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(54) **HUMAN IMMUNODEFICIENCY VIRUS NEUTRALIZING ANTIBODIES AND METHODS OF USE THEREOF**

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§ 371 (c)(1),
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G01N 33/569 (2006.01)

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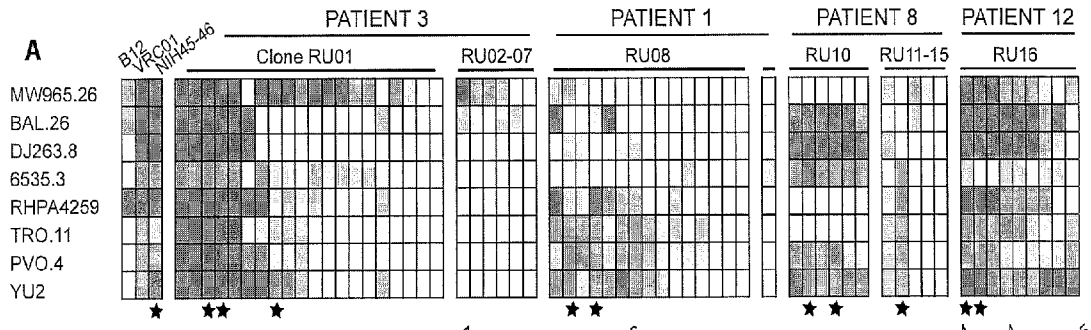
USPC **424/160.1**; 530/389.4; 536/23.53; 435/320.1; 435/69.6; 435/5; 435/339.1

(57) **ABSTRACT**

The invention provides broadly neutralizing antibodies directed to epitopes of Human Immunodeficiency Virus, or HIV. The invention further provides compositions containing HIV antibodies used for prophylaxis, and methods for diagnosis and treatment of HIV infection.

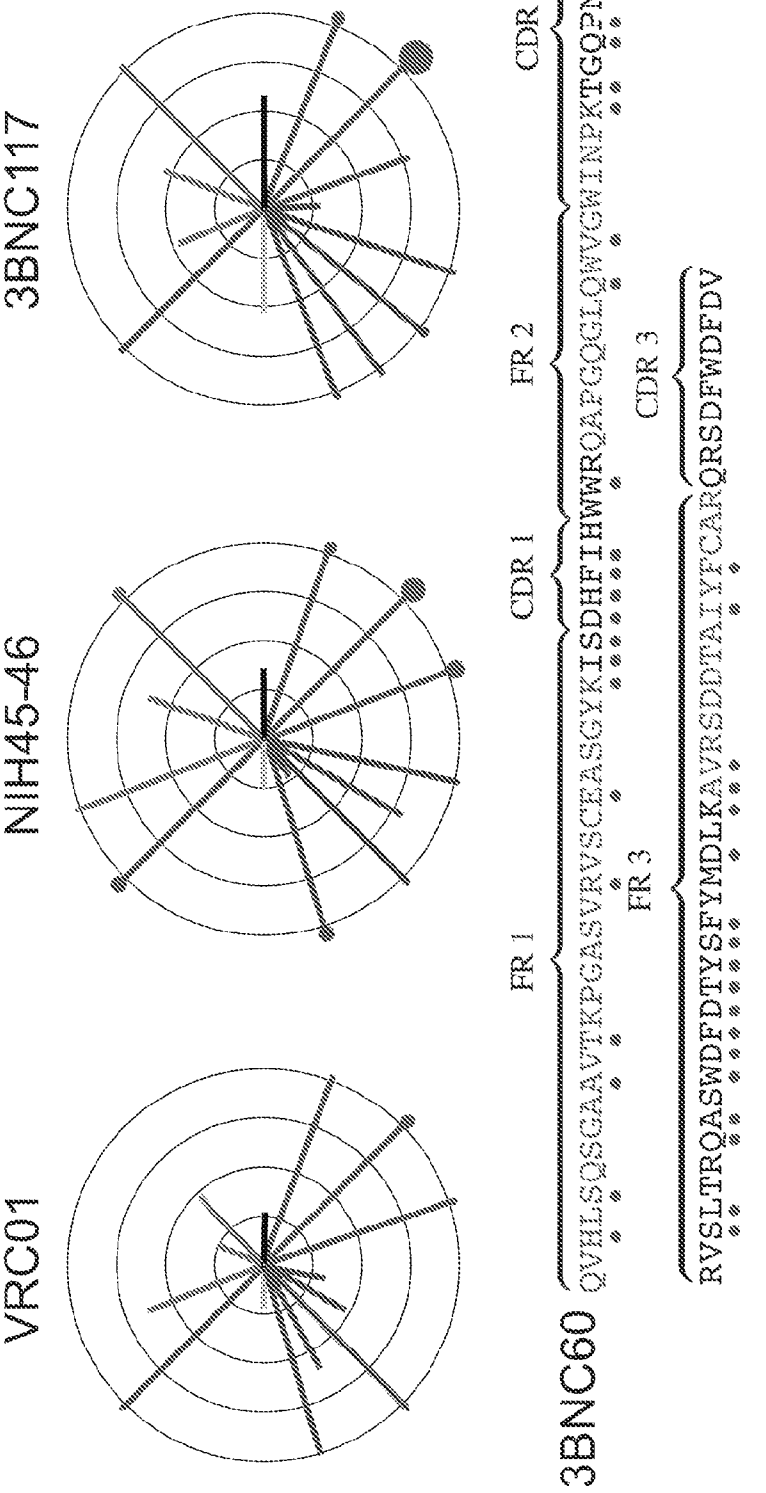
Figure 1A-B



B

		B12	VRC01	3BNC117	3BNC60	3BNC55	NIH45-46	12A12	12A21	1NC9	1B2530	8ANC131	8ANC134	8ANC195
CLADE B	6535.3	1.4	0.539	0.55	0.54	2.6	0.14	21.97	>50	>50	>50	0.20	0.06	0.20
	RHPA4259	0.1	0.06	0.041	<0.05	2.2	<0.05	0.083	0.038	0.09	3.60	>50	>50	0.34
	TRO.11	>50	0.2	0.077	<0.05	18.4	1.9	0.283	0.164	0.20	0.516	>50	>50	0.18
	PVO.4	>50	0.2	<0.09	0.09	3.9	0.17	0.923	0.584	0.34	0.275	0.81	0.46	0.52
	YU2	2.2	0.12	0.054	<0.05	0.9	<0.05	0.084	0.015	0.13	0.209	0.18	0.15	0.79
CLADE A	Q842.d12	>50	0.03	<0.01	0.01	0.011	0.008	0.014	0.015	0.020	0.249	0.053	0.031	>30
	3415.v1.c1	2.5	0.06	0.17	0.10	0.10	0.017	0.124	0.082	0.266	0.065	0.299	0.323	2.404
	3365.v2.c20	>50	0.06	0.08	0.02	0.221	0.029	0.066	0.045	0.329	4.357	>30	>30	>30
CLADE C	ZM53M.PB12	>50	1.3	0.21	0.22	12.549	0.187	0.598	0.420	0.705	0.912	>30	>30	9.626
	ZM109.FPB4	>50	0.128	0.14	0.22	0.083	0.069	0.148	2.104	0.023	>30	>30	>30	>30
CLADE D	3016.v5.c45	1.1	0.16	1.38	1.40	>30	>30	1.163	0.057	>30	>30	>30	>30	0.195
	231965.c1	0.07	0.34	0.05	0.07	0.505	0.021	2.217	>30	0.393	0.168	6.346	>30	0.514
CLADE G	X1254_c3	>50	0.07	0.08	0.05	0.138	0.027	1.032	26.793	>30	>30	>30	>30	1.524
CRF02_AG	251-18	>50	2.5	0.26	0.35	>30	1.445	2.622	1.713	1.234	9.847	0.968	1.560	0.284
CRF01_AE	R1166.c1	>50	1.7	0.17	0.14	0.298	0.445	0.342	0.292	0.551	0.113	>30	>30	0.986
VRC01-resistant	H086.8	>50	>50	>15	>15	>30	>30	>30	>30	>30	>30	>50	>50	0.096
	DU172.17	0.3	>50	1.19	3.81	3.518	>30	0.196	0.126	>30	>30	>30	>30	10.797
	250-4	>50	>50	>15	>15	0.236	>30	>30	>30	>30	>30	>50	>50	>50
	278-50	>50	>50	>15	>15	>30	>30	>30	>30	>30	>30	>50	>50	>50
	620345.c1	>50	>50	>15	>15	>30	>30	>30	>30	>30	>30	>50	>50	>50

FIGURE 1C-D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CDR 2
FR 3
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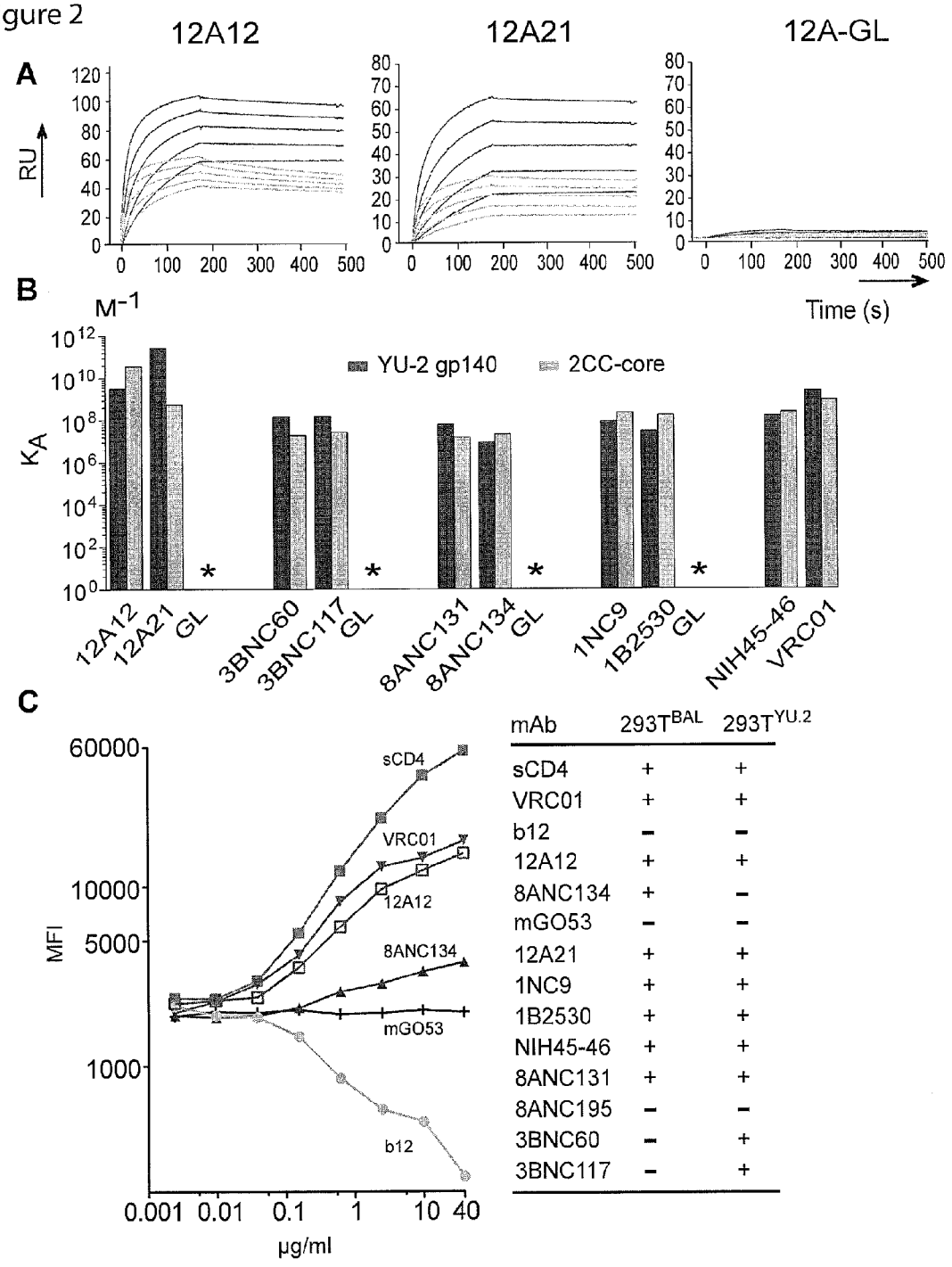
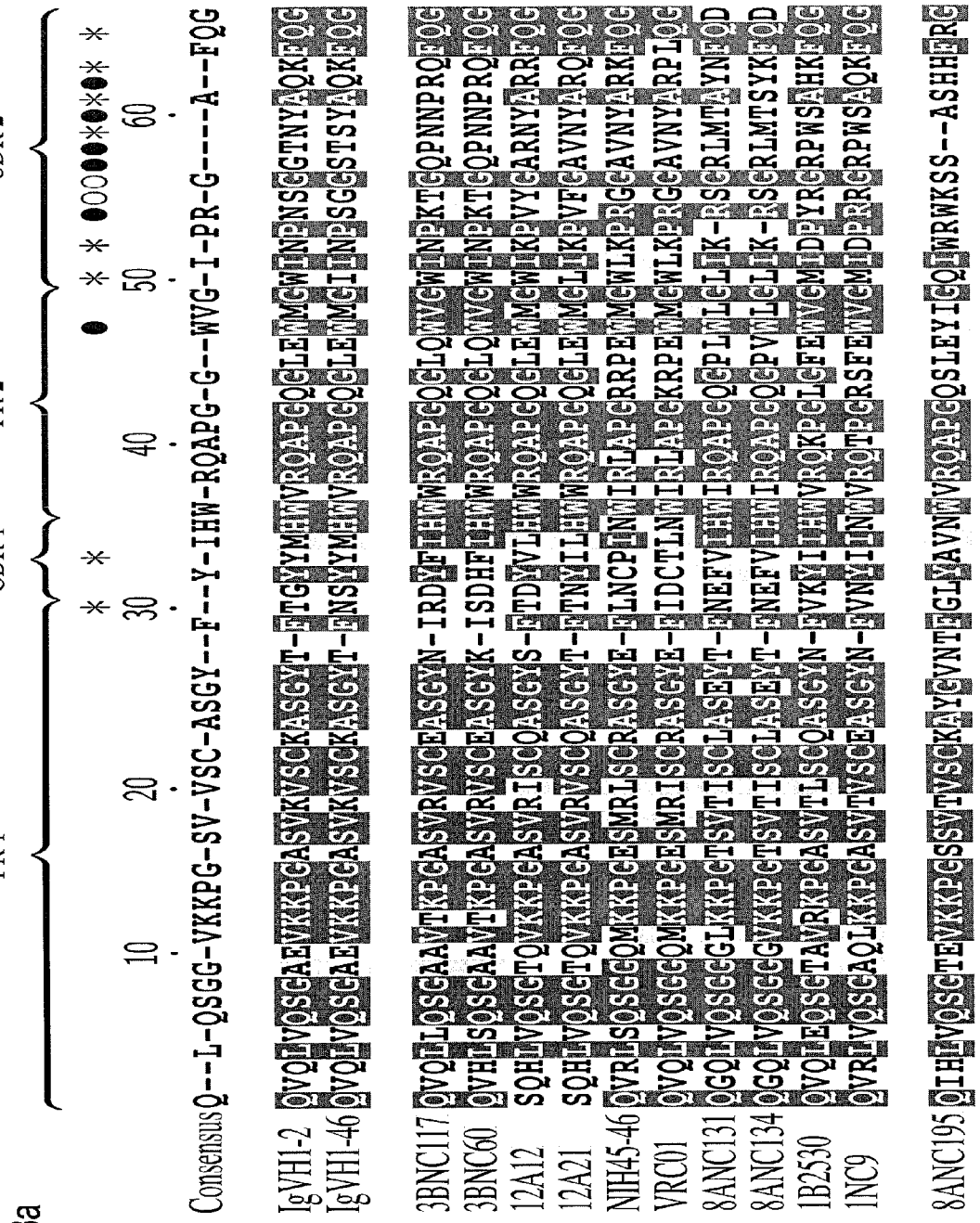
Figure 2



mAb	293T^{BAL}	293T$^{YU.2}$
sCD4	+	+
VRC01	+	+
b12	–	–
12A12	+	+
8ANC134	+	–
mGO53	–	–
12A21	+	+
1NC9	+	+
1B2530	+	+
NIH45-46	+	+
8ANC131	+	+
8ANC195	–	–
3BNC60	–	+
3BNC117	–	+

Figure 3a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CDR 2
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VRC01
8ANC131
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1B2530
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8ANC195

