5 ug each Alum/CpG ODN	tail injection 5 ug each Alum/CpG ODN
bleed		
9th boost	IP injection 5 ug each Titermax Gold	IP injection 5 ug each Titermax Gold
10th boost	tail injection 5 ug each Alum/CpG ODN	tail injection 5 ug each Alum/CpG ODN
11th boost	BIP 5 ug each PBS	BIP 5 ug each PBS
harvest		

The protocol used to titer the XenoMouse animals was as follows: Costar 3368 medium binding plates were coated with neutravidin @ 8 µg/ml (50 µl/well) and incubated at 4°C. in 1XPBS/0.05% azide overnight. They were washed 20 using TiterTek 3-cycle wash with RO water. Plates were blocked using 250 µl of 1XPBS/1% milk and incubated for at least 30 minutes at RT. Block was washed off using TiterTek 3-cycle wash with RO water. One then captured b-human PCSK9 @ 2 µg/ml in 1XPBS/1% milk/10 mM Ca²⁺ (assay diluent) 50 µl/well and incubated for 1 hr at RT. One then 25 washed using TiterTek 3-cycle wash with RO water. For the primary antibody, sera was titrated 1:3 in duplicate from 1:100. This was done in assay diluent 50 µl/well and incubated for 1 hr at RT. One then washed using TiterTek 3-cycle 30 wash with RO water. The secondary antibody was goat anti Human IgG Fc HRP @ 400 ng/ml in assay diluent at 50 µl/well. This was incubated for 1 hr at RT. This was then washed using TiterTek 3-cycle wash with RO water and patted dry on paper towels. For the substrate, one-step TMB solution (Neogen, Lexington, Ky.) was used (50 µl/well) and it was allowed to develop for 30 min at RT.

The protocols followed in the ELISA assays was as follows: For samples comprising b-PCSK9 with no V5H tag the following protocol was employed: Costar 3368 medium 40 binding plates (Corning Life Sciences) were employed. The plates were coated with neutravidin at 8 µg/ml in 1XPBS/0.05% Azide, (50 µl/well). The plates were incubated at 4°C. overnight. The plates were then washed using a TiterTek M384 plate washer (TiterTek, Huntsville, Ala.). A 3-cycle 45 wash was performed. The plates were blocked with 250 µl of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the M384 plate washer. A 3-cycle wash was performed. The capture was b-hu PCSK9, without a V5 tag, and was added at 2 50 µg/ml in 1XPBS/1% milk/10 mM Ca²⁺ (40 µl/well). The plates were then incubated for 1 hour at room temperature. A 3-cycle wash was performed. Sera were titrated 1:3 in duplicate from 1:100, and row H was blank for sera. The titration was done in assay diluent, at a volume of 50 µl/well. The 55 plates were incubated for 1 hour at room temperature. Next, a 3-cycle wash was performed. Goat anti Human IgG Fc HRP at 100 ng/ml (1:4000) in 1XPBS/1% milk/10 mM Ca²⁺ (50 µl/well) was added to the plate and was incubated 1 hour at room temperature. The plates were washed once again, using 60 a 3-cycle wash. The plates were then patted dry with paper towel. Finally, 1 step TMB (Neogen, Lexington, Ky.) (50 µl/well) was added to the plate and was quenched with 1N hydrochloric acid (50 µl/well) after 30 minutes at room temperature. OD's were read immediately at 450 nm using a 65 TiterTek plate reader.

Positive controls to detect plate bound PCSK9 were soluble LDL receptor (R&D Systems, Cat #2148LD/CF) and

a polyclonal rabbit anti-PCSK9 antibody (Caymen Chemical #10007185) titrated 1:3 in duplicate from 3 µg/ml in assay diluent. LDLR was detected with goat anti LDLR (R&D Systems, Cat #AF2148) and rabbit anti goat IgG Fc HRP at a concentration of 400 ng/ml; the rabbit polyclonal was detected with goat anti-rabbit IgG Fc at a concentration of 400 ng/ml in assay diluent. Negative control was naive XMG2-KL and XMG4-KL sera titrated 1:3 in duplicate from 1:100 in assay diluent.

For samples comprising b-PCSK9 with a V5H is tag the following protocol was employed: Costar 3368 medium binding plates (Corning Life Sciences) were employed. The plates were coated with neutravidin at 8 µg/ml in 1XPBS/0.05% Azide, (50 µl/well). The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek M384 plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was performed. The plates were blocked with 250 µl of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the M384 plate washer. A 3-cycle wash was performed. The capture was b-hu PCSK9, with a V5 tag, and was added at 2 µg/ml in 1XPBS/1% milk/10 mM Ca²⁺ (40 µl/well). The plates were then incubated for 1 hour at room temperature. A 3-cycle wash was performed. Sera were titrated 1:3 in duplicate from 1:100, and row H was blank for sera. The titration was done in assay diluent, at a volume of 50 µl/well. The plates were incubated for 1 hour at room temperature. Next, the plates were washed using the M384 plate washer operated using a 3-cycle wash. Goat anti Human IgG Fc HRP at 400 ng/ml in 1XPBS/1% milk/10 mM Ca²⁺ was added at 50 µl/well to the plate and the plate was incubated 1 hour at room temperature. The plates were washed once again, using a 3-cycle wash. The plates were then patted dry with paper towel. Finally, 1 step TMB (Neogen, Lexington, Ky.) (50 µl/well) was added to the plate and the plate was quenched with 1N hydrochloric acid (50 µl/well) after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader.

Positive control was LDLR, rabbit anti-PCSK9 titrated 1:3 in duplicate from 3 µg/ml in assay diluent. LDLR detect with goat anti-LDLR (R&D Systems, Cat #AF2148) and rabbit anti-goat IgG Fc HRP at a concentration of 400 ng/ml; rabbit poly detected with goat anti-rabbit IgG Fc at a concentration of 400 ng/ml in assay diluent. Human anti-His 1.2,3 and anti-V5 1.7.1 titrated 1:3 in duplicate from 1 µg/ml in assay diluent; both detected with goat anti-human IgG Fc HRP at a concentration of 400 ng/ml in assay diluent. Negative control was naive XMG2-KL and XMG4-KL sera titrated 1:3 in duplicate from 1:100 in assay diluent.

Titers of the antibody against human PCSK9 were tested by ELISA assay for mice immunized with soluble antigen as described. Table 4 summarizes the ELISA data and indicates that there were some mice which appeared to be specific for PCSK9. See, e.g., Table 4. Therefore, at the end of the immunization program, 10 mice (in bold in Table 4) were selected for harvest, and splenocytes and lymphocytes were isolated from the spleens and lymph nodes respectively, as described herein.

TABLE 4

Summary of ELISA Results			
	Animal ID	Titer b-hu PCSK9 (V5His) @ 2 ug/ml	Titer b-hu PCSK9 @ 2 ug/ml
Group 1 - IgG2k/l	P175807	>72900 @ OD 2.2	68359
	P175808	>72900 @ OD 2.3	>72900 @ OD 2.5
	P175818	>72900 @ OD 3.2	>72900 @ OD 3.0

TABLE 4-continued

Summary of ELISA Results			
	Animal ID	Titer b-hu PCSK9 (V5His) @ 2 ug/ml	Titer b-hu PCSK9 @ 2 ug/ml
5	P175819	>72900 @ OD 3.4	>72900 @ OD 3.2
	P175820	>72900 @ OD 2.4	>72900 @ OD 2.5
	P175821	>72900 @ OD 3.4	>72900 @ OD 3.0
	P175830	>72900 @ OD 2.6	>72900 @ OD 2.5
	P175831	>72900 @ OD 3.1	>72900 @ OD 3.1
	P175832	>72900 @ OD 3.8	>72900 @ OD 3.6
	P175833	>72900 @ OD 2.6	>72900 @ OD 2.3
	P174501	19369	17109
	P174503	31616	23548
	P174508	48472	30996
10	P174509	23380	21628
	P174510	15120	9673
	P175773	19407	15973
	P175774	54580	44424
	P175775	60713	55667
	P175776	30871	22899
	P175777	16068	12532
	Naïve	<100 @ OD 0.54	<100 @ OD 0.48
	G2		
	Naïve	<100 @ OD 1.57	<100 @ OD 1.32
15	G4		
20			
25			
30			
35			
40			
45			
50			
55			
60			
65			

Example 2

Recovery of Lymphocytes, B-cell Isolations, Fusions and Generation of Hybridomas

This example outlines how the immune cells were recovered and the hybridomas were generated. Selected immunized mice were sacrificed by cervical dislocation and the draining lymph nodes were harvested and pooled from each cohort. The B cells were dissociated from lymphoid tissue by grinding in DMEM to release the cells from the tissues, and the cells were suspended in DMEM. The cells were counted, and 0.9 ml DMEM per 100 million lymphocytes was added to the cell pellet to resuspend the cells gently but completely.

Lymphocytes were mixed with nonsecretory myeloma P3X63Ag8.653 cells purchased from ATCC, cat.# CRL1580 (Kearney et al., (1979) *J. Immunol.* 123, 1548-1550) at a ratio of 1:4. The cell mixture was gently pelleted by centrifugation at 400×g 4 min. After decanting of the supernatant, the cells were gently mixed using a 1 ml pipette. Preheated PEG/DMSO solution from Sigma (cat# P7306) (1 ml per million of B-cells) was slowly added with gentle agitation over 1 min followed by 1 min of mixing. Preheated IDMEM (2 ml per million of B cells) (DMEM without glutamine, L-glutamine, pen/strep, MEM non-essential amino acids (all from Invitrogen), was then added over 2 minutes with gentle agitation. Finally preheated IDMEM (8 ml per 10⁶ B-cells) was added over 3 minutes.

The fused cells were spun down 400×g 6 min and resuspended in 20 ml selection media (DMEM (Invitrogen), 15% FBS (Hyclone), supplemented with L-glutamine, pen/strep, MEM Non-essential amino acids, Sodium Pyruvate, 2-Mercaptoethanol (all from Invitrogen), HA-Azaserine Hypoxanthine and OPI (oxaloacetate, pyruvate, bovine insulin) (both from Sigma) and IL-6 (Boehringer Mannheim)) per million B-cells. Cells were incubated for 20-30 min at 37 C. and then resuspended in 200 ml selection media and cultured for 3-4 days in T175 flask prior to 96 well plating. Thus, hybridomas that produced antigen binding proteins to PCSK9 were produced.

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Example 3

Selection of PCSK9 Antibodies

The present example outlines how the various PCSK9 antigen binding proteins were characterized and selected. The binding of secreted antibodies (produced from the hybridomas produced in Examples 1 and 2) to PCSK9 was assessed. Selection of antibodies was based on binding data and inhibition of PCSK9 binding to LDLR and affinity. Binding to soluble PCSK9 was analyzed by ELISA, as described below. BIAcore® (surface plasmon resonance) was used to quantify binding affinity.

Primary Screen

A primary screen for antibodies which bind to wild-type PCSK9 was performed. The primary screen was performed on two harvests. The primary screen comprised an ELISA assay and was performed using the following protocol:

Costar 3702 medium binding 384 well plates (Corning Life Sciences) were employed. The plates were coated with neutravidin at a concentration of 4 µg/ml in 1XPBS/0.05% Azide, at a volume of 40 µl/well. The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was performed. The plates were blocked with 90 µl of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed. Again, a 3-cycle wash was performed. The capture sample was biotinylated-PCSK9, without a V5 tag, and was added at 0.9 µg/ml in 1XPBS/1% milk/10 mM Ca²⁺ at a volume of 40 µl/well. The plates were then incubated for 1 hour at room temperature. Next, the plates were washed using the Titertek plate washer operated using a 3-cycle wash. 10 µl of supernatant was transferred into 40 µl of 1XPBS/1% milk/10 mM Ca²⁺ and incubated 1.5 hours at room temperature. Again the plates were washed using the Titertek plate washer operated using a 3-cycle wash. 40 µl/well of Goat anti-Human IgG Fc POD at a concentration of 100 ng/ml (1:4000) in 1XPBS/1% milk/10 mM Ca²⁺ was added to the plate and was incubated 1 hour at room temperature. The plates were washed once again, using a 3-cycle wash. Finally, 40 µl/well of One-step TMB (Neogen, Lexington, Ky.) was added to the plate and quenching with 40 µl/well of 1N hydrochloric acid was performed after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader.

The primary screen resulted in a total of 3104 antigen specific hybridomas being identified from the two harvests. Based on highest ELISA OD, 1500 hybridomas per harvest were advanced for a total of 3000 positives.

Confirmatory Screen

The 3000 positives were then rescreened for binding to wild-type PCSK9 to confirm stable hybridomas were established. The screen was performed as follows: Costar 3702 medium binding 384 well plates (Corning Life Sciences) were employed. The plates were coated with neutravidin at 3 µg/ml in 1XPBS/0.05% Azide at a volume of 40 µl/well. The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was performed. The plates were blocked with 90 µl of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the M384 plate washer. A 3-cycle wash was performed. The capture sample was b-PCSK9, without a V5 tag, and was added at 0.9 µg/ml in 1XPBS/1% milk/10 mM Ca²⁺ at a volume of 40 µl/well. The plates were then incubated for 1 hour at room temperature. Next, the plates were washed using a 3-cycle wash. 10 µl of supernatant was transferred into 40 µl

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of 1XPBS/1% milk/10 mM Ca²⁺ and incubated 1.5 hours at room temperature. Again the plates were washed using the Titertek plate washer operated using a 3-cycle wash. 40 µl/well of Goat anti-Human IgG Fc POD at a concentration of 100 ng/ml (1:4000) in 1XPBS/1% milk/10 mM Ca²⁺ was added to the plate, and the plate was incubated 1 hour at room temperature. The plates were washed once again, using the Titertek plate washer operated using a 3-cycle wash. Finally, 40 µl/well of One-step TMB (Neogen, Lexington, Ky.) was added to the plate and was quenched with 40 µl/well of 1N hydrochloric acid after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader. A total of 2441 positives repeated in the second screen. These antibodies were then used in the subsequent screenings.

Mouse Cross-reactivity Screen

The panel of hybridomas was then screened for cross-reactivity to mouse PCSK9 to make certain that the antibodies could bind to both human and mouse PCSK9. The following protocol was employed in the cross-reactivity screen: Costar 3702 medium binding 384 well plates (Corning Life Sciences) were employed. The plates were coated with neutravidin at 3 µg/ml in 1XPBS/0.05% Azide at a volume of 401/well. The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was performed. The plates were blocked with 90 µl of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the Titertek plate washer. A 3-cycle wash was performed. The capture sample was biotinylated-mouse PCSK9, and was added at 1 µg/ml in 1XPBS/1% milk/10 mM Ca²⁺ at a volume of 40 µl/well. The plates were then incubated for 1 hour at room temperature. Next, the plates were washed using the Titertek plate washer operated using a 3-cycle wash. 50 µl of supernatant was transferred to the plates and incubated 1 hour at room temperature. Again the plates were washed using a 3-cycle wash. 40 µl/well of Goat anti-Human IgG Fc POD at a concentration of 100 ng/ml (1:4000) in 1XPBS/1% milk/10 mM Ca²⁺ was added to the plate and the plate was incubated 1 hour at room temperature. The plates were washed once again, using a 3-cycle wash. Finally, 40 µl/well One-step TMB (Neogen, Lexington, Ky.) was added to the plate and was quenched with 40 µl/well of 1N hydrochloric acid after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader. 579 antibodies were observed to cross-react with mouse PCSK9. These antibodies were then used in the subsequent screenings.

D374Y Mutant Binding Screen

The D374Y mutation in PCSK9 has been documented in the human population (e.g., Timms K M et al, "A mutation in PCSK9 causing autosomal-dominant hypercholesterolemia in a Utah pedigree", Hum. Genet. 114: 349-353, 2004). In order to determine if the antibodies were specific for the wild type or also bound to the D374Y form of PCSK9, the samples were then screened for binding to the mutant PCSK9 sequence comprising the mutation D374Y. The protocol for the screen was as follows: Costar 3702 medium binding 384 well plates (Corning Life Sciences) were employed in the screen. The plates were coated with neutravidin at 4 µg/ml in 1XPBS/0.05% Azide at a volume of 40 µl/well. The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was performed. The plates were blocked with 90 µl of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the Titertek plate washer. A 3-cycle wash was per-

fomed. The plates were coated with biotinylated human PCSK9 D374Y at a concentration of 1 μ g/ml in 1XPBS/1% milk/10 mM Ca²⁺ and incubated for 1 hour at room temperature. The plates were then washed using a Titertek plate washer. A 3-cycle wash was perfomed. Late exhaust hybridoma culture supernatant was diluted 1:5 in PBS/milk/Ca²⁺ (10 ml plus 40 ml) and incubated for 1 hour at room temperature. Next, 40 μ l/well of rabbit anti-human PCSK9 (Cayman Chemical) and human anti-His 1.2.3 1:2 at 1 μ g/ml in 1XPBS/1% milk/10 mM Ca²⁺ was titrated onto the plates, which were then incubated for 1 hour at room temperature. The plates were then washed using a Titertek plate washer. A 3-cycle wash was perfomed. 40 μ l/well of Goat anti-Human IgG Fc HRP at a concentration of 100 ng/ml (1:4000) in 1XPBS/1% milk/10 mM Ca²⁺ was added to the plate and the plate was incubated 1 hour at room temperature. 40 μ l/well of Goat anti-rabbit IgG Fc HRP at a concentration of 100 ng/ml (1:4000) in 1XPBS/1% milk/10 mM Ca²⁺ was added to the plate and the plate was incubated 1 hour at room temperature. The plates were then washed using a Titertek plate washer. A 3-cycle wash was perfomed. Finally, 40 μ l/well of One-step TMB (Neogen, Lexington, Ky.) was added to the plate and was quenched with 40 μ l/well of 1N hydrochloric acid after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader. Over 96% of the positive hits on the wild-type PCSK9 also bound mutant PCSK9.

Large Scale Receptor Ligand Blocking Screen

To screen for the antibodies that block PCSK9 binding to LDLR an assay was developed using the D374Y PCSK9 mutant. The mutant was used for this assay because it has a higher binding affinity to LDLR allowing a more sensitive receptor ligand blocking assay to be developed. The following protocol was employed in the receptor ligand blocking screen: Costar 3702 medium binding 384 well plates (Corning Life Sciences) were employed in the screen. The plates were coated with goat anti-LDLR (R&D Cat #AF2148) at 2 μ g/ml in 1XPBS/0.05% Azide at a volume of 40 μ l/well. The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was performed. The plates were blocked with 90 μ l of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the Titertek plate washer. A 3-cycle wash was performed. The capture sample was LDLR (R&D, Cat #2148LD/CF), and was added at 0.4 μ g/ml in 1XPBS/1% milk/10 mM Ca²⁺ at a volume of 40 μ l/well. The plates were then incubated for 1 hour and 10 minutes at room temperature. Contemporaneously, 20 ng/ml of biotinylated human D374Y PCSK9 was incubated with 15 microliters of hybridoma exhaust supernatant in Nunc polypropylene plates and the exhaust supernatant concentration was diluted 1:5. The plates were then pre-incubated for about 1 hour and 30 minutes at room temperature. Next, the plates were washed using the Titertek plate washer operated using a 3-cycle wash. 50 μ l/well of the pre-incubated mixture was transferred onto the LDLR coated ELISA plates and incubated for 1 hour at room temperature. To detect LDLR-bound b-PCSK9, 40 μ l/well streptavidin HRP at 500 ng/ml in assay diluent was added to the plates. The plates were incubated for 1 hour at room temperature. The plates were again washed using a Titertek plate washer. A 3-cycle wash was performed. Finally, 40 μ l/well of One-step TMB (Neogen, Lexington, Ky.) was added to the plate and was quenched with 40 μ l/well of 1N hydrochloric acid after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader. The screen identified 384 antibodies that blocked the

interaction between PCSK9 and the LDLR well, 100 antibodies blocked the interaction strongly (OD<0.3). These antibodies inhibited the binding interaction of PCSK9 and LDLR greater than 90% (greater than 90% inhibition).

5 Receptor Ligand Binding Assay on Blocker Subset

The receptor ligand assay was then repeated using the mutant enzyme on the 384 member subset of neutralizers identified in the first large scale receptor ligand inhibition assay. The same protocol was employed in the screen of the 10 384 member blocker subset assay as was done in the large scale receptor ligand blocking screen. This repeat screen confirmed the initial screening data.

This screen of the 384 member subset identified 85 antibodies that blocked interaction between the PCSK9 mutant enzyme and the LDLR greater than 90%.

15 Receptor Ligand Binding Assay of Blockers that Bind the Wild Type PCSK9 but not the D374Y Mutant

In the initial panel of 3000 supers there were 86 antibodies shown to specifically bind to the wild-type PCSK9 and not to the huPCSK9(D374Y) mutant. These 86 supers were tested for the ability to block wild-type PCSK9 binding to the LDLR receptor. The following protocol was employed: Costar 3702 medium binding 384 well plates (Corning Life Sciences) were employed in the screen. The plates were coated with anti-His 1.2.3 at 10 μ g/ml in 1XPBS/0.05% Azide at a volume of 40 μ l/well. The plates were incubated at 4° C. overnight. The plates were then washed using a Titertek plate washer (Titertek, Huntsville, Ala.). A 3-cycle wash was perfomed. The plates were blocked with 90 μ l of 1XPBS/1% milk and incubated approximately 30 minutes at room temperature. The plates were then washed using the Titertek plate washer. A 3-cycle wash was performed. LDLR (R&D Systems, #2148LD/CF or R&D Systems, #2148LD) was added at 5 μ g/ml in 1XPBS/1% milk/10 mM Ca²⁺ at a volume of 40 μ l/well. The plates were then incubated for 1 hour at room temperature. Next, the plates were washed using the Titertek plate washer operated using a 3-cycle wash. Contemporaneously, biotinylated human wild-type PCSK9 was pre-incubated with hybridoma exhaust supernatant in Nunc polypropylene plates. 22 μ l of hybridoma sup was transferred into 33 μ l of b-PCSK9 at a concentration of 583 ng/ml in 1XPBS/1% milk/10 mM Ca²⁺, giving a final b-PCSK9 concentration=350 ng/ml and the exhaust supernatant at a final dilution of 1:2.5. The plates were pre-incubated for approximately 1 hour and 30 minutes at room temperature. 50 μ l/well of the preincubated mixture was transferred onto LDLR captured ELISA plates and incubated for 1 hour at room temperature. The plates were then washed using the Titertek plate washer. A 3-cycle wash was perfomed. 40 μ l/well streptavidin HRP at 500 ng/ml in assay diluent was added to the plates. The plates were incubated for 1 hour at room temperature. The plates were then washed using a Titertek plate washer. A 3-cycle wash was perfomed. Finally, 40 μ l/well of One-step TMB (Neogen, Lexington, Ky.) was added to the plate and was quenched with 40 μ l/well of 1N hydrochloric acid after 30 minutes at room temperature. OD's were read immediately at 450 nm using a Titertek plate reader.

55 Screening Results

Based on the results of the assays described, several hybridoma lines were identified as producing antibodies with desired interactions with PCSK9. Limiting dilution was used to isolate a manageable number of clones from each line. The clones were designated by hybridoma line number (e.g. 21B12) and clone number (e.g. 21B12.1). In general, no difference among the different clones of a particular line were detected by the functional assays described herein. In a few cases, clones were identified from a particular line that

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behaved differently in the functional assays, for example, 25A7.1 was found not to block PCSK9/LDLR but 25A7.3 (referred to herein as 25A7) was neutralizing. The isolated clones were each expanded in 50-100 ml of hybridoma media and allowed to grow to exhaustion, (i.e., less than about 10% cell viability). The concentration and potency of the antibodies to PCSK9 in the supernatants of those cultures were determined by ELISA and by in vitro functional testing, as described herein. As a result of the screening described herein, the hybridomas with the highest titer of antibodies to PCSK9 were identified. The selected hybridomas are shown in FIGS. 2A-3D and Table 2.

Example 4.1

Production of Human 31H4 IgG4 Antibodies from Hybridomas

This example generally describes how one of the antigen binding proteins was produced from a hybridoma line. The production work used 50 ml exhaust supernatant generation followed by protein A purification. Integra production was for scale up and was performed later. Hybridoma line 31H4 was grown in T75 flasks in 20 ml of media (Integra Media, Table 5). When the hybridoma was nearly confluent in the T75 flasks, it was transferred to an Integra flask (Integra Biosciences, Integra CL1000, cat# 90 005).

The Integra flask is a cell culture flask that is divided by a membrane into two chambers, a small chamber and a large chamber. A volume of 20-30 ml hybridoma cells at a minimum cell density of 1×10^6 cells per ml from the 31H4 hybridoma line was placed into the small chamber of an Integra flask in Integra media (see Table 5 for components of Integra media). Integra media alone (1 L) was placed in the large chambers of the Integra flasks. The membrane separating the two chambers is permeable to small molecular weight nutrients but is impermeable to hybridoma cells and to antibodies produced by those cells. Thus, the hybridoma cells and the antibodies produced by those hybridoma cells were retained in the small chamber.

After one week, media was removed from both chambers of the Integra flask and was replaced with fresh Integra media. The collected media from the small chambers was separately retained. After a second week of growth, the media from the small chamber was again collected. The collected media from week 1 from the hybridoma line was combined with the collected media from week 2 from the hybridoma line. The resulting collected media sample from the hybridoma line was spun to remove cells and debris (15 minutes at 3000 rpm) and the resulting supernatant was filtered (0.22 μ m). Clarified conditioned media was loaded onto a Protein A-Sepharose column. Optionally, the media can be first concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by an extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (such as 50 mM Citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on anion exchanger resin such as Q Sepharose resin. The specific IEX conditions for the 31H4 proteins are Q-Sepharose HP at pH 7.8-8.0. Antibody was eluted with a NaCl gradient of 10 mM-500 mM in 25 column volumes.

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TABLE 5

	Composition of Media INTEGRA MEDIA
5	HSFM 10% Ultra Low IgG serum 2 mmol/L L-glutamine 1% NEAA 4 g/L glucose

Example 4.2

Production of Recombinant 31H4 Human IgG2 Antibodies From Transfected Cells

The present example outlines how 31H4 IgG2 antibodies were produced from transfected cells. 293 cells for transient expression and CHO cells for stable expression were transfected with plasmids that encode 31H4 heavy and light chains. Conditioned media from transfected cells was recovered by removing cells and cell debris. Clarified conditioned media was loaded onto a Protein A-Sepharose column. Optionally, the media can first be concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (such as 50 mM citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on anion exchanger resin such as Q Sepharose resin. The specific IEX conditions for the 31H4 proteins are Q-Sepharose HP at pH 7.8-8.0. The antibody was eluted with a NaCl gradient of 10 mM-500 mM in 25 column volumes.

Example 5

Production of Human 21B12 IgG4 Antibodies from Hybridomas

The present example outlines how antibody 21B12 IgG4 was produced from hybridomas. Hybridoma line 21B12 was grown in T75 flasks in media (Integra Media, Table 5). When the hybridomas were nearly confluent in the T75 flasks, they were transferred to Integra flasks (Integra Biosciences, Integra CL1000, cat# 90 005).

The Integra flask is a cell culture flask that is divided by a membrane into two chambers, a small chamber and a large chamber. A volume of 20-30 ml hybridoma cells at a minimum cell density of 1×10^6 cells per ml from the 31H4 hybridoma line was placed into the small chamber of an Integra flask in Integra media (see Table 5 for components of Integra media). Integra media alone (1 L) was placed in the large chambers of the Integra flasks. The membrane separating the two chambers is permeable to small molecular weight nutrients but is impermeable to hybridoma cells and to antibodies produced by those cells. Thus, the hybridoma cells and the antibodies produced by those hybridoma cells were retained in the small chamber. After one week, media was removed from both chambers of the Integra flask and was replaced with fresh Integra media. The collected media from the small chambers was separately retained. After a second week of growth, the media from the small chamber was again collected. The collected media from week 1 from the hybridoma line was combined with the collected media from week 2 from the hybridoma line. The resulting collected media sample from the hybridoma line was spun to remove cells and debris (15 minutes at 3000 rpm) and the resulting supernatant was filtered (0.22 μ m). Clarified conditioned media was loaded onto a Protein A-Sepharose column. Optionally, the media can be first concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by an extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (such as 50 mM Citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on anion exchanger resin such as Q Sepharose resin. The specific IEX conditions for the 31H4 proteins are Q-Sepharose HP at pH 7.8-8.0. Antibody was eluted with a NaCl gradient of 10 mM-500 mM in 25 column volumes.

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sample from the hybridoma line was spun to remove cells and debris (15 minutes at 3000 rpm) and the resulting supernatant was filtered (0.22 µm). Clarified conditioned media were loaded onto a Protein A Sepharose column. Optionally, the media are first concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by an extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (such as 50 mM Citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on anion exchanger resin such as Q Sepharose resin. The specific IEX conditions for the 21B12 proteins are Q-Sepharose HP at pH 7.8-8.0. The antibody was eluted with a NaCl gradient of 10 mM-500 mM in 25 column volumes.

Example 6

Production of Human 21B12 IgG2 Antibodies from Transfected Cells

The present example outlines how 21B12 IgG2 antibodies were produced from transfected cells. Cells (293 cells for transient expression and CHO cells for stable expression) were transfected with plasmids that encode 21B12 heavy and light chains. Conditioned media from hybridoma cells were recovered by removing cells and cell debris. Clarified conditioned media were loaded onto a Protein A-Sepharose column. Optionally, the media can first be concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (50 mM Citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on cation exchanger resin such as SP-Sepharose resin. The specific IEX conditions for the 21B12 proteins are SP-Sepharose HP at pH 5.2. Antibodies were eluted with 25 column volumes of buffer that contains a NaCl gradient of 10 mM-500 mM in 20 mM sodium acetate buffer.

Example 7

Production of Human 16F12 IgG4 Antibodies from Hybridomas

The present example outlines how antibody 16F12 IgG4 was produced from hybridomas. Hybridoma line 16F12 was grown in T75 flasks in media (see Table 5). When the hybridomas were nearly confluent in the T75 flasks, they were transferred to Integra flasks (Integra Biosciences, Integra CL1000, cat# 90 005).

The Integra flask is a cell culture flask that is divided by a membrane into two chambers, a small chamber and a large chamber. A volume of 20-30 ml Hybridoma cells at a minimum cell density of 1×10^6 cells per ml from the 31H4 hybridoma line was placed into the small chamber of an Integra flask in Integra media (see Table 5 for components of Integra media). Integra media alone (1 L) was placed in the large chambers of the Integra flasks. The membrane separating the two chambers is permeable to small molecular weight nutrients but is impermeable to hybridoma cells and to antibodies produced by those cells. Thus, the hybridoma cells and the antibodies produced by those hybridoma cells were retained in the small chamber.

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After one week, media was removed from both chambers of the Integra flask and was replaced with fresh Integra media. The collected media from the small chambers was separately retained. After a second week of growth, the media from the small chamber was again collected. The collected media from week 1 from the hybridoma line was combined with the collected media from week 2 from the hybridoma line. The resulting collected media sample from the hybridoma line were spun to remove cells and debris (15 minutes at 3000 rpm) and the resulting supernatants were filtered (0.22 µm). Clarified conditioned media were loaded onto a Protein A Sepharose column. Optionally, the media can be first concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (50 mM Citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on anion exchanger resin such as Q Sepharose resin. The specific IEX conditions for the 16F12 proteins are Q Sepharose HP at pH 7.8-8.0. Antibody was eluted with a NaCl gradient of 10 mM-500 mM in 25 column volumes.

Example 8

Production of Human 16F12 IgG2 Antibodies from Transfected Cells

The present example outlines how 16F12 IgG2 antibodies were produced from transfected cells. Cells (293 cells for transient expression and CHO cells for stable expression) were transfected with plasmids that encode 16F12 heavy and light chains. Conditioned media from hybridoma cells were recovered by removing cells and cell debris. Clarified conditioned media were loaded onto a Protein A-Sepharose. Optionally, the media can be first concentrated and then loaded onto a Protein A Sepharose column. Non-specific bindings were removed by extensive PBS wash. Bound antibody proteins on the Protein A column were recovered by standard acidic antibody elution from Protein A columns (50 mM Citrate, pH 3.0). Aggregated antibody proteins in the Protein A Sepharose pool were removed by size exclusion chromatography or binding ion exchange chromatography on cation exchanger resin such as SP Sepharose resin. The specific IEX conditions for the 16F12 proteins are SP Sepharose HP at pH 5.2. Antibody is eluted with 25 column volumes of buffer that contains a NaCl gradient of 10 mM-500 mM in 20 mM sodium acetate buffer.

Example 9

Sequence Analysis of Antibody Heavy and Light Chains

The nucleic acid and amino acid sequences for the light and heavy chains of the above antibodies were then determined by Sanger (dideoxy) nucleotide sequencing. Amino acid sequences were then deduced for the nucleic acid sequences. The nucleic acid sequences for the variable domains are depicted in FIGS. 3E-3JJ.

The cDNA sequences for the lambda light chain variable regions of 31H4, 21B12, and 16F12 were determined and are disclosed as SEQ ID NOs: 153, 95, and 105 respectively.

The cDNA sequences for the heavy chain variable regions of 31H4, 21B12, and 16F12 were determined and are disclosed as SEQ ID NOs: 152, 94, and 104 respectively.

The lambda light chain constant region (SEQ ID NO: 156), and the IgG2 and IgG4 heavy chain constant regions (SEQ ID NOs: 154 and 155) are shown in FIG. 3KK.

The polypeptide sequences predicted from each of those cDNA sequences were determined. The predicted polypeptide sequences for the lambda light chain variable regions of 31H4, 21B12, and 16F12 were predicted and are disclosed as SEQ ID NOs: 12, 23, and 35 respectively, the lambda light chain constant region (SEQ ID NO: 156), the heavy chain variable regions of 31H4, 21B12, and 16F12 were predicted and are disclosed as (SEQ. ID NOs. 67, 49, and 79 respectively. The IgG2 and IgG4 heavy chain constant regions (SEQ ID NOs: 154 and 155).

The FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4 divisions are shown in FIG. 2A-3D.

Based on the sequence data, the germline genes from which each heavy chain or light chain variable region was derived was determined. The identity of the germline genes are indicated next to the corresponding hybridoma line in FIGS. 2A-3D and each is represented by a unique SEQ ID NO. FIGS. 2A-3D also depict the determined amino acid sequences for additional antibodies that were characterized.

Example 8

Determination of Isoelectric Points of Three Antibodies

The theoretical pIs of the antibodies based on amino acid sequence were determined to be 7.36 for 16F12; 8.47 for 21B12; and 6.84 for 31H4.

Example 9

Characterization of Binding of Antibodies to PCSK9

Having identified a number of antibodies that bind to PCSK9, several approaches were employed to quantify and further characterize the nature of the binding. In one aspect of the study, a Biacore affinity analysis was performed. In another aspect of the study a KinExA® affinity analysis was performed. The samples and buffers employed in these studies are presented in Table 6 below.