Figure 3a, cont

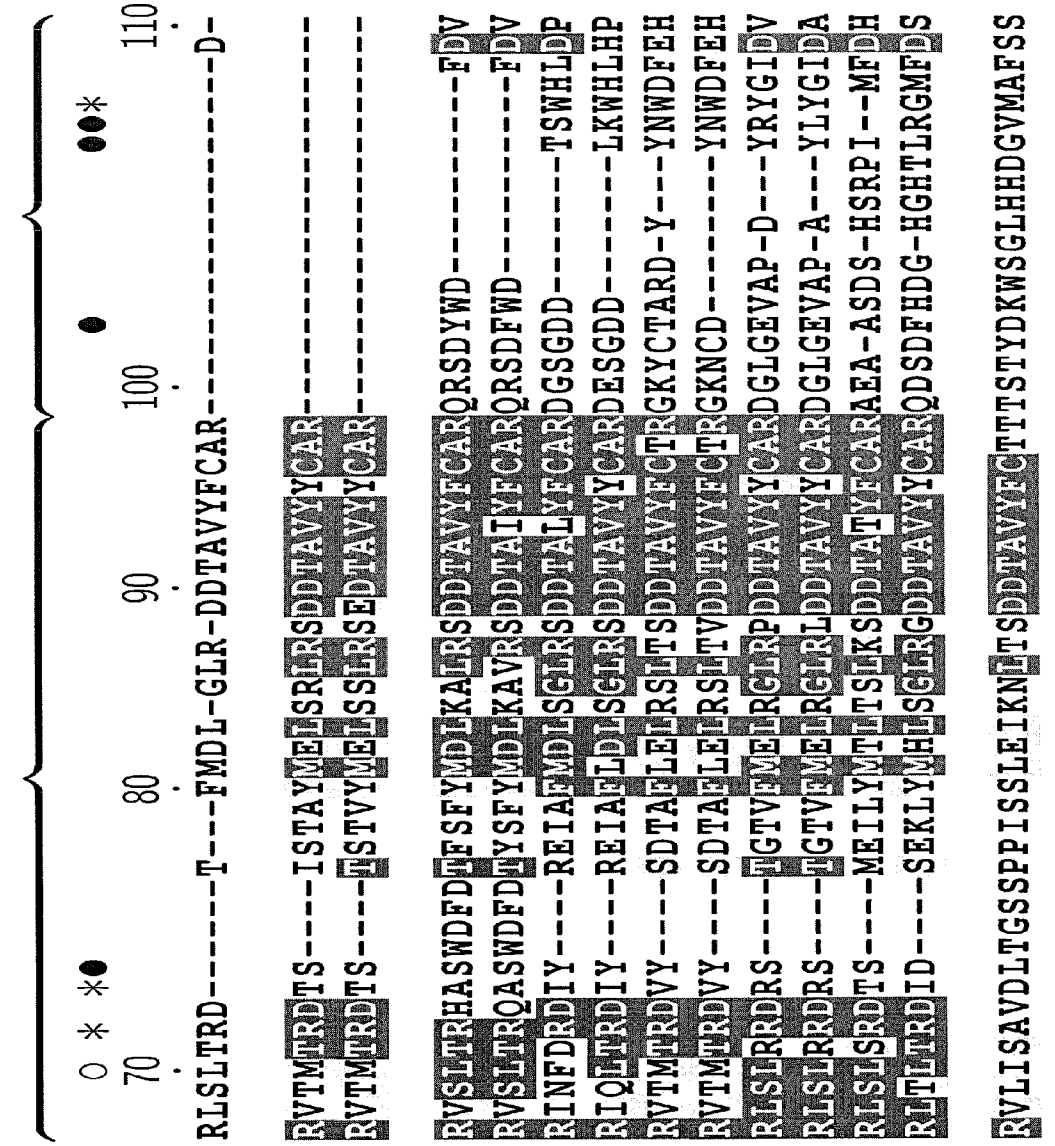
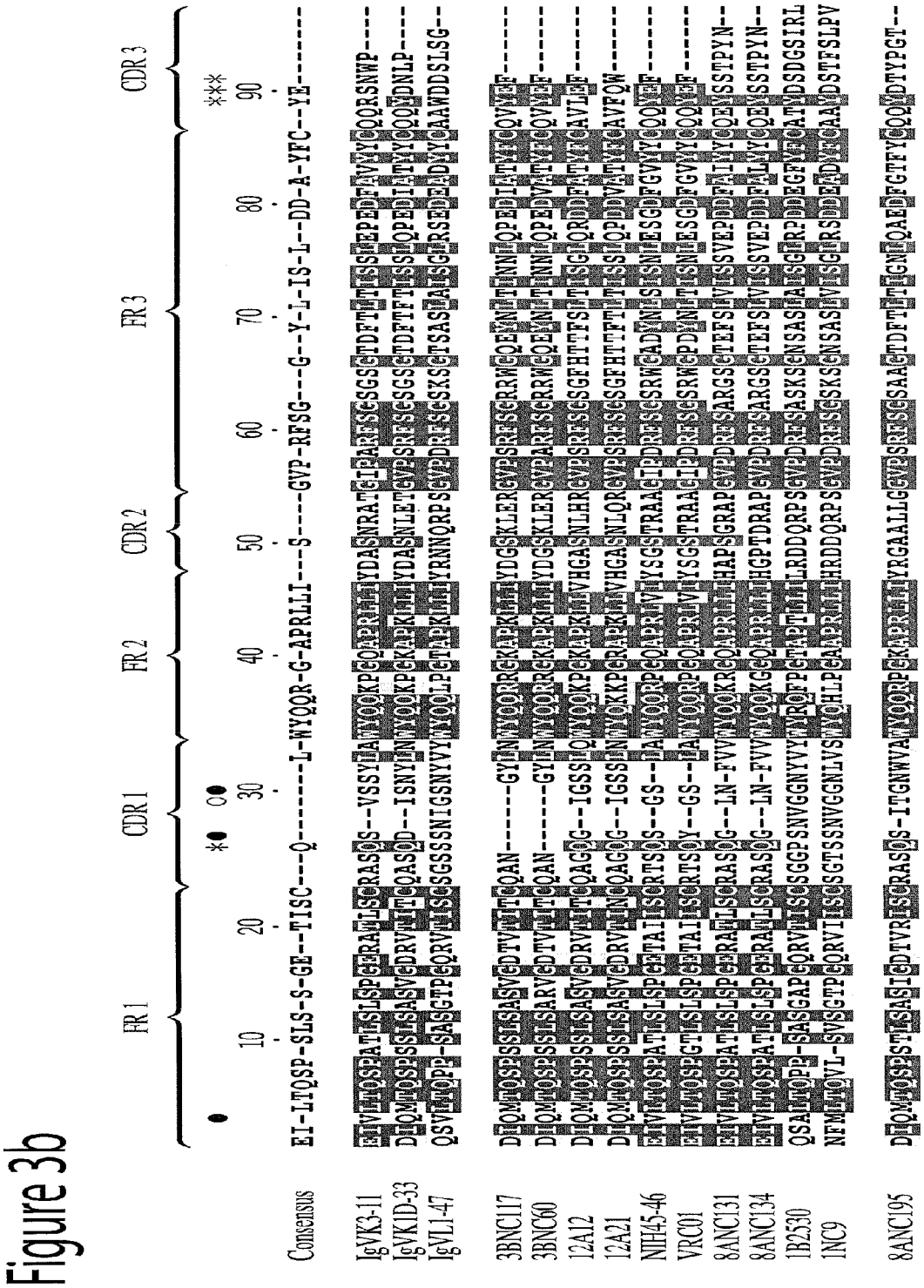


Figure 3b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FR 2
CDR 2
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Consensus
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IgVL1-47
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12A12
12A21
NIH45-46
VRC01
8ANC131
8ANC134
1B2530
1NC9
8ANC195

Figure 4a

NEW PRIMERS ORIGINAL PRIMERS

8A	HEAVY							
	VH	JH	CDR3 (aa)	Mutations				
8A1	1-46	6	D G L G E V A P D Y R Y G I D V	85	X			
8A2	4-61	4/5	Q S L S W Y R P S G Y F E S	57	X			
8A3	1-69	6	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	40	X	X		
8A4	1-69	6	S I N A A V P G L E G V Y Y Y Y G M A V	27	X	X		
8A5	1-69	6	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	37	X			
8A6	1-69	6	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	35	X	X		
8A7	1-69	1/2	W D Y Y D S R G Y Y Y G E Y F D L	23	X			
8A8	3-21	6	D T K V G A P R Q D C Y A M D L	29	X	X		
8A9	1-46	6	D G L G E V A P D Y R Y G I D V	75	X			
8A10	1-24	4	A D R F K V A Q D E G L F V I F D Y	11	X	X		
8A11	1-69	3	D R S S A I G Y C S S I S C Y K G S F D I	12	X	X		
8A12	3-48	6	L A E V P P A I R G S Y Y Y G M D V	18	X	X		
8A13	3-11	6	A Y G T G N W R G L Y Y Y Y Y G M D V	23	X	X		
8A14	3-30	4	S P S Y Y F D Y	9	X	X		
8A15	1-46	6	D G L G E V A P A Y L Y G I D A	85	X			
8A16	1-24	6	[illegible]	12	X	X		
8A17	1-24	6	[illegible]	16	X	X		
8A18	1-46	6	D G L G E V A P A Y L Y G I D A	76	X			
8A19	1-24	4	A D R F K V A Q D E G L F V I F D Y	9	X	X		
8A20	1-46		D G L G E V A P A Y L Y G I D A	81	X			
8A21	3-30	4/5	E G G L R F L E W L F	13	X	X		
8A22	3-21	6	S R P P Q R L Y G M D V	19	X	X		
8A23	1-24	4	A D P F K V A Q D E G L Y V I F D Y	10	X			
8A24	3-30	4	D S S G S N W F D Y	22	X			
8A25	1-46	6	D G L G E V A P A Y L Y G I D A	82	X			
8A26	3-43	5	N G F D V	70	X			
8A27	1-24	4	A D P F K V A Q D E G L Y V I F D Y	12	X			
8A28	1-46	6	D G L G E V A P A Y L Y G I D A	85	X			
8A29	1-46	6	D G L G E L A P A Y H Y G I D V	71	X			
8A30	1-69	3	A R A D S H T P I D A F D I	23	X			

Figure 4a , cont.

8A	HEAVY				NEW PRIMERS	ORIGINAL PRIMERS
	VH	JH	CDR3 (aa)	Mutations		
8A31	1-46	6	DGLGELAPAYHYGIDV	71	X	
8A32	1-69	3	SSGNFEFAFEI	30	X	X
8A33	1-69	6	DRWLPQYYYYGMDV	3	X	X
8A34	3-7	2	NPESRCIVGRNRGWCRYFD	11	X	X
8A35	1-46	6	DGLGELAPAYQYGIDV	71	X	
8A36	3-30	4	PKFLPGADIVVVVAATPFD	2	X	X
8A37	1-46	6	DGLGELAPAYHYGIDV	71	X	
8A38	1-46	6	DGLGEVAPAYLYGIDA	83	X	
8A39	3-43	5	NGFDV	70	X	
8A40	1-24	4	ADPFKVAQDEGLYVIFDY	18	X	
8A41	3-33	4/5	EMAVGGTKALDH	10	X	X
8A42	1-46	4/5	GVSF	41	X	X
8A43	3-11	4/5	DLLHAHDF	13	X	
8A44	3-33	4	DSVAFVLEGPIDY	23	X	X
8A45	1-2	6	YSTRQFFHYYYVTDV	26	X	X
8A46	4-34	6	GKVWGITARPRDAGLD	38	X	X
8A47	3-7	4	VRDPNYNLHFDS	11	X	X
8A48	3-53	4/5	GLRVYFDL	17	X	X
8A49	1-69	3	DRSSAIGYCSSISCYKGSFDI	8	X	X
8A50	4-39	4/5	QKGSGTSLLY	8	X	X
8A51	7-4-1	4/5	DLLESRTYYNDIRDC	7	X	X
8A52	1-69	6	DRGDTRLLDYGDYEDERYYYGMDV	50	X	X
8A53	4-4	4	VRGSWNFDY	15	X	X
8A54	1-24	5	TYLAVVPDGFDGYSSSWYWFDP	19	X	X
8A55	1-69	3	DRSSAIGYCSSISCYKGSFDI	8	X	X
8A56	4-31	4/5	CQDGLASRPIDF	44	X	X
8A57	3-30	4/5	DSVSKSYSAPPEF	39	X	
8A58	1-46	6	DGLGEVAPDYRYGIDV	73	X	
8A59	4-39	5	HVRPYDRSGYPERPNWFD	32	X	X
8A60	1-69	3	NAGAYFYPFDI	35	X	
8A61	1-46	6	EMGTFTLLGVVIDHYDFYPMDV	24	X	X
8A62	4-34	4	GRGKRCSGAYCFAGYFDS	37	X	
8A63	1-46	6	DGLGEVAPAYLYGIDA	83	X	

FIGURE 4B

B

Pt 8 Clones

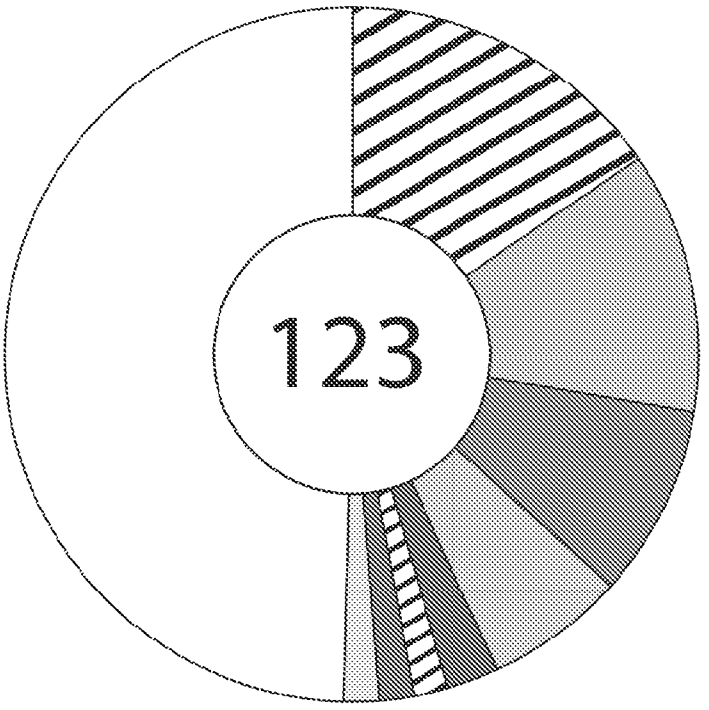
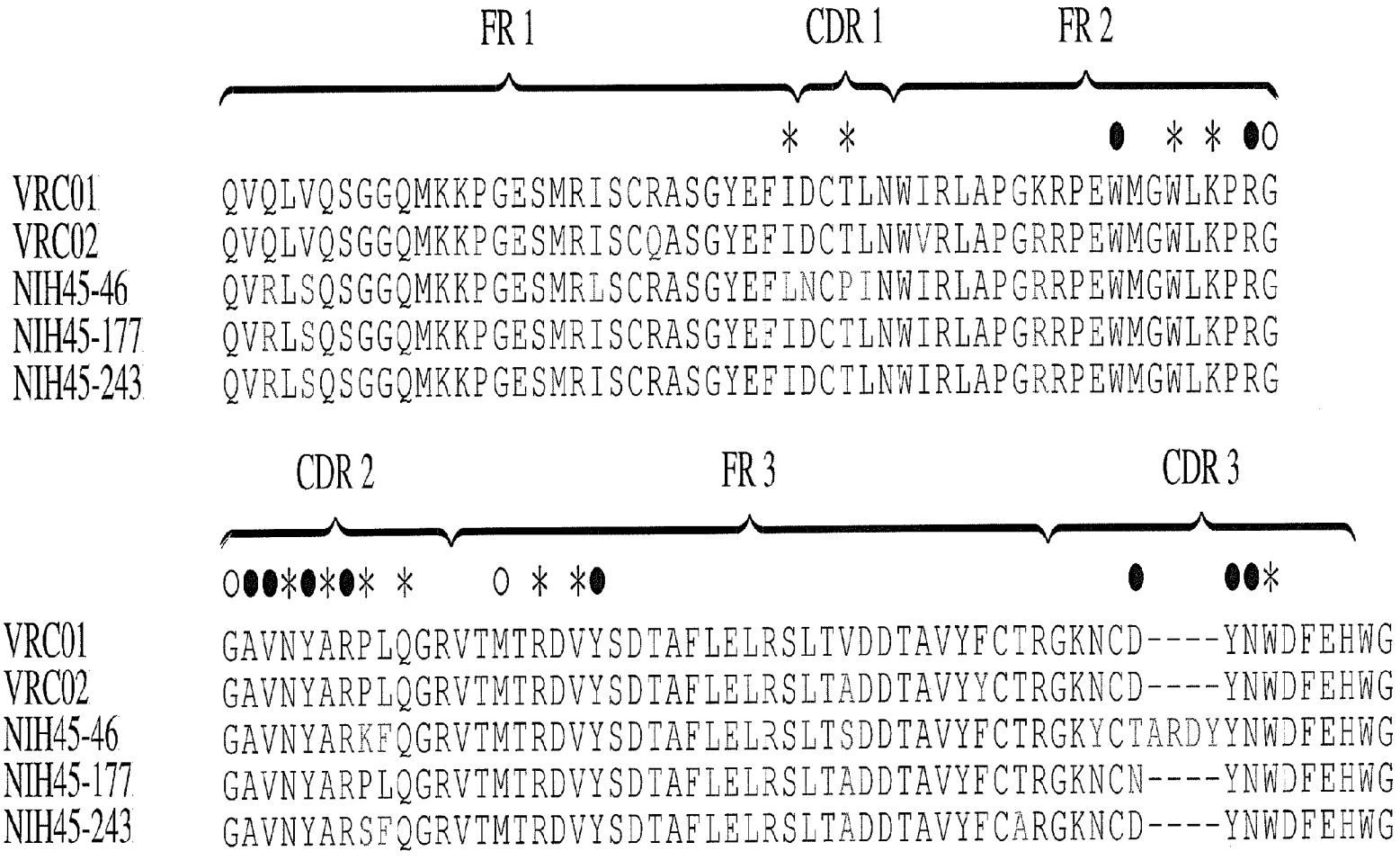


Figure 5a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NIH45-46 QVRLSQSGGQMKKPGESMRLSCRASGYEFLNCPINWIRLAPGRRPEWMGWLKPRG
NIH45-177 QVRLSQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGRRPEWMGWLKPRG
NIH45-243 QVRLSQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGRRPEWMGWLKPRG
CDR 2
FR 3
CDR 3
VRC01 GAVNYARPLQGRVTMTRDVYSDTAFLELRSLTVDDTAVYFCTRGKNCD----YNWDFEHWG
VRC02 GAVNYARPLQGRVTMTRDVYSDTAFLELRSLTADDTAVYYCTRGKNCD----YNWDFEHWG
NIH45-46 GAVNYARKFQGRVTMTRDVYSDTAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWG
NIH45-177 GAVNYARPLQGRVTMTRDVYSDTAFLELRSLTADDTAVYFCTRGKNCN----YNWDFEHWG
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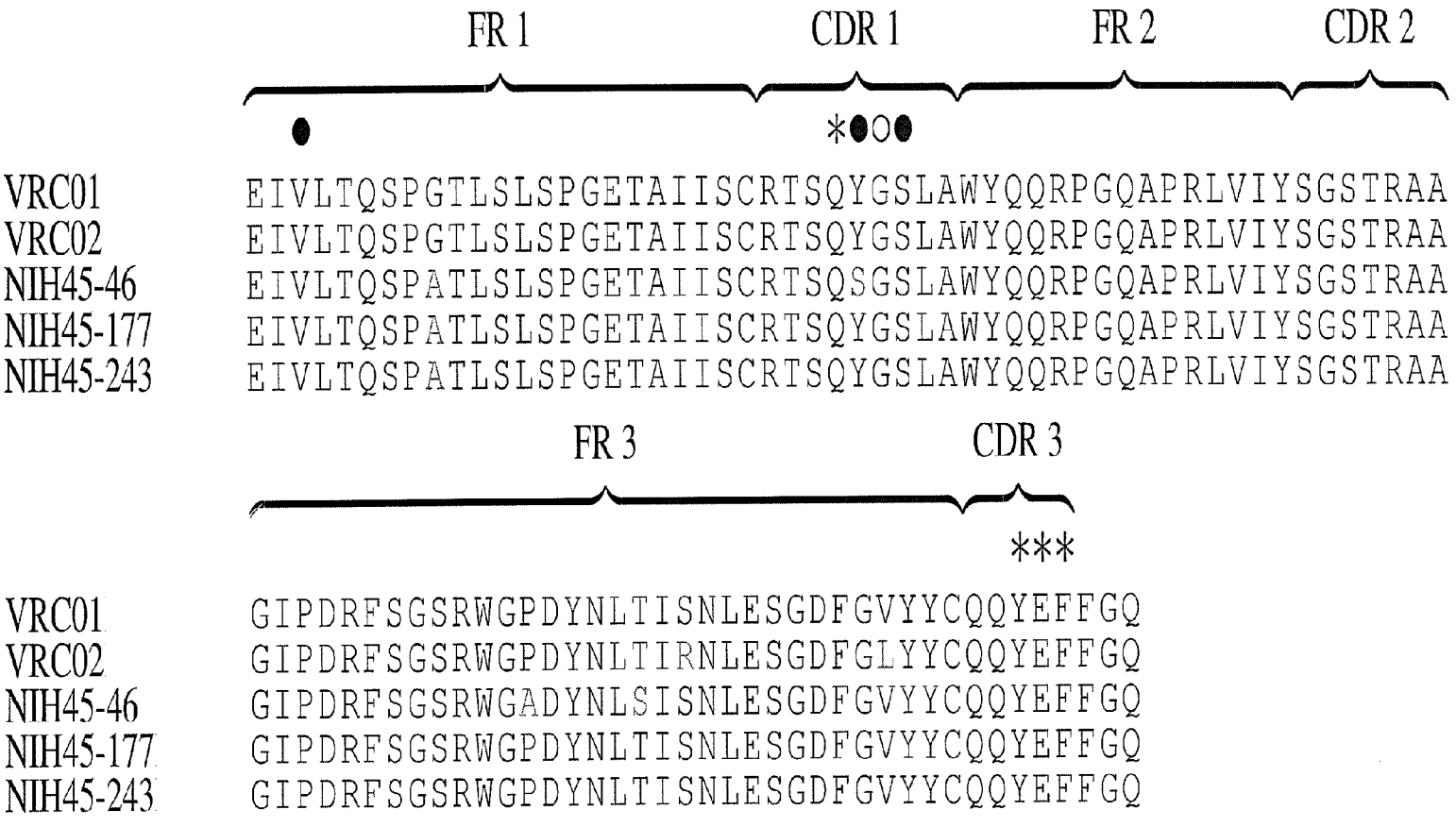
Figure 5b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FR 2
CDR 2
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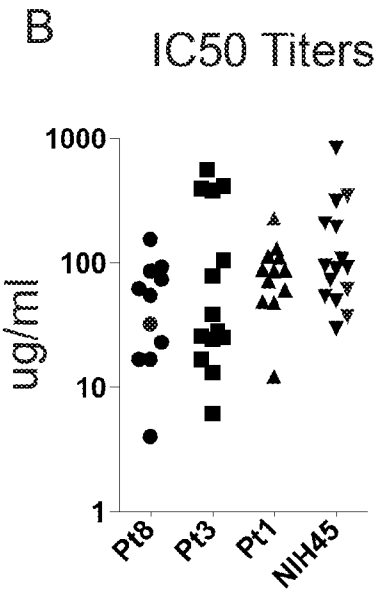
NIH45-46 EIVLTQSPATLSLSPGETAIISCRTSQSGSLAWYQQRPGQAPRLVIYSGSTRAA
NIH45-177 EIVLTQSPATLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAA
NIH45-243 EIVLTQSPATLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAA
FR 3
CDR 3
VRC01 GIPDRFSGSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQ
VRC02 GIPDRFSGSRWGPDYNLTIRNLESGDFGLYYCQQYEFFGQ
NIH45-46 GIPDRFSGSRWGADYNLSISNLESGDFGVYYCQQYEFFGQ
NIH45-177 GIPDRFSGSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQ
NIH45-243 GIPDRFSGSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQ

FIGURE 6A

A

	IC_{50}	Pt 1	Pt 3B	Pt 8	NIH45	Pt 12A
Clade B	6535.3	88	400.4	23.2	61	101.3
	RHPA4259.7	113	16.6	154.1	39	30.1
	SC422661.8	49	25.9	16.6	107	62.7
	PVO.4	89	78.1	74.1	195	116.3
	TRO.11	72	24.5	62.2	208	53.6
	YU2.DG	131	25.4	32.7	92	50.6
	H086.8	>132	>132	>132	37	
Clade C	Du172.17	228.42	418.62	86.463	349	
	ZM53M.PB12	60.70	383.37	>227	317	
	ZM109F.PB4	85.82	12.97	>227	73	
Clade A	Q842.d12	12.196	6.165	4.052	59	
	3415.v1.c1	45.26	38.68	16.63	54	
	3365.v2.c20	111.54	28.46	>227	94	
CRF02_AG	250-4	>132	560.58	55.09	90	
	251-18	>340	104.58	92.28	841	
	278-50	>132	>132	>132	>1000	
CRF01_AE	620345.c1	>132	>132	>132	>1000	
Clade D	3016.v5.c45	>340	185.62	>227	ND	
	231965.c1	304.48	86.54	171.56	ND	
Clade G	X1254_c3	222.01	61.48	>227	ND	
CRF01_AE	R1166.c1	>340	52.01	>227	ND	

FIGURE 6B



A

H S D Y C D F D V W G S G S Q V I V S S A S T K

FIGURE 7A

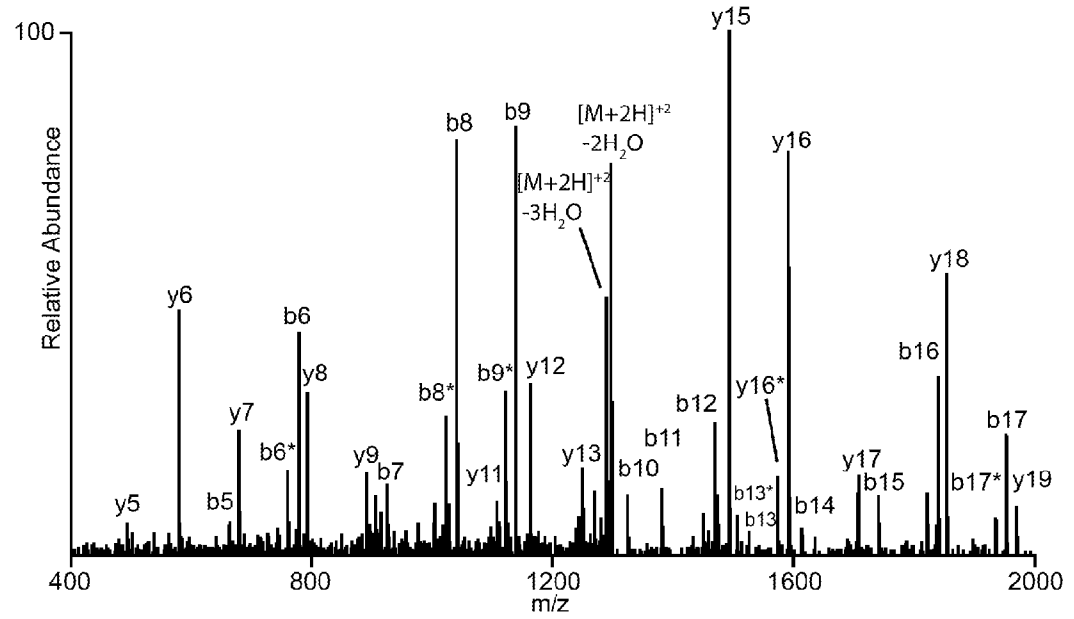


FIGURE 7B

B

D G L G E V A P A Y L Y G I D A W G Q G T T V I V T S A S T K

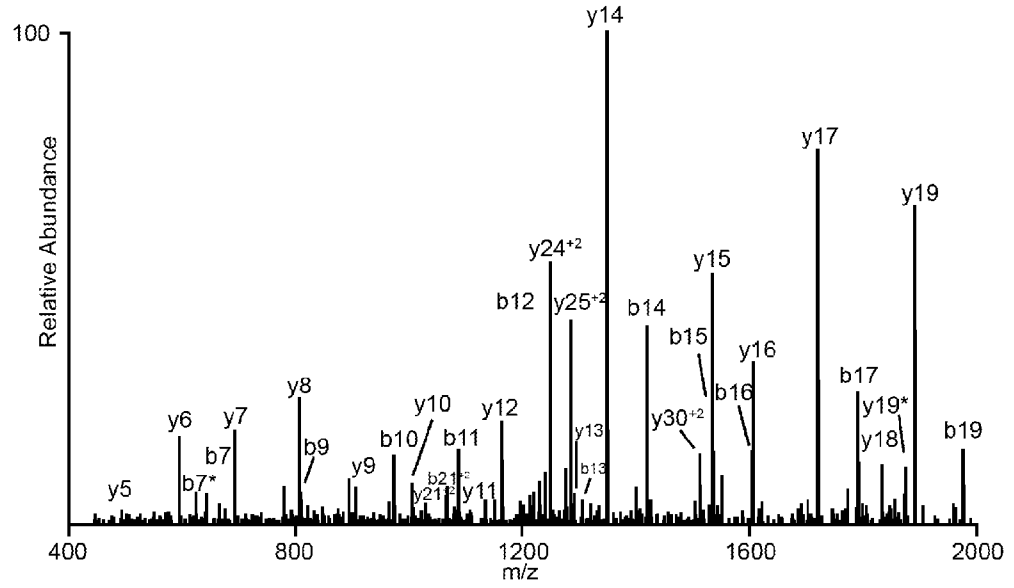
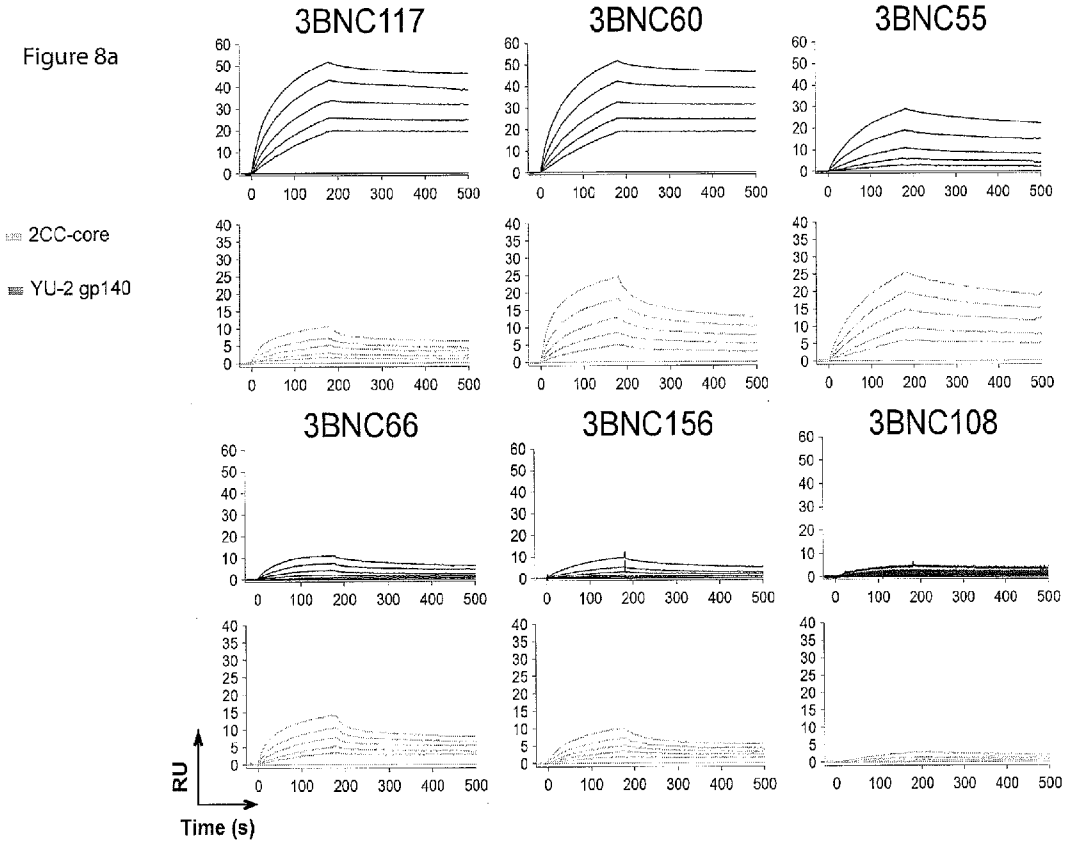


Figure 8a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3BNC55
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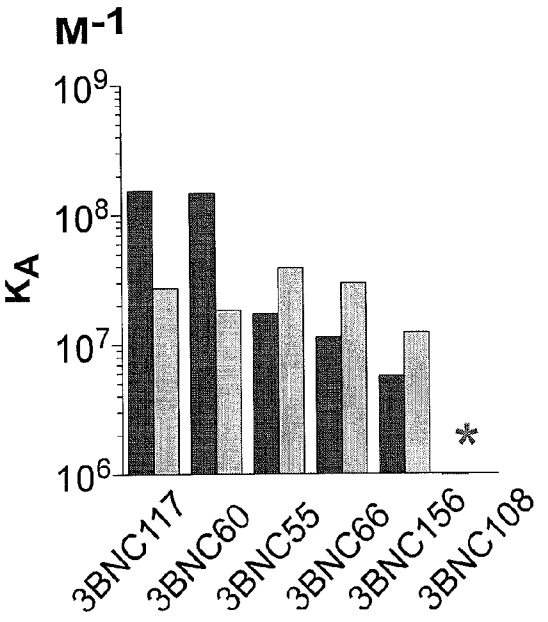
YU-2 gp140
3BNC66
3BNC156
3BNC108
RU
Time (s)

Figure 8b


M-1
10^9
10^8
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10^6
KA
*
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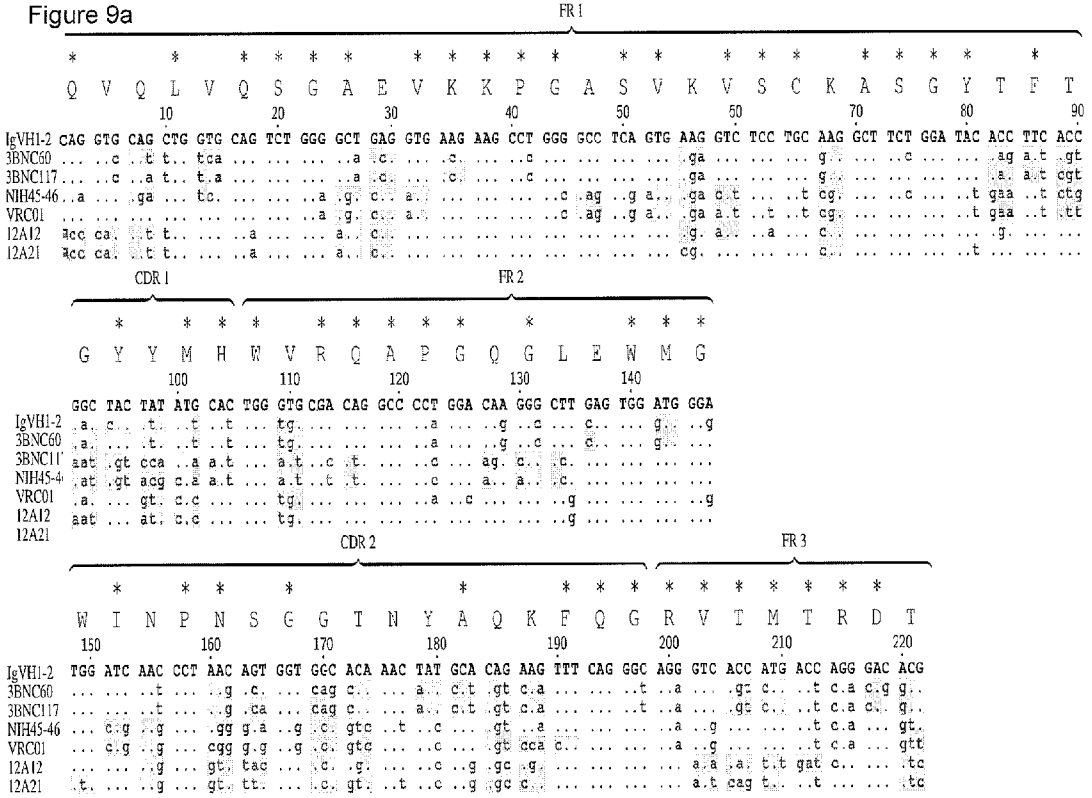
3BNC108

Figure 9a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FR2
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CDR2
FR3
W I N P N S G G T N Y A Q K F Q G R V T M T R D T
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Figure 9a, cont.