TABLE 6

sample	[sample] mg/ml	Buffer	[sample] uM
hPCSK9	1.26	PBS	16.6
mPCSK9-8xHIS	1.44	PBS	18.9
cPCSK9-V5-6xHIS	0.22	PBS	2.9
16F12, anti-PCSK9 huIgG4	4.6	20 mM NaOAC, pH 5.2, 50 mM NaCl	31.9
21B12, anti-PCSK9 huIgG4	3.84	10 mM NAOAC, pH 5.2, 9% Sucrose	27.0
31H4, anti-PCSK9 huIgG4	3.3	10 mM NAOAC, pH 5.2, 9% Sucrose	22.9

BiACore® Affinity Measurements

A BiACore® (surface plasmon resonance device, Biacore, Inc., Piscataway, N.J.) affinity analysis of the 21B12 antibodies to PCSK9 described in this Example was performed according to the manufacturer's instructions.

Briefly, the surface plasmon resonance experiments were performed using Biacore 2000 optical biosensors (Biacore, GE Healthcare, Piscataway, N.J.). Each individual anti-PCSK9 antibody was immobilized to a research-grade CM5 biosensor chip by amine-coupling at levels that gave a maxi-

mum analyte binding response (Rmax) of no more than 200 resonance units (RU). The concentration of PCSK9 protein was varied at 2 fold intervals (the analyte) and was injected over the immobilized antibody surface (at a flow rate of 100 μ l/min for 1.5 minutes). Fresh HBS-P buffer (pH 7.4, 0.01 M Hepes, 0.15 M NaCl, 0.005% surfactant P-20, Biacore) supplemented with 0.01% BSA was used as binding buffer. Binding affinities of each anti-PCSK9 antibody were measured in separate experiments against each of the human, mouse, and cynomolgus monkey PCSK9 proteins at pH 7.4 (the concentrations used were 100, 50, 25, 12.5, 6.25, 3.125, and 0 nM).

In addition, the binding affinities of antibody to human PCSK9 were also measured at pH 6.0 with the pH 6.0 HBS-P buffer (pH 6.0, 0.01 M Hepes, 0.15 M NaCl, 0.005% surfactant P-20, Biacore) supplemented with 0.01% BSA. The binding signal obtained was proportional to the free PCSK9 in solution. The dissociation equilibrium constant (K_D) was obtained from nonlinear regression analysis of the competition curves using a dual-curve one-site homogeneous binding model (KinExA® software, Sapidyne Instruments Inc., Boise, Id.) (n=1 for the 6.0 pH runs). Interestingly, the antibodies appeared to display a tighter binding affinity at the lower pH (where the K_D was 12.5, 7.3, and 29 pM for 31H4, 21B12, and 16F12 respectively).

Antibody binding kinetic parameters including k_a (association rate constant), k_d (dissociation rate constant), and K_D (dissociation equilibrium constant) were determined using the BIA evaluation 3.1 computer program (BIAcore, Inc. Piscataway, N.J.). Lower dissociation equilibrium constants indicate greater affinity of the antibody for PCSK9. The K_D values determined by the BIAcore® affinity analysis are presented in Table 7.1, shown below.

TABLE 7.1

Antibody	hPCSK9	CynoPCSK9	mPCSK9
31H4	210 pM	190 pM	6 nM
21B12	190 pM	360 pM	460 nM
16F12	470 pM	870 pM	6.4 nM

Table 7.2 depicts the k_{on} and k_{off} rates.

TABLE 7.2

—	K_{on} (M-1 s-1)	K_{off} (s-1)	K_D
31H4.1, pH 7.4	2.45e+5	5.348e-5	210 pM
31H4.1, pH 6	5.536e+6	6.936e-5	12.5 pM
21B12.1, pH 7.4	3.4918e+4	6.634e-6	190 pM
21B12.1, pH 6	2.291e+6	1.676e-5	7.3 pM
16F12.1, pH 7.4	1.064e+5	4.983e-5	470 pM
16F12.1, pH 6	2.392e+6	7.007e-5	29 pM

KinExA® Affinity Measurements

A KinExA® (Sapidyne Instruments, Inc., Boise, Id.) affinity analysis of 16F12 and 31H4 was performed according to the manufacturer's instructions. Briefly, Reacti-Gel™ (6x) (Pierce) was pre-coated with one of human, V5-tagged cyno or His-tagged mouse PCSK9 proteins and blocked with BSA. 10 or 100 pM of either antibody 16F12 or antibody 31H4 and one of the PCSK9 proteins was then incubated with various concentrations (0.1 pM-25 nM) of PCSK9 proteins at room temperature for 8 hours before being passed through the PCSK9-coated beads. The amount of the bead-bound 16F12 or 31H4 was quantified by fluorescently (Cy5) labeled goat anti-human IgG (H+L) antibody (Jackson Immuno Research). The binding signal is proportional to the concen-

tration of free 16F12 or 31H4 at binding equilibrium. Equilibrium dissociation constant (K_D) were obtained from non-linear regression of the two sets of competition curves using a one-site homogeneous binding model. The KinExA® Pro software was employed in the analysis. Binding curves generated in this analysis are presented as FIGS. 4A-4F.

Both the 16F12 and 31H4 antibodies showed similar affinity to human and cyno PCSK9, but approximately 10-250 fold lower affinity to mouse PCSK9. Of the two antibodies tested using the KinExA® system, antibody 31H4 showed higher affinity to both human and cyno PCSK9 with 3 and 2 pM K_D respectively. 16F12 showed slightly weaker affinity at 15 pM K_D to human PCSK9 and 16 pM K_D to cyno PCSK9.

The results of the KinExA® affinity analysis are summarized in Table 8.1, shown below.

TABLE 8.1

Sample	hPCSK9		cPCSK		mPCSK	
	K_D (pM)	95% CI	K_D (pM)	95% CI	K_D (pM)	95% CI
16F12	15	11~22	16	14~19	223	106~410
31H4.1	3	1~5	2	1~3	500	400~620

In addition, a SDS PAGE was run to check the quality and quantity of the samples and is shown in FIG. 5A. cPCSK9 showed around 50% less on the gel and also from the active binding concentration calculated from KinExA® assay. Therefore, the K_D of the mAbs to cPCSK9 was adjusted as 50% of the active cPCSK9 in the present.

A BIACore solution equilibrium binding assay was used to measure the K_D values for ABP 21B12. 21B12.1 showed little signal using KinExA assay, therefore, biacore solution equilibrium assay was applied. Since no significant binding was observed on binding of antibodies to immobilized PCSK9 surface, 21B12 antibody was immobilized on the flow cell 4 of a CM5 chip using amine coupling with density around 7000 RU. Flow cell 3 was used as a background control. 0.3, 1, and 3 nM of human PCSK9 or cyno PCSK9 were mixed with a serial dilutions of 21B12.1 antibody samples (ranged from 0.001~25 nM) in PBS plus 0.1 mg/ml BSA, 0.005% P20. Binding of the free PCSK9 in the mixed solutions were measured by injecting over the 21B12.1 antibody surface. 100% PCSK9 binding signal on 21B12.1 surface was determined in the absence of mAb in the solution. A decreased PCSK9 binding response with increasing concentrations of mAb indicated that PCSK9 binding to mAb in solution, which blocked PCSK9 from binding to the immobilized peptide surface. Plotting the PCSK9 binding signal versus mAb concentrations, K_D was calculated from three sets of curves (0.3, 1 and 3 nM fixed PCSK9 concentration) using a one-site homogeneous binding model in KinExA Pro™ software. Although cPCSK9 has lower protein concentration observed from KinExA assay and SDS-gel, its concentration was not adjusted here since the concentration of cPCSK9 was not used for calculation of K_D . The results are displayed in Table 8.2 below and in FIGS. 5B-5D. FIG. 5B depicts the results from the solution equilibrium assay at three different hPCSK9 concentrations for hPCSK9. FIG. 5C depicts a similar set of results for mPCSK9. FIG. 5D depicts the results from the above biacore capture assay.

TABLE 8.2

Sample	hPCSK9		cPCSK		mPCSK	
	K_D (pM)	95% CI	K_D (pM)	95% CI	K_D (pM)	95% CI
21B12.1	15	9~23	11	7~16	17000	—

Example 10

Epitope Binning

Competition ELISA was used for anti-PCSK9 antibody binning. Briefly, to determine if two antibodies belong to the same epitope bin, one of the antibodies (mAb1) was first coated onto an ELISA plate (NUNC) at 2 µg/ml by overnight incubation. The plate was then washed and blocked with 3% BSA. Meanwhile, 30 ng/ml of biotinylated hPCSK9 was incubated with the second antibody (mAb2) for 2 hours at room temperature. The mixture was applied to coated mAb1 and incubated for 1 hour at room temperature. The ELISA plate was then washed and incubated with Neutravidin-HRP (Pierce) at 1:5000 dilutions for 1 hour. After another wash, the plate was incubated with TMB substrate and signal was detected at 650 nm using a Titertek plate reader. Antibodies with the same binding profiles were grouped together into the same epitope bin. The results of the antibody binning studies are presented in Table 8.3.

TABLE 8.3

Clone	Bin
21B12.2	1
31H4	3
20D10	1
25A7.1	2
25A7.3	1
23G1	1
26H5	1
31D1	1
16F12	3
28D6	3
27A6	3
31G11	3
27B2	ND
28B12	3
22E2	3
1A12.2	1
3B6	1
3C4	4
9C9	1
9H6	1
13B5	6
13H1	7
17C2	1
19H9.2	1
23B5	1
25G4	1
26E10	1
27E7	1
27H5	1
30A4	1
30B9	1
31A4	5
31B12	5

Additional examination of the epitope binning was performed using BIACore. Three mAbs, 16F12, 21B12 and 31H4, were immobilized on flow cells 2, 3 and 4 with density around 8000 RU. 5 nM PCSK9 from human, mouse and cyno were injected over the mAb surfaces to reach around 100 to

500 RU. 10 nM mAbs were then injected over the PCSK9 surface. Binding of three mAbs to three different PCSK9 proteins over the three mAbs were then recorded.

If the two mAbs had a similar epitope on the antigen, mAb 1 will not show the binding to the antigen already bound to the mAb 2. If the two mAbs have the different epitope on the antigen, mAb1 will show the binding to the antigen bound to the mAb2. FIG. 5E depicts these epitope binning results in graph form for three mAbs on human PCSk9. A similar pattern was observed for mPCSK9 and cPCSK9. As shown in the graph, 16F12 and 31H4 appear to share a similar epitope, while 21B12 appears to have a different epitope.

Example 11

Efficacy of 31H4 and 21B12 for Blocking D374Y PCSK9/LDLR Binding

This example provides the IC₅₀ values for two of the antibodies in blocking PCSK9 D374Y's ability to bind to LDLR. Clear 384 well plates (Costar) were coated with 2 micrograms/ml of goat anti-LDL receptor antibody (R&D Systems) diluted in buffer A (100 mM sodium cacodylate, pH 7.4). Plates were washed thoroughly with buffer A and then blocked for 2 hours with buffer B (1% milk in buffer A). After washing, plates were incubated for 1.5 hours with 0.4 micrograms/ml of LDL receptor (R&D Systems) diluted in buffer C (buffer B supplemented with 10 mM CaCl₂). Concurrent with this incubation, 20 ng/ml of biotinylated D374Y PCSK9 was incubated with various concentrations of the 31H4 IgG2, 31H4 IgG4, 21B12 IgG2 or 21B12 IgG4 antibody, which was diluted in buffer A, or buffer A alone (control). The LDL receptor containing plates were washed and the biotinylated D374Y PCSK9/antibody mixture was transferred to them and incubated for 1 hour at room temperature. Binding of the biotinylated D374Y to the LDL receptor was detected by incubation with streptavidin-HRP (Biosource) at 500 ng/ml in buffer C followed by TMB substrate (KPL). The signal was quenched with 1N HCl and the absorbance read at 450 nm.

The results of this binding study are shown in FIGS. 6A-6D. Summarily, IC₅₀ values were determined for each antibody and found to be 199 pM for 31H4 IgG2 (FIG. 6A), 156 pM for 31H4 IgG4 (FIG. 6B), 170 pM for 21B12 IgG2 (FIG. 6C), and 169 pM for 21B12 IgG4 (FIG. 6D).

The antibodies also blocked the binding of wild-type PCSK9 to the LDLR in this assay.

Example 12

Cell LDL Uptake Assay

This example demonstrates the ability of various antigen binding proteins to reduce LDL uptake by cells. Human HepG2 cells were seeded in black, clear bottom 96-well plates (Costar) at a concentration of 5×10⁵ cells per well in DMEM medium (Mediatech, Inc) supplemented with 10% FBS and incubated at 37°C. (5% CO₂) overnight. To form the PCSK9 and antibody complex, 2 µg/ml of D374Y human PCSK9 was incubated with various concentrations of antibody diluted in uptake buffer (DMEM with 1% FBS) or uptake buffer alone (control) for 1 hour at room temperature. After washing the cells with PBS, the D374Y PCSK9/antibody mixture was transferred to the cells, followed by LDL-BODIPY (Invitrogen) diluted in uptake buffer at a final concentration of 6 µg/ml. After incubation for 3 hours at 37°C. (5% CO₂), cells were washed thoroughly with PBS and the

cell fluorescence signal was detected by Safire™ (TECAN) at 480-520 nm (excitation) and 520-600 nm (emission).

The results of the cellular uptake assay are shown in FIGS. 7A-7D. Summarily, IC₅₀ values were determined for each antibody and found to be 16.7 nM for 31H4 IgG2 (FIG. 7A), 13.3 nM for 31H4 IgG4 (FIG. 7B), 13.3 nM for 21B12 IgG2 (FIG. 7C), and 18 nM for 21B12 IgG4 (FIG. 7D). These results demonstrate that the applied antigen binding proteins can reduce the effect of PCSK9 (D374Y) to block LDL uptake by cells. The antibodies also blocked the effect of wild-type PCSK9 in this assay.

Example 13

Serum cholesterol Lowering Effect of the 31H4 Antibody in 6 Day Study

In order to assess total serum cholesterol (TC) lowering in wild type (WT) mice via antibody therapy against PCSK9 protein, the following procedure was performed.

Male WT mice (C57BL/6 strain, aged 9-10 weeks, 17-27 g) obtained from Jackson Laboratory (Bar Harbor, Me.) were fed a normal chow (Harland-Teklad, Diet 2918) through out the duration of the experiment. Mice were administered either anti-PCSK9 antibody 31H4 (2 mg/ml in PBS) or control IgG (2 mg/ml in PBS) at a level of 10 mg/kg through the mouse's tail vein at T=0. Naïve mice were also set aside as a naïve control group. Dosing groups and time of sacrifice are shown in Table 9.

TABLE 9

Group	Treatment	Time point after dosing	Number
1	IgG	8 hr	7
2	31H4	8 hr	7
3	IgG	24 hr	7
4	31H4	24 hr	7
5	IgG	72 hr	7
6	31H4	72 hr	7
7	IgG	144 hr	7
8	31H4	144 hr	7
9	Naïve	n/a	7

Mice were sacrificed with CO₂ asphyxiation at the predetermined time points shown in Table 9. Blood was collected via vena cava into eppendorf tubes and was allowed to clot at room temperature for 30 minutes. The samples were then spun down in a table top centrifuge at 12,000×g for 10 minutes to separate the serum. Serum total cholesterol and HDL-C were measured using Hitachi 912 clinical analyzer and Roche/Hitachi TC and HDL-C kits.

The results of the experiment are shown in FIGS. 8A-8D. Summarily, mice to which antibody 31H4 was administered showed decreased serum cholesterol levels over the course of the experiment (FIG. 8A and FIG. 8B). In addition, it is noted that the mice also showed decreased HDL levels (FIG. 8C and FIG. 8D). For FIG. 8A and FIG. 8C, the percentage change is in relation to the control IgG at the same time point (*P<0.01, # P<0.05). For FIG. 8B and FIG. 8D, the percentage change is in relation to total serum cholesterol and HDL levels measured in naïve animals at t=0 hrs (*P<0.01, # P<0.05).

In respect to the lowered HDL levels, it is noted that one of skill in the art will appreciate that the decrease in HDL in mice is not indicative that an HDL decrease will occur in humans and merely further reflects that the serum cholesterol level in the organism has decreased. It is noted that mice transport the majority of serum cholesterol in high density lipoprotein (HDL) particles which is different to humans who carry most

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serum cholesterol on LDL particles. In mice the measurement of total serum cholesterol most closely resembles the level of serum HDL-C. Mouse HDL contains apolipoprotein E (apoE) which is a ligand for the LDL receptor (LDLR) and allows it to be cleared by the LDLR. Thus, examining HDL is an appropriate indicator for the present example, in mice (with the understanding that a decrease in HDL is not expected for humans). For example, human HDL, in contrast, does not contain apoE and is not a ligand for the LDLR. As PCSK9 antibodies increase LDLR expression in mouse, the liver can clear more HDL and therefore lowers serum HDL-C levels.

Example 14

Effect of Antibody 31H4 on LDLR Levels in a 6 Day Study

The present example demonstrates that an antigen binding protein alters the level of LDLR in a subject, as predicted, over time. A Western blot analysis was performed in order to ascertain the effect of antibody 31H4 on LDLR levels. 50-100 mg of liver tissue obtained from the sacrificed mice described in Example 13 was homogenized in 0.3 ml of RIPA buffer (Santa Cruz Biotechnology Inc.) containing complete protease inhibitor (Roche). The homogenate was incubated on ice for 30 minutes and centrifuged to pellet cellular debris. Protein concentration in the supernatant was measured using BioRad protein assay reagents (BioRad laboratories). 100 µg of protein was denatured at 70° C. for 10 minutes and separated on 4-12% Bis-Tris SDS gradient gel (Invitrogen). Proteins were transferred to a 0.45 µm PVDF membrane (Invitrogen) and blocked in washing buffer (50 mM Tris PH7.5, 150 mM NaCl, 2 mM CaCl₂ and 0.05% Tween 20) containing 5% non-fat milk for 1 hour at room temperature. The blot was then probed with goat anti-mouse LDLR antibody (R&D system) 1:2000 or anti-β actin (sigma) 1:2000 for 1 hour at room temperature. The blot was washed briefly and incubated with bovine anti-goat IgG-HRP (Santa Cruz Biotechnology Inc.) 1:2000 or goat anti-mouse IgG-IRP (Upstate) 1:2000. After a 1 hour incubation at room temperature, the blot was washed thoroughly and immunoreactive bands were detected using ECL plus kit (Amersham biosciences). The Western blot showed an increase in LDLR protein levels in the presence of antibody 31H4, as depicted in FIG. 9.

Example 15

Serum cholesterol Lowering Effect of Antibody 31H4 in a 13 Day Study

In order to assess total serum cholesterol (TC) lowering in wild type (WT) mice via antibody therapy against PCSK9 protein in a 13 day study, the following procedure was performed.

Male WT mice (C57BL/6 strain, aged 9-10 weeks, 17-27 g) obtained from Jackson Laboratory (Bar Harbor, Me.) were fed a normal chow (Harland-Teklad, Diet 2918) through out the duration of the experiment. Mice were administered either anti-PCSK9 antibody 31H4 (2 mg/ml in PBS) or control IgG (2 mg/ml in PBS) at a level of 10 mg/kg through the mouse's tail vein at T=0. Naïve mice were also set aside as naïve control group. Dosing groups and time of sacrifice are shown in Table 10. Animals were sacrificed and livers were extracted and prepared as in Example 13.

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TABLE 10

Group	Treatment	Time point after dosing	Number	Dose
1	IgG	72 hr	6	10 mg/kg
2	31H4	72 hr	6	10 mg/kg
3	31H4	72 hr	6	1 mg/kg
4	IgG	144 hr	6	10 mg/kg
5	31H4	144 hr	6	10 mg/kg
6	31H4	144 hr	6	1 mg/kg
7	IgG	192 hr	6	10 mg/kg
8	31H4	192 hr	6	10 mg/kg
9	31H4	192 hr	6	1 mg/kg
10	IgG	240 hr	6	10 mg/kg
11	31H4	240 hr	6	10 mg/kg
12	31H4	240 hr	6	1 mg/kg
13	IgG	312 hr	6	10 mg/kg
14	31H4	312 hr	6	10 mg/kg
15	31H4	312 hr	6	1 mg/kg
16	Naive	n/a	6	n/a

When the 6 day experiment was extended to a 13 day study, the same serum cholesterol lowering effect observed in the 6 day study was also observed in the 13 day study. More specifically, animals dosed at 10 mg/kg demonstrated a 31% decrease in serum cholesterol on day 3, which gradually returned to pre-dosing levels by day 13. FIG. 10A depicts the results of this experiment. FIG. 10C depicts the results of repeating the above procedure with the 10 mg/kg dose of 31H4, and with another antibody, 16F 12, also at 10 mg/kg. Dosing groups and time of sacrifice are shown in Table 11.

TABLE 11

Group	Treatment	Time point after dosing	Number	Dose
1	IgG	24 hr	6	10 mg/kg
2	16F12	24 hr	6	10 mg/kg
3	31H4	24 hr	6	10 mg/kg
4	IgG	72 hr	6	10 mg/kg
5	16F12	72 hr	6	10 mg/kg
6	31H4	72 hr	6	10 mg/kg
7	IgG	144 hr	6	10 mg/kg
8	16F12	144 hr	6	10 mg/kg
9	31H4	144 hr	6	10 mg/kg
10	IgG	192 hr	6	10 mg/kg
11	16F12	192 hr	6	10 mg/kg
12	31H4	192 hr	6	10 mg/kg
13	IgG2	240 hr	6	10 mg/kg
14	16F12	240 hr	6	10 mg/kg
15	31H4	240 hr	6	10 mg/kg
16	IgG2	312 hr	6	10 mg/kg
17	16F12	312 hr	6	10 mg/kg
18	31H4	312 hr	6	10 mg/kg
19	Naive	n/a	6	10 mg/kg

As shown in FIG. 10C both 16F12 and 31H4 resulted in significant and substantial decreases in total serum cholesterol after just a single dose and provided benefits for over a week (10 days or more). The results of the repeated 13 day study were consistent with the results of the first 13 day study, with a decrease in serum cholesterol levels of 26% on day 3 being observed. For FIG. 10A and FIG. 10B, the percentage change is in relation to the control IgG at the same time point (*P<0.01). For FIG. 10C, the percentage change is in relation to the control IgG at the same time point (*P<0.05).

Example 16

Effect of Antibody 31H4 on HDL Levels in a 13 Day Study

The HDL levels for the animals in Example 15 were also examined. HDL levels decreased in the mice. More specific-

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cally, animals dosed at 10 mg/kg demonstrated a 33% decrease in HDL levels on day 3, which gradually returned to pre-dosing levels by day 13. FIG. 10B depicts the results of the experiment. There was a decrease in HDL levels of 34% on day 3. FIG. 10B depicts the results of the repeated 13 day experiment.

As will be appreciated by one of skill in the art, while the antibodies will lower mouse HDL, this is not expected to occur in humans because of the differences in HDL in humans and other organisms (such as mice). Thus, the decrease in mouse HDL is not indicative of a decrease in human HDL.

Example 17

Repeated Administration of Antibodies Produce Continued Benefits of Antigen Binding Peptides

In order to verify that the results obtained in the Examples above can be prolonged for further benefits with additional doses, the Experiments in Examples 15 and 16 were repeated with the dosing schedule depicted in FIG. 11A. The results are displayed in FIG. 11B. As can be seen in the graph in FIG. 11B, while both sets of mice displayed a significant decrease in total serum cholesterol because all of the mice received an initial injection of the 31H4 antigen binding protein, the mice that received additional injections of the 31H4 ABP displayed a continued reduction in total serum cholesterol, while those mice that only received the control injection eventually displayed an increase in their total serum cholesterol. For FIG. 11, the percentage change is in relation to the naïve animals at t=0 hours (*P<0.01, **P<0.001).

The results from this example demonstrate that, unlike other cholesterol treatment methods, in which repeated applications lead to a reduction in efficacy because of biological adjustments in the subject, the present approach does not seem to suffer from this issue over the time period examined. Moreover, this suggests that the return of total serum cholesterol or HDL cholesterol levels to baseline, observed in the previous examples is not due to some resistance to the treatment being developed by the subject, but rather the depletion of the antibody availability in the subject.

Example 18

Epitope Mapping of Human Anti PCSK9 Antibodies

This example outlines methods for determining which residues in PCSK9 are involved in forming or part of the epitope for the antigen binding proteins disclosed herein to PCSK9.

In order to determine the epitopes to which certain of the ABPs of the present invention bind, the epitopes of the ABPs can be mapped using synthetic peptides derived from the specific PCSK9 peptide sequence.

A SPOTs peptide array (Sigma Genosys) can be used to study the molecular interaction of the human anti-PCSK9 antibodies with their peptide epitope. SPOTs technology is based on the solid-phase synthesis of peptides in a format suitable for the systematic analysis of antibody epitopes. Synthesis of custom arrayed oligopeptides is commercially available from Sigma-Genosys. A peptide array of overlapping oligopeptides derived from the amino-acid sequence of the PCSK9 peptide can be obtained. The array can comprise a series of 12-mer peptides as spots on a polypropylene membrane sheets. The peptide array can span the entire length of the PCSK9 mature sequence. Each consecutive peptide can be offset by 1 residue from the previous one, yielding a nested, overlapping library of arrayed oligopeptides. The

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membrane carrying the peptides can be reacted with different anti-PCSK9 antibodies (1 micrograms/ml). The binding of the mAbs to the membrane-bound peptides can be assessed by an enzyme-linked immunosorbent assay using HRP-conjugated secondary antibody followed by enhanced chemiluminescence (ECL).

In addition, functional epitopes can be mapped by combinatorial alanine scanning. In this process, a combinatorial alanine-scanning strategy can be used to identify amino acids in the PCSK9 protein that are necessary for interaction with anti-PCSK9 ABPs. To accomplish this, a second set of SPOTs arrays can be used for alanine scanning. A panel of variant peptides with alanine substitutions in each of the 12 residues can be scanned as above. This will allow for the epitopes for the ABPs to the human PCSK9 to be mapped and identified.

In the alternative, given that it is possible that the epitope is conformational, a combination of alanine scanning and/or arginine scanning, antibody FAB/PCSK9 co-crystallization, and limited proteolysis/LC-MS (liquid chromatography mass spec.) can be employed to indentify the epitopes.

Example 19

Uses of PCSK9 Antibodies for the Treatment of Cholesterol Related Disorders

A human patient exhibiting a Cholesterol Related Disorder (in which a reduction in cholesterol (such as serum cholesterol) can be beneficial) is administered a therapeutically effective amount of PCSK9 antibody, 31H4 (or, for example, 21B12 or 16F12). At periodic times during the treatment, the patient is monitored to determine whether the symptoms of the disorder has subsided. Following treatment, it is found that patients undergoing treatment with the PCSK9 antibody have reduced serum cholesterol levels, in comparison to patients that are not treated.

Example 20

Uses of PCSK9 Antibodies for the Treatment of Hypercholesterolemia

A human patient exhibiting symptoms of hypercholesterolemia is administered a therapeutically effective amount of PCSK9 antibody, such as 31H4 (or, for example, 21B12 or 16F12). At periodic times during the treatment, the human patient is monitored to determine whether the serum cholesterol level has declined. Following treatment, it is found that the patient receiving the treatment with the PCSK9 antibodies has reduced serum cholesterol levels in comparison to arthritis patients not receiving the treatment.

Example 21

Uses of PCSK9 Antibodies for the Prevention of Coronary Heart Disease and/or Recurrent Cardiovascular Events

A human patient at risk of developing coronary heart disease is identified. The patient is administered a therapeutically effective amount of PCSK9 antibody, such as 31H4 (or, for example, 21B12 or 16F12), either alone, concurrently or sequentially with a statin, e.g., simvastatin. At periodic times during the treatment, the human patient is monitored to determine whether the patient's total serum cholesterol level changes. Throughout the preventative treatment, it is found that the patient receiving the treatment with the PCSK9 anti-

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bodies has reduced serum cholesterol thereby reducing their risk to coronary heart diseases or recurrent cardiovascular events in comparison to patients not receiving the treatment.

Example 22

Use of PCSK9 Antibodies as a Diagnostic Agent

An Enzyme-Linked Immunosorbent Assay (ELISA) for the detection of PCSK9 antigen in a sample can be used to diagnose patients exhibiting high levels of PCSK9 production. In the assay, wells of a microtiter plate, such as a 96-well microtiter plate or a 384-well microtiter plate, are adsorbed for several hours with a first fully human monoclonal antibody directed against PCSK9. The immobilized antibody serves as a capture antibody for any of the PCSK9 that may be present in a test sample. The wells are rinsed and treated with a blocking agent such as milk protein or albumin to prevent nonspecific adsorption of the analyte.

Subsequently the wells are treated with a test sample suspected of containing the PCSK9, or with a solution containing a standard amount of the antigen. Such a sample may be, for example, a serum sample from a subject suspected of having levels of circulating antigen considered to be diagnostic of a pathology.

After rinsing away the test sample or standard, the wells are treated with a second fully human monoclonal PCSK9 antibody that is labeled by conjugation with biotin. A monoclonal or mouse or other species origin can also be used. The labeled PCSK9 antibody serves as a detecting antibody. After rinsing away excess second antibody, the wells are treated with avidin-conjugated horseradish peroxidase (HRP) and a suitable chromogenic substrate. The concentration of the antigen in the test samples is determined by comparison with a standard curve developed from the standard samples.

This ELISA assay provides a highly specific and very sensitive assay for the detection of the PCSK9 antigen in a test sample.

Determination of PCSK9 Protein Concentration in Subjects

A sandwich ELISA can quantify PCSK9 levels in human serum. Two fully human monoclonal PCSK9 antibodies from the sandwich ELISA, recognize different epitopes on the PCSK9 molecule. Alternatively, monoclonal antibodies of mouse or other species origin may be used. The ELISA is performed as follows: 50 µL of capture PCSK9 antibody in coating buffer (0.1 M NaHCO₃, pH 9.6) at a concentration of 2 µg/mL is coated on ELISA plates (Fisher). After incubation at 4° C. overnight, the plates are treated with 200 µL of blocking buffer (0.5% BSA, 0.1% Tween 20, 0.01% Thimerosal in PBS) for 1 hour at 25° C. The plates are washed (3×) using 0.05% Tween 20 in PBS (washing buffer, WB). Normal or patient sera (Clinomics, Bioreclamation) are diluted in blocking buffer containing 50% human serum. The plates are incubated with serum samples overnight at 4° C., washed with WB, and then incubated with 100 µL/well of biotinylated detection PCSK9 antibody for 1 hour at 25° C. After washing, the plates are incubated with HRP-Streptavidin for 15 minutes, washed as before, and then treated with 100 µL/well of o-phenylenediamine in H₂O₂ (Sigma developing solution) for color generation. The reaction is stopped with 50 µL/well of H₂SO₄ (2M) and analyzed using an ELISA plate reader at 492 nm. Concentration of PCSK9 antigen in serum samples is calculated by comparison to dilutions of purified PCSK9 antigen using a four parameter curve fitting program.

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Determination of PCSK9 Variant Protein Concentration in Subjects

The steps outlined above can be performed using antibodies noted herein that bind to both the wild type PCSK9 and the variant PCSK9 (D374Y). Next, antibodies that bind to the wild type but not the mutant can be used (again using a similar protocol as outlined above) to determine if the PCSK9 present in the subject is wild type or the D374Y variant. As will be appreciated by one of skill in the art, results that are positive for both rounds will be wild-type, while those that are positive for the first round, but not the second round of antibodies, will include the D374Y mutation. There are high frequency mutations in the population that are known and could benefit particularly from an agent such as the ABPs disclosed herein.

Example 23

Use of PCSK9 Antigen Binding Protein for the Prevention of Hypercholesterolemia

A human patient exhibiting a risk of developing hypercholesterolemia is identified via family history analysis and/or lifestyle, and/or current cholesterol levels. The subject is regularly administered (e.g., one time weekly) a therapeutically effective amount of PCSK9 antibody, 31H4 (or, for example, 21B12 or 16F12). At periodic times during the treatment, the patient is monitored to determine whether serum cholesterol levels have decreased. Following treatment, it is found that subjects undergoing preventative treatment with the PCSK9 antibody have lowered serum cholesterol levels, in comparison to subjects that are not treated.

Example 24

PCSK9 ABPs Further Upregulated LDLR in the Presence of Statins

This example demonstrates that ABPs to PCSK9 produced further increases in LDLR availability when used in the presence of statins, demonstrating that further benefits can be achieved by the combined use of the two.

HepG2 cells were seeded in DMEM with 10% fetal bovine serum (FBS) and grown to ~90% confluence. The cells were treated with indicated amounts of mevinolin (a statin, Sigma) and PCSK9 ABPs (FIGS. 12A-12C) in DMEM with 3% FBS for 48 hours. Total cell lysates were prepared. 50 mg of total proteins were separated by gel electrophoresis and transferred to PVDF membrane. Immunoblots were performed using rabbit anti-human LDL receptor antibody (Fitzgerald) or rabbit anti-human b-actin antibody. The enhanced chemiluminescent results are shown in the top panels of FIGS. 12A-12C. The intensity of the bands were quantified by ImageJ software and normalized by b-actin. The relative levels of LDLR are shown in the lower panels of FIGS. 12A-12C. ABPs 21B12 and 31H4 are PCSK9 neutralizing antibodies, while 25A7.1 is a non-neutralizing antibody.

HepG2-PCSK9 cells were also created. These were stable HepG2 cell line transfected with human PCSK9. The cells were seeded in DMEM with 10% fetal bovine serum (FBS) and grew to 90% confluence. The cells were treated with indicated amounts of mevinolin (Sigma) and PCSK9 ABPs (FIGS. 12D-12F) in DMEM with 3% FBS for 48 hours. Total cell lysates were prepared. 50 mg of total proteins were separated by gel electrophoresis and transferred to PVDF membrane. Immunoblots were performed using rabbit anti-human LDL receptor antibody (Fitzgerald) or rabbit anti-human b-actin antibody. The enhanced chemiluminescent results are

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shown in the top panels. The intensity of the bands were quantified by ImageJ software and normalized by b-actin.

As can be seen in the results depicted in FIGS. 12A-12F, increasing amounts of the neutralizing antibody and increasing amounts of the statin generally resulted in increases in the level of LDLR. This increase in effectiveness for increasing levels of the ABP is especially evident in FIGS. 12D-12F, in which the cells were also transfected with PCSK9, allowing the ABPs to demonstrate their effectiveness to a greater extent.