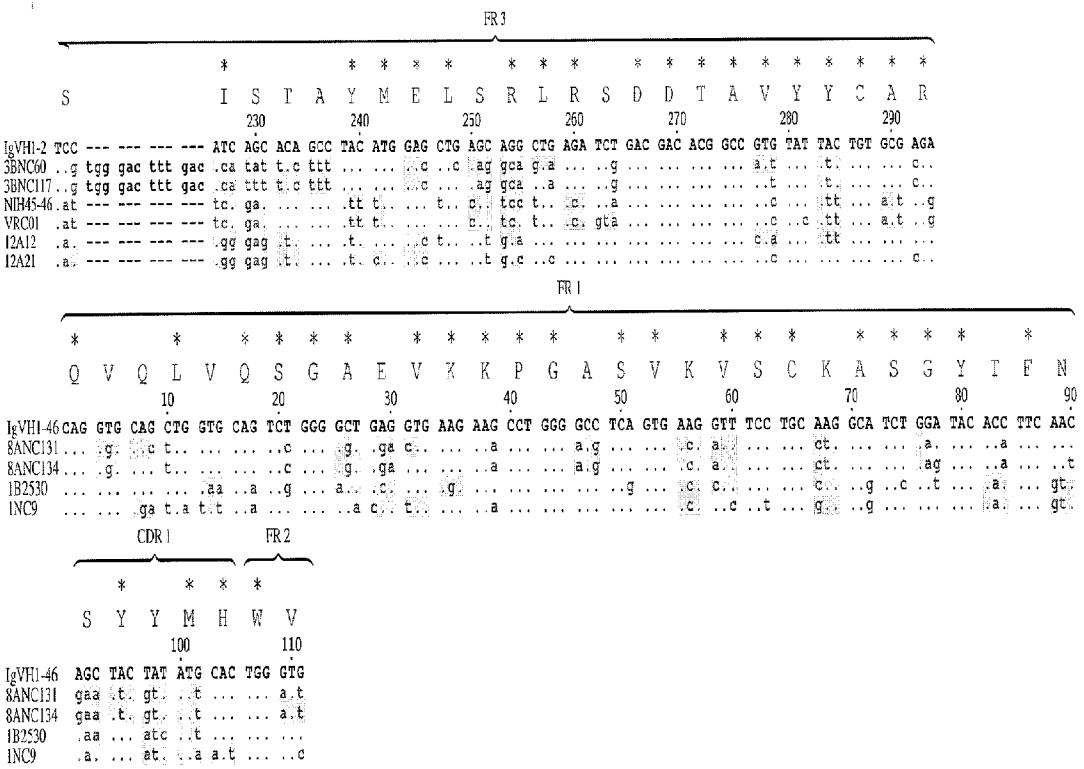


Figure 9a, cont. 2

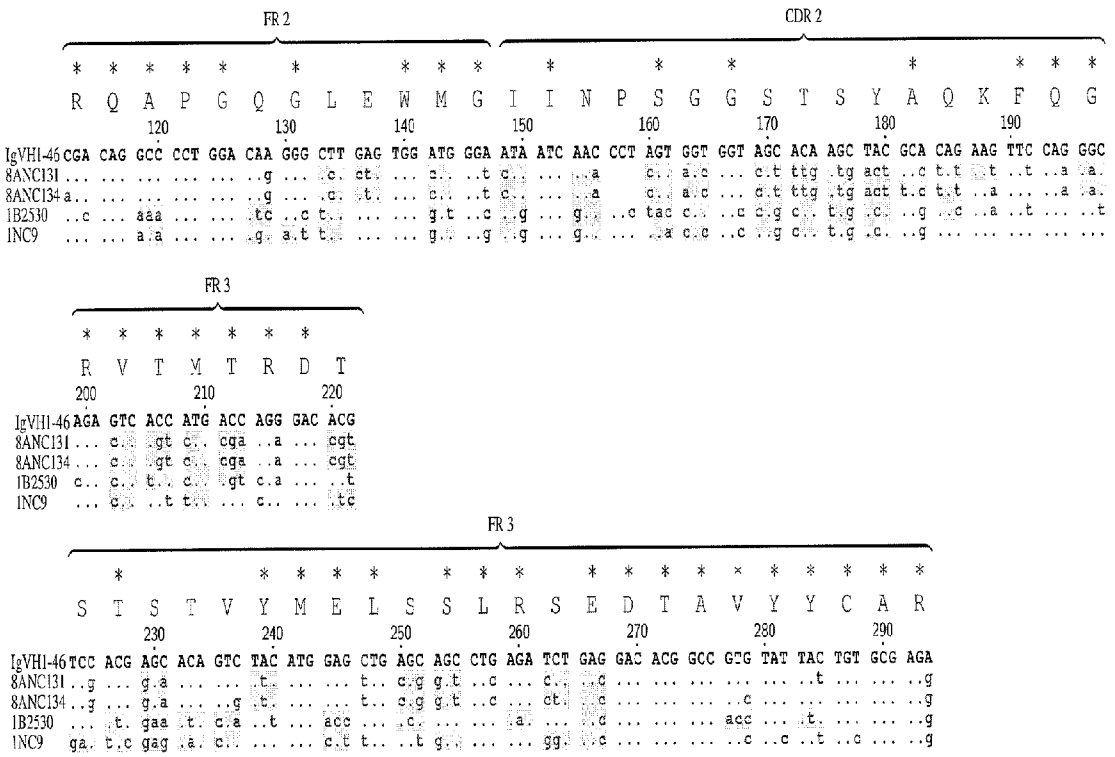


Figure 9b

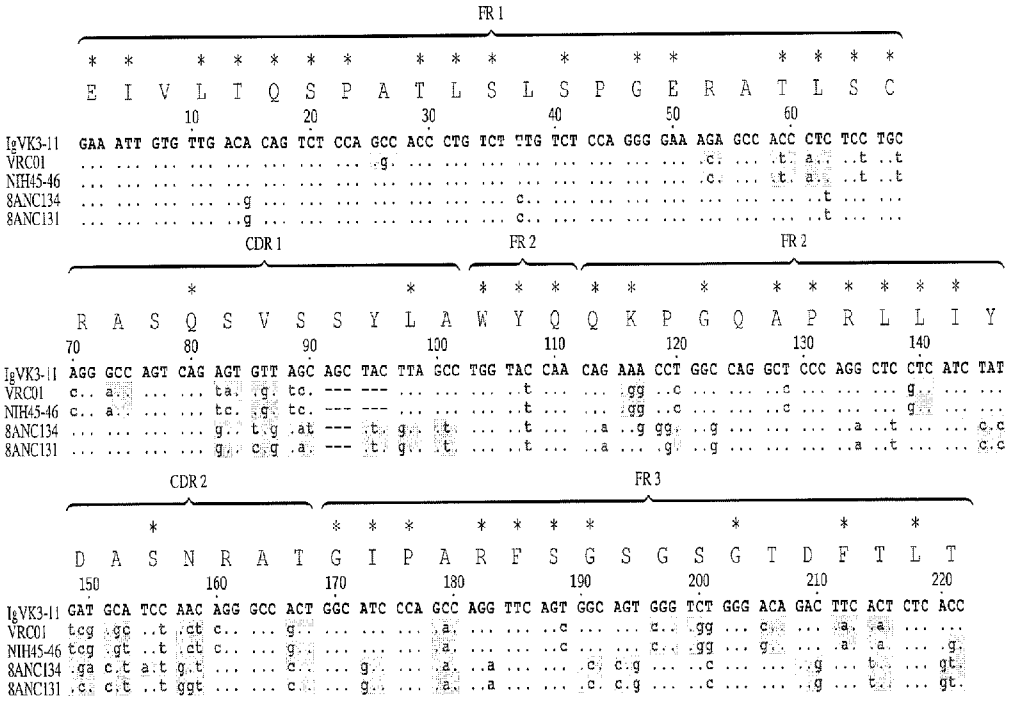

FR 1
E I V L T Q S P A T L S L S P G E R A T L S C
IgVK3-11 GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC
VRC01
NIH45-46
8ANC134
8ANC131
CDR 1
FR 2
FR 2
R A S Q S V S S Y L A W Y Q Q K P G Q A P R L L I Y
IgVK3-11 AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT
VRC01
NIH45-46
8ANC134
8ANC131
CDR 2
FR 3
D A S N R A T G I P A R F S G S G S G T D F T L T
IgVK3-11 GAT GCA TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC
VRC01
NIH45-46
8ANC134
8ANC131

Figure 9b, cont.