Interestingly, as demonstrated by the results in the comparison of FIGS. 12D-12F to 12A-12C, the influence of the ABP concentrations on LDLR levels increased dramatically when PCSK9 was being produced by the cells. In addition, it is clear that the neutralizing ABPs (21B12 and 31H4) resulted in a greater increase in LDLR levels, even in the presence of statins, than the 25A7.1 ABP (a non-neutralizer), demonstrating that additional benefits can be achieved by the use of both statins and ABPs to PCSK9.

Example 25

Consensus Sequences

Consensus sequences were determined using standard phylogenetic analyses of the CDRs corresponding to the V_H and V_L of anti-PCSK9 ABPs. The consensus sequences were determined by keeping the CDRs contiguous within the same sequence corresponding to a V_H or V_L . Briefly, amino acid sequences corresponding to the entire variable domains of either V_H or V_L were converted to FASTA formatting for ease in processing comparative alignments and inferring phylogenies. Next, framework regions of these sequences were replaced with an artificial linker sequence ("bbbbbbbbb" placeholders, non-specific nucleic acid construct) so that examination of the CDRs alone could be performed without introducing any amino acid position weighting bias due to coincident events (e.g., such as unrelated antibodies that serendipitously share a common germline framework heritage) while still keeping CDRs contiguous within the same sequence corresponding to a V_H or V_L . V_H or V_L sequences of this format were then subjected to sequence similarity alignment interrogation using a program that employs a standard ClustalW-like algorithm (see, Thompson et al., 1994, *Nucleic Acids Res.* 22:4673-4680). A gap creation penalty of 8.0 was employed along with a gap extension penalty of 2.0. This program likewise generated phylogenograms (phylogenetic tree illustrations) based on sequence similarity alignments using either UPGMA (unweighted pair group method using arithmetic averages) or Neighbor-Joining methods (see, Saitou and Nei, 1987, *Molecular Biology and Evolution* 4:406-425) to construct and illustrate similarity and distinction of sequence groups via branch length comparison and grouping. Both methods produced similar results but UPGMA-derived trees were ultimately used as the method employs a simpler and more conservative set of assumptions. UPGMA-derived trees were generated where similar groups of sequences were defined as having fewer than 15 substitutions per 100 residues (see, legend in tree illustrations for scale) amongst individual sequences within the group and were used to define consensus sequence collections. The results of the comparisons are depicted in FIGS. 13A-13J. In FIG. 13E, the groups were chosen so that sequences in the light chain that clade are also a dade in the heavy chain and have fewer than 15 substitutions.

As will be appreciated by one of skill in the art, the results presented in FIGS. 13A-13J present a large amount of guid-

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ance as to the importance of particular amino acids (for example, those amino acids that are conserved) and which amino acid positions can likely be altered (for example, those positions that have different amino acids for different ABPs).

Example 26

Mouse Model for PCSK9 and ABP Ability to Lower LDL in vivo

To generate mice which over-expressed human PCSK9, three week old WT C57B1/6 mice were injected via tail vein administration with various concentrations of adenoassociated virus (AAV), recombinantly modified to express human PCSK9, to determine the correct titer which would provide a measurable increase of LDL-cholesterol in the mice. Using this particular virus that expressed human PCSK9, it was determined that 4.5×10^{12} pfu of virus would result in an LDL-cholesterol level of approximately 40 mg/dL in circulating blood (normal levels of LDL in a WT mice are approximately 10 mg/dL). The human PCSK9 levels in these animals was found to be approximately 13 ug/mL. A colony of mice were generated using this injection criteria.

One week after injection, mice were assessed for LDL-cholesterol levels, and randomized into different treatment groups. Animals were then administered, via tail vein injection, a single bolus injection of either 10 mg/kg or 30 mg/kg of 16F12, 21B12, or 31H4 antigen binding proteins. IgG2 ABP was administered in a separate group of animals as a dosing control. Subgroups of animals ($n=6-7$) were then euthanized at 24 and 48 hours after ABP administration. There were no effects on LDL-cholesterol levels following IgG2 administration at either dose. Both 31H4 and 21B12 demonstrated significant LDL-cholesterol lowering up to and including 48 hours post-administration, as compared to IgG2 control (shown in FIGS. 14A and 14B at two different doses). 16F12 shows an intermediary LDL-cholesterol lowering response, with levels returning to baseline of approximately 40 mg/dL by the 48 hour time point. This data is consistent with in vitro binding data (Biacore and Kinexa), which shows near equivalent binding affinity between 31H4 and 21B12, and a lesser affinity of 16F12 to human PCSK9.

As can be seen in the results, total cholesterol and HDL-cholesterol were reduced by the PCSK9 ABPs in the model (both total and HDL-C are elevated above WT mice due to the overexpression of PCSK9). While cholesterol lowering in this model appears to occur over a relatively short period of time, this is believed to be due to the levels of human PCSK9 that are present, which are supraphysiologically high in this model. In addition, given that the expression is governed by AAV, there is no regulation of PCSK9 expression. In these figures, (*) denotes a $P < 0.05$, and (**) denotes a $P < 0.005$ as compared to LDL-cholesterol levels observed in IgG2 control injected animals at the same time point. The 13 microgram/ml level of serum human PCSK9 in the mice corresponds to an approximately 520-fold increase above the endogenous mouse PCSK9 levels (25 ng/ml), and an approximately 75-fold increase above average human serum levels (~175 ng/ml). Thus, the antigen binding proteins should be even more effective in humans.

As will be appreciated by one of skill in the art, the above results demonstrate that appropriateness of the mouse model for testing the antigen binding protein's ability to alter serum cholesterol in a subject. One of skill in the art will also recognize that the use of mouse HDL to monitor serum cholesterol levels in a mouse, while useful for monitoring mouse serum cholesterol levels, is not indicative of the ABPs impact

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on human HDL in humans. For example, Cohen et al. ("Sequence variations in PCSK9, low LDL, and protection against coronary heart disease", N Engl J Med, 354:1264-1272, 2006) demonstrated the lack of any effect of the PCSK9 loss-of-function mutations on human HDL levels (the entirety of which is incorporated by reference). Thus, one of skill in the art will appreciate that the ability of the ABP to lower mouse HDL (which lack LDL) is not indicative of the ABP's ability to lower human HDL. Indeed, as shown by Cohen, this is unlikely to occur for neutralizing antibodies in humans.

Example 27

31H4 and 21B12 Bind to the ProCat Region of PCSK9

The present example describes one method for determining where various antibodies bind to PCSK9.

The ProCat (31-449 of SEQ ID NO: 3) or V domain (450-692 of SEQ ID NO: 3) of the PCSK9 protein was combined with either antibody 31H4 or 21B12. The samples were analyzed by Native PAGE for complex formation. As can be seen in FIG. 16A and FIG. 16B, gel shifts were present for the ProCat/31H4 and ProCat/21B12 samples, demonstrating that the antibodies bound to the ProCat domain.

Example 28

The LDLR EGFa Domain Binds to the Catalytic Domain of PCSK9

The present example presents the solved crystal structure of PCSK9 ProCat (31-454 of SEQ ID NO: 3) bound to the LDLR EGFa domain (293-334) at 2.9 Å resolution (the conditions for which are described in the below Examples).

A representation of the structure of PCSK9 bound to EGFa is shown in FIG. 17. The crystal structure (and its depiction in FIG. 17) reveals that the EGFa domain of LDLR binds to the catalytic domain of PCSK9. In addition, the interaction of PCSK9 and EGFa appears to occur across a surface of PCSK9 that is between residues D374 and S153 in the structure depicted in FIG. 17.

Specific core PCSK9 amino acid residues of the interaction interface with the LDLR EGFa domain were defined as PCSK9 residues that are within 5 Å of the EGFa domain. The core residues are as follows: S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, and S381.

Boundary PCSK9 amino acid residues of the interaction interface with the LDLR EGFa domain were defined as PCSK9 residues that are 5-8 Å from the EGFa domain. The boundary residues are as follows: W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, and Q382. Residues that are underlined are nearly or completely buried within PCSK9.

As will be appreciated by one of skill in the art, the results from this example demonstrate where PCSK9 and EGFa interact. Thus, antibodies that interact with or block any of these residues can be useful as antibodies that inhibit the interaction between PCSK9 and the EGFa domain of LDLR (and/or LDLR generally). In some embodiments, antibodies that, when bound to PCSK9, interact with or block any of the above residues or are within 15-8, 8-5, or 5 angstroms of the above residues are contemplated to provide useful inhibition of PCSK9 binding to LDLR.

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Example 29

31H4 Interacts with Amino Acid Residues from Both the Pro- and Catalytic Domains of PCSK9

The present example presents the crystal structure of full length PCSK9 (N533A mutant of SEQ ID NO: 3) bound to the Fab fragment of 31H4, determined to 2.3 Å resolution (the conditions for which are described in the below Examples).
10 This structure, depicted in FIGS. 18A and 18B, shows that 31H4 binds to PCSK9 in the region of the catalytic site and makes contacts with amino acid residues from both the pro-domain and catalytic domain.

The depicted structure also allows one to identify specific core PCSK9 amino acid residues for the interaction interface of 15 31H4 with PCSK9. This was defined as residues that are within 5 Å of the 31H4 protein. The core residues are as follows: W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, 20 N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, and G384.

The structures were also used to identify boundary PCSK9 amino acid residues for the interaction interface with 31H4. These residues were PCSK9 residues that were 5-8 Å from the 31H4 protein. The boundary residues are as follows: K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, and 30 Q387. Amino acid residues completely buried within the PCSK9 protein are underlined.

As will be appreciated by one of skill in the art, FIG. 18B depicts the interaction between the CDRs on the antigen binding protein and PCSK9. As such, the model allows one of skill in the art to identify the residues and/or CDRs that are especially important in the paratope, and which residues are less critical to the paratope. As can be seen in FIG. 18B, the heavy chain CDR1, CDR2, and CDR3 are most directly involved in the antigen binding protein's binding to the epitope, with the CDRs from the light chain being relatively far away from the epitope. As such, it is probable that larger variations in the light chain CDRs are possible, without unduly interfering with the binding of the antigen binding protein to PCSK9. In some embodiments, residues in the structures that directly interact are conserved (or alternatively conservatively replaced) while residues that are not directly interacting with one another can be altered to a greater extent. As such, one of skill in the art, given the present teachings, can predict which residues and areas of the antigen binding proteins can be varied without unduly interfering with the antigen binding protein's ability to bind to PCSK9. For example, those residues that are located closest to PCSK9 when the antigen binding protein is bound to PCSK9 are those that likely play a more important role in the binding of the antigen binding protein to PCSK9. As above, these residues can be divided into those that are within 5 angstroms of PCSK9 and those that are between 5 and 8 angstroms. Specific core 31H4 amino acid residues of the interaction interface with PCSK9 were defined as 31H4 residues that are within 5 Å of the PCSK9 protein. For the heavy chain, the residues that are within 5 angstroms include the following: T28, S30, S31, Y32, S54, S55, S56, Y57, I58, S59, Y60, N74, A75, R98, Y100, F102, W103, S104, A105, Y106, Y107, D108, A109, and D111. For the light chain, those residues that are within 5 angstroms include the following: L48, S51, Y93, and S98. For the heavy chain, those residues that are 5-8 Å from the PCSK9 protein include the following: G26, F27, F29, W47, S50, I51,

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S52, S53, K65, F68, T69, I70, S71, R72, D73, K76, N77, D99, D101, F110, and V112. For the light chain, those residues that are within 5-8 angstroms of PCSK9 include A31, G32, Y33, D34, H36, Y38, I50, G52, N55, R56, P57, S58, D94, S95, S96, L97, G99, and S100.

As will be appreciated by one of skill in the art, the results from Example 29 demonstrate where antibodies to PCSK9 can interact on PCSK9 and still block PCSK9 from interacting with EGFa (and thus LDLR). Thus, antigen binding proteins that interact with any of these PCSK9 residues, or that block any of these residues (e.g., from other antigen binding proteins that bind to these residues), can be useful as antibodies that inhibit the interaction of PCSK9 and EGFa (and LDLR accordingly). Thus, in some embodiments, antigen binding proteins that interact with any of the above residues or interact with residues that are within 5 Å of the above residues are contemplated to provide useful inhibition PCSK9 binding to LDLR. Similarly, antigen binding proteins that block any of the above residues (which can be determined, for example, via a competition assay) can also be useful for inhibition of the PCSK9/LDLR interaction.

Example 30

21B12 Binds to the Catalytic Domain of PCSK9, has a Distinct Binding Site from 31H4 and can Bind to PCSK9 Simultaneously with 31H4

The present example presents the crystal structure of PCSK9 ProCat (31-449 of SEQ ID NO: 3) bound to the Fab fragments of 31H4 and 21B12, determined at 2.8 Å resolution (the conditions for which are described in the below Examples). This crystal structure, depicted in FIG. 19A and FIG. 19B, shows that 31H4 and 21B12 have distinct binding sites on PCSK9 and that both antigen binding proteins can bind to PCSK9 simultaneously. The structure shows that 21B12 interacts with amino acid residues from PCSK9's catalytic domain. In this structure, the interaction between PCSK9 and 31H4 is similar to what was observed above.

Specific core PCSK9 amino acid residues of the interaction interface with 21B12 were defined as PCSK9 residues that are within 5 Å of the 21B12 protein. The core residues are as follows: S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, and F379.

Boundary PCSK9 amino acid residues of the interaction interface with 21B12 were defined as PCSK9 residues that were 5-8 Å from the 21B12 protein. The boundary residues are as follows: 1154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, and C378. Amino acid residues nearly or completely buried within the PCSK9 protein are underlined.

As will be appreciated by one of skill in the art, FIG. 19B depicts the interaction between the CDRs on the antigen binding protein and PCSK9. As such, the model allows one of skill in the art to identify the residues and/or CDRs which are especially important for the paratope and which residues are less critical to the paratope. As can be seen in the structure, heavy chain CDR2 and light chain CDR1 appear to closely interact with the epitope. Next, heavy chain CDR1, heavy chain CDR3 and light chain CDR3, appear to be close to the epitope, but not as close as the first set of CDRs. Finally, light chain CDR2 appears to be some distance from the epitope. As such, it is probable that larger variations in the more distant CDRs are possible without unduly interfering with the binding of the antigen binding protein to PCSK9. In some embodiments, residues in the structures that directly interact are

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conserved (or alternatively conservatively replaced) while residues that are not directly interacting with one another can be altered to a greater extent. As such, one of skill in the art, given the present teachings, can predict which residues and areas of the antigen binding proteins can be varied without unduly interfering with the antigen binding protein's ability to bind to PCSK9. For example, those residues that are located closest to PCSK9 when the antigen binding protein is bound to PCSK9 are those that likely play a more important role in the binding of the antigen binding protein to PCSK9. As above, these residues can be divided into those that are within 5 angstroms of PCSK9 and those that are between 5 and 8 angstroms. Specific core 21B12 amino acid residues of the interaction interface with PCSK9 were defined as 21B12 residues that are within 5 Å of the PCSK9 protein. For the heavy chain, the residues that are within 5 angstroms include the following: T30, S31, Y32, G33, W50, S52, F53, Y54, N55, N57, N59, R98, G99, Y100, and G101. For the light chain, those residues that are within 5 angstroms include the following: G30, G31, Y32, N33, S34, E52, Y93, T94, S95, T96, and S97. For the heavy chain, those residues that are 5-8 Å from the PCSK9 protein include the following: T28, L29, I34, S35, W47, V51, G56, T58, Y60, T72, M102, and D103. For the light chain, those residues that are within 5-8 angstroms of PCSK9 include the following: S26, V29, V35, Y51, N55, S92, M98, and V99.

As will be appreciated by one of skill in the art, the results from Example 30 demonstrate where antigen binding proteins to PCSK9 can interact on PCSK9 and still block PCSK9 from interacting with EGFa (and thus LDLR). Thus, antigen binding proteins that interact with any of these PCSK9 residues or that block any of these residues can be useful as antibodies that inhibit the interaction of PCSK9 and EGFa (and LDLR accordingly). Thus, in some embodiments, antibodies that interact with any of the above residues or interact with residues that are within 5 Å of the above residues are contemplated to provide useful inhibition PCSK9 binding to LDLR. Similarly, antigen binding proteins that block any of the above residues (which can be determined, for example, via a competition assay) can also be useful for inhibition of the PCSK9/LDLR interaction.

Example 31

Interaction between EGFa, PCSK9, and the Antibodies

The structure of the ternary complex (PCSK9/31H4/21B12) from the above example was overlaid on the PCSK9/EGFa structure (determined as described in Example 28) and the result of this combination is depicted in FIG. 20A. This figure demonstrates areas on PCSK9 which can be usefully targeted to inhibit PCSK9 interaction with EGFa. The figure shows that both 31H4 and 21B12 partially overlap with the position of the EGFa domain of LDLR and sterically interfere with its binding to PCSK9. In addition, as can be seen in the structures, 21B12 directly interacts with a subset of amino acid residues that are specifically involved in binding to the LDLR EGFa domain.

As noted above, analysis of the crystal structures identified specific amino acids involved in the interaction between PCSK9 and the partner proteins (the core and boundary regions of the interface on the PCSK9 surface) and the spatial requirements of these partner proteins to interact with PCSK9. The structures suggest ways to inhibit the interaction between and the LDLR. First, as noted above, binding an agent to PCSK9 where it shares residues in common with the

binding site of the EGFa domain of the LDLR would inhibit the interaction between PCSK9 and the LDLR. Second, an agent that binds outside of the residues in common can sterically interfere with the EGFa domain or regions of the LDLR that are either N- or C-terminal to the EGFa domain to prevent the interaction between PCSK9 and the LDLR.

In some embodiments, the residues that are involved in both EGFa binding and are close to the areas where the above noted antigen binding proteins bind are especially useful for manipulating PCSK9 binding to LDLR. For example, amino acid residues from interfaces in common in both the core region and boundary region for the different binding partners are listed in Table 12 below. Amino acid residues completely buried within the PCSK9 protein are underlined.

TABLE 12

Parameters	Amino acid position(s)
31H4/EGFa both under 5 Å	D374, V380, S381
31H4 under 5 Å/EGFa 5-8 Å	D367, Q382
31H4 at 5-8 Å/EGFa under 5 Å	I369, S372, C378, F379
31H4/EGFa both at 5-8 Å	<u>H</u> 229, S373
21B12/EGFa both under 5 Å	S153, R194, D238, D374, T377, F379
21B12 under 5 Å/EGFa 5-8 Å	R237, K243, S373, S376
21B12 at 5-8 Å/EGFa under 5 Å	I154, A239, I369, S372, C375, C378
21B12/EGFa both at 5-8 Å	H193, E195

As will be appreciated by one of skill in the art, in some embodiments, the antigen binding proteins bind to and/or block at least one of the above noted residues.

Example 32

Structural Interaction of LDLR and PCSK9

A model of full length PCSK9 bound to a full length representation of the LDLR was made using the PCSK9 ProCat (31-454 of SEQ ID NO: 3)/EGFa complex structure. The structure of full length PCSK9¹ (Piper, D. E. et al. The crystal structure of PCSK9: a regulator of plasma LDL-cholesterol. *Structure* 15, 545-52 (2007)) was overlaid onto the PCSK9 ProCat 31-454 from the complex and the structure of the LDLR in its low pH conformation (Rudenko, G. et al. Structure of the LDL receptor extracellular domain at endosomal pH. *Science* 298, 2353-8 (2002)) was overlaid onto the EGFa domain from the complex. Depictions of the model are shown in FIGS. 20B and 20C. The EGFa domain is indicated by the box in the figure. The figures show regions of the LDLR outside of the immediate EGFa binding domain that lie in close proximity to PCSK9. FIGS. 20D-20F show the above interaction, along with mesh surface representations of antibody 31H4 and 21B12 from three different angles. As is clear from the depictions, not only can the antibody interact and/or interfere with LDLR's interaction with PCSK9 at the actual binding site, but other steric interactions appear to occur as well.

In light of the above results, it is clear that antigen binding proteins that bind to PCSK9 can also inhibit the interaction between PCSK9 and the LDLR by clashing with various regions of the LDLR (not just the site at which LDLR and PCSK9 interact). For example, it can clash with repeat 7 (R7), the EGFB domain, and/or the β-propeller domain.

Embodiments of Antigen Binding Molecules that Bind to or Block EGFa Interaction with PCSK9

As will be appreciated by one of skill in the art, Examples 28-32, and their accompanying figures, provide a detailed

description of how and where EGFa interacts with PCSK9 and how two representative neutralizing antigen binding proteins, 21B12 and 31H4 interact with PCSK9 and produce their neutralizing effect. As such, one of skill in the art will readily be able to identify antigen binding molecules that can similarly reduce the binding between EGFa (including LDLR) and PCSK9 by identifying other antigen binding molecules that bind at or near at least one of the same locations on PCSK9. While the relevant locations (or epitopes) on PCSK9 are identified in the figures and the present description, it can also be advantageous to describe these sites as being within a set distance from residues that have been identified as close to the EGFa binding site. In some embodiments, an antigen binding molecule will bind to or within 30 angstroms of one or more of the following residues (numbering in reference to SEQ ID NO: 3): S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, Q382, W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, G384, K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, Q387, S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, F379, I154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, or C378. In some embodiments, the antigen binding molecule binds within 30 angstroms of one or more of the following residues (numbering in reference to SEQ ID NO: 3): S153, I154, P155, R194, D238, A239, I369, S372, D374, C375, T377, C378, F379, V380, S381, W156, N157, L158, E159, H193, E195, H229, R237, G240, K243, D367, I368, G370, A371, S373, S376, or Q382. In some embodiments, the antigen binding molecule binds within 30 angstroms of one or more of the following residues (numbering in reference to SEQ ID NO: 3): W72, F150, A151, Q152, T214, R215, F216, H217, A220, S221, K222, S225, H226, C255, Q256, G257, K258, N317, F318, T347, L348, G349, T350, L351, E366, D367, D374, V380, S381, Q382, S383, G384, K69, D70, P71, S148, V149, D186, T187, E211, D212, G213, R218, Q219, C223, D224, G227, H229, L253, N254, G259, P288, A290, G291, G316, R319, Y325, V346, G352, T353, G365, I368, I369, S372, S373, C378, F379, T385, S386, or Q387. In some embodiments, the antigen binding molecule binds within 30 angstroms of one or more of the following residues (numbering in reference to SEQ ID NO: 3): S153, S188, I189, Q190, S191, D192, R194, E197, G198, R199, V200, D224, R237, D238, K243, S373, D374, S376, T377, F379, I154, T187, H193, E195, I196, M201, V202, C223, T228, S235, G236, A239, G244, M247, I369, S372, C375, or C378. In some embodiments, the antigen binding molecule binds within 30, 30-25, 25-20, 20-15, 15-8, 8, 8-5, 5, 5-4, 4 or less angstroms from one or more of the above residues. In some embodiments, the antigen binding molecule, when bound to PCSK9, is within at least one of the above distances, for more than one of the above noted residues. For example, in some embodiments, the antigen binding molecule is within one of the recited distances (e.g., 30, 30-25, 25-20, 20-15, 15-8, 8, 8-5, 5, 5-4, 4 or less) for at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50, 50-55, 55-60, 60-65, 65-70, 70-75 or more of the above residues. In some embodiments, the antigen bind-

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ing molecule is within one of the recited distances for at least 1-10, 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, 90-95, 95-99, 99-100% of the residues identified in each group of subgroup thereof (such as only those surface residues in the group). Unless specifically stated otherwise, the distance between the antigen binding molecule and PCSK9 is the shortest distance between the covalently bonded atom on PCSK9 and the covalently bonded atom of the antigen binding molecule that are the closest atoms of PCSK9 and the antigen binding molecule. Similarly, unless specifically stated otherwise, the distance between a residue (on the antigen binding molecule or PCSK9) and another protein (either PCSK9 or the antigen binding molecule respectively), is the distance from the closest point on the identified residue to the closest covalently bonded part of the other protein. In some embodiments, the distance can be measured from the backbone of the amino acid chains. In some embodiments, the distance can be measured between an edge of the paratope and an edge (closest to one another) of the epitope. In some embodiments, the distance can be measured between the center of the surface of the paratope and the center of the surface of the epitope. As will be appreciated by one of skill in the art, the present description is applicable for each of the individual sets of residues listed herein. For example, the above ranges are contemplated generally and specifically for the 8 angstrom residues listed in Examples 28-32 and the 5 angstrom residues listed in Examples 28-32.

In some embodiments, the antigen binding molecule binds to a surface on PCSK9 that is bound by at least one of EGFa, 21B12, or 31H4. In some embodiments, the antigen binding molecule binds to PCSK9 at a location that overlaps with the interaction locations between PCSK9 and EFGa, Ab 31H4, and/or Ab 21B12 (as described in the above examples and figures). In some embodiments, the antigen binding molecule binds to PCSK9 at a position that is further away from one of the above recited residues. In some embodiments, such an antigen binding molecule can still be an effective neutralizing antigen binding molecule.

In some embodiments, the structure of the catalytic domain of PCSK9 can be described as generally being triangular (as shown in FIG. 19A). The first side of the triangle is shown as being bound by 31H4. The second side of the triangle is shown as being bound by 21B12, and the third side of the triangle is positioned toward the bottom of the page, immediately above the "FIG. 19A" label. In some embodiments, antigen binding molecules that bind to the first and/or second sides of the catalytic domain of PCSK9 can be useful as neutralizing antibodies as they can either directly or sterically interfere with EGFa's binding to PCSK9. As will be appreciated by one of skill in the art, when the antigen binding molecules are large enough, such as a full antibody, the antigen binding molecule need not directly bind to the EGFa binding site in order to interfere with the binding of EGFa to PCSK9.

As will be appreciated by one of skill in the art, while the EGFa domain of the LDLR has been used in many of the examples, the models and structures are still applicable to how the full length LDLR protein will interact with PCSK9. Indeed, the additional structure present on the full length LDLR protein presents additional protein space that can further be blocked by one of the antigen binding molecules. As such, if the antigen binding molecule blocks or inhibits binding of EGFa to PCSK9, it will likely be at least as, if not more, effective with the full length LDLR protein. Similarly, antigen binding molecules that are within a set distance or block

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various residues that are relevant for inhibiting EGFa binding, will likely be as effective, if not more effective, for the full length LDLR.

As will be appreciated by one of skill in the art, any molecule that blocks or binds to the above noted PCSK9 residues (or within the recited distances), or that inhibits one or more of the interactions noted in the above examples and figures, can be used to inhibit the interaction of EGFa (or LDLR generally) and PCSK9. As such, the molecule need not be limited to an antigen binding "protein," as any antigen binding molecule can also serve the required purpose. Examples of antigen binding molecules include aptamers, which can be either oligonucleic acid or peptide molecules. Other examples of antigen binding molecules include avimers, peptides, small molecules and polymers, and modified versions of EGFa that can increase its affinity to PCSK9 and/or half-life, such as mutation of amino acids, glycosylation, pegylation, Fc fusions, and avimer fusions. As will be appreciated by one of skill in the art, in some embodiments LDLR is not an antigen binding molecule. In some embodiments, binding subsections of LDLR are not antigen binding molecules, e.g., EGFa. In some embodiments, other molecules through which PCSK9 signals in vivo are not antigen binding molecules. Such embodiments will be explicitly identified as such.

Example 33

Expression and Purification of Protein Samples

The present example describes some embodiments for how the various embodiments of the PCSK9 proteins/variants were made and purified (including the LDLR EGFa domain). PCSK9 proteins/variants (e.g., PCSK9 31-692 N533A, PCSK9 449TEV and PCSK9 ProCat 31-454) were expressed in baculovirus infected Hi-5 insect cells with an N-terminal honeybee melittin signal peptide followed by a His₆ tag. The PCSK9 proteins were purified by nickel affinity chromatography, ion exchange chromatography and size exclusion chromatography. The melittin-His₆ tag was removed during purification by cleavage with TEV protease. The construct PCSK9 449TEV was used to generate PCSK9 ProCat (31-449) and V domain (450-692) samples. This construct had a TEV protease cleavage site inserted between PCSK9 residues 449 and 450. For the full length N555A variant for crystallography, the PCSK9 31-454 fragment, and the PCSK9 449TEV variant for crystallography, the post rTEV protein product also included an initial GAMG sequence. Thus, post rTEV cleavage, these proteins were GAMG-PCSK9. Furthermore, the PCSK9 449TEV protein included the sequence "ENLYFQ" (SEQ ID NO: 403) inserted between positions H449 and G450 of SEQ ID NO: 3. After cleavage with rTEV, the PCSK9 ProCat protein generated from this construct was GAMG-PCSK9 (31-449)-ENLYFQ and the V domain generated from this construct was PCSK9 (450-692) of SEQ ID NO: 3.

The 21B12 and 31H4Fab fragments were expressed in *E. coli*. These proteins were purified by nickel affinity chromatography, size exclusion chromatography and ion exchange chromatography.

The LDLR EGFa domain (293-334) was expressed as a GST fusion protein in *E. coli*. The EGFa domain was purified by ion exchange chromatography, glutathione sepharose affinity chromatography and size exclusion chromatography.

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The GST protein was removed during the purification by cleavage with PreScission protease.

Example 34

Complex Formation and Crystallization

The present example describes how complexes and crystals used in the above structure examination Examples were made.

The PCSK9 31-692 N533A/31H4 complex was made by mixing a 1.5 molar excess of the 31H₄Fab with PCSK9. The complex was purified by size exclusion chromatography to remove excess 31H₄Fab. The PCSK9 31-692 N533A/31H4 complex crystallizes in 0.1 M Tris pH 8.3, 0.2 M sodium acetate, 15% PEG 4000, 6% dextran sulfate sodium salt (Mr 5000).

The PCSK9 ProCat 31-449/31H4/21B12 complex was made by first mixing a 1.5 molar excess of 31H₄Fab with PCSK9 31-449. The complex was separated from excess 31H4 by purification on a size exclusion chromatography column. A 1.5 molar excess of 21B12 Fab was then added to the PCSK9 31-449/31H4 complex. The ternary complex was separated from excess 21B12 by purification on a size exclusion chromatography column. The PCSK9 ProCat 31-449/ 15 31H4/21B12 complex crystallizes in 0.1 M Tris pH 8.5, 0.2 M ammonium phosphate monobasic, 50% MPD.

The PCSK9 ProCat 31-454/EGFa complex was made by mixing a 1.2 molar excess of EGFa domain with PCSK9 31-454. The PCSK9 ProCat 31-454/EGFa domain complex crystallizes in 0.2 M potassium formate, 20% PEG 3350.

Example 35

Data Collection and Structure Determination

The present example describes how the datasets were collected and the structures determined for the above structure examination Examples.

Initial datasets for the PCSK9 31-692 N533A/31H4 and PCSK9 ProCat 31-449/31H4/21B12 crystals were collected on a Rigaku FR-E X-ray source. The PCSK9 ProCat 31-454/ EGFa dataset and higher resolution datasets for the PCSK9 31-692 N533A/31H4 and PCSK9 ProCat 31-449/31H4/ 25 21B12 crystals were collected at the Berkeley Advanced Light Source beamline 5.0.2. All datasets were processed with denzo/scalepack or HKL2000 (Otwinowski, Z., Borek, D., Majewski, W. & Minor, W. Multiparametric scaling of diffraction intensities. *Acta Crystallogr A* 59, 228-34 (2003)).

PCSK9/31H4 crystals grew in the C2 space group with unit cell dimensions a=264.9, b=137.4, c=69.9 Å, β=102.8° and diffract to 2.3 Å resolution. The PCSK9/31H4 structure was solved by molecular replacement with the program MOLREP (The CCP4 suite: programs for protein crystallography. *Acta Crystallogr D Biol Crystallogr* 50, 760-3 (1994) using the PCSK9 structure (Piper, D. E. et al. The crystal structure of PCSK9: a regulator of plasma LDL-cholesterol. *Structure* 15, 545-52 (2007)) as the starting search model. Keeping the PCSK9 31-692 solution fixed, an antibody variable domain was used as a search model. Keeping the PCSK9 31-692/ antibody variable domain solution fixed, an antibody constant domain was used as a search model. The complete structure was improved with multiple rounds of model building with Quanta and refinement with cnx. (Brunger, A. T. et al. Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr D Biol Crystallogr* 54, 905-21 (1998)).

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PCSK9/31H4/21B12 crystals grew in the P2₁2₁2 space group with unit cell dimensions a=138.7, b=246.2, c=51.3 Å and diffract to 2.8 Å resolution. The PCSK9/31H4/21B12 structure was solved by molecular replacement with the program MOLREP using the PCSK9 ProCat/31H4 variable domain as the starting search model. Keeping the PCSK9 ProCat 31H4 variable domain fixed, a search for antibody constant domain was performed. Keeping the PCSK9 ProCat/ 5 31H4/21B12 constant domain fixed, an antibody variable domain was used as a search model. The complete structure was improved with multiple rounds of model building with Quanta and refinement with cnx.

PCSK9/EGFa domain crystals grew in the space group P6₃22 with unit cell dimensions a=b=70.6, c=321.8 Å and diffract to 2.9 Å resolution. The PCSK9/EGFa domain structure was solved by molecular replacement with the program MOLREP using the PCSK9 ProCat as the starting search model. Analysis of the electron density maps showed clear electron density for the EGFa domain. The LDLR EGFa domain was fit by hand and the model was improved with multiple rounds of model building with Quanta and refinement with cnx.

Core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the PCSK9 partner protein. 5 Å was chosen as the core region cutoff distance to allow for atoms within a van der Waals radius plus a possible water-mediated hydrogen bond. Boundary interaction interface amino acids were determined as all amino acid residues with at least one atom less than or equal to 8 Å from the PCSK9 partner protein but not included in the core interaction list. Less than or equal to 8 Å was chosen as the boundary region cutoff distance to allow for the length of an extended arginine amino acid. Amino acids that met these distance criteria were calculated 20 with the program PyMOL. (DeLano, W. L. The PyMOL Molecular Graphics System. (Palo Alto, 2002)).

Example 36

Cyrstal Structure of PCSK9 and 31A4

The crystal structure of the 31A4/PCSK9 complex was determined.

Expression and Purification of Protein Samples

PCSK9 449TEV (a PCSK9 construct with a TEV protease cleavage site inserted between residue 449 and 450, numbering according to SEQ ID NO: 3) was expressed in baculovirus infected Hi-5 insect cells with an N-terminal honeybee melittin signal peptide followed by a His₆ tag. The PCSK9 protein was purified by first by nickel affinity chromatography. TEV protease was used to remove the melittin-His₆ tag and cleave the PCSK9 protein between the catalytic domain and V domain. The V domain was further purified by ion exchange chromatography and size exclusion chromatography. The 55 31A4 Fab fragment was expressed in *E. coli*. This protein was purified by nickel affinity chromatography, size exclusion chromatography and ion exchange chromatography.

Complex Formation and Crystallization

The PCSK9 V domain/31A4 complex was made by mixing a 1.5 molar excess of PCSK9 V domain with 31A4 Fab. The complex was separated from excess PCSK9 V domain by purification on a size exclusion chromatography column. The PCSK9 V domain/31A4 complex crystallized in 1.1 M Succinic acid pH 7, 2% PEG MME 2000.