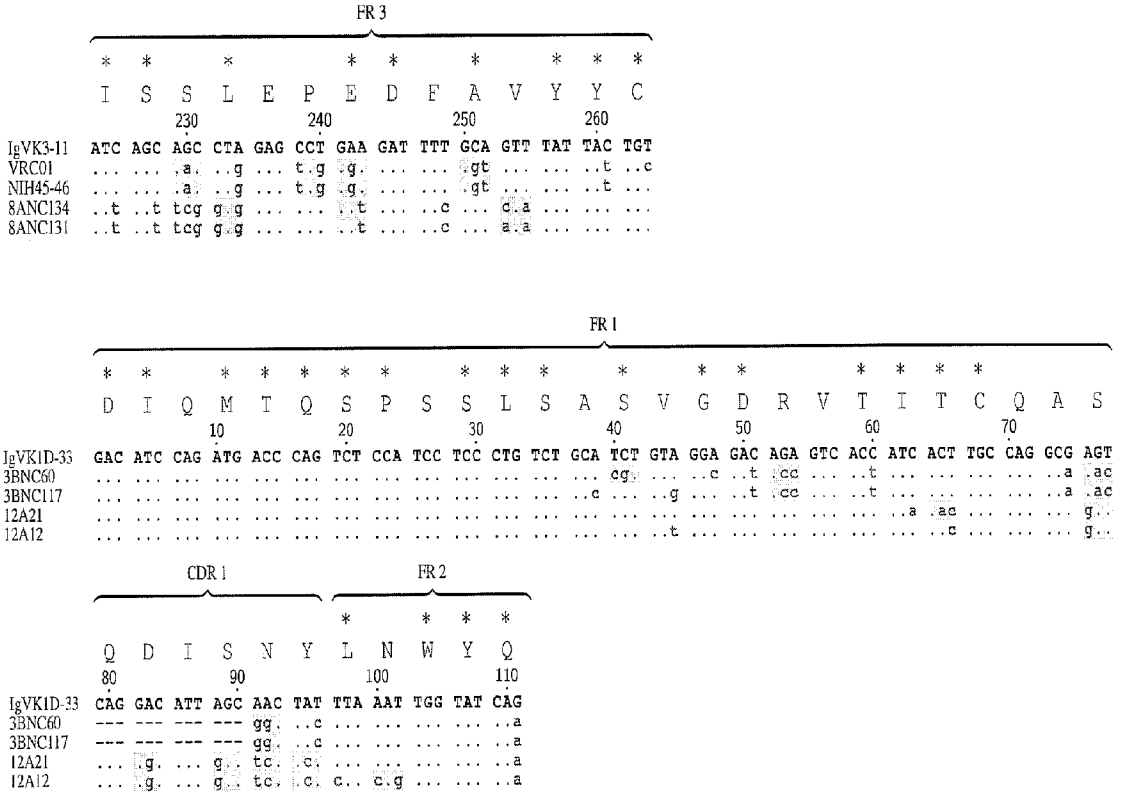


Figure 9b, cont.2

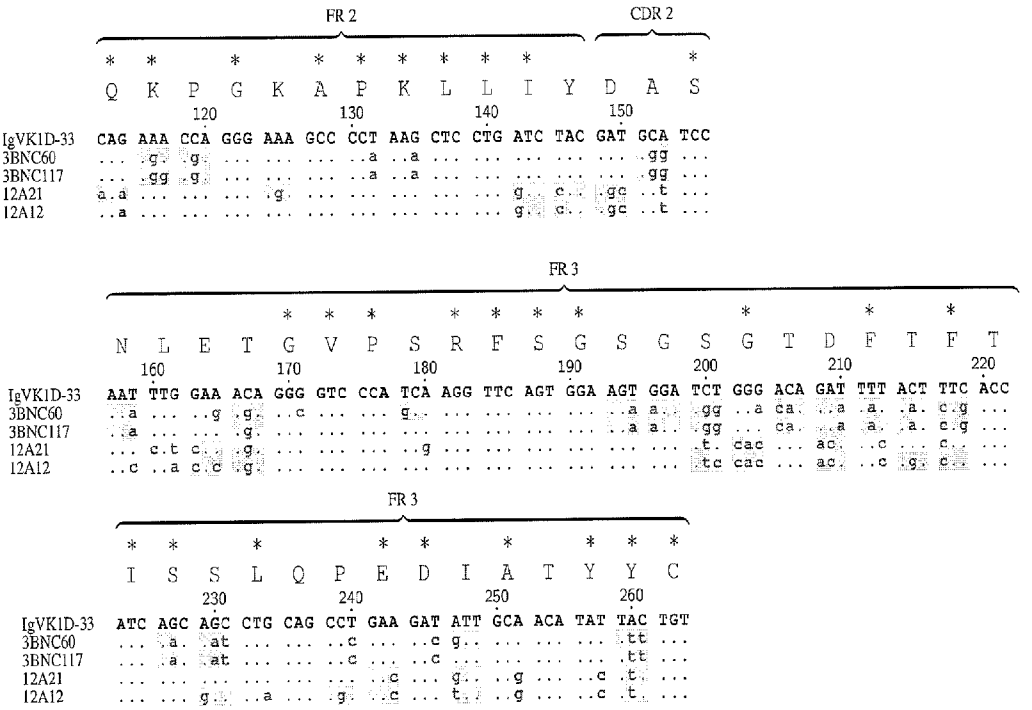


Figure 9c

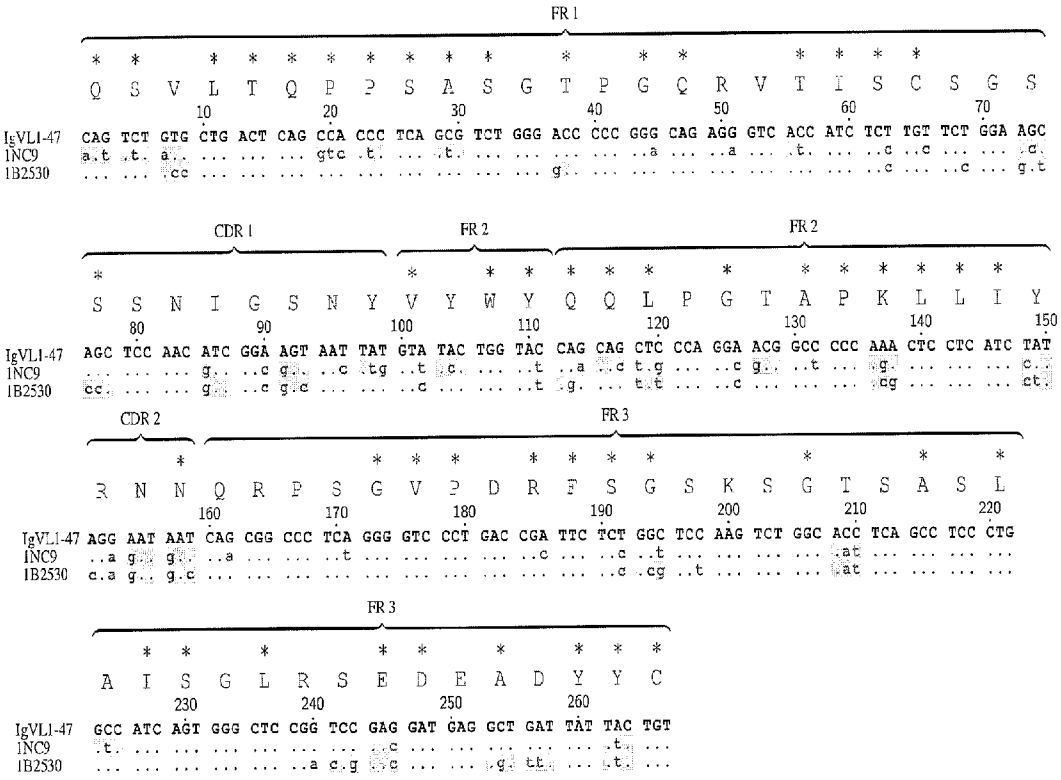
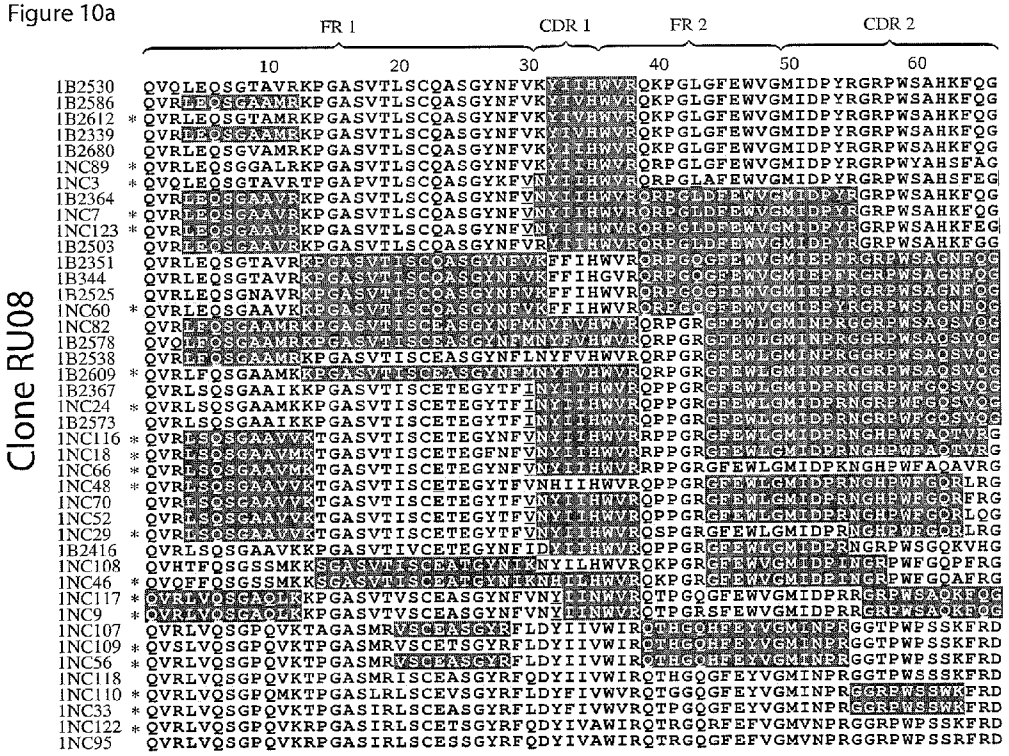


Figure 10a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CDR 1
FR 2
CDR 2
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20
30
40
50
60
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1B2612
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1B344
1B2525
1NC60
1NC82
1B2578
1B2538
1B2609
1B2367
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1B2573
1NC116
1NC18
1NC66
1NC48
1NC70
1NC52
1NC29
1B2416
1NC108
1NC46
1NC117
1NC9
1NC107
1NC109
1NC56
1NC118
1NC110
1NC33
1NC122
1NC95

Figure 10a, cont

Clone RU08

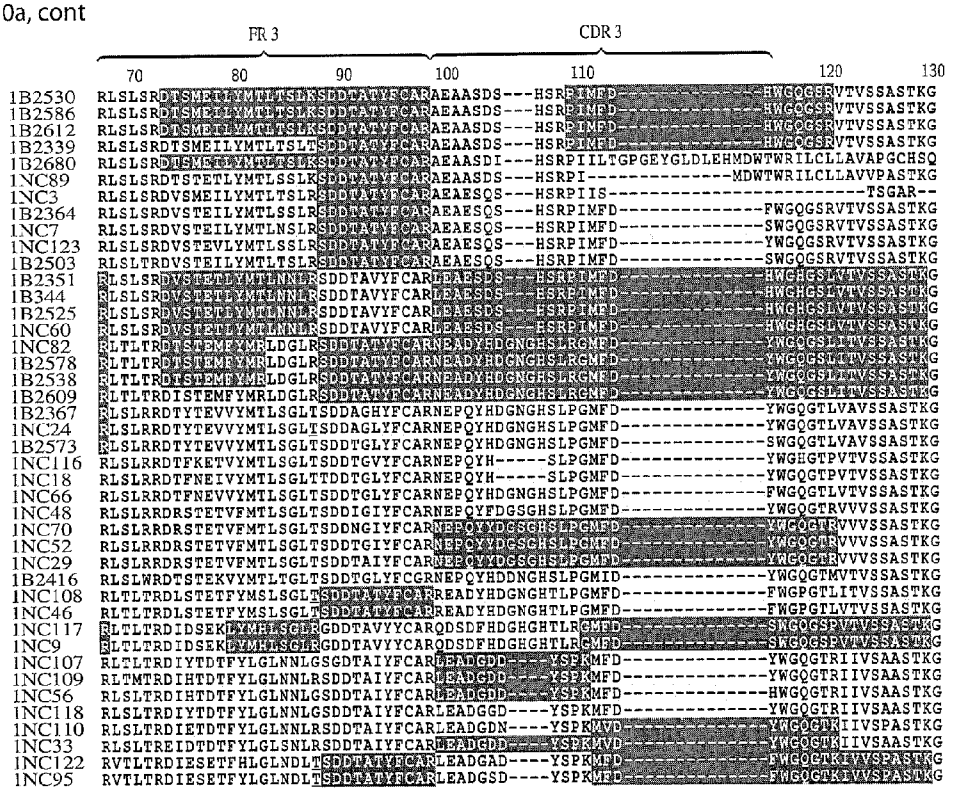
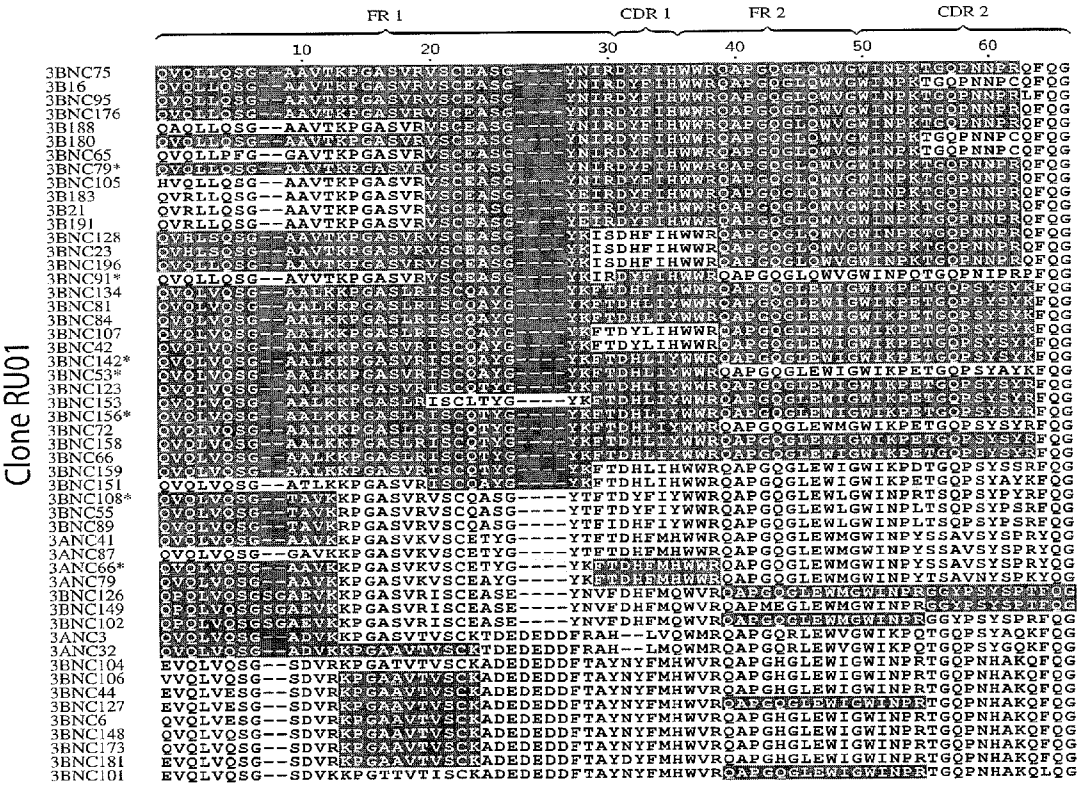


Figure 10b


FR 1
CDR 1
FR 2
CDR 2
10
20
30
40
50
60
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3BNC75
3B16
3BNC95
3BNC176
3B188
3B180
3BNC65
3BNC79*
3BNC105
3B183
3B21
3B191
3BNC128
3BNC23
3BNC196
3BNC91*
3BNC134
3BNC81
3BNC84
3BNC107
3BNC42
3BNC142*
3BNC53*
3BNC123
3BNC153
3BNC156*
3BNC72
3BNC158
3BNC66
3BNC159
3BNC151
3BNC108*
3BNC55
3BNC89
3ANC41
3ANC87
3ANC66*
3ANC79
3BNC126
3BNC149
3BNC102
3ANC3
3ANC32
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3BNC127
3BNC6
3BNC148
3BNC173
3BNC181
3BNC101

Figure 10b, cont

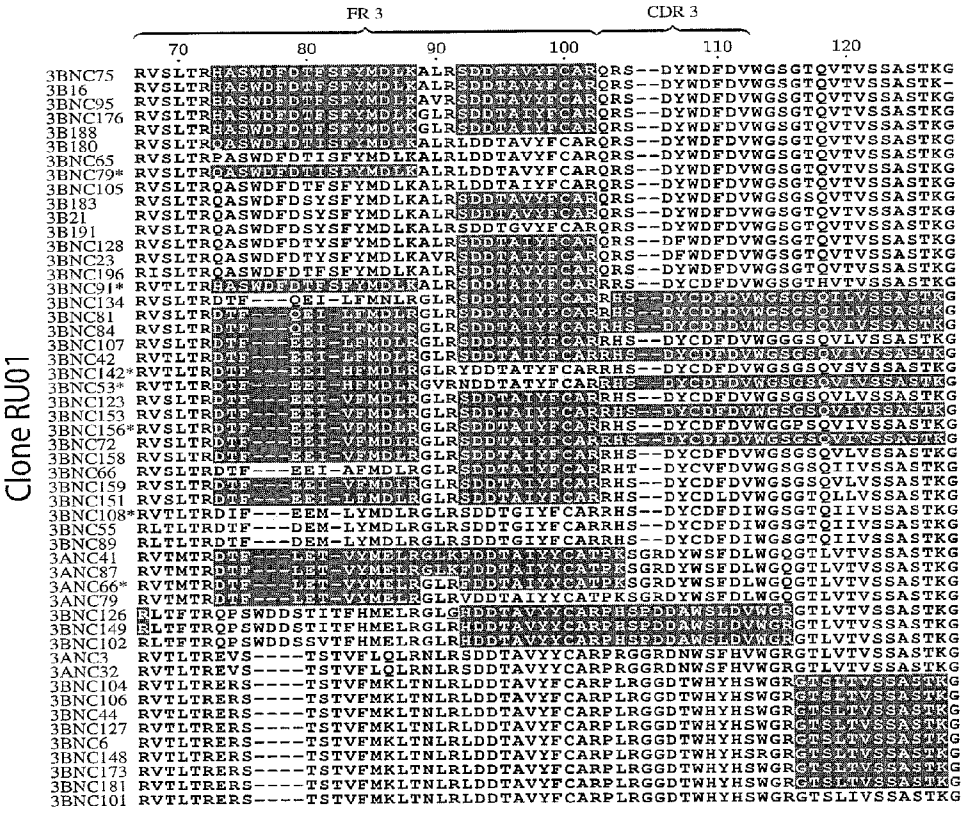
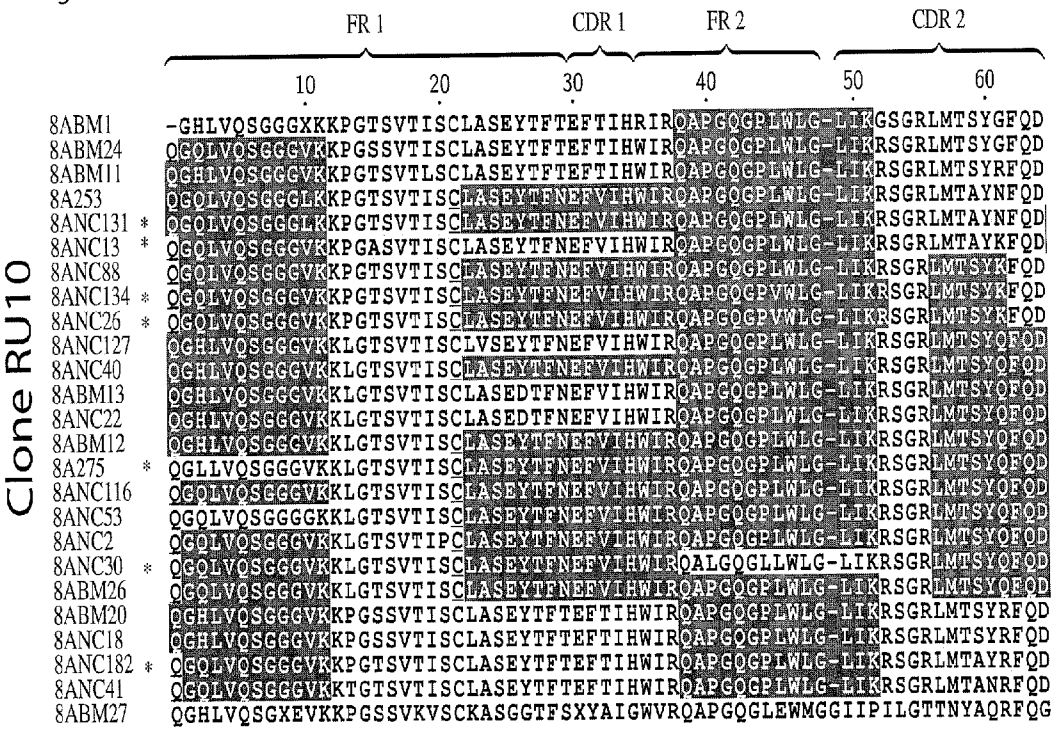


Figure 10c


Clone RU10
FR 1
CDR 1
FR 2
CDR 2
10
20
30
40
50
60
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8ABM24 QGQLVQSGGGVKKPGSSVTISCLASEYTFTEFTIHWIRQAPGQGPLWLG-LIKRSGRLMTSYGFQD
8ABM11 QGHLVQSGGGVKKPGTSVTLSCLASEYTFTEFTIHWIRQAPGQGPLWLG-LIKRSGRLMTSYRFQD
8A253 QGQLVQSGGGLKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTAYNFQD
8ANC131 * QGQLVQSGGGLKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTAYNFQD
8ANC13 * QGQLVQSGGGVKKPGASVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTAYKFQD
8ANC88 QGQLVQSGGGVKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYKFQD
8ANC134 * QGQLVQSGGGVKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGPVWLG-LIKRSGRLMTSYKFQD
8ANC26 * QGQLVQSGGGVKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGPVWLG-LIKRSGRLMTSYKFQD
8ANC127 QGHLVQSGGGVKKLGTSVTISCLVSEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ANC40 QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ABM13 QGHLVQSGGGVKKLGTSVTISCLASEDTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ANC22 QGHLVQSGGGVKKLGTSVTISCLASEDTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
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8A275 * QGLLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ANC116 QGQLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ANC53 QGQLVQSGGGGKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ANC2 QGQLVQSGGGVKKLGTSVTIPCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ANC30 * QGQLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQALGQGLLWLG-LIKRSGRLMTSYQFQD
8ABM26 QGQLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGPLWLG-LIKRSGRLMTSYQFQD
8ABM20 QGHLVQSGGGVKKPGSSVTISCLASEYTFTEFTIHWIRQAPGQGPLWLG-LIKRSGRLMTSYRFQD
8ANC18 QGHLVQSGGGVKKPGSSVTISCLASEYTFTEFTIHWIRQAPGQGPLWLG-LIKRSGRLMTSYRFQD
8ANC182 * QGQLVQSGGGVKKPGTSVTISCLASEYTFTEFTIHWIRQAPGQGPLWLG-LIKRSGRLMTAYRFQD
8ANC41 QGQLVQSGGGVKKTGTSVTISCLASEYTFTEFTIHWIRQAPGQGPLWLG-LIKRSGRLMTANRFQD
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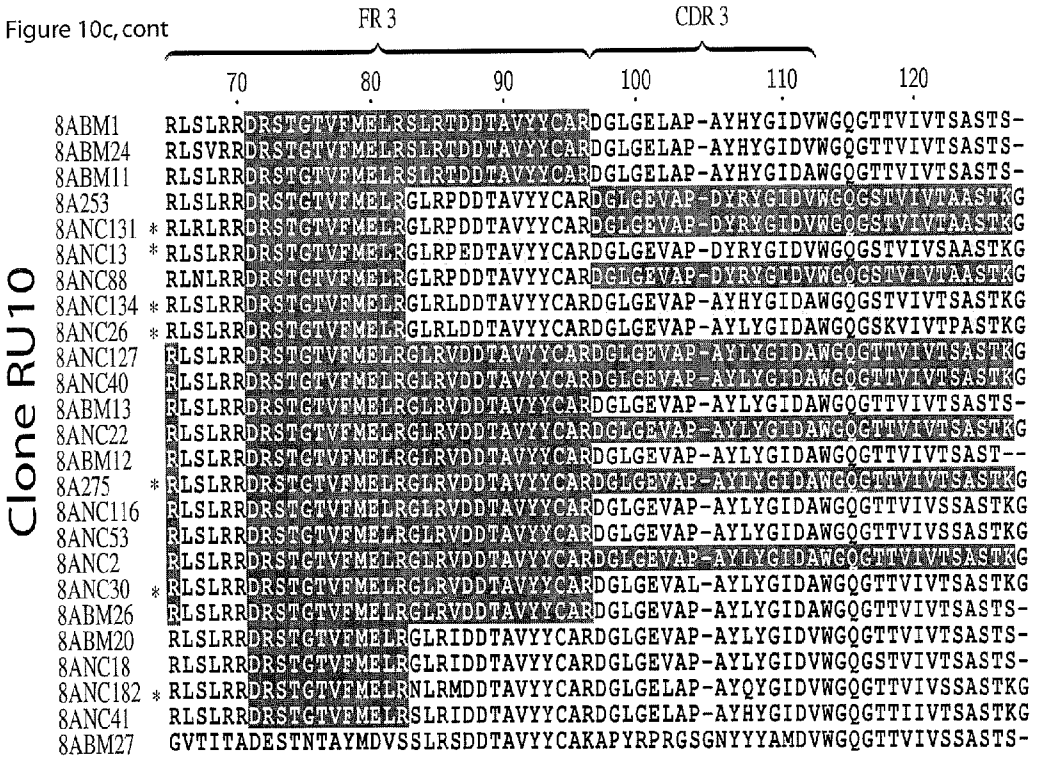
Figure 10c, cont