Data Collection and Structure Determination

The dataset for the PCSK9 V domain/31A4 crystal was collected on a Rigaku FR-E x-ray source and processed with

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denzo/scalepack (Otwinowski, Z., Borek, D., Majewski, W. & Minor, W. Multiparametric scaling of diffraction intensities. *Acta Crystallogr A* 59, 228-34 (2003)).

PCSK9 V domain/31A4 crystals grow in the P₂1₂1₂, space group with unit cell dimensions a=74.6, b=131.1, c=197.9 Å with two complex molecules per asymmetric unit, and diffract to 2.2 Å resolution. The PCSK9 V domain/31A4 structure was solved by molecular replacement with the program MOLREP (CCP4). The CCP4 suite: programs for protein crystallography. *Acta Crystallogr D Biol Crystallogr* 50, 760-3 (1994) using the V domain of the PCSK9 structure (Piper, D. E. et al. The crystal structure of PCSK9: a regulator of plasma LDL-cholesterol. *Structure* 15, 545-52 (2007)) as the starting search model. Keeping the PCSK9 450-692 solution fixed, an antibody variable domain was used as a search model. After initial refinement, the antibody constant domains were fit by hand. The complete structure was improved with multiple rounds of model building with Quanta and refinement with cnx (Brunger, A. T. et al. Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr D Biol Crystallogr* 54, 905-21 (1998)).

Core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the PCSK9 partner protein. 5 Å was chosen as the core region cutoff distance to allow for atoms within a van der Waals radius plus a possible water-mediated hydrogen bond. Boundary interaction interface amino acids were determined as all amino acid residues with at least one atom less than or equal to 8 Å from the PCSK9 partner protein but not included in the core interaction list. Less than or equal to 8 Å was chosen as the boundary region cutoff distance to allow for the length of an extended arginine amino acid. Amino acids that met these distance criteria were calculated with the program PyMOL (DeLano, W. L. The PyMOL Molecular Graphics System. (Palo Alto, 2002)). Distances were calculated using the V domain "A" and 31A4 "L1,H1" complex.

The crystal structure of the PCSK9 V domain bound to the Fab fragment of 31A4 was determined at 2.2 Å resolution. The depictions of the crystal structure are provided in FIGS. 21A-21D. FIGS. 21A-21C shows that the 31A4 Fab binds to the PCSK9 V domain in the region of subdomains 1 and 2.

A model of full length PCSK9 bound the 31A4 Fab was made. The structure of full length PCSK9 was overlaid onto the PCSK9 V domain from the complex. A figure of this model is shown in FIG. 21D. The site of the interaction between the EGFa domain of the LDLR and PCSK9 is highlighted.

Analysis of the structure shows where this antibody interacts with PCSK9 and demonstrated that antibodies that do not bind to the LDLR binding surface of PCSK9 can still inhibit the degradation of LDLR that is mediated through PCSK9 (when the results are viewed in combination with Example 40 and 41 below). In addition, analysis of the crystal structure allows for identification of specific amino acids involved in the interaction between PCSK9 and the 31A4 antibody. Furthermore, the core and boundary regions of the interface on the PCSK9 surface were also determined. Specific core PCSK9 amino acid residues of the interaction interface with 31A4 were defined as PCSK9 residues that are within 5 Å of the 31A4 protein. The core residues are T468, R469, M470, A471, T472, R496, R499, E501, A502, Q503, R510, H512, F515, P540, P541, A542, E543, H565, W566, E567, V568, E569, R592, and E593. Boundary PCSK9 amino acid residues of the interaction interface with 31A4 were defined as PCSK9 residues that are 5-8 Å from the 31A4 protein. The

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boundary residues are as follows: S465, G466, P467, A473, I474, R476, G497, E498, M500, G504, K506, L507, V508, A511, N513, A514, G516, V536, T538, A539, A544, T548, D570, L571, H591, A594, S595, and H597. Amino acid residues nearly or completely buried within the PCSK9 protein are highlighted by underline. As noted herein, the numbering references the amino acid positions of SEQ ID NO: 3 (adjusted as noted herein).

Specific core 31A4 amino acid residues of the interaction interface with PCSK9 were defined as 31A4 residues that are within 5 Å of the PCSK9 protein. The core residues for the 31A4 antibody are as follows: Heavy Chain: G27, S28, F29, S30, A31, Y32, Y33, E50, N52, H53, R56, D58, K76, G98, Q99, L100, and V101; Light Chain: S31, N32, T33, Y50, S51, N52, N53, Q54, W92, and D94. Boundary 31A4 amino acid residues of the interaction interface with PCSK9 were defined as 31A4 residues that are 5-8 Å from the PCSK9 protein. The boundary residues for 31A4 are as follows: Heavy Chain: V2, G26, W34, N35, W47, I51, S54, T57, Y59, A96, R97, P102, F103, and D104; Light Chain: S26, S27, N28, G30, V34, N35, R55, P56, K67, V91, D93, S95, N97, G98, and W99.

The crystal structure also displayed the spatial requirements of this ABP in its interaction with PCSK9. As shown in this structure, surprisingly, antibodies that bind to PCSK9 without directly preventing PCSK9's interaction with the LDLR can still inhibit PCSK9's function.

In some embodiments, any antigen binding protein that binds to, covers, or prevents 31A4 from interacting with any of the above residues can be employed to bind to or neutralize PCSK9. In some embodiments, the ABP binds to or interacts with at least one of the following PCSK9 (SEQ ID NO: 3) residues: T468, R469, M470, A471, T472, R496, R499, E501, A502, Q503, R510, H512, F515, P540, P541, A542, E543, H565, W566, E567, V568, E569, R592, and E593. In some embodiments, the ABP is within 5 angstroms of one or more of the above residues. In some embodiments, the ABP binds to or interacts with at least one of the following PCSK9 (SEQ ID NO: 3) residues: S465, G466, P467, A473, 1474, R476, G497, E498, M500, G504, K506, L507, V508, A511, N513, A514, G516, V536, T538, A539, A544, T548, D570, L571, H591, A594, S595, and H597. In some embodiments, the ABP is 5 to 8 angstroms from one or more of the above residues. In some embodiments, the ABP interacts, blocks, or is within 8 angstroms of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, I1, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, or 50 of the above residues.

The coordinates for the crystal structures discussed in the above Examples are presented in Table 35.1 (full length PCSK9 and 31H4), Table 35.2 (PCSK9 and EGFa), Table 35.3 (PCSK9, 31H4, and 21B12), and Table 35.4 (PCSK9 and 31A4). Antigen binding proteins and molecules that interact with the relevant areas or residues of the structure of PCSK9 (including those areas or residues within 15, 15-8, 8, 8-5, 5, or fewer angstroms from where EGFa, or the antibodies, interact with PCSK9) depicted in the figures and/or their corresponding positions on the structures from the coordinates are also contemplated.

The antibodies that are described in the coordinates were raised in *E. coli* and thus possess some minor amino acid differences from the fully human antibodies. The first residue in the variable region was a glutamic acid instead of a glutamine for the heavy and light chains of 21B12 and for the light chain for 31H4. In addition to the differences in the sequence of variable region, there were also some differences in the constant region of the antibodies described by the coordinates (again due to the fact that the antibody was raised in *E. coli*). FIG. 22 highlights (via underlining shading, or bold) the differences between the constant regions of the

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21B12, 31H4, and 31A4 Fabs (raised in *E. coli*) when compared to SEQ ID NOs: 156, and 155. For 21B12 31H4, and 31A4, the light chain constant sequence is similar to human lambda (SEQ ID NO: 156). The underlined glycine residue is an insertion between where the 21B12 and 31H4 variable sequences stop and the lambda sequence starts.

For both 21B12 and 31H4, the heavy chain constant is similar to human IgG4 (SEQ ID NO: 155). The highlighted differences in FIG. 22 are shown in Table 36.1:

TABLE 36.1

CRYSTAL	SEQ ID NO: 155
S	C
K	R
G	E
G	S
Q	K
I	T
N	D
K	R
P	S

In regard to 31A4, while it also has the same distinctions noted above, there are three additional differences. As shown in FIG. 22, there are two additional amino acids at the start, which comes from incomplete processing of the signal peptide in *E. coli* expression. In addition, there is one additional substitution in the 31A4 heavy chain constant region when compared to SEQ ID NO: 155, which is the adjustment of a L (in SEQ ID NO: 155) to a H. Finally, 31A4 does have a glutamine as the initial amino acid of the Fab, rather than the adjustment to glutamic acid noted above for 21B12 and 31H4.

For all three antibodies, the end of the heavy chain (boxed in dark grey) differs as well, but the amino acids are not ordered in the structure so they do not appear in the coordinates. As will be appreciated by one of skill in the art, his-tags are not a required part of the ABP and should not be considered as part of the ABP's sequence, unless explicitly called out by reference to a specific SEQ ID NO that includes a histidine tag and a statement that the ABP sequence "includes the Histidine tag."

Example 37

Epitope Mapping—Binning

An alternative set of binning experiments was conducted in addition to the set in Example 10. As in Example 10, ABPs that compete with each other can be thought of as binding to the same site on the target and in common parlance are said to "bin" together.

A modification of the Multiplexed Binning method described by Jia, et al (J. Immunological Methods, 288 (2004) 91-98) was used. Individual bead codes of streptavidin-coated Luminesex beads was incubated in 100 ul 0.5 ug/ml biotinylated monovalent mouse-anti-human IgG capture antibody (BD Pharmingen, #555785) for 1 hour at room temperature in the dark, then washed 3x with PBSA, phosphate buffered saline (PBS) plus 1% bovine serum albumin

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(BSA). Each bead code was separately incubated with 100 ul 2 ug/ml anti-PCSK9 antibody (Coating Antibody) for 1 hour then washed 3x with PBSA. The beads were pooled then dispensed to a 96-well filter plate (Millipore, #MSBVN1250). 100 ul of 2 ug/ml purified PCSK9 protein was added to half the wells. Buffer was added to the other half as control. The reaction was incubated for 1 hour then washed. 100 ul of a 2 ug/ml anti-PCSK9 antibody (Detection Ab) was added to all the wells, incubated for 1 hour then washed. An irrelevant human-IgG (Jackson, #009-000-003) was run as another control. 20 ul PE-conjugated monovalent mouse-anti-human IgG (BD Pharmingen, #555787) was added to each well and incubated for 1 hour then washed. Beads were resuspended in 100 ul PBSA and a minimum of 100 events/bead code were collected on the BioPlex instrument (BioRad).

Median Fluorescent Intensity (MFI) of the antibody pair without PCSK9 was subtracted from signal of the corresponding reaction containing PCSK9. For the antibody pair to be considered bound simultaneously, and therefore in different bins, the subtracted signal had to be greater than 3 times the signal of the antibody competing with itself and the 3 times the signal of the antibody competing with the irrelevant antibody.

The data from the above is depicted in FIGS. 23A-23D. The ABPs fell into five bins. The shaded boxes indicate ABPs that can bind simultaneously to PCSK9. The nonshaded boxes indicate those ABPs that compete with each other for binding. A summary of the results is shown in Table 37.1.

TABLE 37.1

BIN 1	BIN 2	BIN 3	BIN 4	BIN 5
01A12.2	27B2.1	16F12.1	11G1.5	30A4.1
03B6.1	27B2.5	22E2.1	03C4.1	13B5.1
09C9.1	12H11.1	27A6.1		13H1.1
17C2.1		28B12.1		31A4.1
21B12.2		28D6.1		31B12.1
23G1.1		31G11.1		
25G4.1		31H4.1		
26E10.1		08A1.2		
11H4.1		08A3.1		
11H8.1		11F1.1		
19H9.2				
26H5.1				
27E7.1				
27H5.1				
30B9.1				
02B5.1				
23B5.1				
27B2.6				
09H6.1				

50 Bins 1 (competes with ABP 21B12) and 3 (competes with 31H4) are exclusive of each other; bin 2 competes with bins 1 and 3; and Bin 4 does not compete with bins 1 and 3. Bin 5, in this example, is presented as a "catch all" bin to describe those 55 ABPs that do not fit into the other bins. Thus, the above identified ABPs in each of the bins are representative of different types of epitope locations on PCSK9, some of which overlap with each other.

As will be appreciated by one of skill in the art, if the 60 reference ABP prevents the binding of the probe ABP then the antibodies are said to be in the same bin. The order in which the ABPs are employed can be important. If ABP A is employed as the reference ABP and blocks the binding of ABP B the converse is not always true: ABP B used as the 65 reference ABP will not necessarily block ABP A. There are a number of factors in play here: the binding of an ABP can cause conformational changes in the target which prevent the

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binding of the second ABP, or epitopes which overlap but do not completely occlude each other may allow for the second ABP to still have enough high-affinity interactions with the target to allow binding. ABPs with a much higher affinity may have a greater ability to bump a blocking ABP out of the way. In general, if competition is observed in either order the ABPs are said to bin together, and if both ABPs can block each other then it is likely that the epitopes overlap more completely.

Example 38

Epitope Mapping—Western Blot

The present example demonstrates whether or not the epitopes for the examined ABPs were linear or conformational. Denaturing reducing and denaturing non-reducing western blots were run to determine which antibodies have a conformational epitope. Antibodies that bind to a denaturing reducing western blot have a linear epitope and are not conformational. The results are presented in FIG. 24A and FIG. 24B. For the blot, 0.5 ug/lane of purified full-length human PCSK9 was run on a 4-12% NuPAGE Bis-Tris gel and MES SDS Running Buffer. 1 ug/ml anti-PCSK9 antibodies, except 0.5 ug/ml 31G11, were used to probe the blot. 1:5000 donkey-anti-human-IR700 secondary was used and read on a LiCOR instrument. Antibody 13H1 bound to a linear epitope on the pro-domain of PCSK9. All other antibodies displayed results that were consistent with conformational epitopes. These gels split apart the pro-domain from the rest of the protein, and the pro domain ran at about 15 kDa. In addition, 3C4 and 31A4 appeared to bind to conformational epitopes which were preserved by disulfide bonds, as these antibodies bound to PCSK-9 under denaturing conditions where the disulfide bonds had been preserved (left) but reducing the samples (right) eliminated binding.

Example 39

Epitope Mapping—Arginine/Glutamic Acid Scanning

Representative ABPs from each bin (from Example 37) were selected for further epitope analysis. An arginine/glutamic acid-scanning strategy was performed for mapping ABP binding to PCSK9. By way of background, this method determines if a residue is part of the structural epitope, meaning those residues in the antigen which contact or are buried by the antibody. Arginine and glutamic acid sidechains are charged and bulky and can disrupt antibody binding even if the mutated residue is not directly involved in antibody binding.

Residue Selection

The crystal structure of PCSK9 was used to select the residues to be mutated for epitope mapping. The method used to choose residues to mutate involved both computational mechanisms and interactive structure analysis. The PCSK9 structure contained gaps of missing residues and was missing 30 amino acids in the N—(i.e., the signal sequence) and 10 amino acids in the C-termini. The internal missing residues were modeled onto the structure, but the N- and C-terminal missing residues were not. The solvent exposure ratio for each residue was calculated: the surface area of each residue in the context of the protein (SA1) was divided by the surface area of the residue in a trimer with flanking glycines (SA2) with a conserved backbone structure. Residues with solvent exposure ratio greater than 10% (R10) were selected as well as the 40 missing terminal residues. From these, prolines and

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glycines with positive Φ angles were excluded to reduce the possibility of misfolding. The number of residues to be mutated in the V domain was reduced by using a solvent exposure ratio of 37% along with visual inspection of the entire protein to bring the total number of mutations to 285. Various orientations of the surface of PCSK9 with these various classes identifies are shown in FIG. 25A-25F. In these figures, lightest gray denotes areas that were not selected or were deselected, darker gray denotes those residues selected).

10 Cloning and Expression

Once the residues to be altered were identified, the various residues were altered. Human PCSK9 was cloned into the pTT5 vector with a C-terminal Flag-His tag. Mutants were made from this original construct by site-directed mutagenesis using a QuikChange II kit from Stratagene. Sense and anti-sense oligonucleotides used for mutagenesis were designed using Amgen's MutaGenie software. All PCSK9 constructs were expressed in transiently-transfected 293-6E cells in 24-well plates and re-racked into three 96-well plates 15 with a non-mutated PCSK9 control (wild-type, WT) in each plate. Expression levels and integrity of the recombinant proteins in conditioned media were checked by Western blot. Of the 285 mutants originally selected, 41 failed in cloning or expression. 244 mutants were used for epitope mapping. An alignment of the PCSK9 parent sequence with the 244 mutated residues is shown in FIG. 26. Separate constructs were made containing a single mutation. For the purposes of the epitope sequences and the epitope based inventions involving changes in binding, the 20 sequences are provided in reference to SEQ ID NO: 1 and/or SEQ ID NO: 303. The sequences in FIG. 26 were the sequences used for the present binding epitope studies. One of skill in the art will appreciate that the present results apply to other PCSK9 variants disclosed herein as well (e.g., SEQ 25 ID NO: 1 and 3, as well as the other allelic variants).

Five antibodies, a representative of each bin, were chosen for fine epitope mapping. They were 21B12, 31H4, I2H₁₁, 31A4, 3C4. All conformational epitope antibodies. Three, 21B12, 31H4, and 31A4 were also crystallized with PCSK9, 30 as described above.

Structural and Functional Epitopes

Epitopes can be further defined as structural or functional. Functional epitopes are generally a subset of the structural epitopes and have those residues that directly contribute to the affinity of the interaction (e.g. hydrogen bonds, ionic interactions). Structural epitopes can be thought of as the patch of the target which is covered by the antibody.

The scanning mutagenesis employed was an arginine and glutamic acid scan. These two sidechains were chosen due to their large steric bulk and their charge, which allows mutations that occur in the structural epitope to have a greater effect on antibody binding. Arginine was generally employed except when the WT residue was arginine, and in these cases the residue was mutated to glutamic acid to switch the charge.

55 For the purpose of epitope mapping, a bead-based multiplexed assay was used to measure antibody binding to PCSK9 and PCSK9 mutants simultaneously. Antibody binding to mutants was then compared to its binding to the wild-type in the same well. The variants were split into three groups: Group 1: 81 variants+2 wt controls+1 negative control+1 other PCSK9 supernatant; Group 2: 81 variants+2 wt controls+2 negative controls; and Group 3: 82 variants+2 wt controls+1 negative control.

The assay was run as follows: 85 sets of color-coded streptavidin-coated LumAvidin beads (Luminex) were bound 60 with biotinylated anti-pentaHis antibody (Qiagen, #1019225) for 1 hour at room temperature (RT) then washed three times

in PBS, 1% BSA, 0.1% Tween 20. Each color-coded bead set was then allowed to bind to a PCSK9 mutant, wild-type, or negative control in 150 ul supernatant overnight at 4° C.

The color-coded bead sets, each associated to a specific protein, were washed and pooled. At this point, there were 3 pools of 85 bead sets, one pool for each group of mutants and controls. The beads from each pool were aliquoted to 24 wells (3 columns) of a 96-well filter plate (Millipore, #MSBVN1250). 100 ul of anti-PCSK9 antibodies in 4-fold dilutions were added to nine columns for triplicate points and incubated for 1 hour at RT and washed. 100 ul of 1:200 dilution phycoerythrin (PE)-conjugated anti-human IgG Fc (Jackson Immunoresearch, #109-116-170) was added to each well and incubated for 1 hour at RT and washed.

Beads were resuspended in 1% BSA in PBS, shaken for 10 mins and read on the BioPlex instrument (Bio-Rad). The instrument identifies each bead by its color-code thereby identifying the specific protein associated with the color code. At the same time, it measures the amount of antibody bound to the beads by fluorescence intensity of the PE dye. Antibody binding to each mutant can then be compared directly to its binding to the wild type in the same pool. IL-17R chimera E was used as a negative control. A summary of all of the mutants examined is shown in Table 39.1 (with reference to the sequence numbering used in FIGS. 1A and 26).

ment, all beads were conjugated with the same wild type control protein. Therefore, the difference between beads regions was due to purely B-B variance and was not confounded by difference between wild type and mutant proteins. The titration of antibody was run with twelve replications in different wells.

The objective of this statistical analysis was to estimate the B-B variability of the estimated EC50 of binding curves. The estimated B-B standard deviation (SD) was then used to build the EC50 confidence intervals of wild type and mutant proteins during curve comparison experiments.

A four-parameter logistic model was fitted to the binding data for each bead region. The resulting file, containing curve quality control (QC) results and parameter estimates for top (max), bottom (min), Hillslope (slope), and natural log of EC50 (xmid) of the curves, was used as the raw data for the analysis. B-B variability for each parameter was then estimated by fitting mixed effect model using SAS PROC MIXED procedure. Only curves with "good" QC status were included in the analysis. The final mixed effect model included only residual (i.e. individual bead regions) as random effect. Least squares means (LS-mean) for each parameter were estimated by the mixed effect model as well. B-B SD was calculated by taking square root of B-B variance.

TABLE 39.1

	1	2	3	4	5	6	7	8	9	10	11	12
A	WT PCSK9	Y8R	E18R	P26R	A38R	T56R	A70R	H83R	E102R	L128R	D145R	
B	Q1R	E9R	E19R	E27R	K39R	H57R	Q71R	V84R	L105R	E129R	S148R	
C	E2R	E10R	D20R	G29R	D40R	L58R	A73R	H86R	K106R	R130E	pesk9 supe test	
D	D3R	L11R	G21R	T30R	L44R	Q60R	R74E	K95R	H109R	T132R	IL17R chimera E	
E	E4R	V12R	L22R	T31R	T47R	E62R	R75E	S97R	D111R	D139R	WT PCSK9	
F	D5R	A14R	A23R	A32R	K53R	R63E	Y77R	G98R	A121R	E140R		
G	G6R	L15R	E24R	T33R	E54R	R66E	L78R	D99R	S123R	Y141R		
H	D7R	S17R	A25R	H35R	E55R	R67E	L82R	L101R	W126R	Q142R		
A	WT PCSK9	M171R	E181R	Q189R	K213R	R242E	G251R	L294R	L321R	Q352R	E380R	
B	L149R	V172R	D182R	A190R	G214R	K243R	G262R	A311R	E336R	M368R	R384E	
C	S158R	T173R	G183R	S191R	S216R	S244R	R265E	Q312R	D337R	S371R	IL17R chimera E	
D	Q160R	D174R	T184R	K192R	R221E	Q245R	A269R	D313R	D344R	A372R	IL17R chimera E	
E	S161R	E176R	R185E	S195R	Q226R	L246R	Q272R	Q314R	T347R	E373R	WT PCSK9	
F	D162R	N177R	F186R	H196R	K228R	V247R	R276E	T317R	F349R	E375R		
G	R164E	V178R	H187R	R207E	T230R	Q248R	A277R	L318R	V350R	T377R		
H	E167R	E180R	R188E	D208R	F240R	V250R	R289E	T320R	S351R	L378R		
A	WT PCSK9	N395R	V405R	W423R	R446E	E513R	Q525R	Q554R	Q589R	S632R	A641R	
B	I386R	E396R	N409R	Q424R	D450R	A514R	E537R	N556R	Q591R	T633R	R650E	
C	H387R	A397R	A413R	A433R	A472R	S515R	V538R	K579R	A595R	T634R	R652E	
D	F388R	W398R	S417R	H434R	F485R	M516R	E539R	V580R	E597R	G635R	IL17R chimera E	
E	A390R	E401R	T418R	T438R	G486R	R519E	L541R	K581R	E598R	S636R	WT PCSK9	
F	K391R	D402R	H419R	R439E	E488R	H521R	H544R	E582R	V620R	T637R		
G	D392R	Q403R	G420R	M440R	N503R	H523R	V548R	H583R	R629E	S638R		
H	V393R	R404E	A421R	T442R	T508R	Q524R	R552E	G584R	V631R	E639R		

Bead Variability Study

Before running the epitope mapping binding assay, a validation experiment was conducted to assess the "bead region" to "bead region" (B-B) variability. In the validation experi-

Fold change between LS-mean +2SD and LS-mean -2SD, which represent approximately upper and lower 97.5 percentile of the population, was also calculated. The results are displayed in Table 39.2

TABLE 39.2

Least square mean and bead-to-bead variance estimations						
Assay ID	parname	Ls Mean	B-B Variance	-2SD	+2SD	Fold Change*
PCSK9	max	15000	997719	13002.3	16997.7	1.3
PCSK9	min	162.09	1919.66	74.5	249.7	3.4
PCSK9	slope	0.8549	0.000599	0.8	0.9	1.1
PCSK9	xmid	3.1715	0.002098	3.1	3.3	1.2

*xmid is natural log of the EC50. Fold change for xmid was converted back to original scale.

Identifying Residues in the Structural Epitope

A residue was considered part of the structural epitope (a "hit") when mutating it to arginine or glutamic acid alters antibody binding. This is seen as a shift in the EC50 or a reduction of maximum signal compared to antibody binding to wild type. Statistical analyses of antibody binding curves to wild type and mutants were used to identify statistically significant EC50 shifts. The analysis takes into consideration variation in the assay and curve fitting.

Hit Identification Based on EC50 Comparison

The EC50 and Bmax values were generated from a Weighted 4-Parameter Logistical model fitted to the binding data using S-PLUS with VarPower software (Insightful Corporation, Seattle Wash.). The EC50s of the mutant binding curves and wild type binding curves were compared. Statistically significant differences were identified as hits for further consideration. The curves with "nofit" or "badfit" flags were excluded from the analysis.

The Variations in EC50 Estimates

Two sources of variations were considered in the comparison of EC50 estimates, variation from the curve fit and the bead-bead variation. Wild types and mutants were linked to different beads, hence their difference are confounded with the bead-bead difference (described above). The curve fit variation was estimated by the standard error of the log EC50 estimates. Bead-bead variation was experimentally determined using an experiment where wild type controls were

Multiplicity adjustments were important to control the false positive(s) while conducting a large number of tests simultaneously. Two forms of multiplicity adjustment were implemented for this analysis: family wise error (FWE) control and false discovery rate (FDR) control. The FWE approach controls the probability that one or more hits are not real; FDR approach controls the expected proportion of false positive among the selected hits. The former approach is more conservative and less powerful than the latter one. There are many methods available for both approaches, for this analysis, the Hochberg's (1988) method for FWE analysis and Benjamini-Hochberg's (1995) FDR method for FDR analysis were selected. Adjusted p-values for both approaches were calculated.

Results

EC50 Shift

Mutations whose EC50 is significantly different from wild type, e.g., having a False Discovery Rate adjusted p-value for the whole assay of 0.01 or less, were considered part of the structural epitope. All the hits also had a Familywise type I error rate adjusted p-value for each antibody of less than 0.01 except residue R185E for antibody 31H4 which had an FWE adjusted p-value per antibody of 0.0109. The residues in the structural epitope of the various antibodies determined by EC50 shift are shown in Table 39.3 (point mutations are with reference to SEQ ID NO: 1 and 303)

TABLE 39.3

Antibody	Mutation	FDR.Adjusted.	FWE.Adjusted.	Low99	Low95	FoldChange	High95	High99	RawPval
		Pval	By.Pval						
21B12	D208R	0.0000	0.0000	0.3628	0.3844	0.4602	0.5509	0.5837	0.0000
21B12	R207E	0.0000	0.0000	1.7148	1.8488	2.3191	2.9090	3.1364	0.0000
31H4	R185E	0.0024	0.0109	1.2444	1.3525	1.7421	2.2439	2.4388	0.0000
31A4	E513R	0.0001	0.0003	1.4764	1.6219	2.1560	2.8660	3.1485	0.0000
31A4	E539R	0.0000	0.0000	1.6014	1.7461	2.2726	2.9578	3.2252	0.0000
31A4	R439E	0.0000	0.0000	3.1565	3.6501	5.5738	8.5113	9.8420	0.0000
31A4	V538R	0.0004	0.0013	1.4225	1.5700	2.1142	2.8471	3.1423	0.0000
12H11	A390R	0.0000	0.0001	1.4140	1.5286	1.9389	2.4594	2.6588	0.0000
12H11	A413R	0.0009	0.0028	1.2840	1.3891	1.7653	2.2434	2.4269	0.0000
12H11	S351R	0.0009	0.0028	1.2513	1.3444	1.6761	2.0896	2.2452	0.0000
12H11	T132R	0.0000	0.0001	1.3476	1.4392	1.7631	2.1599	2.3068	0.0000
3C4	E582R	0.0016	0.0069	1.3523	1.5025	2.0642	2.8359	3.1509	0.0000

linked to each one of the beads (described above). The bead variation in EC50 estimates of wild type binding curve from this experiment was used to estimate the bead-bead variation in the actual epitope mapping experiment.

Testing for EC50 Shift between Mutants and Wild Type

The comparisons of two EC50s (in log scale) was conducted using Student's t-test. The t-statistic was calculated as the ratio between delta (the absolute differences between EC50 estimates) and the standard deviation of delta. The variance of delta was estimated by the sum of the three components, variance estimate of EC50 for mutant and wild type curves in the nonlinear regression and two times the bead-bead variance estimated from a separate experiment. The multiple of two for the bead-bead variance was due to the assumption that both mutant and wild type beads had the same variance. The degree of freedom of the standard deviation of delta was calculated using the Satterthwaite's (1946) approximation. Individual p-values and confidence intervals (95% and 99%) were derived based on Student's t distribution for each comparison. In the case of multiple wild type controls, a conservative approach was taken by picking the wild type control that was most similar to the mutant, i.e., picking the ones with the largest p-values.

Maximum Signal Reduction

The percent maximum signal was calculated using the maximum signal from the curve fitting (BmaxPerWT) and raw data point (RawMaxPerWT). Mutations that reduced the antibody binding maximum signal by $\geq 70\%$ as compared to wild type signal or that reduced the signal of one antibody compared to other antibodies by $>50\%$ when all other antibodies are at least 40% of wild type were considered hits and part of the epitope. Table 39.4 displays the residues that are in the structural epitope (*italics*) as determined by reduction of maximum signal.

TABLE 39.4

antibody	Mutants	BmaxPerWT	RawMaxPerWT
21B12	A311R	141.6388	139.7010
31H4	A311R	145.2189	147.8244
31A4	A311R	103.4377	96.2214
<i>12H11</i>	<i>A311R</i>		<i>14.9600</i>
3C4	A311R	129.0460	131.2060
<i>21B12</i>	<i>D162R</i>		<i>7.0520</i>
31H4	D162R	108.8308	112.4904
31A4	D162R	98.8873	95.9268

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TABLE 39.4-continued

antibody	Mutants	BmaxPerWT	RawMaxPerWT
12H11	D162R	94.6280	97.4928
3C4	D162R	101.4281	100.1586
21B12	D313R	45.8356	45.0011
31H4	D313R	45.6242	44.9706
31A4	D313R	47.9728	44.7741
12H11	D313R	16.1811	18.4262
3C4	D313R	58.5269	57.6032
21B12	D337R	61.9070	62.2852
31H4	D337R	63.1604	64.1029
31A4	D337R	62.9124	59.4852
12H11	D337R		10.8443
3C4	D337R	73.0326	73.9961
21B12	E129R	139.9772	138.9671
31H4	E129R	141.6792	139.1764
31A4	E129R	77.3005	74.8946
12H11	E129R	28.6398	29.3751
3C4	E129R	85.7701	85.7802
21B12	E167R		15.1082
31H4	E167R	127.4479	128.2698
31A4	E167R	115.3403	112.6951
12H11	E167R	111.0979	109.6813
3C4	E167R	109.3223	108.7864
21B12	H521R	133.8480	133.9791
31H4	H521R	130.2068	128.4879
31A4	H521R	124.5091	129.3218
12H11	H521R	130.7979	134.4355
3C4	H521R		22.1077
21B12	Q554R	125.9594	125.2103
31H4	Q554R	122.2045	128.7304
31A4	Q554R	113.6769	121.3369
12H11	Q554R	116.1789	118.4170
3C4	Q554R		31.8416
21B12	R164E	17.3807	19.8505
31H4	R164E	97.8218	99.6673
31A4	R164E	98.2595	96.3352
12H11	R164E	88.0067	89.8807
3C4	R164E	105.0589	105.7286
21B12	R519E	139.4598	141.2949
31H4	R519E	135.5609	140.0000
31A4	R519E	134.2303	137.1110
12H11	R519E	135.4755	137.0824
3C4	R519E		44.0091
21B12	S123R	87.6431	88.1356
31H4	S123R	85.5312	84.7668
31A4	S123R	68.4371	66.6131
12H11	S123R	20.8560	20.6910
3C4	S123R	73.6475	71.5959

(Point mutations are with reference to SEQ ID NO: 1 and FIG. 26).

Table 39.5 displays a summary of all of the hits for the various antibodies.

TABLE 39.5

EC50 shift hits						Bmax shift hits			
12H11	31H4	31A4	12H11	3C4	21B12	12H11	31H4	31A4	
R207E	R185E	R439E	T132R	E582R	D162R			S123R	R519E
D208R*		E513R	S351R		R164E			E129R	H521R
		V538R	A390R		E167R			A311R	Q554R
		E539R	A413R					D313R	
								D337R	

*decreases EC50

To further examine how these residues form part of or all of the relevant epitopes, the above noted positions were mapped onto various crystal structure models, the results are shown in FIG. 27A through 27E. FIG. 27A depicts the 21B12 epitope hits, as mapped onto a crystal structure of PCSK9 with the 21B12 antibody. The structure identifies PCSK9 residues as follows: light gray indicates those residues that were not

mutated (with the exception of those residues that are explicitly indicated on the structure) and darker gray indicates those residues mutated (a minority of which failed to express). Residues that are explicitly indicated were tested (regardless of the shading indicated on the figure) and resulted in a significant change in EC50 and/or Bmax. The epitope hits were based on Bmax shift. In this figure, 31H4 is behind 21B12.

FIG. 27B depicts the 31H4 epitope hits, as mapped onto a crystal structure of PCSK9 with 31H4 and 21B12 antibodies. The structure identifies PCSK9 residues as follows: light gray indicates those residues that were not mutated (with the exception of those residues that are explicitly indicated on the structure) and darker gray indicates those residues mutated (a minority of which failed to express). Residues that are explicitly indicated were tested (regardless of the shading indicated on the figure) and resulted in a significant change in EC50 and/or Bmax. The epitope hits were based on the EC50 shift.

FIG. 27C depicts the 31A4 epitope hits, as mapped onto a crystal structure of PCSK9 with 31H4 and 21B12 antibodies. The structure identifies PCSK9 residues as follows: light gray indicates those residues that were not mutated (with the exception of those residues that are explicitly indicated on the structure) and darker gray indicates those residues mutated (a minority of which failed to express). Residues that are explicitly indicated were tested (regardless of the shading indicated on the figure) and resulted in a significant change in EC50 and/or Bmax. The epitope hits were based on the EC50 shift. 31A4 antibody is known to bind to the V-domain of PCSK9, which appears consistent with the results presented in FIG. 27C.

FIG. 27D depicts the 12H11 epitope hits, as mapped onto the crystal structure of PCSK9 with 31H4 and 21B12 antibodies. The structure identifies PCSK9 residues as follows: light gray indicates those residues that were not mutated (with the exception of those residues that are explicitly indicated on the structure) and darker gray indicates those residues mutated (a minority of which failed to express). Residues that are explicitly indicated were tested (regardless of the shading indicated on the figure) and resulted in a significant change in EC50 and/or Bmax. The epitope hits were based on the EC50 shift. 12H11 competes with 21B12 and 31H4 in the binning assay described above.

FIG. 27E depicts the 3C4 epitope hits, as mapped onto the crystal structure of PCSK9 with 31H4 and 21B12 antibodies. The structure identifies PCSK9 residues as follows: light gray

indicates those residues that were not mutated (with the exception of those residues that are explicitly indicated on the structure) and darker gray indicates those residues mutated (a minority of which failed to express). Residues that are explicitly indicated were tested (regardless of the shading indicated on the figure) and resulted in a significant change in EC50 and/or Bmax.

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3C4 does not compete with 21B12 and 31H4 in the binning assay. 3C4 binds to the V-domain in the domain binding assay (see results from Example 40, FIGS. 28A and 28B).

While there were approximately a dozen mutants that could have been expected to have an effect on binding (based upon the crystal structure), the present experiment demonstrated that, surprisingly, they did not. As will be appreciated by one of skill in the art, the results presented above are in good agreement with the crystal structures and PCSK-9's binding of these antibodies. This demonstrates that the provided structural and corresponding functional data adequately identifies the key residues and areas of interaction of the neutralizing ABPs and PCSK9. Thus, variants of the ABPs that possess the ability to bind to the above noted areas are adequately provided by the present description.

As will be appreciated by one of skill in the art, while the B-max drop and EC50 shift hits can be considered manifestations of the same phenomenon, strictly speaking, a B-max drop alone does not reflect a loss of affinity per se but, rather, the destruction of some percentage of the epitope of an antibody. Although there is no overlap in the hits determined by B-max and EC50, mutations with a strong affect on binding may not allow for the generation of a useful binding curve and hence, no EC50 can be determined for such variants.

As will be appreciated by one of skill in the art, ABPs in the same bin (with the exception of bin 5, which as noted above, is a general catch all bin) likely bind to overlapping sites on the target protein. As such, the above epitopes and relevant residues can generally be extended to all such ABPs in the same bin.

To further examine the above results in regard to ABP 31H4, position E181R, which, according to the above crystal structure, was predicted to interact with R185 to form part of the surface that interacts with the ABP, was also altered (E181R). The results, while not statistically significant on their own, were, when combined with the crystal structure, demonstrative of 31H4 interacting with E181R (data not shown). Thus, position 181 also appears to form part of the epitope for the 31H4 ABP.

As noted above, the above binding data and epitope characterization references a PCSK9 sequence (SEQ ID NO: 1) that does not include the first 30 amino acids of PCSK9. Thus, the numbering system of this protein fragment, and the SEQ ID NO:s that refer to this fragment, are shifted by 30 amino acids compared to the data and experiments that used a full length PCSK9 numbering system (such as that used in the crystal study data described above). Thus, to compare these results, an extra 30 amino acids should be added to the positions in each of the above epitope mapping results. For example, position 207 of SEQ ID NO: 1 (or SEQ ID NO: 303), correlates to position 237 of SEQ ID NO: 3 (the full length sequence, and the numbering system used throughout the rest of the specification). Table 39.6 outlines how the above noted positions, which reference SEQ ID NO: 1 (and/or SEQ ID NO: 303) correlate with SEQ ID NO: 3 (which includes the signal sequence).

TABLE 39.6

AMINO ACID POSITION IN SEQ ID NO: 1 (EPITOPE DATA)	AMINO ACID POSITION IN SEQ ID NO: 3 (EPITOPE DATA)
207	237
208	238
185	215
181	211
439	469
513	543

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TABLE 39.6-continued

	AMINO ACID POSITION IN SEQ ID NO: 1 (EPITOPE DATA)	AMINO ACID POSITION IN SEQ ID NO: 3 (EPITOPE DATA)
5	538	568
	539	569
	132	162
	351	381
	390	420
10	413	443
	582	612
	162	192
	164	194
	167	197
15	123	153
	129	159
	311	341
	313	343
	337	367
	519	549
	521	551
20		584

Thus, those embodiments described herein with reference to SEQ ID NO: 1 can also be described, by their above noted corresponding position with reference to SEQ ID NO: 3.

Example 40

PCSK9 Domain Binding Assay

The present example examined where on PCSK9 the various ABPs bound.

Clear, 96 well maxisorp plates (Nunc) were coated overnight with 2 ug/ml of various anti-PCSK9 antibodies diluted in PBS. Plates were washed thoroughly with PBS/0.05% Tween-20 and then blocked for two hours with 3% BSA/PBS. After washing, plates were incubated for two hours with either full length PCSK9 (aa 31-692 SEQ ID NO: 3, procat PCSK9 (aa 31-449 SEQ ID NO: 3) or v-domain PCSK9 (aa 450-692 of SEQ ID NO: 3) diluted in general assay diluent (Immunochemistry Technologies, LLC). Plates were washed and a rabbit polyclonal biotinylated anti-PCSK9 antibody (D8774), which recognizes the procat and v-domain as well as full-length PCSK9, was added at 1 ug/ml (in 1% BSA/PBS). Bound full-length, procat or v-domain PCSK9 was detected by incubation with neutravidin-HRP (Thermo Scientific) at 200 ng/ml (in 1% BSA/PBS) followed by TMB substrate (KPL) and absorbance measurement at 650 nm. The results, presented in FIGS. 28A and 28B, demonstrate the ability of the various ABS to bind to various parts of PCSK9. As shown in FIG. 28B, ABP 31A4 binds to the V domain of PCSK9.

Example 41

Neutralizing, Non-competitive Antigen Binding Proteins

The present example demonstrates how to identify and characterize an antigen binding protein that is non-competitive with LDLR for binding with PCSK9, but is still neutralizing towards PCSK9 activity. In other words, such an antigen binding protein will not block PCSK9 from binding to LDLR, but will prevent or reduce PCSK9 mediated LDLR degradation.

Clear, 384 well plates (Costar) were coated with 2 ug/ml of goat anti-LDL receptor antibody (R&D Systems) diluted in buffer A (100 mM sodium cacodylate, pH 7.4). Plates were washed thoroughly with buffer A and then blocked for 2 hours

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with buffer B (1% milk in buffer A). After washing, plates were incubated for 1.5 hours with 0.4 ug/ml of LDL receptor (R&D Systems) diluted in buffer C (buffer B supplemented with 10 mM CaCl₂). Concurrent with this incubation, 20 ng/ml of biotinylated D374Y PCSK9 was incubated with 100 ng/ml of antibody diluted in buffer A or buffer A alone (control). The LDL receptor containing plates were washed and the biotinylated D374Y PCSK9/antibody mixture was transferred to them and incubated for 1 hour at room temperature. Binding of the biotinylated D374Y to the LDL receptor was detected by incubation with streptavidin-HRP (Biosource) at 500 ng/ml in buffer C followed by TMB substrate (KPL). The signal was quenched with 1N HCl and the absorbance read at 450 nm. The results are presented in FIG. 28C, which shows that while ABP 31H4 inhibits LDLR binding, ABP 31A4 does not inhibit LDLR binding to PCSK9. In combination with the results from Example 40 and shown in FIGS. 28A and 28B, it is clear that 31A4 ABP binds to the V domain of PCSK9 and does not block the interaction of PCSK9 with LDLR.

Next, the Ability of ABP 31A4 to serve as a neutralizing ABP was further confirmed via a cell LDL uptake assay (as described in the examples above). The results of this LDL uptake assay are presented in FIG. 28D. As shown in FIG.

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28D, ABP 31A4 displays significant PCSK9 neutralizing ability. Thus, in light of Example 40 and the present results, it is clear that ABPs can bind to PCSK9 without blocking the PCSK9 and LDLR binding interaction, while still being useful as neutralizing PCSK9 ABPs.

Incorporation by Reference

All references cited herein, including patents, patent applications, papers, text books, and the like, and the references cited therein, to the extent that they are not already, are hereby incorporated herein by reference in their entirety. To the extent that any of the definitions or terms provided in the references incorporated by reference differ from the terms and discussion provided herein, the present terms and definitions control.

15 Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The foregoing description and examples detail certain preferred embodiments of the invention and describe the best mode contemplated by the inventors. It will be appreciated, however, that no matter how detailed the foregoing may appear in text, the invention may be practiced in many ways and the invention should be construed in accordance with the appended claims and any equivalents thereof.

SEQUENCE LISTING

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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

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200

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Ala Gly Val Ala Lys Gly Ala Ser Met Arg Ser Leu Arg Val Leu Asn
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Cys Gln Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe
 225 230 235 240

Ile Arg Lys Ser Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu
 245 250 255

Leu Pro Leu Ala Gly Gly Tyr Ser Arg Val Leu Asn Ala Ala Cys Gln
 260 265 270

Arg Leu Ala Arg Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe
 275 280 285

Arg Asp Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile
 290 295 300

Thr Val Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr
 305 310 315 320

Leu Gly Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Glu
 325 330 335

Asp Ile Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln
 340 345 350

Ser Gly Thr Ser Gln Ala Ala His Val Ala Gly Ile Ala Ala Met
 355 360 365

Met Leu Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg
 370 375 380

Leu Ile His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro
 385 390 395 400

Glu Asp Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro
 405 410 415

Ser Thr His Gly Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser
 420 425 430

Ala His Ser Gly Pro Thr Arg Met Ala Thr Ala Ile Ala Arg Cys Ala
 435 440 445

Pro Asp Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Lys
 450 455 460

Arg Arg Gly Glu Arg Met Glu Ala Gln Gly Lys Leu Val Cys Arg
 465 470 475 480

Ala His Asn Ala Phe Gly Glu Gly Val Tyr Ala Ile Ala Arg Cys
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Cys Leu Leu Pro Gln Ala Asn Cys Ser Val His Thr Ala Pro Pro Ala
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Glu Ala Ser Met Gly Thr Arg Val His Cys His Gln Gln Gly His Val
 515 520 525

Leu Thr Gly Cys Ser Ser His Trp Glu Val Glu Asp Leu Gly Thr His
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Lys Pro Pro Val Leu Arg Pro Arg Gly Gln Pro Asn Gln Cys Val Gly
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His Arg Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly Leu
 565 570 575

Glu Cys Lys Val Lys Glu His Gly Ile Pro Ala Pro Gln Gly Gln Val
 580 585 590

Thr Val Ala Cys Glu Glu Gly Trp Thr Leu Thr Gly Cys Ser Ala Leu
 595 600 605

Pro Gly Thr Ser His Val Leu Gly Ala Tyr Ala Val Asp Asn Thr Cys
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-continued

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1920

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<400> SEQUENCE: 3

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 20          25          30

Asp Glu Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg Ser Glu
 35          40          45

Glu Asp Gly Leu Ala Glu Ala Pro Glu His Gly Thr Thr Ala Thr Phe
 50          55          60

His Arg Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr Val Val
 65          70          75          80

Val Leu Lys Glu Glu Thr His Leu Ser Gln Ser Glu Arg Thr Ala Arg
 85          90          95

Arg Leu Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys Ile Leu
100         105         110

His Val Phe His Gly Leu Leu Pro Gly Phe Leu Val Lys Met Ser Gly
115         120         125

Asp Leu Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr Ile Glu
130         135         140

Glu Asp Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu Arg
145         150         155         160

Ile Thr Pro Pro Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro Asp Gly
165         170         175

Gly Ser Leu Val Glu Val Tyr Leu Leu Asp Thr Ser Ile Gln Ser Asp
180         185         190

His Arg Glu Ile Glu Gly Arg Val Met Val Thr Asp Phe Glu Asn Val
195         200         205

Pro Glu Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser Lys Cys Asp
210         215         220

Ser His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp Ala Gly
225         230         235         240

Val Ala Lys Gly Ala Ser Met Arg Ser Leu Arg Val Leu Asn Cys Gln
245         250         255

Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe Ile Arg
260         265         270

Lys Ser Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu Leu Pro
275         280         285

Leu Ala Gly Gly Tyr Ser Arg Val Leu Asn Ala Ala Cys Gln Arg Leu
290         295         300

Ala Arg Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe Arg Asp
305         310         315         320

Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile Thr Val
325         330         335

Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr Leu Gly
340         345         350

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Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Glu Asp Ile
 355 360 365
 Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln Ser Gly
 370 375 380
 Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met Met Leu
 385 390 395 400
 Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile
 405 410 415
 His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro Glu Asp
 420 425 430
 Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro Ser Thr
 435 440 445
 His Gly Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser Ala His
 450 455 460
 Ser Gly Pro Thr Arg Met Ala Thr Ala Ile Ala Arg Cys Ala Pro Asp
 465 470 475 480
 Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Lys Arg Arg
 485 490 495
 Gly Glu Arg Met Glu Ala Gln Gly Lys Leu Val Cys Arg Ala His
 500 505 510
 Asn Ala Phe Gly Gly Glu Gly Val Tyr Ala Ile Ala Arg Cys Cys Leu
 515 520 525
 Leu Pro Gln Ala Asn Cys Ser Val His Thr Ala Pro Pro Ala Glu Ala
 530 535 540
 Ser Met Gly Thr Arg Val His Cys His Gln Gln Gly His Val Leu Thr
 545 550 555 560
 Gly Cys Ser Ser His Trp Glu Val Glu Asp Leu Gly Thr His Lys Pro
 565 570 575
 Pro Val Leu Arg Pro Arg Gly Gln Pro Asn Gln Cys Val Gly His Arg
 580 585 590
 Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly Leu Glu Cys
 595 600 605
 Lys Val Lys Glu His Gly Ile Pro Ala Pro Gln Gly Gln Val Thr Val
 610 615 620
 Ala Cys Glu Glu Gly Trp Thr Leu Thr Gly Cys Ser Ala Leu Pro Gly
 625 630 635 640
 Thr Ser His Val Leu Gly Ala Tyr Ala Val Asp Asn Thr Cys Val Val
 645 650 655
 Arg Ser Arg Asp Val Ser Thr Thr Gly Ser Thr Ser Glu Glu Ala Val
 660 665 670
 Thr Ala Val Ala Ile Cys Cys Arg Ser Arg His Leu Ala Gln Ala Ser
 675 680 685
 Gln Glu Leu Gln
 690

<210> SEQ ID NO 4

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

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Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95

Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105 110

<210> SEQ ID NO 5
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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

Glu Pro Pro Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

Asn Gly Tyr Asn Phe Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser His Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Val
 85 90 95

Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105 110

<210> SEQ ID NO 6
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

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

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

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

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

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

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

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

<210> SEQ ID NO 7
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 7

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

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

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

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

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

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

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

<210> SEQ ID NO 8

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

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

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

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

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

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

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

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

<210> SEQ ID NO 9

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

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

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

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

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

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

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

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

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<210> SEQ ID NO 10
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

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

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

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

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

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

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

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

<210> SEQ ID NO 11
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

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

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

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

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

<210> SEQ ID NO 12
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

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

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

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

Leu Ile Ser Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

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65	70	75	80
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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser			
85	90	95	

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

<210> SEQ ID NO 13

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

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

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

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu			
65	70	75	80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asn Ser			
85	90	95	

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

<210> SEQ ID NO 14

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

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

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

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

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

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

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

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

<210> SEQ ID NO 15

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

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

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

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Asn	Ser	Val	Ser	Trp	Tyr	Gln	His	His	Pro	Gly	Lys	Ala	Pro	Lys	Val
35						40					45				

Met	Ile	Tyr	Glu	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Thr	Arg	Phe
50						55					60				

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

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

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

<210> SEQ ID NO 16

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

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

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

Asn	Ser	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Pro	Pro	Lys	Leu
35						40					45				

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

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

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

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

<210> SEQ ID NO 17

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

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

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

Asn	Ser	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Pro	Pro	Lys	Leu
35						40					45				

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

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

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

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

<210> SEQ ID NO 18

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

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

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

```
Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Pro Pro Lys Leu
 35          40          45
```

```
Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50          55          60
```

```
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65          70          75          80
```

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

```
Ser Met Val Phe Gly Gly Thr Lys Leu Ala Val Leu
 100         105
```

<210> SEQ ID NO 19

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

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

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

```
Asn Ser Val Ser Trp Tyr Gln Tyr Pro Gly Lys Pro Pro Lys Leu
 35          40          45
```

```
Lys Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50          55          60
```

```
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65          70          75          80
```

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

```
Ser Met Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 100         105
```

<210> SEQ ID NO 20

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

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

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

```
Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Pro Pro Lys Leu
 35          40          45
```

```
Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50          55          60
```

```
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65          70          75          80
```

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

```
Ser Met Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 100         105
```

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<210> SEQ ID NO 21
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

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

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

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Pro Pro Lys Leu
35 40 45

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

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

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

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

```

```

<210> SEQ ID NO 22
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

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

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

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Pro Pro Lys Leu
 35          40          45

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

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

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

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

```

```

<210> SEQ ID NO 23
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

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

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

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

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

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

```

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

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

<210> SEQ ID NO 24

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

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

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

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Arg
 35 40 45

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

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

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

Asn Met Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO 25

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

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

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

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

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

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

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

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

<210> SEQ ID NO 26

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

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

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

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu

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35

40

45

Met Ile Tyr Glu Val Thr Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60

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

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

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

<210> SEQ ID NO 27

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

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

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

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

Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
 85 90 95

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

<210> SEQ ID NO 28

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

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

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

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

Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
 85 90 95

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

<210> SEQ ID NO 29

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

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-continued

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

<210> SEQ ID NO 30
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

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

<210> SEQ ID NO 31
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

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

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-continued

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
 85 90 95

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

<210> SEQ ID NO 35

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
 20 25 30

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

Ile Tyr Asp Tyr Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
 85 90 95

Ser Ala Tyr Val Phe Gly Thr Gly Thr Arg Val Thr Val Leu
 100 105 110

<210> SEQ ID NO 36

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
 20 25 30

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

Ile Tyr Asp Tyr Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
 85 90 95

Ser Gly Tyr Val Phe Gly Thr Gly Thr Arg Val Thr Val Leu
 100 105 110

<210> SEQ ID NO 37

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
 20 25 30

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

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-continued

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

<210> SEQ ID NO 38
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

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

<210> SEQ ID NO 39
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 39

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

<210> SEQ ID NO 40
 <211> LENGTH: 110
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln

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-continued

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

<210> SEQ ID NO 41

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

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

<210> SEQ ID NO 42

<211> LENGTH: 110

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

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

<210> SEQ ID NO 43

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-continued

<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

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Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Pro Gly Gln
 1           5          10          15

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

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

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

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65          70          75          80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
85          90          95

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

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<210> SEQ ID NO 44
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

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Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Pro Gly Gln
 1           5          10          15

Thr Ala Arg Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
20          25          30

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

Gln Asn Thr Lys Trp Pro Leu Gly Ile Pro Glu Arg Phe Ser Gly Ser
50          55          60

Lys Ser Gly Asn Thr Val Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65          70          75          80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Val Val
85          90          95

Phe Gly Gly Thr Lys Leu Thr Val Leu
100         105

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<210> SEQ ID NO 45
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

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

Ser Val Thr Leu Thr Cys Thr Leu Ser Ser Gly Tyr Ser Asn Tyr Lys
20          25          30

Val Asp Trp Tyr Gln Gln Arg Pro Gly Lys Gly Pro Arg Phe Val Met
35          40          45

Arg Val Gly Thr Gly Gly Ile Val Gly Ser Lys Gly Asp Gly Ile Pro
50          55          60

Asp Arg Phe Ser Val Leu Gly Ser Gly Leu Asn Arg Tyr Leu Thr Ile
65          70          75          80

Lys Asn Ile Gln Glu Glu Asp Glu Ser Asp Tyr His Cys Gly Ala Asp

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-continued

85

90

95

His Gly Ser Gly Ser Asn Phe Val Val Val Phe Gly Gly Thr Lys
100 105 110

Leu Thr Val Leu
115

<210> SEQ ID NO 46
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

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

Ser Val Thr Leu Thr Cys Thr Leu Ser Ser Gly Tyr Ser Ser Tyr Glu
20 25 30

Val Asp Trp Tyr Gln Gln Arg Pro Gly Lys Gly Pro Arg Phe Val Met
35 40 45

Arg Val Asp Thr Gly Gly Ile Val Gly Ser Lys Gly Glu Gly Ile Pro
50 55 60

Asp Arg Phe Ser Val Leu Gly Ser Gly Leu Asn Arg Tyr Leu Thr Ile
65 70 75 80

Lys Asn Ile Gln Glu Glu Asp Glu Ser Asp Tyr His Cys Gly Ala Asp
85 90 95

His Gly Ser Gly Thr Asn Phe Val Val Phe Gly Gly Thr Lys
100 105 110

Leu Thr Val Leu
115

<210> SEQ ID NO 47
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> SEQ ID NO 48
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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-continued

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

<210> SEQ ID NO 49
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49

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

<210> SEQ ID NO 50
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

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

-continued

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

Val Ser Ser
115

<210> SEQ ID NO 51
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Phe Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

Val Ser Ser
115

<210> SEQ ID NO 52
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Val Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

Val Ser Ser
115

<210> SEQ ID NO 53
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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

<210> SEQ ID NO 54
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

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

<210> SEQ ID NO 55
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55

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

-continued

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

Val Ser Ser
115

<210> SEQ ID NO 56

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Leu Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

Val Ser Ser
115

<210> SEQ ID NO 57

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Val Ser Ser
115

<210> SEQ ID NO 58

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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

<210> SEQ ID NO 59
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

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

Ser

<210> SEQ ID NO 60
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

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

-continued

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

Val Ser Ser
 115

<210> SEQ ID NO 61
 <211> LENGTH: 116
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 61

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

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

Thr Val Ser Ser
 115

<210> SEQ ID NO 62
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30

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

Ala Asn Ile Lys His Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Ser Asn Trp Gly Phe Ala Phe Asp Val Trp Gly His Gly
 100 105 110

Thr Met Val Thr Val Ser Ser
 115

<210> SEQ ID NO 63
 <211> LENGTH: 116
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

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

-continued

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Asn Trp Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
 100 105 110

Thr Val Ser Ser
 115

<210> SEQ ID NO 64
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

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

Ser Leu Arg Leu Ser Cys Val Val Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
 115

<210> SEQ ID NO 65
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Asn Phe
 20 25 30

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

-continued

Thr Arg Glu Ser Asn Trp Gly Phe Ala Phe Asp Ile Trp Gly Gln Gly
 100 105 110

Thr Met Val Thr Val Ser Ser
 115

<210> SEQ ID NO 66

<211> LENGTH: 123

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Asp Tyr Asp Phe Trp Ser Gly Tyr Tyr Thr Ala Phe Asp Val
 100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 67

<211> LENGTH: 123

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Asp Tyr Asp Phe Trp Ser Ala Tyr Tyr Asp Ala Phe Asp Val
 100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 68

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

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

-continued

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

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

Ala Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 100 105 110

<210> SEQ ID NO 69

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

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

Ala Lys Glu Val Gly Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> SEQ ID NO 70

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

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

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

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

-continued

Val Thr Val Ser Ser
115

<210> SEQ ID NO 71
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Lys Lys Phe Val Leu Met Val Tyr Ala Met Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 72
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Lys Lys Phe Val Leu Met Val Tyr Ala Met Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 73
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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-continued

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

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

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

Thr Val Ser Ser
 115

<210> SEQ ID NO 74

<211> LENGTH: 123

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Thr Gly Pro Leu Lys Leu Tyr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 75

<211> LENGTH: 116

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

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

-continued

Thr Val Ser Ser
115

<210> SEQ ID NO 76
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

Gln Val His Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Phe
20 25 30

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

Ala Leu Ile Trp Ser Asp Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Ala Ile Ala Ala Leu Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

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

<210> SEQ ID NO 77
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

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

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

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

Ala Arg Ala Ile Ala Ala Leu Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

Gly His Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 78
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 78

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

<210> SEQ ID NO 79
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 79

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

<210> SEQ ID NO 80
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

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

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-continued

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

<210> SEQ ID NO 81
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Arg Gly Gly Leu Ala Ala Arg Pro Gly Gly Met Asp Val Trp
100 105 110

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

<210> SEQ ID NO 82
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Ile Ala Val Ala Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

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

<210> SEQ ID NO 83
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

-continued

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

Ala Leu Ile Trp His Asp Gly Ser Asn Thr Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Ile Ala Val Ala Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110

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

<210> SEQ ID NO 84

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 84

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

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

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

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

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

Val Thr Val Ser Ser
 115

<210> SEQ ID NO 85

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 85

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

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

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

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

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

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

<210> SEQ ID NO 86

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 86

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

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

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 87

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 87

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

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

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

Trp Ile Gly Tyr Ile Tyr Asn Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Glu Asp Thr Ala Met Val Pro Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 88

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 88

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

-continued

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

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

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

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

Arg Gly Gln Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> SEQ ID NO 89

<211> LENGTH: 116

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 89

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Ala Tyr
 20 25 30

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

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

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

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

Arg Gly Gln Leu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> SEQ ID NO 90

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 90

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

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

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

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

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-continued

Val Ser Ser
115

<210> SEQ ID NO 91
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 91

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1															15

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

Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Ser	Arg	Gly	Leu	Glu
															45
35															40

Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Lys	Asn	Tyr	Ser
															50
															55

Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	Thr	Ser	Lys	Asn
															65
															70

Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Gly	Asp	Thr	Ala	Val
															85
															90

Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Pro	Thr	Ala	Ala	Phe	Asp	Tyr	Trp	Gly
															100
															105

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
115								120

<210> SEQ ID NO 92

<211> LENGTH: 345

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 92

cagattcagc	tggtgccagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
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tcctgcaagg	tttctggta	ccccttgacc	agctatggta	tcaagctgggt	gcgcacaggcc	120
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cctggacaag	gggtttagtg	gatggatgg	atcagcgctt	acaatggtaa	cacaaactat	180
------------	------------	-----------	------------	------------	------------	-----

gcacagaagg	tccagggcag	cgtcaccatg	accacagaca	catccacgag	cacagtctac	240
------------	------------	------------	------------	------------	------------	-----

atggagctga	gggacctgag	atctgacgac	acggccgtgt	attactgtgc	gagaggctac	300
------------	------------	------------	------------	------------	------------	-----

ggtatggacg	tctggggcca	agggaccacg	gtcacccgtct	cctct		345
------------	------------	------------	-------------	-------	--	-----

<210> SEQ ID NO 93

<211> LENGTH: 327

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 93

cagtctgccc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gtacaccatc	60
------------	------------	------------	------------	------------	------------	----

tcctgcactg	gaaccagcag	tgacgttgggt	ggttataact	ctgtctccctg	gtaccaacag	120
------------	------------	-------------	------------	-------------	------------	-----

taccaggcga	aaccccccua	actcaagatt	tatgagggtca	gtaatcgcc	ctcagggggtt	180
------------	------------	------------	-------------	-----------	-------------	-----

tctaattcgct	tctctggetc	caagtctggc	aacacggcct	ccctgaccat	ctctgggctc	240
-------------	------------	------------	------------	------------	------------	-----

caggctgagg	acgaggcgtga	ttattttctgc	agctcatata	caagcaccag	catggtcttc	300
------------	-------------	-------------	------------	------------	------------	-----

ggcggagggga	ccaagctgac	cgtccta				327
-------------	------------	---------	--	--	--	-----

<210> SEQ ID NO 94

<211> LENGTH: 345

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 94

caggttcagc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggc	60	
tcctgcaagg	cttctggta	cacctaacc	agctatggta	tcaagctgggt	gcgacaggcc	120
cctggacaag	ggcttgagtg	gatgggatgg	gtcagtttt	ataatggtaa	cacaactat	180
gcacagaagc	tccagggcag	aggcaccatg	accacagacc	catccacgag	cacagctac	240
atggagctga	ggagcctgag	atctgacgac	acggccgtgt	attactgtgc	gagaggctac	300
ggtatggacg	tctggggcca	agggaccacg	gtcacccgtct	cctct	345	

<210> SEQ ID NO 95

<211> LENGTH: 327

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 95

cagtctgccc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gtacaccatc	60
tcctgcactg	gaaccagcag	tgacgttggt	ggttataact	ctgtctcctg	gtaccaacag	120
caccaggca	aagcccccaa	actcatgatt	tatgagggtca	gtaatcgcc	ctcaggggtt	180
tctaatcgct	tctctggctc	caagtctggc	aacacggcct	ccctgaccat	ctctgggctc	240
caggctgagg	acgaggctga	ttattactgc	aattcatata	caagcaccag	catggattc	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 96

<211> LENGTH: 345

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 96

caggttcagc	tggagctgaa	gtgaagaagc	ctggggcctc	agtgaaggc	60	
tcctgcaagg	cttctggta	cacctaacc	agctatggta	tcaagctgggt	gcgacaggcc	120
cctggacaag	ggcttgagtg	gatgggatgg	atcagtttt	acaatggtaa	cacaactat	180
gcacagaagg	tccagggcag	agtacccatg	accacagaca	catccacgag	cacagctac	240
atggagctga	ggagcctgag	atctgacgac	acggccgtgt	attactgtgc	gagaggctac	300
ggtatggacg	tctggggcca	agggaccacg	gtcacccgtct	cctct	345	

<210> SEQ ID NO 97

<211> LENGTH: 327

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 97

cagtctgccc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gtacaccatc	60
tcctgcactg	gaaccagcag	tgacgttggt	ggttataact	ctgtctcctg	gtaccaacag	120
caccaggca	aaccccccaa	actcatgatt	tatgagggtca	gtaatcgcc	ctcaggggtt	180
tctattcgct	tctctggctc	caagtctggc	aacacggcct	ccctgaccat	ctctgggctc	240
caggctgagg	acgaggctga	ttatttctgc	agctcatata	caagcaccag	catggcttc	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 98

<211> LENGTH: 345

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 98

cagattcagc	tggtgcagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggc	60		
tcctgcaagg	cttctggta	caccttgcacc	agctatggta	tca	gctgggt	g	cgacaggcc	120
cctggacaag	ggcttgagtg	gatggatgg	atcagctttt	acaatggtaa	cacaactat	180		
gcacagaagg	tccaggcag	agt	caccatg	accacagaca	catccacgag	240		
atggagctga	ggagcctgag	atctgacgac	acggccgtgt	atttctgtgc	gagaggtac	300		
ggtatggacg	tctgggcca	agggaccacg	gtcacccgtct	cctca		345		

<210> SEQ ID NO 99

<211> LENGTH: 327

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 99

cagtctgccc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gatcaccatc	60
tcctgcactg	gaaccagcag	tgacgttgg	gttataact	ctgtctcg	gtaccaacag	120
caccaggca	aacccccc	aa	actcatgatt	tatgagg	tca gtaatcg	180
tcta	aatcg	ct	tctgg	ctca	ggttgc	240
caggctgagg	acgaggc	gt	ttatttctgc	ag	tcata	300
ggcggaggga	ccaagctggc	cgtccta				327

<210> SEQ ID NO 100

<211> LENGTH: 345

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 100

caggttcagc	tggtgcagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggc	60		
tcctgcaagg	cttctggta	cacctaacc	agctatggta	tca	gctgggt	g	cgacaggcc	120
cctggacaag	ggcttgagtg	gatggatgg	gtcagttttt	ataatggtaa	cacaactat	180		
gcacagaagg	tccaggcag	aggcaccatg	accacagacc	catccacgag	cacagctac	240		
atggagctga	ggagcctgag	atctgacgac	acggccgtgt	atttctgtgc	gagaggtac	300		
ggtatggacg	tctgggcca	agggaccacg	gtcacccgtct	cctca		345		

<210> SEQ ID NO 101

<211> LENGTH: 327

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 101

cagtctgccc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gatcaccatc	60
tcctgcactg	gaaccagcag	tgacgttgg	gttataact	ctgtctcg	gtaccaacag	120
caccaggca	aacccccc	aa	actcatgatt	tatgagg	tca aatcg	180
tcta	aatcg	ct	tctgg	ctca	ggttgc	240
caggctgagg	acgaggc	gt	ttatttactgc	aact	catata	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 102

<211> LENGTH: 363

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 102

caggtgcagc	tgcaggagtc	gggcccagga	ctggtaaagc	cttcacagac	cctgtccctc	60
acctgcactg	tctctgggt	ctccatcagc	agtgggtgg	actactggag	ctggatccgc	120
cagcacccag	ggaagggcct	ggagtggtt	gggtacatat	ataacagtgg	gagcacctac	180
tacaacccgt	ccctcaagag	tcgagttacc	atatcagtag	acacgtctaa	gaaccaggttc	240
tccctgaagc	tgagcttgt	gactgccccg	gacacggccg	tgtattactg	tgcgagagag	300
gatacagcta	tggttcctta	ctttgactac	tggggccagg	gaaccctgg	caccgtctcc	360
tca						363

<210> SEQ ID NO 103

<211> LENGTH: 333

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 103

cagtctgtac	tgacgcagcc	gccctcagtg	tctggggccc	cagggcagag	ggtcaccatc	60
tcctgcactg	ggagcagtc	caacatcggt	gcacattatg	atgtgcactg	gtaccaggcag	120
gttccaggaa	cagcccccaa	actcctcatc	tatggtaaca	cctatggcc	ctcaggggtc	180
cctgaccgat	tctctggctc	caagtctggc	acctcagcct	ccctggccat	cactgggctc	240
caggctgagg	atgaggctga	ttattactgc	cagtcctatg	acaacagcct	gagtgggtgt	300
gtattcggcg	gagggaccaa	gtgaccgtc	ctta			333

<210> SEQ ID NO 104

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 104

caggtgcacc	tggtgaggc	tggggaggc	gtggtccagc	ctgggaggc	cctgagactc	60
tcctgtgcag	cgtctggatt	caccttcaac	agctttggca	tgcactgggt	ccggccaggct	120
ccaggcaagg	ggctggagtg	ggtggcaatt	atctggctg	atggaagtga	tgaataactat	180
gcagactccg	tgaagggcgg	attcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaata	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagccata	300
gcagccctct	actactacta	cggatggac	gtctggggcc	aagggaccac	ggtcacccgtc	360
tcctca						366

<210> SEQ ID NO 105

<211> LENGTH: 330

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 105

cagtctgtgt	tgacgcagcc	gccctcagtg	tctggggccc	caggacagaa	ggtcaccatc	60
tcctgctctg	gaagcagtc	caacattggg	aataattttg	tatcctggta	ccagcagtc	120
ccaggaacag	cccccaaact	cctcatttat	gactataata	agcgaccctc	agggattcct	180
gacggattct	ctggctcaa	gtctggcacg	tcagccaccc	tgggcacac	cgactccag	240
actggggacg	aggccgatta	ttactgcca	acatggata	gcagcctgag	tgcttatgtc	300
ttcggaactg	ggaccagggt	caccgtctta				330

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<210> SEQ ID NO 106
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