HUMAN IMMUNODEFICIENCY VIRUS NEUTRALIZING ANTIBODIES AND METHODS OF USE THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a U.S. National Phase of International Application No. PCT/US2012/038400, filed May 17, 2012, which claims priority under 35 U.S.C. §119(e) to U.S. Provisional Application No. 61/486,960 filed on May 17, 2011. The disclosures of which are hereby incorporated in their entirety.

STATEMENT REGARDING FEDERALLY FUNDED RESEARCH

[0002] The research leading to the present invention was supported in part, by National Institutes of Health Grant No. P01 AI08677-01. Accordingly, the U.S. Government has certain rights in this invention.

FIELD OF THE INVENTION

[0003] The present invention relates to antibodies directed to epitopes of Human Immunodeficiency Virus ("HIV"). The present invention further relates to the preparation and use of broadly neutralizing antibodies directed to the HIV gp120 envelope protein for the prevention and treatment of HIV infection.

BACKGROUND OF THE INVENTION

[0004] HIV causes Acquired Immunodeficiency Syndrome ("AIDS"). The immune response to HIV infection in long-term non-progressors suggests that specific viral immunity may limit infection and the symptoms of disease. Some HIV infected individuals show broadly neutralizing IgG antibodies in their serum; little is known regarding the specificity and activity of these antibodies, despite their potential importance in designing effective vaccines, and no single characteristic has of yet been correlated with protective immunity. In animal models, passive transfer of neutralizing antibodies can contribute to protection against virus challenge. Neutralizing antibody responses also can be developed in HIV-infected individuals but the detailed composition of the serologic response is yet to be fully uncovered.

[0005] A number of immunologic abnormalities have been described in AIDS. These include, but are not limited to, abnormalities in B-cell function, abnormal antibody response, defective monocyte cell function, impaired cytokine production, depressed natural killer and cytotoxic cell function, defective ability of lymphocytes to recognize and respond to soluble antigens, and the depletion of the T4 helper/inducer lymphocyte population.

[0006] The amino acid and RNA sequences encoding HIV env from a number of HIV strains are known (Modrow, S. et al., J. Virology 61(2): 570 (1987)). The HIV virion is covered by a membrane or envelope derived from the outer membrane of host cells. This membrane contains a population of envelope glycoproteins (gp 160) anchored in the membrane bilayer at their carboxyl terminal region. Each glycoprotein contains two segments: the N-terminal segment, and the C-terminal segment. The N-terminal segment, called gp 120 by virtue of its relative molecular weight of about 120 kD, protrudes into the aqueous environment surrounding the virion. The C-terminal segment, called gp41, spans the membrane. The N-terminal gp120 and the C-terminal gp41 are covalently linked by a peptide bond that is particularly susceptible to proteolytic cleavage. See European Patent Application Publication No. 0 335 635 to McCune et al and the references cited therein, each incorporated herein by reference in its entirety.

[0007] Several approaches to an AIDS vaccine have been proposed, including, but not limited to, inactivated and attenuated virus vaccines, subunit vaccines from virus-infected cells, recombinantly produced viral antigens, vaccines based on synthetic peptides, anti-idiotypic vaccines, and viral carrier-based vaccines. An additional approach to HIV therapeutic and prophylactic treatment includes making highly potent, broadly neutralizing monoclonal antibodies. Multiple studies have reported cloning and making monoclonal antibodies by various techniques for targeting the CD4 binding site as well as other parts of the virion spike and for neutralizing HIV. Generally, these techniques involve self-fusion or phage display techniques. Typically, in making HIV neutralizing antibodies using phage display techniques, random combinations of heavy and light chains are combined and a random pair is selected. Studies have reported a limited number of monoclonal antibodies, such as, for example, the phage display antibody b12, that are broadly highly potent, and broadly neutralizing (meaning antibodies that can neutralize multiple strains of HIV in sera) against HIV. The monoclonal antibody b12 is a broadly neutralizing antibody which has been reported to prevent HIV infection in macaques. Another broadly neutralizing antibody includes 2G12, which, atypically, has a structure which has yet to be seen in any other antibody with three combining sites. VRC01 is recently discovered broadly neutralizing antibody that targets the CD4 binding site (CD4bs) on the HIV spike. VRC01 was isolated by purifying single B cells that bind to a soluble, biotin labeled, stabilized, and re-surfaced core fragment of HIV gp120 (X. Wu et al., Science 329, 856 (Aug. 13, 2010)). Although successful, the isolation was inefficient, producing only 3 closely related HIV-binding antibodies from 25 million peripheral blood mononuclear cells from one individual. Like other anti-HIV antibodies obtained by the single cell antigen capture method, VRC01-3 showed very high levels of somatic mutations that were essential for potency and breadth. This high frequency of mutation is a potential impediment to antibody cloning because the mutated sequences may no longer be complementary to the primers used for cloning.

[0008] Some studies have reported that certain patients develop antibodies to HIV that are broadly neutralizing. Studies have reported that antibodies can be protective against initial HIV infection in passive transfer experiments in non-human primates and can modulate viral load during infection. See, for example, Mascola, 2000; Shibata, 1999; Veazey, 2003; Parren, 2001; Mascola, 1999; Trkola, 2005; Wei, 2003; Frost, 2005; Burton, 2004; Mascola, 2007; Karlsson Hedestam, 2008; McMichael, 2006; Zolla-Pazner, 2004.

BRIEF SUMMARY OF THE INVENTION

[0009] The present invention, in one embodiment, provides broadly neutralizing antibodies against HIV. In one embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain comprising the consensus amino acid sequence: QXXLXQSGGXVKKPGXSVX-VSCXASGYXXFXXYXIHWXRQAPGXGXXWVGXI XPRXGXXXXAXXFQGRLSLTRDXXXXXX-

TXXXFMDLXGLRXDDTAVYFCARX XXXXXXXXXXXXXXXXXDX (SEQ ID NO:1) wherein X indicates any amino acid or no amino acid.

[0010] In another embodiment, the present invention provides an isolated HIV antibody comprising a light chain comprising the consensus amino sequence: EIXLTQSPXSLSX-SXGEXXTISCXXXQXXXXXXXLXWYQQRXGXARPL LIXXXSX XXXGVPXRFSGXXXGXXYXLXISXLXXD-DXAXYFCXXYEXXXXXXX (SEQ ID NO:2) wherein X indicates any amino acid or no amino acid.

[0011] In another embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain comprising a highly conserved consensus sequence and a light chain comprising a highly conserved consensus sequence. The present invention further provides a method of producing an isolated HIV antibody comprising a heavy chain comprising a highly conserved consensus sequence and a light chain comprising a highly conserved consensus sequence.

[0012] In another embodiment, the present invention provides an isolated HIV antibody comprising the heavy chain consensus sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2. In a further embodiment, the present invention provides an isolated HIV antibody comprising one or both of the heavy chain consensus sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2, or sequences having at least 70%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 97%, or at least 98%, or at least 99% identity thereto, with the proviso that the antibody does not have the amino acid sequence of VRC01.

[0013] In another embodiment, the present invention provides an isolated HIV antibody comprising one or both of the heavy chain consensus sequence of SEQ ID NO:1 and the light chain consensus sequence of SEQ ID NO:2 and wherein the antibody neutralizes HIV virus ZM53M.PB12 at an IC_{50} concentration of less than 1.0 μg/ml, or HIV virus R1166.c1 at an IC_{50} concentration of less than 1.0 μg/ml, or DU172.17 at an IC_{50} concentration of less than 30 μg/ml. In another embodiment, the present invention provides an isolated HIV antibody comprising one or both of the heavy chain consensus sequence of SEQ ID NO:1 and the light chain consensus sequence of SEQ ID NO:2, wherein the antibody neutralizes a VRC01-resistant HIV virus at an IC_{50} concentration of less than 30 μg/ml.

[0014] In another embodiment, the present invention provides an isolated HIV antibody selected from the group consisting of 3BNC117, 3BNC60, 12A12, 12A21, NIH45-46, 8ANC131, 8ANC134, IB2530, INC9 and 8ANC196.

[0015] In another embodiment, the present invention provides an isolated HIV antibody comprising heavy chain CDR1, CDR2 and CDR3 regions and light chain CDR1, CDR2 and CDR3 regions comprising the amino acid sequences of the corresponding regions of an HIV antibody selected from the group consisting of 3BNC117, 3BNC60, 12A12, 12A21, NIH45-46, bANC131, 8ANC134, IB2530, INC9 and 8ANC196.

[0016] In another embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-438.

[0017] In another embodiment, the present invention provides an isolated HIV antibody comprising a light chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 439-583.

[0018] In another embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain and a light chain comprising an amino acid sequence set forth in Table A or Table B.

[0019] In another embodiment, the present invention provides an isolated HIV antibody comprising an insertion sequence comprising the amino acid sequence: ASWDFDF (SEQ ID NO:3).

[0020] In another embodiment, the present invention provides an isolated HIV antibody comprising an insertion sequence comprising the amino acid sequence: TARDY (SEQ ID NO:4).

[0021] In another embodiment, the present invention provides an isolated HIV antibody comprising insertion sequences SEQ ID No: 3 and SEQ ID No: 4.

[0022] In another embodiment, the present invention provides a method to improve the HIV neutralization potency and breadth of an isolated HIV antibody comprising inserting at least one of insertion sequences SEQ ID No: 3 and SEQ ID No: 4.

[0023] According to another embodiment, the present invention provides compositions comprising an isolated HIV antibody of the invention.

[0024] According to another embodiment, the present invention provides pharmaceutical compositions comprising an antibody of the invention and a pharmaceutically acceptable carrier.

[0025] According to another embodiment, the present invention provides nucleic acid molecules encoding an isolated HIV antibody of the invention.

[0026] According to other embodiments, the present invention provides vectors comprising nucleic acid molecules encoding an isolated HIV antibody of the invention, and cells comprising such vectors.

[0027] According to another embodiment, the present invention provides a method of preventing or treating HIV infection or an HIV-related disease comprising the steps of: identifying a mammalian subject in need of such prevention or treatment, and administering to said subject a therapeutically effective amount of at least one HIV antibody of the invention.

[0028] According to another embodiment, the method further comprises the administration of a second therapeutic agent. According to another embodiment, the second therapeutic agent is an antiviral agent.

[0029] Another embodiment of the present invention provides a method of reducing virus replication or spread of infection to additional host cells or tissues comprising contacting a mammalian cell with at least one antibody of the invention. According to another aspect, the present invention provides for a method for treating a mammalian subject infected with HIV, the method comprising administering to said subject a pharmaceutical composition comprising at least one antibody according to the invention.

[0030] According to another embodiment, the present invention provides a method for the preparation and administration of an HIV antibody preparation which is suitable for administration to a mammalian subject having or at risk of HIV infection, in an amount and according to a schedule sufficient to induce a protective immune response against HIV or reduction of the HIV virus in a mammalian subject. In another embodiment, the present invention provides a method

for detecting an HIV antibody comprising a heavy chain comprising a highly conserved consensus sequence and a light chain comprising a highly conserved consensus sequence in a biological sample.

[0031] In another embodiment, the present invention provides the isolated antibodies of the invention for use in the treatment of HIV.

[0032] In another embodiment, the present invention provides a kit comprising a pharmaceutically acceptable dose unit of a pharmaceutically effective amount of at isolated HIV antibody of the invention, and a pharmaceutically acceptable dose unit of a pharmaceutically effective amount of an HIV agent selected from the group consisting of a non-nucleoside reverse transcriptase inhibitor, a protease inhibitor, a entry or fusion inhibitor and an integrase inhibitors, wherein the two pharmaceutically acceptable dose units can optionally take the form of a single pharmaceutically acceptable dose unit.

[0033] In another embodiment, the present invention provides a kit for the diagnosis, prognosis or monitoring the treatment of HIV in a subject comprising one or more detection reagents which specifically bind to anti-HIV neutralizing antibodies in a biological sample from a subject. In another aspect of the invention, the kit further provides reagents for performing PCR or mass spectrometry.

BRIEF DESCRIPTION OF THE DRAWINGS

[0034] FIGS. **1**A-D show the HIV antibody neutralizing activity IC_{50}. (A) Limited panel. Top line indicates the donor number, then clone or antibody (Table 4); viruses are shown on the left. Colors indicate concentration at IC_{50}: red≤0.1 μg/ml; orange 0.1-1 μg/ml; yellow 1-10 μg/ml; green≤10 μg/ml; white not neutralized at any concentration tested. (B) Extended panel. (C) Neutralization summary graph comparing VRC01, NIH45-46, 3BNC117. Length of lines and size of circles inversely proportional to IC_{50}. Colors indicate viral clades: red A; blue B; green C; fucia D; black AE; gold AG. (D) Sequence of 3BNC60, 1B2530 and 8ANC134 heavy chains with coverage by peptides found by Mass Spec in light grey. Red dots indicate differences from respective germline sequences.

[0035] FIGS. **2**A-C show the binding properties of the HIV antibodies. (A) Representive SPR sensograms for binding to YU2-gp140 and 2CC-core by 12A12, 12A21 and 12A-germline (GL) reverted antibodies. (B) Graph shows K_A for representative antibodies. (C) Graph shows mean fluorescence intensity of anti-CD4i antibody binding to Ba1.26 expressing 293T cells after incubation with the indicated antibodies. Table indicates whether or not an antibody induces CD4i site accessibility.

[0036] FIGS. **3**A and B show the HIV antibody consensus sequence, and HIV antibody amino acid sequences. (A) Amino acid alignment relative to framework (FR) and CDR regions for consensus, germline genes, 10 selected antibodies and 8ANC195. Residues are numbered according to the 3BNC60 structure. (B) As in (A) for light chains. (C, D, and E) Crystal structure of 3BNC60 Fab.

[0037] FIGS. **4**A and B show recovery of highly mutated immunoglobulin heavy chains with specific primers. (A) side by side comparison of new and old primer set. Red boxes indicate successful amplification of IgV_H genes. (B) HIV antibodies that bind to 2CC-core from Pt 8. Clonal families are shown by differently expanded slices. Two highly mutated clones that were not amplified with the old primer set are shown in striped pie slices.

[0038] FIG. **5** shows Ig V heavy (A) and light chain (B) sequences of new VRC01 clonal members.

[0039] FIG. **6** shows patient serum neutralizing activity. (A) Table summarizes purified serum IgG neutralizing activity against a panel of Tier 2 viruses in a Tzm-b1 assay. Dark red boxes indicate IC_{50} values below 10 μg/ml, orange between 10 and 100 μg/ml and yellow above 100 μg/ml. (B) dot plot summarizes the IC_{50} values shown in A for the 4 more extensively tested patients.

[0040] FIG. **7** demonstrates detection of antibodies by mass spectrometry. Collision activated dissociation MS/MS spectrum recorded on the doubly charged peptides HSDYCDFDVWGSGSQVIVSSASTK from 3BNC153HC (A) and DGLGEVAPAYLYGIDAWGQGTTVIVTSASTK from 8ANC134HC. (B. Observed b-type fragment ions (containing the N-terminus) and y-type fragment ions (containing the C-terminus) are labeled in the spectrum. Loss of water from fragment ions is indicated by *. Ions corresponding to the loss of water from the parent ion are labeled in the spectrum. Observed backbone cleavages are indicated in the sequence with ⌉ for b-type ions and ⌋ for y type ions.