```
caggtgcagc tgggggaggc gtggccagc ctgggaggc cctgagactc      60
tcctgtgcag cgtctggatt cacccatcagc agctttggca tgcactgggt ccggccaggct    120
ccaggcaagg ggctggagtg ggtggcactt atatggaaatg atggaaatgaa taaataactat    180
gcagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa cacgctgtat    240
ctgcaaataatgaa acagcctgag agccgaggac acggctgtgtt attactgtgc gagagocata    300
gcagccctct actactacta cggtatggac gtctggggcc aaggaccac ggtcacccgtc    360
tcctca                                              366
```

<210> SEQ ID NO 107
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

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cagtctgtgt tgacgcagcc gcctcagtg tctgcggccc caggacagaa ggtcaccatc      60
tcctgctctg gaagcagtc caacattggg aataattttg tatcctggta ccagcagctc    120
ccaggaacag cccccaaact cctcatttt gactataata agcgaccctc agggattcct    180
gaccgattct ctggctccaa gtctggcagc tcagccaccc tgggcacac ccggactccag    240
actggggacg aggccgatta ttactgcggaa acatgggata gcagtctgag tggttatgtc    300
ttcggaaactg ggaccagggt caccgtctca                                              330
```

<210> SEQ ID NO 108
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 108

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caggtgcacc tgggggaggc gtggccagc ctgggaggc cctgagactc      60
tcctgtgcag cgtctggatt cacccatcagc agctttggca tgcactgggt ccggccaggct    120
ccaggcaagg ggctggagtg ggtggcactt atatggctcg atggaaatgaa taaataactat    180
gcagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa cacgctgtat    240
ctgcaaataatgaa acagcctgag agccgaggac acggctgtgtt attactgtgc gagagocata    300
gcagccctct actactacta cggtatggac gtctggggcc aaggaccac ggtcacccgtc    360
tcctca                                              366
```

<210> SEQ ID NO 109
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 109

```
cagtctgtgt tgacgcagcc gcctcagtg tctgcggccc caggacagaa ggtcaccatc      60
tcctgctctg gaagcagtc caacattggg aataattttg tatcctggta ccagcagttc    120
ccaggaacag cccccaaact cctcatttt gactataata agcgaccctc agggattcct    180
gaccgattct ctggctccaa gtctggcagc tcagccaccc tgggcacac ccggactccag    240
actggggacg aggccgatta ttactgcggaa acatgggata gcagtctgag ttcttatgtc    300
```

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ttcggaaactg ggaccagggt caccgtcctta	330
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<210> SEQ ID NO 110
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 110

caggtgcagc tggtggagtc tgggggaggc gtggccagc ctgggaggc cctgagactc	60
tcctgtgcag cgtctggatt cacccatcagc agctttggca tgcactgggt ccggcaggct	120
ccaggcaagg ggctggagtg ggtggcactt atatggaatg atggaagtaa taaatactat	180
gcagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaata gacgcctgag agccgaggac acggctgtgtt attactgtgc gagagccata	300
gcagccctct actactacta cggtatggac gtctggggcc acgggaccac ggtcaccgtc	360
tcctca	366

<210> SEQ ID NO 111
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 111

cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc	60
tcctgctctg gaagcagtc caacattggg aataattttg tatcctggta ccagcagctc	120
ccaggaacag cccccaaact cctcatttt gactataata agcgaccctc agggattct	180
gaccgattct ctggctccaa gtctggcagc tcagccaccc tgggcatcac cggactccag	240
actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tggttatgtc	300
ttcggaaactg ggaccagggt caccgtcctta	330

<210> SEQ ID NO 112
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 112

caggtgcagc tggtggagtc tgggggaggc gtggccagc ctgggaggc cctgagactc	60
tcctgtgcag cgtctggatt cacccatcagc agctttggca tgcactgggt ccggcaggct	120
ccaggcaagg ggctggagtg ggtggcactt atatggaatg atggaagtaa taaatactat	180
gcagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaata gacgcctgag agccgaggac acggctgtgtt attactgtgc gagagccata	300
gcagccctct actactacta cggtatggac gtctggggcc acgggaccac ggtcaccgtc	360
tcctca	366

<210> SEQ ID NO 113
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 113

cagtctgtgt tgacgcagcc gcccacagtg tctgcggccc caggacagaa ggtcaccatc	60
tcctgctctg gaagcagtc caacattggg aataattttg tatcctggta ccagcagctc	120
ccaggaacag cccccaaact cctcatttt gactataata agcgaccctc agggattct	180

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gaccgattct ctggctccaa gtctggcact tcagccaccc tgggcatac cggactccag 240
 actggggacg aggccgatta ctactgcca acatggata gcagcctgag tggttatgtc 300
 ttcggaaactg ggaccagggt caccgtccta 330

<210> SEQ ID NO 114
 <211> LENGTH: 366
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 114

caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctggggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt caccttcagg agctatggca tgcactgggt ccggcaggct 120
 ccaggcaagg ggctggagtg ggtggcactt atatggcatg atggaagtaa tacatactat 180
 gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagaggata 300
 gcagtggctt actactacta cggtatggac gtctgggccc aaggaccac ggtcaccgtc 360
 tcctca 366

<210> SEQ ID NO 115
 <211> LENGTH: 330
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 115

cagtctgtgt tgacgcagcc gcctcagtg tctgcggccc caggacagaa ggtcaccatc 60
 tcctgctctg gaagcagtc caacattggg aataattttt tattcctggta ccagcagctc 120
 ccaggaacag cccccaaact cctcattttt gacagtaata agcgaccctc agggattcct 180
 gaccgattct ctggctccaa gtctggcact tcagccaccc tggacatcac cggactccag 240
 actggggacg aggccgatta ttactgcca acatggata gcagcctgag tggttatgtt 300
 ttcggaaactg ggaccaaggt caccgtccta 330

<210> SEQ ID NO 116
 <211> LENGTH: 363
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 116

gaggtgcagc tggtggagtc tgggggaggc ttgggtacagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttagc agctatgcca tgaactgggt ccggcaggct 120
 ccagggaaagg ggctggagtg ggtctcaact attagtggtt gtgggtataa cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaaagttt 300
 gtactaatgg tgtatgctat gcttgactac tggggccagg gaaccctgggt caccgtctcc 360
 tca 363

<210> SEQ ID NO 117
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 117

gacatcctga tgacccagtc tccatcctcc ctgtctgcat ctgttggaga cagagtccacc 60

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atcaacttgc	gggcaagtca	gagcattagc	agttatttaa	attggtatca	gcagaaacca	120
gggaaagccc	ctaaggctc	gatctatgct	gcctccagg	tgcaaagtgg	ggtcccatca	180
aggttcagtg	gcagtggatc	tggcacat	ttcactctca	ccatcaacag	tctgcaacct	240
gaagatttt	caacttacta	ctgtcaacag	agttacagtt	cccccatcac	cttcggccaa	300
gggacacgac	tggagattaa	a				321

<210> SEQ ID NO 118
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 118

gaggtgcagc	tgttggagtc	tgggggaggc	ttggtagc	cgggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacctttagc	agctatgcca	tgaactgggt	ccgcccaggct	120
ccagggaaagg	ggctggagtg	ggtctcaact	attagtggta	gtgggtgtaa	cacatactac	180
gcagactccg	tgaaggggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtat	attactgtgc	aaaaaagttt	300
gtactaatgg	tgtatgctat	gcttactac	tggggccagg	gaaccctgg	caccgtctcc	360
tca						363

<210> SEQ ID NO 119
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

gacatccaga	tgacccagtc	tccatcctcc	ctatctgcat	ctgtaggaga	cagagtccacc	60
atcaacttgc	gggcaagtca	gagcattagc	atctatttaa	attggtatca	gcagaagcca	120
gggaaagccc	cttacctct	gatctatgct	gcagccagg	tgcaaagtgg	ggtcccatca	180
aggttcagtg	gcagtggatc	tggcacat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagatttt	caacttacta	ctgtcaacag	agttacagtg	cccccatcac	cttcggccaa	300
gggacacgac	tggagattaa	a				321

<210> SEQ ID NO 120
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 120

caggttcagc	tggtgca	tggagctgag	gtgaagaagc	ctggggc	actgaagg	60
tcctgcaagg	cttctgg	tta	cagtttacc	agctatggta	tca	120
cctggacaag	ggcttgagtg	gatggatgg	atcagcg	ctt	acaatggtaa	180
gcacagaagg	tccaggc	ag	tcaccat	accacagaca	catccac	240
atggaggtga	ggagtctgag	atctgac	gac	acggccgt	tgt	300
ggtatggacg	tctggg	ccca	agggacc	ac	gtcaccg	345

<210> SEQ ID NO 121
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 121

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cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc	60
tccctgcactg gaaccagcag tgacgttggg gtgtataact ctgtctcctg gtaccaacag	120
caccaggca aaccccccua actcatgatt tatgagggtca gtaatcgcc ctcaggggtt	180
tctaattcgct tctctggctc caagtctggc aatacggcct ccctgaccat ctctgggctc	240
caggctgagg acgaggctga ttatttctgc agtcataca aagcaccag catggtcttc	300
ggcggaggga ccaagctgac cgtccta	327

<210> SEQ ID NO 122
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 122

caggttcagc tgggtcagtc tggagcttagt gtgaagaggc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta caccttggacc agctatggta tcagctgggt gcgcacaggcc	120
cctggacaag ggcttgagtg gatggatgg atcagcggtt acaatggtaa cacaactat	180
gcacagaagg tccaggcagc agtcaccatg accacagaca catccacgag cacagtctac	240
atggagctga ggagccttagt ctctgacgac acggccgtgtt attactgtgc gagaggctac	300
ggtatggacg tctggggcca agggaccacg gtcaccgtct cctca	345

<210> SEQ ID NO 123
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc	60
tccctgcaactg gaaccagcag tgacgttggg gtgtataact ctgtctcctg gtaccaacag	120
caccaggca aaccccccua actcatgatt tatgagggtca gtaatcgcc ctcaggggtt	180
tctattcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc	240
caggctgagg acgaggctga ttatttctgc agtcataca aagcaccag catggtcttc	300
ggcggaggga ccaagctgac cgtccta	327

<210> SEQ ID NO 124
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

caggttcagc tgggtcagtc tggagcttagt gtgaagaaggc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta ccccttggacc agctatggta tcagctgggt gcgcacaggcc	120
cctggacaag ggcttgagtg gatggatgg atcagcggtt acaatggtaa cacaactat	180
gcacagaagg tccaggcagc agtcaccatg accacagaca catccacgag cacagtctac	240
atggagttga ggagccttagt ctctgacgac acggccgtgtt attactgtgc gagaggctac	300
ggtatggacg tctggggcca agggaccacg gtcaccgtct cctca	345

<210> SEQ ID NO 125
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 125

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cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc	60
tccctgcactg gaaccagcag tgacgttggg ggttataact ctgtctcctg gtaccaacag	120
caccaggca aaccccccua actcatgatt tatgagggtca gtaatcgcc ctcaggggtt	180
tctaatacgct tctctggctc caagtctggc aatacggcct ccctgaccat ctctgggctc	240
caggctgagg acgaggctga ttatttctgc agtcataca aagcaccag catggtcttc	300
ggcggaggaga ccaagctgac cgtccta	327

<210> SEQ ID NO 126
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

caggttcagt tggtgcaagt tggagcttagt gtgaagaagc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta cgccttggacc agctatggta tcagctgggt gcgacaggcc	120
cctggacaag ggcttggatgt gatgggatgg atcagcgctt acaatggtaa cacaaactat	180
gcacagaagg tccaggcggcag agtcaccatg accacagaca catccacgag cacagctac	240
atggagctga ggagccttagt atctgacgac acggccgtgtt attactgtgc gagaggctac	300
ggtatggacg tctggggcca agggaccacg gtcaccgtct cctca	345

<210> SEQ ID NO 127
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 127

cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc	60
tccctgcaactg gaaccaacag tgacgttggg ggttataact ctgtctcctg gtaccaacag	120
caccaggca aaccccccua actcatgatt tatgagggtca gtaatcgcc ctcagggatt	180
tctaatacgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc	240
caggctgagg acgaggctga ttatttctgc agtcataca aagcaccag catggtcttc	300
ggcggaggaga ccaagctgac cgtccta	327

<210> SEQ ID NO 128
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

caggttcagc tggtgcaagt tggagcttagt gtgaagaagc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta cagcttacc agctatggta tcagctgggt gcgacaggcc	120
cctggacaag ggcttggatgt gatgggatgg gtcagcgctt acaatggtaa cacaaactat	180
gcacagaagt tccaggcggcag agtcaccatg accacagaca catccacgag cacagctac	240
atggaaactga ggagccttagt atctgacgac acggccgtgtt attactgtgc gagaggctac	300
ggttatggacg tctggggcca agggaccacg gtcaccgtct cctca	345

<210> SEQ ID NO 129
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

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cagtctgccc tgactcagcc tgcctccgtt tctgggtctc ctggacagtc gatcaccatc	60
tcctgtcactg gaaccagcag tgacgttggg gcttataact ctgtctcctg gtaccaacag	120
caccaggca aagcccccaa acgcatgatt tatgaggtca gtaatcgcc ctcaggggtt	180
tctaatacgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc	240
caggctgagg acgaggctga ttattactgc agctcatata caagcaccaa catggattc	300
ggcggaggga ccaagctgac cgcccta	327

<210> SEQ ID NO 130
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 130

caggtacagt tgcagcagtc aggtccagga ctggtaagc cctcgacac cctctcaactc	60
acctgtgcca tctccgggaa cagtgtctct agcaacagtg ctgcttgaa ctggatcagg	120
cagtccccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggat	180
aaaaattatt cagtatctgt gaaaagtgcg ataaccatca acccagacac atccaagaac	240
cagttctctc tgcaactgaa ctctgtgact cccgggaca cggctgtgta ttactgtgca	300
agaggggggc caactgctgc ttttactac tggggccagg gaaccctggg caccgtctcc	360
tca	363

<210> SEQ ID NO 131
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 131

ctttctgccc tgactcagcc tgcctccgtt tctgggtctc ctggacagtc gatcaccatc	60
tcctgtcactg gaaccagcag ttagtgggg aattataacc ttgtctcctg gtaccaacag	120
tattcaggca aagcccccaa actcatgatt tatgaggtca gtaagcgcc ctcaggggtt	180
tctaatacgct tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc	240
caggctgagg acgaggctga ttattactgc tgctcatatg caggttagtag cactttggtt	300
tccggcggag ggaccaagct gaccgtctca	330

<210> SEQ ID NO 132
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 132

gaggtgcagt tggtggagtc tggggggggc ttggtccagc ctggggggc cctgagactc	60
tcctgtgttag tctctggatt caccttagt agctattgga tgagctgggt ccgccaggct	120
ccagggaaagg ggctggagtg ggtggccaa ataaagcaag atggaagtga gaaatactat	180
gtggactctg tgaaggcccg attcaccatc tccagagaca acgccaagaa ctcactgtat	240
ctgcaaatacgac acggcctgag agccgaggac acggctgtat attactgtgc gagagagtca	300
aactggggat ttgctttga tatctggggc caagggacaa tggtcaccgt ctcttca	357

<210> SEQ ID NO 133
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 133

cagtctgtgc	tgactcagcc	accctcagcg	tctgggaccc	ccgggcagag	ggtcaccatc	60
tcttgttctg	gaaggcagtc	caacatcgga	agtaagactg	taaactggta	ccaacaggtc	120
ccaggaacgg	cccccaaact	cctcatctat	aggaataatc	agcggccctt	aggggtccct	180
gaccgattct	ctggctccaa	gtctggcacc	tcagcctccc	tggccatcg	tgggctccag	240
tctgaggatg	aggctgatta	ttattgtgca	gcatggatg	acagcctgaa	ttgggtgttc	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 134

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

gaggtgcagc	tggtggagtc	tgggggaggc	ttggtccagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttttagt	cgctatttga	tgagctgggt	ccgcccaggct	120
ccagggaaagg	ggctggagtg	ggtggccaaac	ataaaagcatg	atggaaagtga	gaaataactat	180
gtggactctg	tgaaggccg	attcaccatt	tccagagaca	acgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagagtca	300
aactgggat	ttgctttga	tgtctggggc	cacgggacaa	tggtcaccgt	ctcttca	357

<210> SEQ ID NO 135

<211> LENGTH: 327

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 135

cagtctgtgc	tgactcagcc	accctcagcg	tctgggcccc	ccggacagag	ggtcaccatc	60
tcttgttctg	gaaggcagtc	caacatcgga	agtaataactg	taaactggta	ccagcagtc	120
ccaggaacgg	cccccaaact	cctcatctat	agtaataatc	ggcggccctt	aggggtccct	180
gaccgattct	ctggctccaa	gtctggcacc	tcagcctccc	tggccatcg	tgggctccag	240
tctgaggatg	aggctgatta	ttactgtgca	gcatggatg	acagcctgaa	ttgggtgttc	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 136

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

gaggtgcagc	tgtggagtc	tgggggaggc	ttggtacagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttttagc	agctatgcac	tgagctgggt	ccgcccaggct	120
ccagggaaagg	ggctggagtg	ggctctcaact	attagtggta	gtgggtggtag	gacatattac	180
gcagactccg	tgaaggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtat	attactgtgc	gaaagaagtt	300
ggcagtcctt	ttgactactg	gggccaggga	accctggtca	ccgtctcctc	a	351

<210> SEQ ID NO 137

<211> LENGTH: 330

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 137

cagtcgtgt	tgacgcagcc	gcctcagtg	tctgcggccc	caggacagaa	ggtcaccatc	60
tcctgctctg	gaagcaactc	caacattggg	aataattatg	tatcctggta	ccagcagctc	120
ccaggaacag	cccccaaact	cctcatttat	gacaataata	agcgaccctc	agggattcct	180
gaccgattct	ctggctccaa	ctctggcagc	ttagccaccc	tgggcatcac	cggaactccag	240
actggggacg	aggccgatta	ttactgcegga	acatgggata	gcagectgag	tgctgtggta	300
ttcggcggag	ggaccaagct	gaccgtctta				330

<210> SEQ ID NO 138

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

caggtgcagc	tggtggagtc	tgggggaggc	gtggtccagc	ctgggaggtc	cctgagactc	60
tcctgtcag	cgtctggatt	cacccctcagt	agctatggca	tgcactgggt	ccggccaggct	120
ccaggcaagg	ggctggagtg	ggctggcaatt	atatggatg	atggaaagtaa	taaataactat	180
gcagactccg	tgaaggccg	attcaccatc	tccagagaca	attccaagaa	cacactgtat	240
cttcaaata	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gaggaggggg	300
ggtctggcag	ctcgccggg	cggtatggac	gtctggggcc	aagggaccac	ggtcaccgtc	360
tcctca						366

<210> SEQ ID NO 139

<211> LENGTH: 318

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

tcctatgagc	tgactcagcc	accctcagtg	tctgtgtccc	caggacagac	agccagaatc	60
acctgctctg	gagataaatt	ggggataaa	tatgcttgc	ggtatcagca	gaaaccaggc	120
cagtccctg	tgttgtcat	ctatcaaaat	accaagtggc	ccttagggat	ccctgagcga	180
ttctctggct	ccaaagtctgg	gaacacagtc	actctgacca	tcagcgggac	ccaggtatg	240
gatgaggctg	actattactg	tcaggcgtgg	gacagcagca	ctgtggatt	cgccggaggg	300
accaagctga	ccgtctta					318

<210> SEQ ID NO 140

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

caggtgcagc	tgcaggagtc	ggcccccagga	ctggtgaagc	cttcacagac	cctgtccctc	60
acctgcactg	tctctggtgg	ctccatcagc	agtagtgatt	actactggag	ctggatccgc	120
cagcacccag	ggaagggect	ggagtggatt	gggtacatct	attacagtgg	gagcacctac	180
tacaaccgt	ccctcaagag	tgcattacc	atatcgatag	acacgtctaa	gaacctgttc	240
tccctgaagt	tgagctctgt	gactgcccgc	gacacggccg	tgtattactg	tgcgagaggg	300
ggggtgacta	cgtactacta	cgctatggac	gtctggggcc	aagggaccac	ggtcaccgtc	360
tcctca						366

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<210> SEQ ID NO 141
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 141

gacatacaga tgacccagtc tccatctcc ctgtctgc	60
atcaactgcc gggcaagtca gcgcatttgc aactattaa	120
gggattgcc ctaagctctt gatctatgct gcatccagg	180
aggttcagtg gcagtggatc tgggacagat ttca	240
gaagattttg caacttacta ctgtcaacag agttacagta	300
gggaccaagg tggagatcaa a	321

<210> SEQ ID NO 142
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc	60
tcctgtgcag cgtctggatt caccttcagt agctatggca	120
ccaggcaagg ggctggagtg ggtggcaggat atatggatg	180
gcagactccg tgaaggggcg attcaccatc tccagagaca	240
ctgcaaatga acagcctgag agccgaggac acggctgtgt	300
ggtcccttga aacttacta ctacggatg gacgtctggg	360
gttccttca	369

<210> SEQ ID NO 143
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

gatattgtga tgactcagtc tccactctcc ctgtccgtca	60
atctcctgca ggtcttagtca gagcctctg catalgat	120
tacctgcaga agccagggca gtctccacaa ctccgtatct	180
tccggggtcc ctgacagggtt cagtggcagt ggtcaggca	240
agcagagtgg aggctgagga tttttttttt tattactgca	300
ttcactttcg gccctggac caaaatggat atcaaa	336

<210> SEQ ID NO 144
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 144

gaggtgcagc tgggtggagtc tgggggaggc ttgggtccagc	60
tcctgtgcag cctctggact cacctttagt aacttttgg	120
ccaggaaagg ggctggagtg ggtggccaac ataaagcaag	180
gtggactctg tgaaggggcg attcaccatc tccagagaca	240
ctgcaaatga acagcctgag agccgaggac acggctgtgt	300
aactggggat ttgttttga tatctggggc caagggacaa	357
ttggcacccgt ctcttca	

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<210> SEQ ID NO 145
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 145

```
cagtctgtgc tgactcagcc accctcagcg tctgggaccc cggggcagag ggtcaccatc      60
tcttgttctg gaagcagctc caacatcgga agtaaaaactg taaactggta ccagcagttc      120
ccaggaacgg ccccccaaact cctcatatat agtaataatc ggccgcctc aggggtccct      180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240
tctgaggatg aggctgatta ttactgtgca gcatggatg acagcctgaa ttgggtgttc      300
ggcgcaggga ccaagctgac cgtccta                                         327
```

<210> SEQ ID NO 146
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 146

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caggttcagc tggtgcaagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta cacctttacc agctatggta tcagctgggt gcgcacaggcc      120
cctggacaag ggcttgagtg gatgggatgg atcagcacctt acaatggtaa cacaactat      180
gcacagaagg tccaggcag agtcaccatg accacagaca catccacggag cacaactac      240
atggagctga ggagcctgag atctgacgac acggccgtt attactgtgc gagagggtat      300
actcgggact actggggcca gggAACCTG gtcaccgtct cctca                                         345
```

<210> SEQ ID NO 147
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 147

```
cagectgtgc tgactcagcc actttttgca tcagcctccc tgggagcctc ggtcacactc      60
acctgcaccc tgagcagggc ctacagtagt tatgaagtgg actggatcga gcagagacca      120
gggaaggggcc cccgggttgc catgcgagtg gacactgggt ggattgtggg atccaagggg      180
gaaggcatcc ctgatcgctt ctcagttttg ggctcaggcc tgaatcggtt tctgaccatc      240
aagaacatcc aggaagagga tgagagtgac taccactgtg gggcagacca tggcagtgg      300
accaacttcg tggtggtatt cggcggaggg accaagctga ccgtccta                                         348
```

<210> SEQ ID NO 148
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 148

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caggtgcagc tacagcagtg gggcgccagga ctgttgaagc ctccggagac cctgtccctc      60
acctgcgcgtg tctatggtgg gtccttcagt gcgtactact ggaactggat ccggccagccc      120
ccagggaaagg ggctggagtg gattggggaa atcaatcata gtggaagaac cgactacaac      180
ccgtccctca agagtcgagt caccatcata gtagacacgt ccaagaagca gttcccttg      240
aagctgaact ctgtgaccgc cgccggacacg gctgtgtatt actgtgcgag agggcagctc      300
gtcccccttg actactgggg ccagggaaacc ctggtcaccg tctttca                                         348
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<210> SEQ ID NO 149
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 149

cagtctgtgc tgactcagcc accctcagcg tctgggaccc cggggcagag ggtcaccatc      60
tcttgttctg gaagcagctc caacatcgga agtaatactg taaattggta tcagcaactc      120
ccaggaacgg ccccccaaact cctcatatat agtaataatc agcggccctc aggggtccct      180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240
tctgaggatg aggctgatta ttactgtgca gtatggatg acagcctgaa tggttgggtg      300
ttcggcggag ggaccaagct gaccgtctta                                         330

<210> SEQ ID NO 150
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 150

caggttcagc tggtgcaagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta cacctttccc agctatggta tcagctgggt gcgcacaggcc      120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaactat      180
gcagagaagc tccaggcag agtcaccatg accacagaca catccacgag cacagctac      240
atggaggtga ggagcctgag atctgacgac acggccgtgt tttactgtgc gagaggtac      300
gttatggacg tctggggcca agggaccacg gtcaccgtct cctct                                         345

<210> SEQ ID NO 151
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 151

cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc      60
tcctgcaactg gaaccagcag tgacggtggt cgttataatt ctgtctctg gtaccaacac      120
cacccaggca aagcccccaa agtcatgatt tatgaggtca gtaatggcc ctcaggggtt      180
tctactcgct tctctggctc caagtctggc aacacggctt ccctgaccat ctctggctc      240
caggctgagg acgaggctga ttattactgc agtcataata caagcagcag cgttgtattc      300
ggcggaggaga ccaaactgac cgtctta                                         327

<210> SEQ ID NO 152
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 152

gaggtgcagc tggtgaggatc tgggggaggc ctggtcaagc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacttcagt agctatagca tgaactgggt ccggcaggct      120
ccagggaaagg ggctggagtg ggtctcatcc attagtagta gtagtagtta catttctac      180
gcagactcag tgaaggcccg attcaccatc tccagagaca acggcaagaa ctcactgtat      240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt atttctgtgc gagagattac      300
gatttttggta gtgcttacta ttagtgcctttt gatgtctggg gccaaggac aatggtcacc      360

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gtctcttca	369
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<210> SEQ ID NO 153
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 153

cagtctgtgc tgacgcagcc	60
gccttcagtg tctggggccc	
cagggcagag ggtcaccatc	
tcctgcactg ggaggcagtc	120
caacatcgaa gcagggttatg	
atgtacactg gtaccaggcag	
cttccaggaa cagcccccaa	180
actcctcatc tctggtaaca	
gcaatcgcc ctcaggggtc	
cctgaccgat tctctggc	240
caagtctggc acctcagcct	
ccctggccat cactgggctc	
caggctgagg atgaggctga	300
ttattactgc cagtcctatg	
acagcagcct gagtggttcg	
gtattcggcg gagggaccaa	333
gctgaccgtc cta	

<210> SEQ ID NO 154
<211> LENGTH: 326
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 154

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg	
1 5 10 15	

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr	
20 25 30	

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser	
35 40 45	

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr	
65 70 75 80	

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys	
85 90 95	

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro	
100 105 110	

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	
115 120 125	

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	
130 135 140	

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly	
145 150 155 160	

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn	
165 170 175	

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp	
180 185 190	

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro	
195 200 205	

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu	
210 215 220	

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn	
225 230 235 240	

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	
245 250 255	

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
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320

Leu Ser Leu Ser Leu Gly Lys
325

<210> SEQ ID NO 156

<211> LENGTH: 105

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 156

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
20 25 30

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
35 40 45

Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> SEQ ID NO 157

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> SEQ ID NO 158

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 158

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Ser Val Ser
1 5 10

<210> SEQ ID NO 159

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 159

Thr Gly Thr Asn Ser Asp Val Gly Gly Tyr Asn Ser Val Ser
 1 5 10

<210> SEQ ID NO 160

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

Thr Gly Thr Ser Ser Asp Val Gly Ala Tyr Asn Ser Val Ser
 1 5 10

<210> SEQ ID NO 161

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

Thr Gly Thr Ser Ser Asp Val Gly Arg Tyr Asn Ser Val Ser
 1 5 10

<210> SEQ ID NO 162

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 162

Glu Val Ser Asn Arg Pro Ser
 1 5

<210> SEQ ID NO 163

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 163

Glu Val Thr Asn Arg Pro Ser
 1 5

<210> SEQ ID NO 164

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 164

Ser Ser Tyr Thr Ser Thr Ser Met Val
 1 5

<210> SEQ ID NO 165

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 165

Asn Ser Tyr Thr Ser Thr Ser Met Val
 1 5

<210> SEQ ID NO 166

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 166

Ser Ser Tyr Thr Ser Thr Asn Met Val

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1 5

<210> SEQ ID NO 167
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 167

Ser Ser Tyr Thr Ser Ser Ser Val Val
1 5

<210> SEQ ID NO 168
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

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

<210> SEQ ID NO 169
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 169

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

<210> SEQ ID NO 170
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 170

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

<210> SEQ ID NO 171
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 171

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

<210> SEQ ID NO 172
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 172

Gly Tyr Ser Phe Thr Ser Tyr Gly Ile Ser
1 5 10

<210> SEQ ID NO 173
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

Gly Tyr Thr Phe Pro Ser Tyr Gly Ile Ser
1 5 10

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<210> SEQ ID NO 174
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 174

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val Gln
1 5 10 15

Gly

<210> SEQ ID NO 175
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

Trp Val Ser Phe Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> SEQ ID NO 176
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

Trp Ile Ser Phe Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val Gln
1 5 10 15

Gly

<210> SEQ ID NO 177
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 177

Trp Ile Ser Val Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val Gln
1 5 10 15

Gly

<210> SEQ ID NO 178
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

Trp Val Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 179
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Glu Lys Leu Gln
1 5 10 15

Gly

<210> SEQ ID NO 180
<211> LENGTH: 6

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 180

Gly Tyr Gly Met Asp Val
1 5

<210> SEQ ID NO 181
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 181

Gly Tyr Val Met Asp Val
1 5

<210> SEQ ID NO 182
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182

Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Asn Phe Val Ser
1 5 10

<210> SEQ ID NO 183
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 183

Asp Tyr Asn Lys Arg Pro Ser
1 5

<210> SEQ ID NO 184
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 184

Asp Ser Asn Lys Arg Pro Ser
1 5

<210> SEQ ID NO 185
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

Gly Thr Trp Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> SEQ ID NO 186
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

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

<210> SEQ ID NO 187
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 187

Gly	Thr	Trp	Asp	Ser	Ser	Leu	Ser	Ser	Tyr	Val
1		5				10				

<210> SEQ ID NO 188

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 188

Gly	Phe	Thr	Phe	Ser	Ser	Phe	Gly	Met	His
1		5				10			

<210> SEQ ID NO 189

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 189

Gly	Phe	Thr	Phe	Asn	Ser	Phe	Gly	Met	His
1		5				10			

<210> SEQ ID NO 190

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

Gly	Phe	Thr	Phe	Arg	Ser	Tyr	Gly	Met	His
1		5				10			

<210> SEQ ID NO 191

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

Leu	Ile	Trp	Asn	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1		5			10		15								

Gly

<210> SEQ ID NO 192

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

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

Gly

<210> SEQ ID NO 193

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

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

Gly

<210> SEQ ID NO 194

<211> LENGTH: 17

-continued

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

Leu	Ile	Trp	His	Asp	Gly	Ser	Asn	Thr	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5				10				15			

Gly

<210> SEQ ID NO 195

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

Ala	Ile	Ala	Ala	Leu	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
1				5				10			

<210> SEQ ID NO 196

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

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

<210> SEQ ID NO 197

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

Ser	Gly	Ser	Ser	Asn	Ile	Gly	Ser	Asn	Thr	Val	Asn
1				5				10			

<210> SEQ ID NO 198

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 198

Ser	Gly	Ser	Ser	Asn	Ile	Gly	Ser	Lys	Thr	Val	Asn
1				5				10			

<210> SEQ ID NO 199

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 199

Ser	Asn	Asn	Arg	Arg	Pro	Ser
1			5			

<210> SEQ ID NO 200

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 200

Arg	Asn	Asn	Gln	Arg	Pro	Leu
1			5			

<210> SEQ ID NO 201

<211> LENGTH: 10

<212> TYPE: PRT

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 201

Ala	Ala	Trp	Asp	Asp	Ser	Leu	Asn	Trp	Val
1		5				10			

<210> SEQ ID NO 202

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 202

Gly	Phe	Thr	Phe	Ser	Arg	Tyr	Trp	Met	Ser
1		5			10				

<210> SEQ ID NO 203

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 203

Gly	Leu	Thr	Phe	Ser	Asn	Phe	Trp	Met	Ser
1		5			10				

<210> SEQ ID NO 204

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 204

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Trp	Met	Ser
1		5			10				

<210> SEQ ID NO 205

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 205

Asn	Ile	Lys	His	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1		5			10			15							

Gly

<210> SEQ ID NO 206

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 206

Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1		5			10			15							

Gly

<210> SEQ ID NO 207

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 207

Glu	Ser	Asn	Trp	Gly	Phe	Ala	Phe	Asp	Val
1		5			10				

<210> SEQ ID NO 208

<211> LENGTH: 10

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 208

Glu Ser Asn Trp Gly Phe Ala Phe Asp Ile
1 5 10

<210> SEQ ID NO 209

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 209

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> SEQ ID NO 210

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 210

Arg Ala Ser Gln Ser Ile Ser Ile Tyr Leu Asn
1 5 10

<210> SEQ ID NO 211

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 211

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> SEQ ID NO 212

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 212

Ala Ala Ala Ser Leu Gln Ser
1 5

<210> SEQ ID NO 213

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 213

Gln Gln Ser Tyr Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 214

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 214

Gln Gln Ser Tyr Ser Ala Pro Ile Thr
1 5

<210> SEQ ID NO 215

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 215

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Asn
1			5					10	

<210> SEQ ID NO 216

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 216

Thr	Ile	Ser	Gly	Ser	Gly	Asp	Asn	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10				15			

Gly

<210> SEQ ID NO 217

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 217

Thr	Ile	Ser	Gly	Ser	Gly	Gly	Asn	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10				15			

Gly

<210> SEQ ID NO 218

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 218

Lys	Phe	Val	Leu	Met	Val	Tyr	Ala	Met	Leu	Asp	Tyr
1				5				10			

<210> SEQ ID NO 219

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 219

Arg	Ala	Ser	Gln	Arg	Ile	Ser	Asn	Tyr	Leu	Ser
1				5				10		

<210> SEQ ID NO 220

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 220

Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Tyr	Asn	Phe	Leu	Asn
1				5				10			15				

<210> SEQ ID NO 221

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 221

Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Asn	Tyr	Asn	Leu	Val	Ser
1				5				10				15	

<210> SEQ ID NO 222

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 222

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
 1 5 10

<210> SEQ ID NO 223

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 223

Thr Gly Ser Ser Ser Asn Ile Gly Ala His Tyr Asp Val His
 1 5 10

<210> SEQ ID NO 224

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 224

Ser Gly Ser Asn Ser Asn Ile Gly Asn Asn Tyr Val Ser
 1 5 10

<210> SEQ ID NO 225

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 225

Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala Cys
 1 5 10

<210> SEQ ID NO 226

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 226

Thr Leu Ser Ser Gly Tyr Ser Ser Tyr Glu Val Asp
 1 5 10

<210> SEQ ID NO 227

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 227

Leu Gly Ser His Arg Ala Ser
 1 5

<210> SEQ ID NO 228

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 228

Glu Val Ser Lys Arg Pro Ser
 1 5

<210> SEQ ID NO 229

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 229

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Gly Asn Ser Asn Arg Pro Ser
1 5

<210> SEQ ID NO 230
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 230

Gly Asn Thr Tyr Arg Pro Ser
1 5

<210> SEQ ID NO 231
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 231

Ser Asn Asn Gln Arg Pro Ser
1 5

<210> SEQ ID NO 232
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 232

Asp Asn Asn Lys Arg Pro Ser
1 5

<210> SEQ ID NO 233
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 233

Gln Asn Thr Lys Trp Pro Leu
1 5

<210> SEQ ID NO 234
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 234

Val Asp Thr Gly Gly Ile Val
1 5

<210> SEQ ID NO 235
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 235

Gln Gln Ser Tyr Ser Thr Pro Leu Ile
1 5

<210> SEQ ID NO 236
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 236

Met Gln Val Leu Gln Thr Pro Phe Thr
1 5

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<210> SEQ ID NO 237
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 237

Cys	Ser	Tyr	Ala	Gly	Ser	Ser	Thr	Leu	Val
1			5				10		

<210> SEQ ID NO 238
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 238

Gln	Ser	Tyr	Asp	Ser	Ser	Leu	Ser	Gly	Ser	Val
1			5			10				

<210> SEQ ID NO 239
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 239

Gln	Ser	Tyr	Asp	Asn	Ser	Leu	Ser	Gly	Val	Val
1			5			10				

<210> SEQ ID NO 240
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 240

Ala	Val	Trp	Asp	Asp	Ser	Leu	Asn	Gly	Trp	Val
1			5			10				

<210> SEQ ID NO 241
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 241

Gly	Thr	Trp	Asp	Ser	Ser	Leu	Ser	Ala	Val	Val
1			5			10				

<210> SEQ ID NO 242
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 242

Gln	Ala	Trp	Asp	Ser	Ser	Thr	Val	Val
1			5					

<210> SEQ ID NO 243
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 243

Ser	Asp	Tyr	His	Cys	Gly	Ala	Asp	His	Gly	Ser	Gly	Thr	Asn	Phe	Val
1				5			10		15						

Val Val

-continued

<210> SEQ ID NO 244
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 244

Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser
1 5 10

<210> SEQ ID NO 245
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 245

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

<210> SEQ ID NO 246
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 246

Gly Phe Thr Phe Ser Ser Tyr Gly Met His
1 5 10

<210> SEQ ID NO 247
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 247

Gly Phe Thr Phe Ser Ser Tyr Ser Met Asn
1 5 10

<210> SEQ ID NO 248
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 248

Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr Trp Ser
1 5 10

<210> SEQ ID NO 249
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 249

Gly Gly Ser Ile Ser Ser Ser Asp Tyr Tyr Trp Ser
1 5 10

<210> SEQ ID NO 250
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 250

Gly Gly Ser Phe Ser Ala Tyr Tyr Trp Asn
1 5 10

<210> SEQ ID NO 251
<211> LENGTH: 12
<212> TYPE: PRT

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 251

Gly	Asp	Ser	Val	Ser	Ser	Asn	Ser	Ala	Ala	Trp	Asn
1			5			10					

<210> SEQ ID NO 252

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 252

Trp	Ile	Ser	Thr	Tyr	Asn	Gly	Asn	Thr	Tyr	Asn	Ala	Gln	Lys	Val	Gln
1			5		10			15							

Gly

<210> SEQ ID NO 253

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 253

Thr	Ile	Ser	Gly	Ser	Gly	Gly	Arg	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1			5			10		15							

Gly

<210> SEQ ID NO 254

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 254

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

Gly

<210> SEQ ID NO 255

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 255

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

Gly

<210> SEQ ID NO 256

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 256

Ser	Ile	Ser	Ser	Ser	Ser	Ser	Tyr	Ile	Ser	Tyr	Ala	Asp	Ser	Val	Lys
1			5			10		15							

Gly

<210> SEQ ID NO 257

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 257

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Tyr	Ile	Tyr	Asn	Ser	Gly	Ser	Thr	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5				10					15		

<210> SEQ ID NO 258
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 258

Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5				10					15		

<210> SEQ ID NO 259
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

Glu	Ile	Asn	His	Ser	Gly	Arg	Thr	Asp	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5				10					15		

<210> SEQ ID NO 260
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 260

Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Lys	Asn	Tyr	Ser	Val	Ser	Val
1				5				10					15		

Lys Ser

<210> SEQ ID NO 261
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 261

Gly	Tyr	Thr	Arg	Asp	Tyr
1				5	

<210> SEQ ID NO 262
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

Glu	Val	Gly	Ser	Pro	Phe	Asp	Tyr
1							5

<210> SEQ ID NO 263
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 263

Glu	Thr	Gly	Pro	Leu	Lys	Leu	Tyr	Tyr	Gly	Met	Asp	Val
1				5				10				

<210> SEQ ID NO 264
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 264

Arg Gly Gly Leu Ala Ala Arg Pro Gly Gly Met Asp Val

1 5 10

<210> SEQ ID NO 265

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 265

Asp Tyr Asp Phe Trp Ser Ala Tyr Tyr Asp Ala Phe Asp Val
1 5 10

<210> SEQ ID NO 266

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 266

Glu Asp Thr Ala Met Val Pro Tyr Phe Asp Tyr
1 5 10

<210> SEQ ID NO 267

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 267

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

<210> SEQ ID NO 268

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 268

Gly Gln Leu Val Pro Phe Asp Tyr
1 5

<210> SEQ ID NO 269

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 269

Gly Gly Pro Thr Ala Ala Phe Asp Tyr
1 5

<210> SEQ ID NO 270

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 270

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

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

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

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

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

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

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

<210> SEQ ID NO 271

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 271

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

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

Asn Ser Val Ser Trp Tyr Gln His Pro Gly Lys Ala Pro Lys Arg
 35 40 45

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

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

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

Asn Met Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO 272

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 272

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

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

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

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

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

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO 273

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 273

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

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

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

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

```

<210> SEQ ID NO 274
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 274

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

```

<210> SEQ ID NO 275
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 275

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

```

<210> SEQ ID NO 276
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 276

```
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Pro Gly Gln
```

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

<210> SEQ ID NO 277

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 277

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

<210> SEQ ID NO 278

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 278

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

```

<210> SEQ ID NO 279
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 279

Thr Leu Ser Ser Gly Tyr Ser Ser Tyr Glu Val Asp
1           5           10

<210> SEQ ID NO 280
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 280

Val Asp Thr Gly Gly Ile Val Gly Ser Lys Gly Glu
1           5           10

<210> SEQ ID NO 281
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 281

Gly Ala Asp His Gly Ser Gly Thr Asn Phe Val Val Val
1           5           10           15

<210> SEQ ID NO 282
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 282

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

Ser Val Thr Leu Thr Cys
20

<210> SEQ ID NO 283
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 283

Trp Tyr Gln Gln Arg Pro Gly Lys Gly Pro Arg Phe Val Met Arg
1           5           10           15

<210> SEQ ID NO 284
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 284

Gly Ile Pro Asp Arg Phe Ser Val Leu Gly Ser Gly Leu Asn Arg Tyr
1           5           10           15

Leu Thr Ile Lys Asn Ile Gln Glu Glu Asp Glu Ser Asp Tyr His Cys
20          25           30

<210> SEQ ID NO 285
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 285

```

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 1 5 10

<210> SEQ ID NO 286

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 286

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

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

Asn Ser Val Ser Trp Tyr Gln His His Pro Gly Lys Ala Pro Lys Val
 35 40 45

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Val Ser Thr Arg Phe
 50 55 60

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

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

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

<210> SEQ ID NO 287

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 287

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

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

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Pro Pro Lys Leu
 35 40 45

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

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

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

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

<210> SEQ ID NO 288

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 288

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

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

Asn Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Pro Pro Lys Leu
 35 40 45

Met Ile Tyr Glu Val Ser Asn Arg Pro Ser Gly Ile Ser Asn Arg Phe

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50 55 60

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

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

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

<210> SEQ ID NO 289

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 289

Gln Val His Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
 20 25 30

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

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

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

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

Ala Arg Ala Ile Ala Ala Leu Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110

Gly His Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 290

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 290

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Arg Gly Gly Leu Ala Ala Arg Pro Gly Gly Met Asp Val Trp
 100 105 110

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

<210> SEQ ID NO 291

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 291

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20          25          30

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

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

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

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

Ala Arg Ala Ile Ala Ala Leu Tyr Tyr Tyr Gly Met Asp Val Trp
100         105         110

Gly Gln Gly Thr Thr Val Thr Val Ser
115         120

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<210> SEQ ID NO 292

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<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 292

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20          25          30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50          55          60

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

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

Ala Arg Arg Gly Gly Leu Pro Gly Gly Met Asp Val Trp Gly Gln Gly
100         105         110

Thr Thr Val Thr Val Ser Ser
115

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<210> SEQ ID NO 293

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<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 293

cagtctgccc tgactcagcc tgcctccgtt tctgggtctc ctggacagtc gatcaccatc 60
tcctgcactg gaaccagcag tgacgttggt ggttataact ctgtctcctg gtaccaacag 120
cacccaggca aagcccccaa actcatgatt tatgagggtca gtaatcggtt ctcagggtt 180
tctaatacgct tctctggctc caagtctggc aacacggctt ccctgaccat ctctgggtc 240
caggctgagg acgaggctga ttattactgc aactcatata caagcaccag catggattc 300
ggcggaggaa ccaagctgac cgtccta 327

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<210> SEQ ID NO 294
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 294

cagtctgcc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gatcaccatc	60
tcctgcactg	gaaccagcag	tgacgttgg	ggttataact	ctgtctcctg	gtaccaacag	120
caccaggca	aacccccc	aaactcatgatt	tatgagggtca	gtaatcgcc	ctcagggtt	180
tctaatacgct	tctctggctc	caagtctggc	aacacggct	ccctgaccat	ctctggctc	240
caggctgagg	acgaggctga	ttatttctgc	agctcatata	caagcaccag	catggtctc	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 295
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 295

tcctatgagc	tgactcagcc	accctcagtg	tccgtgtccc	caggacagac	agccagaatc	60
acctgctctg	gagataaatt	ggggataaaa	tatgcttgct	ggtatcagca	gaagccaggc	120
cagtccccctg	tgctggtcat	ctatcaaata	accaagtggc	cccttagggat	ccctgagcga	180
ttctctggct	ccaagtctgg	gaacacagtc	actctgacca	tcagcggac	ccaggctatg	240
gataggctg	actattactg	tcaggcgtgg	gacagcagca	ctgtggatt	cgccggaggg	300
accaagctga	cgtccta					318

<210> SEQ ID NO 296
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 296

cagtctgcc	tgactcagcc	tgcctccgtg	tctgggtctc	ctggacagtc	gatcaccatc	60
tcctgcactg	gaaccagcag	tgacgttgg	ggttataact	ctgtctcctg	gtaccaacag	120
caccaggca	aagccccc	aaactcatgatt	tatgagggtca	gtaatcgcc	ctcagggtt	180
tctaatacgct	tctctggctc	caagtctggc	aacacggct	ccctgaccat	ctctggctc	240
caggctgagg	acgaggctga	ttatttactgc	aattcatata	caagcaccag	catggtattc	300
ggcggaggga	ccaagctgac	cgtccta				327

<210> SEQ ID NO 297
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 297

Glu	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1															15
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
	20														30
Asn	Ser	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
	35														45
Met	Ile	Tyr	Glu	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50														60
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu

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

<210> SEQ ID NO 298
<211> LENGTH: 230
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 298

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

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<210> SEQ ID NO 299
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 299

Glu	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1															
															15

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

Tyr	Asp	Val	His	Trp	Tyr	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu

Leu	Ile	Ser	Gly	Asn	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe
															60

Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu
															80

Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser
															95

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

Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu
															125

Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe
															140

Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val
															160

Lys	Ala	Gly	Val	Glu	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys

Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser
															190

His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu
															205

Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser

<210> SEQ ID NO 300
<211> LENGTH: 238
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 300

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1														

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
															30

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

Ser	Ser	Ile	Ser	Ser	Ser	Ser	Ser	Tyr	Ile	Ser	Tyr	Ala	Asp	Ser	Val
															60

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
															80

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

Ala	Arg	Asp	Tyr	Asp	Phe	Trp	Ser	Ala	Tyr	Tyr	Asp	Ala	Phe	Asp	Val
															110

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Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125

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

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

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

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

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

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

Ser Cys Ala Ala Asp Glu Val Asp His His His His His His
 225 230 235

<210> SEQ ID NO 301

<211> LENGTH: 218

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 301

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

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

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

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

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

Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Val Trp Asp Asp
 85 90 95

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

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

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

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

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

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

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

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> SEQ ID NO 302

<211> LENGTH: 231

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 302

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Ala Tyr
 20 25 30

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

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

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

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

Arg Gly Gln Leu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ala Ala Asp Glu Val
 210 215 220

Asp His His His His His
 225 230

<210> SEQ ID NO 303

<211> LENGTH: 680

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 303

Gln Glu Asp Glu Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg
 1 5 10 15

Ser Glu Glu Asp Gly Leu Ala Glu Ala Pro Glu His Gly Thr Thr Ala
 20 25 30

Thr Phe His Arg Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr
 35 40 45

Val Val Val Leu Lys Glu Glu Thr His Leu Ser Gln Ser Glu Arg Thr
 50 55 60

Ala Arg Arg Leu Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys
 65 70 75 80

Ile Leu His Val Phe His Gly Leu Leu Pro Gly Phe Leu Val Lys Met
 85 90 95

Ser Gly Asp Leu Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr
 100 105 110

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

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Glu Arg Ile Thr Pro Pro Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro
 130 135 140
 Asp Gly Gly Ser Leu Val Glu Val Tyr Leu Leu Asp Thr Ser Ile Gln
 145 150 155 160
 Ser Asp His Arg Glu Ile Glu Gly Arg Val Met Val Thr Asp Phe Glu
 165 170 175
 Asn Val Pro Glu Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser Lys
 180 185 190
 Cys Asp Ser His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp
 195 200 205
 Ala Gly Val Ala Lys Gly Ala Ser Met Arg Ser Leu Arg Val Leu Asn
 210 215 220
 Cys Gln Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe
 225 230 235 240
 Ile Arg Lys Ser Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu
 245 250 255
 Leu Pro Leu Ala Gly Gly Tyr Ser Arg Val Leu Asn Ala Ala Cys Gln
 260 265 270
 Arg Leu Ala Arg Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe
 275 280 285
 Arg Asp Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile
 290 295 300
 Thr Val Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr
 305 310 315 320
 Leu Gly Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Glu
 325 330 335
 Asp Ile Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln
 340 345 350
 Ser Gly Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met
 355 360 365
 Met Leu Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg
 370 375 380
 Leu Ile His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro
 385 390 395 400
 Glu Asp Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro
 405 410 415
 Ser Thr His Gly Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser
 420 425 430
 Ala His Ser Gly Pro Thr Arg Met Ala Thr Ala Ile Ala Arg Cys Ala
 435 440 445
 Pro Asp Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Lys
 450 455 460
 Arg Arg Gly Glu Arg Met Glu Ala Gln Gly Gly Lys Leu Val Cys Arg
 465 470 475 480
 Ala His Asn Ala Phe Gly Gly Glu Val Tyr Ala Ile Ala Arg Cys
 485 490 495
 Cys Leu Leu Pro Gln Ala Asn Cys Ser Val His Thr Ala Pro Pro Ala
 500 505 510
 Glu Ala Ser Met Gly Thr Arg Val His Cys His Gln Gln Gly His Val
 515 520 525
 Leu Thr Gly Cys Ser Ser His Trp Glu Val Glu Asp Leu Gly Thr His
 530 535 540
 Lys Pro Pro Val Leu Arg Pro Arg Gly Gln Pro Asn Gln Cys Val Gly
 545 550 555 560

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His Arg Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly Leu
 565 570 575
 Glu Cys Lys Val Lys Glu His Gly Ile Pro Ala Pro Gln Glu Gln Val
 580 585 590
 Thr Val Ala Cys Glu Glu Gly Trp Thr Leu Thr Gly Cys Ser Ala Leu
 595 600 605
 Pro Gly Thr Ser His Val Leu Gly Ala Tyr Ala Val Asp Asn Thr Cys
 610 615 620
 Val Val Arg Ser Arg Asp Val Ser Thr Thr Gly Ser Thr Ser Glu Glu
 625 630 635 640
 Ala Val Thr Ala Val Ala Ile Cys Cys Arg Ser Arg His Leu Ala Gln
 645 650 655
 Ala Ser Gln Glu Leu Gln Gly Ser Ser Asp Tyr Lys Asp Asp Asp Lys
 660 665 670
 His His His His His His His
 675 680

<210> SEQ ID NO 304
 <211> LENGTH: 680
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 304

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

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Leu Pro Leu Ala Gly Arg Tyr Ser Glu Val Leu Asn Arg Ala Cys Arg
 260 265 270
 Arg Leu Ala Glu Arg Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe
 275 280 285
 Glu Asp Asp Ala Cys Arg Tyr Ser Pro Ala Arg Ala Pro Glu Val Ile
 290 295 300
 Thr Val Gly Ala Thr Asn Arg Arg Arg Pro Val Arg Arg Gly Arg
 305 310 315 320
 Arg Gly Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Arg
 325 330 335
 Arg Ile Ile Gly Ala Ser Ser Arg Cys Ser Arg Cys Arg Arg Arg Arg
 340 345 350
 Ser Gly Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Arg
 355 360 365
 Met Leu Arg Arg Arg Pro Arg Leu Arg Arg Ala Arg Leu Arg Gln Glu
 370 375 380
 Leu Arg Arg Arg Ser Arg Arg Arg Arg Ile Arg Arg Arg Arg Phe Pro
 385 390 395 400
 Arg Arg Arg Glu Arg Leu Thr Pro Arg Leu Val Ala Arg Leu Pro Pro
 405 410 415
 Arg Arg Arg Arg Gly Arg Arg Leu Phe Cys Arg Thr Val Trp Ser
 420 425 430
 Arg Arg Ser Gly Pro Arg Glu Arg Ala Arg Ala Ile Ala Glu Cys Ala
 435 440 445
 Pro Arg Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Lys
 450 455 460
 Arg Arg Gly Glu Arg Met Glu Arg Gln Gly Lys Leu Val Cys Arg
 465 470 475 480
 Ala His Asn Ala Arg Arg Gly Arg Gly Val Tyr Ala Ile Ala Arg Cys
 485 490 495
 Cys Leu Leu Pro Gln Ala Arg Cys Ser Val His Arg Ala Pro Pro Ala
 500 505 510
 Arg Arg Arg Arg Gly Thr Glu Val Arg Cys Arg Arg Arg Gly His Val
 515 520 525
 Leu Thr Gly Cys Ser Ser His Trp Arg Arg Arg Asp Arg Gly Thr Arg
 530 535 540
 Lys Pro Pro Arg Leu Arg Pro Glu Gly Arg Pro Arg Gln Cys Val Gly
 545 550 555 560
 His Arg Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly Leu
 565 570 575
 Glu Cys Arg Arg Arg Arg Arg Ile Pro Ala Pro Arg Glu Arg Val
 580 585 590
 Thr Val Arg Cys Arg Arg Gly Trp Thr Leu Thr Gly Cys Ser Ala Leu
 595 600 605
 Pro Gly Thr Ser His Val Leu Gly Ala Tyr Ala Arg Asp Asn Thr Cys
 610 615 620
 Val Val Arg Ser Glu Asp Arg Arg Arg Arg Arg Arg Arg Arg Glu
 625 630 635 640
 Arg Val Thr Ala Val Ala Ile Cys Cys Glu Ser Glu His Leu Ala Gln
 645 650 655
 Ala Ser Gln Glu Leu Gln Gly Ser Ser Asp Tyr Lys Asp Asp Asp Lys
 660 665 670
 His His His His His His His

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<210> SEQ ID NO 305
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 305

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Ser Val Ser
1 5 10

<210> SEQ ID NO 306
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 306

Glu Val Ser Asn Arg Pro Ser
1 5

<210> SEQ ID NO 307
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 307

Ser Ser Tyr Thr Ser Thr Ser Met Val
1 5

<210> SEQ ID NO 308
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 308

Ser Tyr Gly Ile Ser
1 5

<210> SEQ ID NO 309
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 309

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Val Gln
1 5 10 15

Gly

<210> SEQ ID NO 310
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 310

Gly Tyr Gly Met Asp Val
1 5

<210> SEQ ID NO 311
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 311

Thr Gly Thr Ser Ser Asp Val Gly Arg Tyr Asn Ser Val Ser
1 5 10

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<210> SEQ ID NO 312
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 312

Glu Val Ser Asn Arg Pro Ser
1 5

<210> SEQ ID NO 313
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 313

Ser Ser Tyr Thr Ser Ser Ser Val Val
1 5

<210> SEQ ID NO 314
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 314

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Glu Lys Leu Gln
1 5 10 15

Gly

<210> SEQ ID NO 315
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 315

Gly Tyr Val Met Asp Val
1 5

<210> SEQ ID NO 316
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 316

Thr Gly Thr Ser Ser Asp Val Gly Ala Tyr Asn Ser Val Ser
1 5 10

<210> SEQ ID NO 317
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 317

Ser Ser Tyr Thr Ser Thr Asn Met Val
1 5

<210> SEQ ID NO 318
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 318

Trp Val Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

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Gly

<210> SEQ ID NO 319
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 319

Asn	Ser	Tyr	Thr	Ser	Thr	Ser	Met	Val
1							5	

<210> SEQ ID NO 320
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 320

Trp	Val	Ser	Phe	Tyr	Asn	Gly	Asn	Thr	Asn	Tyr	Ala	Gln	Lys	Leu	Gln
1				5				10					15		

Gly

<210> SEQ ID NO 321
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 321

Glu	Val	Thr	Asn	Arg	Pro	Ser
1					5	

<210> SEQ ID NO 322
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 322

Thr	Gly	Thr	Asn	Ser	Asp	Val	Gly	Gly	Tyr	Asn	Ser	Val	Ser
1					5				10				

<210> SEQ ID NO 323
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 323

Trp	Ile	Ser	Val	Tyr	Asn	Gly	Asn	Thr	Asn	Tyr	Ala	Gln	Lys	Val	Gln
1				5				10					15		

Gly

<210> SEQ ID NO 324
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 324

Trp	Ile	Ser	Phe	Tyr	Asn	Gly	Asn	Thr	Asn	Tyr	Ala	Gln	Lys	Val	Gln
1				5				10					15		

Gly

<210> SEQ ID NO 325
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 325

Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Phe Val Ser
 1 5 10

<210> SEQ ID NO 326

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

Asp Tyr Asn Lys Arg Pro Ser
 1 5

<210> SEQ ID NO 327

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 327

Gly Thr Trp Asp Ser Ser Leu Ser Gly Tyr Val
 1 5 10

<210> SEQ ID NO 328

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 328

Ser Phe Gly Met His
 1 5

<210> SEQ ID NO 329

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 329

Leu Ile Trp Asn Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> SEQ ID NO 330

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 330

Ala Ile Ala Ala Leu Tyr Tyr Tyr Gly Met Asp Val
 1 5 10

<210> SEQ ID NO 331

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 331

Asp Ser Asn Lys Arg Pro Ser
 1 5

<210> SEQ ID NO 332

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

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

<210> SEQ ID NO 333
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 333

Ser Tyr Gly Met His
 1 5

<210> SEQ ID NO 334
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 334

Leu Ile Trp His Asp Gly Ser Asn Thr Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> SEQ ID NO 335
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 335

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

<210> SEQ ID NO 336
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 336

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

Gly

<210> SEQ ID NO 337
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 337

Gly Thr Trp Asp Ser Ser Leu Ser Ser Tyr Val
 1 5 10

<210> SEQ ID NO 338
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 338

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

Gly

<210> SEQ ID NO 339
 <211> LENGTH: 13
 <212> TYPE: PRT

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 339

Ser Gly Ser Ser Ser Asn Ile Gly Ser Lys Thr Val Asn
 1 5 10

<210> SEQ ID NO 340

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

Ser Asn Asn Arg Arg Pro Ser
 1 5

<210> SEQ ID NO 341

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 341

Ala Ala Trp Asp Asp Ser Leu Asn Trp Val
 1 5 10

<210> SEQ ID NO 342

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 342

Tyr Trp Met Ser
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<210> SEQ ID NO 343

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 343

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> SEQ ID NO 344

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

Glu Ser Asn Trp Gly Phe Ala Phe Asp Ile
 1 5 10

<210> SEQ ID NO 345

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 345

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
 1 5 10

<210> SEQ ID NO 346

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 346

Arg Tyr Trp Met Ser
1 5

<210> SEQ ID NO 347

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 347

Asn Ile Lys His Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> SEQ ID NO 348

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 348

Glu Ser Asn Trp Gly Phe Ala Phe Asp Val
1 5 10

<210> SEQ ID NO 349

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 349

Arg Asn Asn Gln Arg Pro Leu
1 5

<210> SEQ ID NO 350

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 350

Ser Tyr Trp Met Ser
1 5

<210> SEQ ID NO 351

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 351

Asn Phe Trp Met Ser
1 5

<210> SEQ ID NO 352

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 352

Arg Ala Ser Gln Ser Ile Ser Tyr Leu Asn
1 5 10

<210> SEQ ID NO 353

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 353

Ala Ala Ser Leu Gln Ser
1 5

<210> SEQ ID NO 354

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 354

Gln Gln Ser Tyr Ser Pro Ile Thr
1 5

<210> SEQ ID NO 355

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 355

Arg Ala Ser Gln Ser Ile Ser Ile Tyr Leu Asn
1 5 10

<210> SEQ ID NO 356

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 356

Ala Ala Ala Ser Leu Gln Ser
1 5

<210> SEQ ID NO 357

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 357

Gln Gln Ser Tyr Ser Ala Pro Ile Thr
1 5

<210> SEQ ID NO 358

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 358

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> SEQ ID NO 359

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 359

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> SEQ ID NO 360

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 360

Gln Gln Ser Tyr Ser Ser Pro Ile Thr

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1 5

<210> SEQ ID NO 361
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

Ser Tyr Ala Met Asn
1 5

<210> SEQ ID NO 362
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 362

Thr Ile Ser Gly Ser Gly Asn Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 363
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 363

Lys Phe Val Leu Met Val Tyr Ala Met Leu Asp Tyr
1 5 10

<210> SEQ ID NO 364
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 364

Thr Ile Ser Gly Ser Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> SEQ ID NO 365
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 365

Thr Ile Ser Gly Ser Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> SEQ ID NO 366
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366

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

<210> SEQ ID NO 367
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 367

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

<210> SEQ ID NO 368
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

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

<210> SEQ ID NO 369
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

Gly Tyr Ser Phe Thr Ser Tyr Gly Ile Ser
1 5 10

<210> SEQ ID NO 370
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 370

Gly Tyr Thr Phe Pro Ser Tyr Gly Ile Ser
1 5 10

<210> SEQ ID NO 371
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 371

Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser
1 5 10

<210> SEQ ID NO 372
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 372

Gly Phe Thr Phe Ser Arg Tyr Trp Met Ser
1 5 10

<210> SEQ ID NO 373
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 373

Gly Leu Thr Phe Ser Asn Phe Trp Met Ser
1 5 10

<210> SEQ ID NO 374
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 374

Gly Phe Thr Phe Ser Ser Tyr Ala Met Asn
1 5 10

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<210> SEQ ID NO 375
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 375

Gly Phe Thr Phe Asn Ser Phe Gly Met His
1 5 10

<210> SEQ ID NO 376
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 376

Gly Phe Thr Phe Arg Ser Tyr Gly Met His
1 5 10

<210> SEQ ID NO 377
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 377

Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Val Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 378
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

Asn Ile Lys His Asp Gly Ser Glu Lys Tyr Val Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 379
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

Thr Ile Ser Gly Ser Gly Asp Asn Thr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 380
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 380

Thr Ile Ser Gly Ser Gly Gly Asn Thr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 381
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

Leu Ile Trp Asn Asp Gly Ser Asn Lys Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 382
<211> LENGTH: 16

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

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

<210> SEQ ID NO 383

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

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

<210> SEQ ID NO 384

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 384

Leu Ile Trp His Asp Gly Ser Asn Thr Tyr Val Asp Ser Val Lys Gly
1 5 10 15

<210> SEQ ID NO 385

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 385

Glu Ser Asn Trp Gly Phe Ala Phe Asp Ile
1 5 10

<210> SEQ ID NO 386

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

Glu Ser Asn Trp Gly Phe Ala Phe Asp Val
1 5 10

<210> SEQ ID NO 387

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 387

Gly Tyr Val Met Asp Val
1 5

<210> SEQ ID NO 388

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

Arg Ala Ser Gln Ser Ile Ser Ile Tyr Leu Asn
1 5 10

<210> SEQ ID NO 389

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 389

Thr Gly Thr Asn Ser Asp Val Gly Gly Tyr Asn Ser Val Ser
 1 5 10

<210> SEQ ID NO 390

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

Thr Gly Thr Ser Ser Asp Val Gly Ala Tyr Asn Ser Val Ser
 1 5 10

<210> SEQ ID NO 391

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 391

Thr Gly Thr Ser Ser Asp Val Gly Arg Tyr Asn Ser Val Ser
 1 5 10

<210> SEQ ID NO 392

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

Arg Asn Asn Gln Arg Pro Leu
 1 5

<210> SEQ ID NO 393

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 393

Ala Ala Ala Ser Leu Gln Ser
 1 5

<210> SEQ ID NO 394

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 394

Gln Gln Ser Tyr Ser Ala Pro Ile Thr
 1 5

<210> SEQ ID NO 395

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 395

Asn Ser Tyr Thr Ser Thr Ser Met Val
 1 5

<210> SEQ ID NO 396

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 396

Ser Ser Tyr Thr Ser Ser Ser Val Val

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

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

Thr Met Val Thr Val Ser
 115

<210> SEQ ID NO 402
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 402

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Asn Trp Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
 100 105 110

Thr Val Ser
 115

<210> SEQ ID NO 403
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 403

Glu Asn Leu Tyr Phe Gln
 1 5

<210> SEQ ID NO 404
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 1
 <223> OTHER INFORMATION: Xaa= D, A, R or no amino acid

<220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 2
 <223> OTHER INFORMATION: Xaa=Y, I, G or no amino acid

<220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 3
 <223> OTHER INFORMATION: Xaa=D, A, G or no amino acid

<220> FEATURE:

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<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=F, A, L or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=W, L, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=S, Y, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa=A, Y, R or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa=Y, P or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa=Y, G or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Xaa=D, G or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)...(11)
<223> OTHER INFORMATION: Xaa=A, M or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(12)
<223> OTHER INFORMATION: Xaa=F,D or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(13)
<223> OTHER INFORMATION: Xaa=D, V or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(14)
<223> OTHER INFORMATION: Xaa=V or no amino acid

<400> SEQUENCE: 404

Xaa Xaa
 1           5           10

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<210> SEQ ID NO 405
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=Q or G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=S, T, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=Y, W or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=D or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=S or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=S or no amino acid
<220> FEATURE:
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<222> LOCATION: (7) ... (7)
<223> OTHER INFORMATION: Xaa=L, T or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8) ... (8)
<223> OTHER INFORMATION: Xaa=A, S or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9) ... (9)
<223> OTHER INFORMATION: Xaa=G, A, V or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10) ... (10)
<223> OTHER INFORMATION: Xaa=S, Y, V or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11) ... (11)
<223> OTHER INFORMATION: Xaa=V or no amino acid

<400> SEQUENCE: 405

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Xaa Xaa
1           5           10

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<210> SEQ ID NO 406
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=Y, F or G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=L or F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=T, S or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=S or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7) ... (7)
<223> OTHER INFORMATION: Xaa=Y or F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8) ... (8)
<223> OTHER INFORMATION: Xaa=G, S or Y
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9) ... (9)
<223> OTHER INFORMATION: Xaa=I, M or W
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10) ... (10)
<223> OTHER INFORMATION: Xaa=S, N or H

<400> SEQUENCE: 406

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1           5           10

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<210> SEQ ID NO 407
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=T or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=G or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=S, T or G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=N, D or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7) ... (7)
<223> OTHER INFORMATION: Xaa=I, V or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8) ... (8)
<223> OTHER INFORMATION: Xaa=G or I
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9) ... (9)
<223> OTHER INFORMATION: Xaa=A or G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10) ... (10)
<223> OTHER INFORMATION: Xaa=G, Y, S or N
<220> FEATURE:
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<222> LOCATION: (11) ... (11)
<223> OTHER INFORMATION: Xaa=Y or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12) ... (12)
<223> OTHER INFORMATION: Xaa=D, S, T or F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13) ... (13)
<223> OTHER INFORMATION: Xaa=V
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14) ... (14)
<223> OTHER INFORMATION: Xaa=S, N or H

<400> SEQUENCE: 407

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Xaa												
1												10

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<210> SEQ ID NO 408
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=W, S, L or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=V, I or E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=S, W or I
<220> FEATURE:

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<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=F, S or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=Y, S, D or H
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=N, S or G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa=S or G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa=N, Y, D or R
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa=T, I or E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Xaa=N, S, Y or D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)...(11)
<223> OTHER INFORMATION: Xaa=Y
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)...(12)
<223> OTHER INFORMATION: Xaa=A and N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(13)
<223> OTHER INFORMATION: Xaa=Q, D or P
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(14)
<223> OTHER INFORMATION: Xaa=K or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (15)...(15)
<223> OTHER INFORMATION: Xaa=L or V
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(16)
<223> OTHER INFORMATION: Xaa=Q or K
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (17)...(17)
<223> OTHER INFORMATION: Xaa=G or S

<400> SEQUENCE: 408

Xaa Xaa
 1           5           10          15

Xaa

```

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<210> SEQ ID NO 409
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=G, E, S or D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=N, V or Y
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=S or N

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=N, Q or K
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=R
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=P
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7) ... (7)
<223> OTHER INFORMATION: Xaa=S