[0041] FIGS. **8**A and B demonstrate affinity of HIV antibodies. (A) Antibody binding to gp140 and 2CC-core measured by surface plasmon resonance (SPR). The SPR sensograms for antibody binding of the selected 3BNC-antibody clones are shown over time. (B) Bar graphs show the binding affinity (K_A) for gp140 and 2CC-core antigens for the selected IgG antibodies shown in A. RU, response units.

[0042] FIGS. **9**A-C illustrate the somatic hypermutation analysis of selected HIV antibodies for (A) immunoglobulin heavy chain gene, (B) light chain kappa and (C) light chain lambda gene sequences. Sequences are aligned with their respective germline nucleotide sequences. Somatic mutations are shown in red letters, additionally gray boxes designate replacement mutations. Germline amino acid sequences with * indicating consensus residues are shown above the nucleotide alignment.

[0043] FIGS. **10** A-C shows antibody sequences from one expanded neutralizing clone in each (A) Patient (Pt)1, (B) Pt3 and (C) Pt8. Peptides identified by mass spectrometry are indicated in color. The variants marked with an asterisk are uniquely defined by one or more mass spectrometrically observed peptides (shown in light grey). The remaining mass spectrometrically observed peptides map non-uniquely to multiple variants as shown in dark grey. Underlined amino acids indicate non-tryptic cleavage sites in the variants shown. The cleavages are presumed to occur through chymotryptic cleavage or additional mutations (not observed among the cloned variants) that place a lysine or arginine residue at these sites.

DETAILED DESCRIPTION OF THE INVENTION

I. HIV Neutralizing Antibodies

[0044] The present invention, in one embodiment, provides broadly neutralizing antibodies against HIV. In one embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain comprising the consensus amino acid sequence: QXXLXQSGGXVKKPGXSVXVSCXASGYXXFXXYXIHWXRQAPGXGXXWVGXI
XPRXGXXXAXXFQGRLSLTRDXXXXXX-
TXXXFMDLXGLRXDDTAVYFCARX
XXXXXXXXXXXXXXXXXDX (SEQ ID NO:1) wherein X indicates any amino acid or no amino acid.

[0045] In another embodiment, the present invention provides an isolated HIV antibody comprising a light chain comprising the consensus amino sequence: EIXLTQSPXSLSX-SXGEXXTISCXXXQXXXXXXXLXWYQQRXGXARPL LIXXXSX XXXGVPXRFSGXXXGXXYXLXISXLXXD-DXAXYFCXXYEXXXXXXX (SEQ ID NO:2) wherein X indicates any amino acid or no amino acid.

[0046] In another embodiment, the present invention provides an isolated HIV antibody comprising the heavy chain sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2. In a further embodiment, the present invention provides an isolated HIV antibody comprising one or both of the heavy chain sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2, or sequences having at least 70%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 97%, or at least 98%, or at least 99% identity thereto, with the proviso that the antibody does not have the amino acid sequence of VRC01. Percentage identity is determined as disclosed hereinbelow.

[0047] The present invention provides, in other embodiments, an isolated HIV antibody comprising a heavy chain comprising an highly conserved heavy chain amino acid sequence and a light chain comprising a highly conserved light chain amino acid sequence. A highly conserved heavy chain amino acid sequence is defined herein as an amino acid sequence having at least 70%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 97%, or at least 98%, or at least 99% identity with the sequence of SEQ ID NO:1. A highly conserved light chain amino acid sequence is defined herein as an amino acid sequence having at least 70%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 97%, or at least 98%, or at least 99% identity with the sequence of SEQ ID NO:2. Percentage identity is determined as disclosed hereinbelow.

[0048] In another embodiment, present invention provides an isolated HIV antibody comprising a heavy chain comprising an highly conserved heavy chain amino acid sequence and a light chain comprising a highly conserved light chain amino acid sequence, with the proviso that the antibody does not have the sequence of VRC01.

[0049] In another embodiment, the present invention provides an isolated HIV antibody comprising one or both of the heavy chain sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2 and wherein the antibody neutralizes HIV virus ZM53M.PB12 at an IC_{50} concentration of less than 1.0 μg/ml, or HIV virus R1166.c1 at an IC_{50} concentration of less than 1.0 μg/ml, or DU172.17 at an IC_{50} concentration of less than 30 μg/ml. In another embodiment, the present invention provides an isolated HIV antibody comprising one or both of the heavy chain sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2, wherein the antibody neutralizes a VRC01-resistant HIV virus at an IC_{50} concentration of less than 30 μg/ml. A VRC01-resistant HIV virus is defined herein as an HIV virus that is resistant to neutralization by VRC01 at an IC_{50} value of 50 μg/ml. VRC01-resistant HIV viruses include, for example, HO86.8, DU172.17, 250-4, 278-50, and 620345.c1.

[0050] In another embodiment, the present invention provides an isolated HIV antibody selected from the group consisting of 3BNC117, 3BNC60, 12A12, 12A21, NIH45-46, bANC131, 8ANC134, IB2530, INC9 and 8ANC196.

[0051] In another embodiment, the present invention provides an isolated HIV antibody comprising heavy chain CDR1, CDR2 and CDR3 regions and light chain CDR1, CDR2 and CDR3 regions comprising the amino acids sequences of the corresponding regions of an HIV antibody selected from the group consisting of 3BNC117, 3BNC60, 12A12, 12A21, NIH45-46, bANC131, 8ANC134, IB2530, INC9 and 8ANC196.

[0052] In another embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-438.

[0053] In another embodiment, the present invention provides an isolated HIV antibody comprising a light chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 439-583.

[0054] In another embodiment, the present invention provides an isolated HIV antibody comprising a heavy chain and a light chain comprising an amino acid sequence set forth in Table A or Table B.

[0055] In another embodiment, the present invention provides an isolated HIV antibody comprising an insertion sequence comprising the amino acid sequence: ASWDFDF (SEQ ID NO:3). In a further embodiment, the present invention provides an isolated HIV antibody wherein insertion sequence SEQ ID No: 3, which corresponds to the FR3 region of the heavy chain commencing at amino acid 74 of 3BNC117 and 3BNC60 as shown in FIG. **5**A, is substituted for the corresponding region, as determined by sequence alignment, of an HIV antibody of the invention. For example, SEQ ID No: 3 may be inserted after the seventh amino acid of FR3 of the heavy chain.

[0056] In another embodiment, the present invention provides an isolated HIV antibody comprising an insertion sequence comprising the amino acid sequence: TARDY (SEQ ID NO:4). In a further embodiment, the present invention provides an isolated HIV antibody wherein insertion sequence SEQ ID No: 4, which corresponds to the CDR3 region of the heavy chain commencing at amino acid 103 of NIH45-46 as shown in FIG. **5**A, is substituted for the corresponding region, as determined by sequence alignment, of an HIV antibody of the invention. For example, SEQ ID No: 4 may be inserted after the fourth amino acid of CDR3 of the heavy chain.

[0057] In another embodiment, the present invention provides an isolated HIV antibody wherein insertion sequence SEQ ID No: 3, which corresponds to the FR3 region of the heavy chain commencing at amino acid 74 of 3BNC117 and 3BNC60 as shown in FIG. **5**A, is substituted for the corresponding region, as determined by sequence alignment, of an HIV antibody of the invention, and insertion sequence SEQ ID No: 4, which corresponds to the CDR3 region of the heavy chain commencing at amino acid 103 of NIH45-46 as shown in FIG. **5**A, is substituted for the corresponding region, as determined by sequence alignment, of an HIV antibody of the invention. For example, SEQ ID No: 3 may be inserted after the seventh amino acid of FR3 of the heavy chain and SEQ ID No: 4 may be inserted after the fourth amino acid of CDR3 of the heavy chain.

[0058] In a further embodiment, the present invention provides a method to improve the HIV neutralization potency and breadth of an isolated HIV antibody comprising making an isolated HIV antibody wherein insertion sequence SEQ ID No: 3, which corresponds to the FR3 region of the heavy commencing at amino acid 74 of 3BNC117 and 3BNC60 as shown in FIG. **5**A, is substituted for the corresponding region, as determined by sequence alignment, of an HIV antibody of

the invention and/or the insertion sequence SEQ ID No: 4, which corresponds to the CDR3 region of the heavy chain commencing at amino acid 103 of NIH45-46 as shown in FIG. **5**A, is substituted for the corresponding region, as determined by sequence alignment, of an HIV antibody of the invention. For example, SEQ ID No: 3 may be inserted after the seventh amino acid of FR3 of the heavy chain, and/or SEQ ID No: 4 may be inserted after the fourth amino acid of CDR3 of the heavy chain. One skilled in this art can modify the amino acid sequence of an antibody utilizing recombinant methods and/or synthetic chemistry techniques for the production of a polypeptide or an antibody. Also, one skilled in the art can identify an improved HIV antibody with greater neutralization potency and breadth by using a HIV neutralization assay, as described below.

[0059] In another embodiment, the present invention provides an improved isolated HIV antibody comprising at least one of insertion sequences SEQ ID NO: 3 and SEQ ID NO: 4, wherein the improved isolated HIV antibody has greater HIV neutralization potency and breadth, than said isolated HIV antibody without insertion sequences SEQ ID NO: 3 and SEQ ID NO: 4. One skilled in the art can identify the improved HIV antibody with greater HIV neutralization potency and breadth by using the HIV neutralization assay, as described below.

[0060] One skilled in this art can modify the amino acid sequence of an antibody utilizing recombinant methods and/or synthetic chemistry techniques for the production of a polypeptide or an antibody.

[0061] In another embodiment, the present invention provides for a method to make an isolated HIV antibody comprising the heavy chain consensus sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2. In a further embodiment, the present invention provides for a method of producing an isolated HIV antibody comprising one or both of the heavy chain consensus sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2, or sequences having at least 70%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 97%, or at least 98%, or at least 99% identity thereto, with the proviso that the antibody does not have the amino acid sequence of VRC01. Percentage identity is determined as disclosed hereinbelow.

[0062] In another embodiment, the present invention provides a method for detecting an isolated HIV antibody comprising obtaining an immunoglobulin-containing biological sample from a mammalian subject, isolating an HIV antibody from said sample, determining the amino sequence of the HIV antibody and identifying the presence of the heavy chain sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2. In a further embodiment, the present invention provides for a method of selecting an isolated HIV antibody comprising determining the presence of one or both of the heavy chain consensus sequence of SEQ ID NO:1 and the light chain sequence of SEQ ID NO:2, or sequences having at least 70%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 97%, or at least 98%, or at least 99% identity thereto, with the proviso that the antibody does not have the amino acid sequence of VRC01. Percentage identity is determined as disclosed herein below. The biological sample may be blood, serum, saliva, urine, sputum, a cell swab sample, or a tissue biopsy. The amino acid sequences may be determined by methods known in the art including, for example, PCR and mass spectrometry.

[0063] The term "antibody" (Ab) as used herein includes monoclonal antibodies, polyclonal antibodies, multispecific antibodies (for example, bispecific antibodies and polyreactive antibodies), and antibody fragments. Thus, the term "antibody" as used in any context within this specification is meant to include, but not be limited to, any specific binding member, immunoglobulin class and/or isotype (e.g., IgG1, IgG2, IgG3, IgG4, IgM, IgA, IgD, IgE and IgM); and biologically relevant fragment or specific binding member thereof, including but not limited to Fab, F(ab')2, Fv, and scFv (single chain or related entity). It is understood in the art that an antibody is a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen binding portion thereof. A heavy chain is comprised of a heavy chain variable region (VH) and a heavy chain constant region (CH1, CH2 and CH3). A light chain is comprised of a light chain variable region (VL) and a light chain constant region (CL). The variable regions of both the heavy and light chains comprise framework regions (FWR) and complementarity determining regions (CDR). The four FWR regions are relatively conserved while CDR regions (CDR1, CDR2 and CDR3) represent hypervariable regions and are arranged from NH2 terminus to the COOH terminus as follows: FWR1, CDR1, FWR2, CDR2, FWR3, CDR3, FWR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen while, depending of the isotype, the constant region(s) may mediate the binding of the immunoglobulin to host tissues or factors.

[0064] Also included in the definition of "antibody" as used herein are chimeric antibodies, humanized antibodies, and recombinant antibodies, human antibodies generated from a transgenic non-human animal, as well as antibodies selected from libraries using enrichment technologies available to the artisan.

[0065] The term "variable" refers to the fact that certain segments of the variable (V) domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and defines specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable regions. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable regions of native heavy and light chains each comprise four FRs, largely adopting a beta sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the beta sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see, for example, Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)).

[0066] The term "hypervariable region" as used herein refers to the amino acid residues of an antibody that are responsible for antigen binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" ("CDR").

[0067] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies

comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. The term "polyclonal antibody" refers to preparations that include different antibodies directed against different determinants ("epitopes").

[0068] The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with, or homologous to, corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with, or homologous to, corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see, for example, U.S. Pat. No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). The described invention provides variable region antigen-binding sequences derived from human antibodies. Accordingly, chimeric antibodies of primary interest herein include antibodies having one or more human antigen binding sequences (for example, CDRs) and containing one or more sequences derived from a non-human antibody, for example, an FR or C region sequence. In addition, chimeric antibodies included herein are those comprising a human variable region antigen binding sequence of one antibody class or subclass and another sequence, for example, FR or C region sequence, derived from another antibody class or subclass.

[0069] A "humanized antibody" generally is considered to be a human antibody that has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues often are referred to as "import" residues, which typically are taken from an "import" variable region. Humanization may be performed following the method of Winter and co-workers (see, for example, Jones et al., Nature, 321:522-525 (1986); Reichmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting import hypervariable region sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (see, for example, U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable region has been substituted by the corresponding sequence from a non-human species.

[0070] An "antibody fragment" comprises a portion of an intact antibody, such as the antigen binding or variable region of the intact antibody. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, and Fv fragments; diabodies; linear antibodies (see, for example, U.S. Pat. No. 5,641,870; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0071] "Fv" is the minimum antibody fragment that contains a complete antigen-recognition and antigen-binding site. This fragment contains a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (three loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable region (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0072] "Single-chain Fv" ("sFv" or "scFv") are antibody fragments that comprise the VH and VL antibody domains connected into a single polypeptide chain. The sFv polypeptide can further comprise a polypeptide linker between the VH and VL domains that enables the sFv to form the desired structure for antigen binding. For a review of sFv, see, for example, Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, infra.

[0073] The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments with short linkers (about 5-10 residues) between the VH and VL domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the VH and VL domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

[0074] Domain antibodies (dAbs), which can be produced in fully human form, are the smallest known antigen-binding fragments of antibodies, ranging from about 11 kDa to about 15 kDa. dAbs are the robust variable regions of the heavy and light chains of immunoglobulins (VH and VL, respectively). They are highly expressed in microbial cell culture, show favorable biophysical properties including, for example, but not limited to, solubility and temperature stability, and are well suited to selection and affinity maturation by in vitro selection systems such as, for example, phage display. dAbs are bioactive as monomers and, owing to their small size and inherent stability, can be formatted into larger molecules to create drugs with prolonged serum half-lives or other pharmacological activities. Examples of this technology have been described in, for example, WO9425591 for antibodies derived from Camelidae heavy chain Ig, as well in US20030130496 describing the isolation of single domain fully human antibodies from phage libraries.

[0075] Fv and sFv are the only species with intact combining sites that are devoid of constant regions. Thus, they are suitable for reduced nonspecific binding during in vivo use. sFv fusion proteins can be constructed to yield fusion of an effector protein at either the amino or the carboxy terminus of an sFv. See, for example, Antibody Engineering, ed. Borrebaeck, supra. The antibody fragment also can be a "linear antibody", for example, as described in U.S. Pat. No. 5,641, 870 for example. Such linear antibody fragments can be monospecific or bispecific.

[0076] In certain embodiments, antibodies of the described invention are bispecific or multi-specific. Bispecific antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies can bind to two different epitopes of a single antigen. Other such antibodies can combine a first antigen binding site with a binding site for a second antigen. Alternatively, an anti-HIV arm can be combined with an arm that binds to a triggering molecule on a leukocyte, such as a T-cell receptor molecule (for example, CD3), or Fc receptors for IgG (Fc gamma R), such as Fc gamma RI (CD64), Fc gamma RII (CD32) and Fc gamma RIII (CD16), so as to focus and localize cellular defense mechanisms to the infected cell. Bispecific antibodies also can be used to localize cytotoxic agents to infected

cells. Bispecific antibodies can be prepared as full length antibodies or antibody fragments (for example, F(ab')2 bispecific antibodies). For example, WO 96/16673 describes a bispecific anti-ErbB2/anti-Fc gamma RIII antibody and U.S. Pat. No. 5,837,234 discloses a bispecific anti-ErbB2/anti-Fc gamma RI antibody. For example, a bispecific anti-ErbB2/Fc alpha antibody is reported in WO98/02463; U.S. Pat. No. 5,821,337 teaches a bispecific anti-ErbB2/anti-CD3 antibody. See also, for example, Mouquet et al., Polyreactivity Increases The Apparent Affinity Of Anti-HIV Antibodies By Heteroligation. *NATURE.* 467, 591-5 (2010).