<400> SEQUENCE: 409

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

```

<210> SEQ ID NO 410
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=D or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=Y, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=D, I or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=F, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=W, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=S, L or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7) ... (7)
<223> OTHER INFORMATION: Xaa=A, Y, G or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8) ... (8)
<223> OTHER INFORMATION: Xaa=Y, Q or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9) ... (9)
<223> OTHER INFORMATION: Xaa=G, Y or L
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10) ... (10)
<223> OTHER INFORMATION: Xaa=Y, D or V
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11) ... (11)
<223> OTHER INFORMATION: Xaa=G, A or P
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12) ... (12)
<223> OTHER INFORMATION: Xaa=M or F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13) ... (13)
<223> OTHER INFORMATION: Xaa=D
<220> FEATURE:

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<221> NAME/KEY: VARIANT
 <222> LOCATION: (14)...(14)
 <223> OTHER INFORMATION: Xaa=V or Y

<400> SEQUENCE: 410

Xaa
 1 5 10

<210> SEQ ID NO 411
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 1
 <223> OTHER INFORMATION: Xaa=Q, A, G or no amino acid
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 2
 <223> OTHER INFORMATION: Xaa=S, V, T or no amino acid
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 3
 <223> OTHER INFORMATION: Xaa=Y, N or W
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 4
 <223> OTHER INFORMATION: Xaa=S or D
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 5
 <223> OTHER INFORMATION: Xaa=S, Y or D
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 6
 <223> OTHER INFORMATION: Xaa=S or T
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (7)...(7)
 <223> OTHER INFORMATION: Xaa=L or S
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (8)...(8)
 <223> OTHER INFORMATION: Xaa=S, T or N
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (9)...(9)
 <223> OTHER INFORMATION: Xaa=G, S or A
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (10)...(10)
 <223> OTHER INFORMATION: Xaa=S, M, W or Y
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (11)...(11)
 <223> OTHER INFORMATION: Xaa=V

<400> SEQUENCE: 411

Xaa
 1 5 10

<210> SEQ ID NO 412
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 1
 <223> OTHER INFORMATION: Xaa=G, P or A
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 2
 <223> OTHER INFORMATION: Xaa=Y, W, F, T or S
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 3

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<223> OTHER INFORMATION: Xaa=T, P, S, A, C, V, L or I
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=L, F, I, V, M, A or Y
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=T, P, S or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa=Y, W, F, T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa=G, P or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa=I, L, V, M, A or F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Xaa=S, T, A or C

<400> SEQUENCE: 412

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Xaa	Xaa	Xaa	Xaa
1	5	10	

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<210> SEQ ID NO 413
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=G, P or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=S, N, T, A, C or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=D or E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa=V, I, M, L, F or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa=G, P or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa=G, A, R, P, V, L, I, K, Q or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Xaa=Y, W, F, T or S

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11) ... (11)
<223> OTHER INFORMATION: Xaa=N or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12) ... (12)
<223> OTHER INFORMATION: Xaa=Y, S, W, F, T, S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13) ... (13)
<223> OTHER INFORMATION: Xaa=V, I, M, L, F, or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (14) ... (14)
<223> OTHER INFORMATION: Xaa=S, T, A or C

<400> SEQUENCE: 413

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Xaa Xaa
1           5           10

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<210> SEQ ID NO 414
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=W, Y or F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=V, I, M, L, F or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=A, F, V, L, I, Y or M
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=Y, W, F, T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=N or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7) ... (7)
<223> OTHER INFORMATION: Xaa=G, P or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8) ... (8)
<223> OTHER INFORMATION: Xaa=N or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9) ... (9)
<223> OTHER INFORMATION: Xaa=T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10) ... (10)
<223> OTHER INFORMATION: Xaa=N or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11) ... (11)
<223> OTHER INFORMATION: Xaa=Y, W, F, T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12) ... (12)
<223> OTHER INFORMATION: Xaa=A, V, L or I
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13) ... (13)
<223> OTHER INFORMATION: Xaa=Q, E, N or D
<220> FEATURE:

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<221> NAME/KEY: VARIANT
<222> LOCATION: (14)...(14)
<223> OTHER INFORMATION: Xaa=K, R, Q or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (15)...(15)
<223> OTHER INFORMATION: Xaa=L, F, V, I, M, A or Y
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (16)...(16)
<223> OTHER INFORMATION: Xaa=Q or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (17)...(17)
<223> OTHER INFORMATION: Xaa=G, P or A

<400> SEQUENCE: 414

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Xaa Xaa
1           5           10          15

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Xaa

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<210> SEQ ID NO 415
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=E or D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=V, I, M, L, F or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=N or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=R, K, Q or N
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=P or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa=S, T, A or C

<400> SEQUENCE: 415

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1           5

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<210> SEQ ID NO 416
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=G, P, A or no amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=Y, W, F, T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=G, V, P, A, I, M, L or F
<220> FEATURE:

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<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=M, L, F or I
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=D or E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=V, I, M, L, F or A

<400> SEQUENCE: 416

```

```

Xaa Xaa Xaa Xaa Xaa Xaa
1           5

```

```

<210> SEQ ID NO 417
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa=S, N, T, A, C or Q
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa=Y, W, F, T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa=T or S
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa=S, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Xaa=N, S, Q, T, A or C
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: Xaa=M, V, L, F, I or A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: Xaa=V, I, M, L, F or A

<400> SEQUENCE: 417

```

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1           5

```

```

<210> SEQ ID NO 418
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 418
```

caggtgcagg tggcgcagtc tggggctgag gtgaagaagc ctggggccctc agtgaaggtc	60
tcctgcaagg cttctggata caccttcacc ggctactata tacactgggt gcgacaggcc	120
cctggacaag ggcttgatgt gatggatgg atcaaccctc acagtggatgg cgcaaactat	180
gcacagaagt ttcaaggcag ggtcaccatg accagggaca cgtccatcg cacagctac	240

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atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaggcaac	300
tggaaactacg actactacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc	360
tca	363

<210> SEQ ID NO 419
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

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

<210> SEQ ID NO 420
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

gacatccaga tgacccagtgc tccatcctcc ctgtctgcat ctgttaggaga cagagtacc	60
atcaacttgcc gggcgagtca ggacatttgc aattatttag cctggtatca gcagaaacca	120
ggaaaggttc ctaagctctt gatctatgct gcatccactt tgcaatcagg ggtccatct	180
cggttcagtg gcagtggatc tggcacatg ttcaactctca ccatcagcag cctacagcct	240
gaagatgtt caaccttattt ctgtcaaagg tatcagatg ccccattcac ttccggccct	300
gggaccaagg tggatatcaa a	321

<210> SEQ ID NO 421
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 421

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

-continued

Glu Asp Val Ala Thr Tyr Phe Cys Gln Arg Tyr Gln Ile Ala Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> SEQ ID NO 422

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 422

caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctggggaggtc cctgagactc	60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccggcaggct	120
ccaggcaagg ggctggagtg ggtggcagtt atctggatg atggaagttac taaatactat	180
gcagactccg tgaagggccg atccaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatacg acaggcctgag agccgaggac acggctgtgtt attactgtgc gaggtcagtg	300
gctggtttacc actactacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc	360
tcctca	366

<210> SEQ ID NO 423

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 423

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Ser Val Ala Gly Tyr His Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110

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

<210> SEQ ID NO 424

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc	60
acatgccaag gagacagcct cagaggctat tatgcaacct ggtaccagca gaagccaaga	120
caggccccctg tacttgtcat ctatggtaaa aactaccggc cctcaggat cccagaccga	180
ttctctggct ccacactcagg aaacacagct tccttgacca tcactggggc tcaggcggaa	240
gatgaggctg actattactg taactcccg gacagcatg gtaaccatct ggtgttccgc	300
ggagggacca agctgaccgt ccta	324

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<210> SEQ ID NO 425
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 425

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

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

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

Gly Lys Asn Tyr Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Thr Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ile Gly Asn His
85 90 95

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

<210> SEQ ID NO 426
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 426

cagggtgcagc	tgggtggagtc	tgggggagggc	gtgggtccagc	ctggggaggtc	cctgagactc	60
tccctgtgcag	cgtctggatt	cacccatcgat	agctatggct	tgcactgggt	ccggccaggct	120
ccaggcaagg	ggctggagtg	ggtggcagt	atatggttag	atggaaagtaa	taaatactat	180
gcagactccg	tgaaggcccg	atccaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gaggtaactgt	300
gctggttacc	actactacta	cggtatggac	gtctggggcc	aagggaccac	ggtcaccgtc	360
tcctca						366

<210> SEQ ID NO 427
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 427

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Arg Ser Val Ala Gly Tyr His Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

-continued

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

<210> SEQ ID NO 428
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 428

tcttcgtgac	tgactcagga	ccotgctgtg	tctgtggcct	tgggacagac	agtcaggatc	60
acatgc	caag	gaga	cgtt	tttt	aa	120
caggccc	ctg	tactt	gtcat	cttggtaaa	aacaaccggc	180
ttctctggc	ccacctcagg	aaacacagct	tccttgacca	tcactggggc	tcaggcggaa	240
gatgaggc	tg	actattactg	taactcacgg	gacatcat	gtgaccatct	300
ggagggacca	agctgac	cttca				324

<210> SEQ ID NO 429
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 429

Ser	Ser	Glu	L	Leu	Thr	Gln	A	sp	P	ro	A	l	V	al	A	l	eu	G	ln															
1				5			10					15																						
Th	r	V	a	l	R	I	l	h	C	y	G	ln	G	sp	S	er	L	e	u	R	T	Y	T	Y	G									
20					25				30																									
Ser	T	r	p	T	y	G	ln	G	ln	L	y	s	P	o	R	G	ln	A	l	P	o	V	l	u	E									
35						40				45																								
G	ly	L	ys	A	n	A	n	R	g	P	o	S	er	G	ly	I	l	le	P	o	A	sp	S	er	G	ly								
50						55				60																								
Th	r	S	e	R	G	ly	A	n	S	er	L	e	u	T	h	R	I	l	h	G	ly	A	l	u	E									
65						70				75																								
A	s	p	G	lu	A	l	A	s	T	y	R	C	ys	A	n	S	er	g	A	sp	I	l	I	le	G	ly	A	l	u	E				
85						90				95																								
L	e	u	E	P	h	G	ly	T	h	R	I	l	h	G	ly	S	er	L	e	u	R	I	l	h	G	ly	A	l	u	E				
100						105																												

<210> SEQ ID NO 430
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 430

cagg	tggtggagtc	tgggggaggc	gtggtccagt	ctgggaggc	cctgagactc	60
tcct	gtgcag	cgtctggatt	cacccagg	aactatggca	tgcactgggt	120
ccagg	caagg	ggctggagtg	ggtggcagtt	atatggttt	atggaaat	180
gcag	actcc	tgaaggcgc	atccaccatc	tccagagaca	attccaagaa	240
ctg	cta	acagcctgag	agccgaggac	acggctgtgt	attactgtc	300
gct	gggttacc	actactacta	cggtatggac	gtctggggcc	aagggaccac	360
tcctca						366

<210> SEQ ID NO 431
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 431

```

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
 1           5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr
 20          25          30

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

Ala Val Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50          55          60

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

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

Ala Arg Ser Val Ala Gly Tyr His Tyr Tyr Gly Met Asp Val Trp
100         105         110

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

```

<210> SEQ ID NO 432

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

```

tcttcgtggc tgactcgagg ccctgctgtg tctgtggcct tggggacagac agtcaggatc      60
acatgccagg gagacagccct cagaagctat tatgcacatc ggtaccagca gaagccaaga      120
caggccccctg tacttgtcat ctatggtaaa aacaaccggc cctcaggatcccagaccga      180
atctctggct ccacctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa      240
gatgaggctg actattactg taaatcccg gacatcatcg gtgaccatct ggtgttcggc      300
ggagggacca aactgaccgt ccta                                         324

```

<210> SEQ ID NO 433

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 433

```

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Ile Ser Gly Ser
 50          55          60

Thr Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65          70          75          80

Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Ile Ile Gly Asp His
 85          90          95

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

```

<210> SEQ ID NO 434

<211> LENGTH: 342

<212> TYPE: DNA

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-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 434

caggtgcagc	tggtgaggc	tggggaggc	gtggccagc	ctggaggc	cctgagactc	60
tcctgtcag	cgtctggatt	cacccatgt	agctatggca	tgcactgggt	ccggcaggct	120
ccaggcaagg	ggctggagtg	ggtggcagtt	atatggtatg	atggaagtaa	taataactat	180
gcagactccg	tgaaggcccg	attcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgt	gagagatcgg	300
ggactggact	ggggccaggg	aaccctggtc	accgtctcct	ca		342

<210> SEQ ID NO 435

<211> LENGTH: 114

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 435

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

<210> SEQ ID NO 436

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 436

tcttcgtggc	tgactcgagga	ccctgctgtg	tctgtggcct	tgggacagac	agtcaggatc	60
acatgccaag	gagacagccct	cagaggctat	tatgcaagct	ggtaccagca	gaagccaaaga	120
caggccccctg	tacttgtcat	ctatggtaaa	aacaaccggc	cctcaggat	cccagaccga	180
ttctctggct	ccacacctcagg	aaacacacgt	tccttgacca	tcactggggc	tcaggoggaa	240
gatgaggctg	actattactg	taagtcccg	gacagcagtg	gtgaccatct	ggtgttccgc	300
ggagggacca	agctgaccgt	ccta				324

<210> SEQ ID NO 437

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 437

Ser	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln
1				5				10					15		
Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Gly	Tyr	Tyr	Ala
	20				25					30					

-continued

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Thr Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Ser Ser Gly Asp His
 85 90 95

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

<210> SEQ ID NO 438

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 438

caggtgcagg tggtgaggc tggggggaggc gtggccagc ctggggggtc cctgagactc 60
 tcctgtcagc cgtctggatt cacccatcg aactatggca tgcactgggt ccggcaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtag taaatactat 180
 gcagactccg tgaagggccg atccaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagccttag agccgaggac acggctgtgtt attactgtgc gaggtcagtg 300
 gctgggttacc actactacta cggtatggac gtctggggcc aagggaccac ggtcacccgtc 360
 tcctca 366

<210> SEQ ID NO 439

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 439

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

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

Ala Arg Ser Val Ala Gly Tyr His Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110

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

<210> SEQ ID NO 440

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 440

tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

-continued

acatgccaaag gagacagccct cagaggctat tatgcaagct ggtaccagca gaagccaaga	120
caggccccctg tacttgtcat ctatggtaaa aacaaccggc cctcaggatcccagaccga	180
ttctctggct ccacctcagg aaacacagct tccttgacca tcactggggc tcaggcgaa	240
gatgaggctg actattactg taagtcccg gacagcagtg gtgaccatct ggtgttcggc	300
ggagggacca agetgaccgt ccta	324

<210> SEQ ID NO 441

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 441

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

<210> SEQ ID NO 442

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 442

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggc cctgagtc	60
tcctgtcagc cgtctggatt cacttcagt agctatggca tgcactgggt ccgcaggct	120
ccaggcaagg ggctggagtg ggtggcaggat atatggatg atggaaagtttaaaaactat	180
gcagactccg tgaaggcccg atccaccatc tccagagaca actccaagaa cacgctgtat	240
ctgcaaatacga acagcctgag agccgaggac acggctgtgtt attattgtgc gaggtaagt	300
gctggttacc actactacta cggtatggac gtctggggcc aagggaccac ggtcacccgtc	360
tcctca	366

<210> SEQ ID NO 443

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 443

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

-continued

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

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

Ala Arg Ser Val Ala Gly Tyr His Tyr Tyr Gly Met Asp Val Trp
 100 105 110

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

<210> SEQ ID NO 444

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 444

```
tcttctgagc tgactcgaga ccctgctgtg tctgtggcct tgggacagac agtcaggatc        60
acatgccaaag gagacagccct cagaacctat tatgcaagct ggtaccagca gaagccaaga        120
caggcccccta ttcttgtcat ctatggtaaa aacaaccggc cctcaggatcccagaccga        180
ttctctggct ccacccctagg aatcacagct tccttgacca tcactggggc tcaggccgaa        240
gatgaggctg actattactg taaaatcccg gacatcattt gtaaccatct gctgttcggc        300
ggaggggacta agctgaccgt ccta                                                        324
```

<210> SEQ ID NO 445

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 445

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Thr Ser Gly Ile Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Ile Ile Gly Asn His
 85 90 95

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

<210> SEQ ID NO 446

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 446

```
caggtgcagc tggggcgctc tgggggaggc gtgggtccagc ctggggaggc cctgagactc        60
tcctgtgcag cgtctggatt caccctcagt agctatggca tgcactgggt ccggccaggct        120
ccaggccagg ggctggagtg ggtggcagtc atatggtatg atggaagtaa caaatactat        180
gcagccctccg tgaaggcccg attcaccatc tccagagaca attccaagaa cacgctgtat        240
ctgcaaatga acagtcttag agccgaggac acggctgtgtt attactgtgc gagaggggg        300
```

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ggttcgaaaa gtcatcgata ctactactac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctca	375

<210> SEQ ID NO 447
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 447

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

<210> SEQ ID NO 448
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 448

tcttctgagc	tgactcgagga	ccctgctgtg	tctgtggcct	tgggacagac	agtcaaggatc		60
acatgccaag	gagacagcct	cagaacctat	tatgcaagct	ggtaccagca	gaagccaaga		120
caggcccccta	ttcttgcata	ctatggtaaa	aacaaccggc	cctcaggat	cccagaccga		180
ttctctggct	ccacactcagg	aatcacagct	tccttgacca	tcactggggc	tcaggcggaa		240
gatgaggctg	actattactg	taaatccgg	gacatcatg	gtaaccatct	gctgttcggc		300
ggagggacta	agctgaccgt	ccta					324

<210> SEQ ID NO 449
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 449

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

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370

85	90	95
Leu Leu Phe Gly Gly Thr Lys	Leu Thr Val	Leu
100	105	

<210> SEQ ID NO 450
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 450

caggtgcaag	tggtgaggc	tgggtccagc	ctgggaggtc	cctgagactc	60
tcctgtgcag	cgtctggatt	caccttcagt	aactatggca	tgcactgggt	120
ccaggcaagg	ggctggagtg	ggtggcagtt	atatggtatg	atggaggtaa	180
gcagactccg	tgaaggcccg	atccatcatc	tccagagaca	attccaagag	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgttt	attattgtgc	300
gctggttacc	attattacta	cgttatggac	gtctggggcc	aagggaccac	360
gcctca					366

<210> SEQ ID NO 451
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 451

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

<210> SEQ ID NO 452
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 452

cagtctgccc	tgactcagcc	tgcctccgtt	tctgggtctc	ctggacagtc	gatcaccatc	60
tcctgcactg	gaaccagcag	tgacgttgg	ggttataact	ctgtctccgt	gtaccaacag	120
caccaggc	aacccccc	aaactcatatt	tatgagggtca	gtaatcgcc	ctcaggatt	180
tctaatacgt	tctctggc	caagtctggc	aacacggc	ccctgaccat	ctctgggctc	240
caggctgagg	acgaggctga	ttattttcgc	agctcatata	caagcaccag	catggcttc	300
ggcggaggga	ccaagctggc	cgtccta				327

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<210> SEQ ID NO 453
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 453

Gln	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1															
															15

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

Asn	Ser	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Pro	Pro	Lys	Leu
															45
35															

Met	Ile	Tyr	Glu	Val	Ser	Asn	Arg	Pro	Ser	Gly	Ile	Ser	Asn	Arg	Phe
															60
50															

Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
															80
65															

Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Phe	Cys	Ser	Ser	Tyr	Thr	Ser	Thr
															95
85															

Ser	Met	Val	Phe	Gly	Gly	Thr	Lys	Leu	Ala	Val	Leu
100											

<210> SEQ ID NO 454

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 454

caggtgcaag	tggtgaggc	tggggaggc	gtggccagc	ctgggaggc	cctgagactc		60
tcctgtgcag	cgtctggatt	cacttcagt	aactatggca	tgcactgggt	ccgccaggct		120
ccaggcaagg	ggctggagtg	ggtggcagtt	atatggatg	atggaggtaa	taaatactat		180
gcagactccg	tgaagggecg	atccatcatc	tccagagaca	attccaagag	cacgctgtat		240
ctgcaaatga	acagcctgag	agccgaggac	acggctgttt	attattgtgc	gaggctcgt		300
gctggttacc	attattacta	cggtatggac	gtctggggcc	aagggaccac	ggtcaccgtc		360
gcctca							366

<210> SEQ ID NO 455

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 455

Gln	Val	Gln	Val	Val	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1														
														15

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr
															30
20															

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

Ala	Val	Ile	Trp	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
															60
50															

Lys	Gly	Arg	Ser	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Ser	Thr	Leu	Tyr
															80
65															

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

Ala	Arg	Ser	Val	Ala	Gly	Tyr	His	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp
															110
100															

Gly Gln Gly Thr Thr Val Thr Val Ala Ser

-continued

115

120

<210> SEQ ID NO 456
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 456

tcttctgagc tgactcgagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc	60
acatgc当地 gagacagccat cagaggctat tatgcaagct ggtaccagca gaagcoaaga	120
caggccccctg tacttgtcat ctatggtaaa aacaaccggc cctcaggat cccagaccga	180
ttctctggct ccacgtcagg aaacacagct tccttgacca tcactggggc tcaggoggaa	240
gatgaggctg actattactg taactcccgg gacaacatgt gtgaccatct ggtgttccgc	300
ggagggacca agctgaccgt ccta	324

<210> SEQ ID NO 457
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 457

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

<210> SEQ ID NO 458
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 458

gaggtgcagc tgggtggagtc tgggggaggc ttgggtccagc ctggggggtc cctgagactc	60
tcctgtgcag cctccggatt caccttagt agctattgga tgagctgggt ccgccaggct	120
ccagggaaagg ggctggagtg ggtggccagc ataaaacaag atggaagtga gaaatactat	180
gtggactctg tgaaggcccg attcaccatc tccagagaca acgccaggaa ctcactgtat	240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagatctt	300
gttataatgg tgtatgatat agactactac tactacggta tggacgtctg gggccaagg	360
accacggta ccgtctccct a	381

<210> SEQ ID NO 459
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 459

-continued

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Ser Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60

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

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

Ala Arg Asp Leu Val Leu Met Val Tyr Asp Ile Asp Tyr Tyr Tyr Tyr
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 460
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 460

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc 60
 atctccctgca ggtcttagtca gagcctcctg catactaatacg gataacaacta tttggatttg 120
 tacctgcaga agccaggcgtca gtctccacag ctcctgatct atttgggttc taatcgggccc 180
 tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
 agcagagtggtgg aggctgagga tgggggtt tattactgca tgcaagctct acaaaactccg 300
 ctcactttcg gcggaggac caaggttagag atcaaa 336

<210> SEQ ID NO 461
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 461

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 462
 <211> LENGTH: 381
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 462

```

gagggtgcagc tgggtggagtc tggggggagc ttgggtccagc ctggggggtc cctgagactc      60
tcctgtgcag cctccggatt caccttagt aactattgga tgagctgggt ccgccaggct      120
ccagggaaagg ggctggagtg ggtggccagc ataaaacaag atggaagtga gaaatactat      180
gtggactctg tgaagggecg attcgccatc tccagagaca acgccaagaa ctcactgttt      240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagatctt      300
gtactaatgg tgtatgatat agactactac tactacggta tggacgtctg gggccaaggg      360
accacggtca ccgtctccctc a                                         381

```

<210> SEQ ID NO 463

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 463

```

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20          25          30

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

Ala Ser Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50          55          60

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

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

Ala Arg Asp Leu Val Leu Met Val Tyr Asp Ile Asp Tyr Tyr Tyr Tyr
100         105         110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115         120         125

```

<210> SEQ ID NO 464

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 464

```

gatattgtga tgactcagtc tccactctcc ctgcctgtca cccctggaga gccggccctcc      60
atctcttgca ggtctagtca gagcctctgtc catagtaatg ggtacaacta tttggattgg      120
tacctgcaga agccaggcgtc gtctccacag ctccctgatct atttgggttc taatcgggccc     180
tccggggtcc ctgacaggtt cagttggcgtt ggatcaggca cacatcttac actgaaaaatc     240
agcagagtggtt aggctgaggtt tattactgca tgcaaactct acaaactccg      300
ctcactttcg gcggaggac caaggtggag atcaaa                                         336

```

<210> SEQ ID NO 465

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 465

```

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser

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20

25

30

Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
35															

Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro
50															

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	His	Leu	Thr	Leu	Lys	Ile
65															

Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Thr
85															

Leu	Gln	Thr	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys
100															

<210> SEQ ID NO 466

<211> LENGTH: 342

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 466

caggtgcagc	tgggtggagtc	tgggggaggc	gtggccca	ctgggagg	tcctgagactc	60
tcctgtgcag	cgtctggatt	caccc	ttcagt	agctatggca	tgcactgggt	120
ccaggcaagg	ggctggagtg	ggtggcagtt	atatactatg	atggaaattaa	taaacactat	180
gcagactccg	tgaaggggccg	attcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatcg	300
ggactggact	ggggccaggg	aaccctgg	tc accgtctc	ca		342

<210> SEQ ID NO 467

<211> LENGTH: 114

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 467

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Val	Ala	Gln	Pro	Gly	Arg
1														

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
20															

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
35															

Ala	Val	Ile	Tyr	Tyr	Asp	Gly	Ile	Asn	Lys	His	Tyr	Ala	Asp	Ser	Val
50															

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65															

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

Ala	Arg	Asp	Arg	Gly	Leu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
100															

Ser Ser

<210> SEQ ID NO 468

<211> LENGTH: 339

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 468

gacatcgta	tgacccagtc	tccagactcc	ctggctgtgt	ctctggcga	gaggccacc	60
-----------	------------	------------	------------	-----------	-----------	----

atcaactgca	agtccagcca	gagtgtttta	tacagctcca	acagtaagaa	ctacttagtt	120
------------	------------	------------	------------	------------	------------	-----

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tggtaccagg agaaaccagg acagcctcct aagctgctca tttactgggc ctctacccgg	180
gaatccgggg tccttgacgg attcagtggc agcgggtctg ggacagattt cactctacc	240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagta	300
ccgtggacgt tcggccaagg gaccaaggtg gaaatcaa	339

<210> SEQ ID NO 469

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 469

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

Lys

<210> SEQ ID NO 470

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 470

gaggtgcagc tggtggagtc tgggggaggc ttgggtccagc ctggggggtc cctgagactc	60
tcctgtcgag cctctggact caccttagt aacctttgga tgagctgggt ccgccaggct	120
ccagggaaagg ggctggagtg ggtggccaa ataaagcaag atggaaatga taaatactat	180
gtggactctg tgaaggcccg attcaccatc tccagagaca acgccaagaa ttcactgtat	240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagagtca	300
aactggggat ttgctttga tatctggggc caagggacaa tggtcaccgt ctcttca	357

<210> SEQ ID NO 471

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 471

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

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

<210> SEQ ID NO 472
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 472

cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccate	60
tcttggctcg gaagcagctc caacatcgga agtaaaaactg taaactggta ccagcagttc	120
ccaggaacgg ccccccaaact cctcatatat agtaataatc ggccggccctc aggggtccct	180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag	240
tctgaggatg aggctgatta ttactgtgca gcatggatg acagcctgaa ttgggtgttc	300
ggcgcaggga ccaagctgac cgtccta	327

<210> SEQ ID NO 473
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 473

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

<210> SEQ ID NO 474
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 474

gaggtgcagc tgggtggagtc tggggggaggt ttgggtccagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggact caccttttagt aacttttggta tgagctgggt ccgcaggct	120
ccagggaaagg ggctggagtg ggtggccaaat aaaaagcaag atggaaagtga gaaataactat	180
gtggactctg tgaaggggccg attcaccatc tccagagaca acgccaagaa ttcaactgtat	240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagatca	300
aactggggat ttgctttga tatctggggc caagggacaa tggtcaccgt ctcttca	357

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<210> SEQ ID NO 475
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 475

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Asn Phe
 20 25 30

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

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Thr Met Val Thr Val Ser Ser
115

<210> SEQ ID NO 476
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: *Homo sapiens*

<400> SEQUENCE: 476

```

cagtcgtgc tgactcagcc accctcagcg tctgggaccc cggggcagag ggtcaccatc 60
tcttgttctg gaagcagctc caacatcgga agtaaaaactg taaactggta ccagcagttc 120
ccaggaacgg cccccaact cctcatctat agtaataatc ggccccccctc aggggtccct 180
gaccgattct ctgggtccaa gtctggacc tcagcctccc tggccatcag tgggttccag 240
tctgaggatg aggctgatta ttactgtgca acatggatg acagactgaa ttgggtgttc 300
ggcgcagggg ccaagctgac cgtctcta 327

```

<210> SEQ ID NO 477

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: *Homo sapiens*

<400> SEQUENCE: 477

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

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

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

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

65 70 75 80

85	90
Asn Trp Val Phe Gly Ala Gly Thr Lys Leu Thr Val Leu	

-continued

<210> SEQ ID NO 478
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 478

```
caggtcacct tgaaggagtc tggcctgtg ctggtaaac ccacagagac cctcacgctg      60
acctgcaccg tctctgggtt ctcactcagc aatgttagaa tgggtgtgag ctggatccgt     120
cagccccccag ggaaggccct ggagtggctt gcacacattt ttctgaatga cgaaaattcc    180
tacagaacat ctctgaagag caggctcacc atctccaagg acacctccaa aagccaggtg    240
gtccttacca tgaccaacat ggaccctgtg gacacagcca catattactg tgcacggata   300
gtgggagcta caacggatga tgctttgtat atctggggcc aaggacaat ggtcacccgtc   360
tcttca                                              366
```

<210> SEQ ID NO 479
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 479

Gln	Val	Thr	Leu	Lys	Glu	Ser	Gly	Pro	Val	Leu	Val	Lys	Pro	Thr	Glu
1															

Thr	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser	Asn	Val
20															

Arg	Met	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
35															

Trp	Leu	Ala	His	Ile	Phe	Ser	Asn	Asp	Glu	Asn	Ser	Tyr	Arg	Thr	Ser
50															

Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Ser	Gln	Val
65															

Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr
85															

Cys	Ala	Arg	Ile	Val	Gly	Ala	Thr	Thr	Asp	Asp	Ala	Phe	Asp	Ile	Trp
100															

Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser						
115															

<210> SEQ ID NO 480
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 480

```
tcctatgtgc tgactcagcc accctcggtg tcagtgccc caggacagac ggccaggatt     60
acctgtgggg gaaacaacat tggaaataaa agtgtgcaact ggtaccagca gaagccaggc    120
caggccccctg tgctggtegt ctatgtat agcgaccggc cctcaggat ccctgagcga    180
ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg    240
gatgaggcccg actttactg tcaggtgtgg gatagtagta gtgatcctgt ggtattccgc   300
ggagggacca agctgaccgt ccta                                              324
```

<210> SEQ ID NO 481
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 481

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

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

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

Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
	50					55				60					

Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Gly
	65					70			75				80		

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

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

<210> SEQ ID NO 482

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 482

gaggtgcagc	tgggtggagtc	tgggggaggc	ttgggtccagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttttagt	aactatttgg	tgacctgggt	ccggcaggct	120
ccagggaaagg	ggcttggagtg	ggtgtggccagc	ataaagcaag	atggaagtga	gagatactat	180
gtggactctg	tgaaggggccg	attcaccatc	tcccagagaca	ccgccaagaa	ctctctgtat	240
ctccaaatga	acagcctcg	agccgaggac	acggctgtgt	attactgtgc	gagacctt	300
gtactaatgg	tgttatgtct	acactactac	tactacggta	tggacgtctg	gggccacggg	360
accacggta	ccgtctcc	ta				381

<210> SEQ ID NO 483

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 483

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr
	20				25			30							

Trp	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Ley	Glu	Trp	Val
	35				40					45					

Ala	Ser	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Arg	Tyr	Tyr	Val	Asp	Ser	Val
	50				55				60						

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

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

Ala	Arg	Pro	Leu	Val	Leu	Met	Val	Tyr	Ala	Leu	His	Tyr	Tyr	Tyr	Tyr
	100					105			110						

Gly	Met	Asp	Val	Trp	Gly	His	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
	115				120					125					

<210> SEQ ID NO 484

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-continued

<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 484

```
gatatttgta tgactcagtc tccactctcc ctgccccgtca cccctggaga gcccggctcc      60
atctcctgtca ggtcttagtca gagcctctcg catagtaaatg gataacaacta tttggattgg     120
tacacctgcaga agccagggtca gtctccacag ctccctgatct atttgggttc taatcggggcc    180
tccggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc      240
agcagagtgg aggctgagga tttttgggtt tattactgca tgcaagctct acaaaactccg      300
ctcactttcg gcggaggggac caaggtggag atcaaa                                336
```

<210> SEQ ID NO 485

<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 485

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

<210> SEQ ID NO 486

<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 486

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

<210> SEQ ID NO 487

<211> LENGTH: 98
<212> TYPE: PRT

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 487

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
									20			25			30

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

Ala	Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val
									50			55		60	

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

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

Ala Arg

<210> SEQ ID NO 488

<211> LENGTH: 98

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 488

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
									20		25		30		

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

Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
									50		55		60		

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

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

Ala Arg

<210> SEQ ID NO 489

<211> LENGTH: 93

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 489

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

Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
									20		25		30		

Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
									35		40		45		

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

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

Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys			
									85		90				

<210> SEQ ID NO 490

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 493

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

Gly

<210> SEQ ID NO 494

<211> LENGTH: 98

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 494

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

Ala Arg

<210> SEQ ID NO 495

<211> LENGTH: 98

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 495

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

Ala Arg

<210> SEQ ID NO 496

<211> LENGTH: 88

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 496

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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399**400**

-continued

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

<210> SEQ ID NO 497
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 497

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

<210> SEQ ID NO 498
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 498

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

<210> SEQ ID NO 499
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 499

1	5	10
Ser Gly Ser Ser Ser Asn Ile Gly Ser Lys Thr Val Asn		

401**402**

What is claimed is:

1. An isolated monoclonal antibody, wherein, when bound to PCSK9, said monoclonal antibody binds to at least one residue within the sequence set forth by residues 123-132 of SEQ ID NO: 1, and wherein said monoclonal antibody reduces binding between PCSK9 and an EGFa domain of LDLR protein antagonizes PCSK9's inhibition of cellular LDL uptake. 5
2. The isolated monoclonal antibody of claim 1, wherein the monoclonal antibody comprises a humanized or human antibody. 10
3. The isolated monoclonal antibody of claim 1, wherein the monoclonal antibody comprises a full length monoclonal antibody. 15
4. The isolated monoclonal antibody of claim 3, wherein said monoclonal antibody is of the IgG4- or the IgG2-type.
5. A pharmaceutical composition comprising the monoclonal antibody of claim 1.
6. The isolated monoclonal antibody of claim 1, wherein the monoclonal antibody is an immunologically functional fragment. 20

* * * * *