[0077] Methods for making bispecific antibodies are known in the art. Traditional production of full length bispecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (see, for example, Millstein et al., Nature, 305:537-539 (1983)). Similar procedures are disclosed in, for example, WO 93/08829, Traunecker et al., EMBO J., 10:3655-3659 (1991) and see also; Mouquet et al., Polyreactivity Increases The Apparent Affinity Of Anti-HIV Antibodies By Heteroligation. NATURE. 467, 591-5 (2010).

[0078] Alternatively, antibody variable regions with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion is with an Ig heavy chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. According to some embodiments, the first heavy-chain constant region (CH1) containing the site necessary for light chain bonding, is present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host cell. This provides for greater flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yield of the desired bispecific antibody. It is, however, possible to insert the coding sequences for two or all three polypeptide chains into a single expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios have no significant affect on the yield of the desired chain combination.

[0079] Techniques for generating bispecific antibodies from antibody fragments also have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. For example, Brennan et al., Science, 229: 81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')2 fragments. These fragments are reduced in the presence of the dithiol complexing agent, sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated then are converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives then is reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0080] Other modifications of the antibody are contemplated herein. For example, the antibody can be linked to one of a variety of nonproteinaceous polymers, for example, polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol. The antibody also can be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate)microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules), or in macroemulsions. Such techniques are disclosed in, for example, Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

[0081] Typically, the antibodies of the described invention are produced recombinantly, using vectors and methods available in the art. Human antibodies also can be generated by in vitro activated B cells (see, for example, U.S. Pat. Nos. 5,567,610 and 5,229,275). General methods in molecular genetics and genetic engineering useful in the present invention are described in the current editions of Molecular Cloning: A Laboratory Manual (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), Gene Expression Technology (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, Calif.), "Guide to Protein Purification" in Methods in Enzymology (M. P. Deutshcer, ed., (1990) Academic Press, Inc.); PCR Protocols: A Guide to Methods and Applications (Innis, et al. 1990. Academic Press, San Diego, Calif.), Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed. (R. I. Freshney. 1987. Liss, Inc. New York, N.Y.), and Gene Transfer and Expression Protocols, pp. 109-128, ed. E. J. Murray, The Humana Press Inc., Clifton, N.J.). Reagents, cloning vectors, and kits for genetic manipulation are available from commercial vendors such as BioRad, Stratagene, Invitrogen, ClonTech and Sigma-Aldrich Co.

[0082] Human antibodies also can be produced in transgenic animals (for example, mice) that are capable of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (JH) gene in chimeric and germline mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array into such germ-line mutant mice results in the production of human antibodies upon antigen challenge. See, for example, Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in Immuno., 7:33 (1993); U.S. Pat. Nos. 5,545,806, 5,569,825, 5,591,669 (all of GenPharm); U.S. Pat. No. 5,545,807; and WO 97/17852. Such animals can be genetically engineered to produce human antibodies comprising a polypeptide of the described invention.

[0083] Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, for example, Morimoto et al., Journal of Biochemical and Biophysical Methods 24:107-117 (1992); and Brennan et al., Science, 229:81 (1985)). However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and ScFv antibody fragments can all be expressed in and secreted from *E. coli*, thus allowing the facile production of large amounts of these fragments. Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab')2 fragments (see, for example, Carter et al., Bio/Technology 10:163-167 (1992)). According to another approach, F(ab')2 fragments can be isolated directly from recombinant host cell culture. Fab and F(ab')2 fragment with

increased in vivo half-life comprising a salvage receptor binding epitope residues are described in U.S. Pat. No. 5,869,046. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner.

[0084] Other techniques that are known in the art for the selection of antibody fragments from libraries using enrichment technologies, including but not limited to phage display, ribosome display (Hanes and Pluckthun, 1997, *Proc. Nat. Acad. Sci.* 94: 4937-4942), bacterial display (Georgiou, et al., 1997, *Nature Biotechnology* 15: 29-34) and/or yeast display (Kieke, et al., 1997, *Protein Engineering* 10: 1303-1310) may be utilized as alternatives to previously discussed technologies to select single chain antibodies. Single-chain antibodies are selected from a library of single chain antibodies produced directly utilizing filamentous phage technology. Phage display technology is known in the art (e.g., see technology from Cambridge Antibody Technology (CAT)) as disclosed in U.S. Pat. Nos. 5,565,332; 5,733,743; 5,871,907; 5,872,215; 5,885,793; 5,962,255; 6,140,471; 6,225,447; 6,291650; 6,492,160; 6,521,404; 6,544,731; 6,555,313; 6,582,915; 6,593,081, as well as other U.S. family members, or applications which rely on priority filing GB 9206318, filed 24 May 1992; see also Vaughn, et al. 1996, Nature Biotechnology 14: 309-314). Single chain antibodies may also be designed and constructed using available recombinant DNA technology, such as a DNA amplification method (e.g., PCR), or possibly by using a respective hybridoma cDNA as a template.

[0085] Variant antibodies also are included within the scope of the invention. Thus, variants of the sequences recited in the application also are included within the scope of the invention. Further variants of the antibody sequences having improved affinity can be obtained using methods known in the art and are included within the scope of the invention. For example, amino acid substitutions can be used to obtain antibodies with further improved affinity. Alternatively, codon optimization of the nucleotide sequence can be used to improve the efficiency of translation in expression systems for the production of the antibody.

[0086] Such variant antibody sequences will share 70% or more (i.e., 80%, 85%, 90%, 95%, 97%, 98%, 99% or greater) sequence identity with the sequences recited in the application. Such sequence identity is calculated with regard to the full length of the reference sequence (i.e., the sequence recited in the application). Percentage identity, as referred to herein, is as determined using BLAST version 2.1.3 using the default parameters specified by the NCBI (the National Center for Biotechnology Information; http://www.ncbi.nlm.nih.gov/) [Blosum 62 matrix; gap open penalty=11 and gap extension penalty=1]. For example, peptide sequences are provided by this invention that comprise at least about 5, 10, 15, 20, 30, 40, 50, 75, 100, 150, or more contiguous peptides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. As used herein, the term "intermediate lengths" is meant to describe any length between the quoted values, such as 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, etc.; 21, 22, 23, etc.; 30, 31, 32, etc.; 50, 51, 52, 53, etc.; 100, 101, 102, 103, etc.; 150, 151, 152, 153, etc.

[0087] The present invention provides for antibodies, either alone or in combination with other antibodies, such as, but not limited to, VRC01 and PG9, that have broad neutralizing activity in serum.

[0088] According to another embodiment, the present invention provides methods for the preparation and administration of an HIV antibody composition that is suitable for administration to a human or non-human primate patient having HIV infection, or at risk of HIV infection, in an amount and according to a schedule sufficient to induce a protective immune response against HIV, or reduction of the HIV virus, in a human.

[0089] According to another embodiment, the present invention provides a vaccine comprising at least one antibody of the invention and a pharmaceutically acceptable carrier. According to one embodiment, the vaccine is a vaccine comprising at least one antibody described herein and a pharmaceutically acceptable carrier. The vaccine can include a plurality of the antibodies having the characteristics described herein in any combination and can further include antibodies neutralizing to HIV as are known in the art.

[0090] It is to be understood that compositions can be a single or a combination of antibodies disclosed herein, which can be the same or different, in order to prophylactically or therapeutically treat the progression of various subtypes of HIV infection after vaccination. Such combinations can be selected according to the desired immunity. When an antibody is administered to an animal or a human, it can be combined with one or more pharmaceutically acceptable carriers, excipients or adjuvants as are known to one of ordinary skilled in the art. The composition can further include broadly neutralizing antibodies known in the art, including but not limited to, VRC01, PG9 and b12.

[0091] Further, with respect to determining the effective level in a patient for treatment of HIV, in particular, suitable animal models are available and have been widely implemented for evaluating the in vivo efficacy against HIV of various gene therapy protocols (Sarver et al. (1993b), supra). These models include mice, monkeys and cats. Even though these animals are not naturally susceptible to HIV disease, chimeric mice models (for example, SCID, bg/nu/xid, NOD/SCID, SCID-hu, immunocompetent SCID-hu, bone marrow-ablated BALB/c) reconstituted with human peripheral blood mononuclear cells (PBMCs), lymph nodes, fetal liver/thymus or other tissues can be infected with lentiviral vector or HIV, and employed as models for HIV pathogenesis. Similarly, the simian immune deficiency virus (SIV)/monkey model can be employed, as can the feline immune deficiency virus (FIV)/cat model. The pharmaceutical composition can contain other pharmaceuticals, in conjunction with a vector according to the invention, when used to therapeutically treat AIDS. These other pharmaceuticals can be used in their traditional fashion (i.e., as antiviral agents to treat HIV infection). Examples of HIV agents include without limitation non-nucleoside reverse transcriptase inhibitors, protease inhibitors, entry or fusion inhibitors and integrase inhibitors

[0092] According to another embodiment, the present invention provides an antibody-based pharmaceutical composition comprising an effective amount of an isolated HIV antibody, or an affinity matured version, which provides a prophylactic or therapeutic treatment choice to reduce infection of the HIV virus. The antibody-based pharmaceutical composition of the present invention may be formulated by any number of strategies known in the art (e.g., see McGoff and Scher, 2000, Solution Formulation of Proteins/Peptides: In McNally, E. J., ed. Protein Formulation and Delivery. New York, N.Y.: Marcel Dekker; pp. 139-158; Akers and Defilippis, 2000, Peptides and Proteins as Parenteral Solutions. In: Pharmaceutical Formulation Development of Peptides and Proteins. Philadelphia, Pa.: Talyor and Francis; pp. 145-177; Akers, et al., 2002, Pharm. Biotechnol. 14:47-127). A phar-

maceutically acceptable composition suitable for patient administration will contain an effective amount of the antibody in a formulation which both retains biological activity while also promoting maximal stability during storage within an acceptable temperature range. The pharmaceutical compositions can also include, depending on the formulation desired, pharmaceutically acceptable diluents, pharmaceutically acceptable carriers and/or pharmaceutically acceptable excipients, or any such vehicle commonly used to formulate pharmaceutical compositions for animal or human administration. The diluent is selected so as not to affect the biological activity of the combination. Examples of such diluents are distilled water, physiological phosphate-buffered saline, Ringer's solutions, dextrose solution, and Hank's solution. The amount of an excipient that is useful in the pharmaceutical composition or formulation of this invention is an amount that serves to uniformly distribute the antibody throughout the composition so that it can be uniformly dispersed when it is to be delivered to a subject in need thereof. It may serve to dilute the antibody to a concentration which provides the desired beneficial palliative or curative results while at the same time minimizing any adverse side effects that might occur from too high a concentration. It may also have a preservative effect. Thus, for the antibody having a high physiological activity, more of the excipient will be employed. On the other hand, for any active ingredient(s) that exhibit a lower physiological activity, a lesser quantity of the excipient will be employed.

[0093] The above described antibodies and antibody compositions or vaccine compositions, comprising at least one or a combination of the antibodies described herein, can be administered for the prophylactic and therapeutic treatment of HIV viral infection.

[0094] The present invention also relates to isolated polypeptides comprising the amino acid sequences of the light chains and heavy chains listed in Tables A,B and FIGS. **10** A-C; the consensus sequences for the heavy and light chains of SEQ ID NOs: 1 and 2; and insertion sequences SEQ ID NOs:3 and 4.

[0095] In other related embodiments, the invention provides polypeptide variants that encode the amino acid sequences of the HIV antibodies listed in Tables A,B and FIG. **10** A-C; the consensus sequences for the heavy and light chains of SEQ ID NOs: 1 and 2; and insertion sequences SEQ ID NOs:3 and 4. These polypeptide variants have at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, or greater, sequence identity compared to a polypeptide sequence of this invention, as determined using the methods described herein, (for example, BLAST analysis using standard parameters). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by taking into amino acid similarity and the like.

[0096] The term "polypeptide" is used in its conventional meaning, i.e., as a sequence of amino acids. The polypeptides are not limited to a specific length of the product. Peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms can be used interchangeably herein unless specifically indicated otherwise. This term also includes post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide can be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising CDRs, VH and VL, being capable of binding an antigen or HIV-infected cell.

[0097] A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants can be naturally occurring or can be synthetically generated, for example, by modifying one or more of the above polypeptide sequences of the invention and evaluating one or more biological activities of the polypeptide as described herein and/or using any of a number of techniques well known in the art.

[0098] For example, certain amino acids can be substituted for other amino acids in a protein structure without appreciable loss of its ability to bind other polypeptides (for example, antigens) or cells. Since it is the binding capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, accordingly, its underlying DNA coding sequence, whereby a protein with like properties is obtained. It is thus contemplated that various changes can be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences that encode said peptides without appreciable loss of their biological utility or activity.

[0099] In many instances, a polypeptide variant will contain one or more conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged.

[0100] Amino acid substitutions generally are based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

[0101] "Homology" or "sequence identity" refers to the percentage of residues in the polynucleotide or polypeptide sequence variant that are identical to the non-variant sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology. In particular embodiments, polynucleotide and polypeptide variants have at least about 70%, at least about 75%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% polynucleotide or polypeptide homology with a polynucleotide or polypeptide described herein.

[0102] Such variant polypeptide sequences will share 70% or more (i.e. 80%, 85%, 90%, 95%, 97%, 98%, 99% or more) sequence identity with the sequences recited in the application. In additional embodiments, the described invention provides polypeptide fragments comprising various lengths of contiguous stretches of amino acid sequences disclosed herein. For example, peptide sequences are provided by this invention that comprise at least about 5, 10, 15, 20, 30, 40, 50, 75, 100, 150, or more contiguous peptides of one or more of the sequences disclosed herein as well as all intermediate lengths there between.

[0103] The invention also includes nucleic acid sequences encoding part or all of the light and heavy chains of the described inventive antibodies, and fragments thereof. Due to redundancy of the genetic code, variants of these sequences will exist that encode the same amino acid sequences.

[0104] The present invention also includes isolated nucleic acid sequences encoding the polypeptides for the heavy and light chains of the HIV antibodies listed in Tables A,B and FIG. **10** A-C; the consensus sequences for the heavy and light chains of SEQ ID NOs: 1 and 2; and insertion sequences SEQ ID NOs:3 and 4.

[0105] In other related embodiments, the described invention provides polynucleotide variants that encode the peptide sequences of the heavy and light chains of the HIV antibodies listed in Tables A,B and FIGS. **10** A-C; the consensus sequences for the heavy and light chains of SEQ ID NOs: 1 and 2; and insertion sequences SEQ ID NOs:3 and 4. These polynucleotide variants have at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, or greater, sequence identity compared to a polynucleotide sequence of this invention, as determined using the methods described herein, (for example, BLAST analysis using standard parameters). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like.

[0106] The terms "nucleic acid" and "polynucleotide" are used interchangeably herein to refer to single-stranded or double-stranded RNA, DNA, or mixed polymers. Polynucleotides can include genomic sequences, extra-genomic and plasmid sequences, and smaller engineered gene segments that express, or can be adapted to express polypeptides.

[0107] An "isolated nucleic acid" is a nucleic acid that is substantially separated from other genome DNA sequences as well as proteins or complexes such as ribosomes and polymerases, which naturally accompany a native sequence. The term encompasses a nucleic acid sequence that has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates and chemically synthesized analogues or analogues biologically synthesized by heterologous systems. A substantially pure nucleic acid includes isolated forms of the nucleic acid. Accordingly, this refers to the nucleic acid as originally isolated and does not exclude genes or sequences later added to the isolated nucleic acid by the hand of man.

[0108] A polynucleotide "variant," as the term is used herein, is a polynucleotide that typically differs from a polynucleotide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants can be naturally occurring or can be synthetically generated, for example, by modifying one or more of the polynucleotide sequences of the invention and evaluating one or more biological activities of the encoded polypeptide as described herein and/or using any of a number of techniques well known in the art.

[0109] Modifications can be made in the structure of the polynucleotides of the described invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, variant or portion of a polypeptide of the invention, one skilled in the art typically will change one or more of the codons of the encoding DNA sequence.

[0110] Typically, polynucleotide variants contain one or more substitutions, additions, deletions and/or insertions, such that the immunogenic binding properties of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein.

[0111] In additional embodiments, the described invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between and encompass any length between the quoted values, such as 16, 17, 18, 19, etc.; 21, 22, 23, etc.; 30, 31, 32, etc.; 50, 51, 52, 53, etc.; 100, 101, 102, 103, etc.; 150, 151, 152, 153, etc.; and including all integers through 200-500; 500-1,000.

[0112] In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderate stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5×SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50-60° C., 5×SSC, overnight; followed by washing twice at 65° C. for 20 minutes with each of 2×, 0.5×, and 0.2×SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, for example, to 60-65° C. or 65-70° C.

[0113] In some embodiments, the polypeptide encoded by the polynucleotide variant or fragment has the same binding specificity (i.e., specifically or preferentially binds to the same epitope or HIV strain) as the polypeptide encoded by the native polynucleotide. In some embodiments, the described polynucleotides, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that have a level of binding activity of at least about 50%, at least about 70%, and at least about 90% of that for a polypeptide sequence specifically set forth herein.

[0114] The polynucleotides of the described invention, or fragments thereof, regardless of the length of the coding sequence itself, can be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length can vary considerably. A nucleic acid fragment of almost any length is employed. For example, illustrative polynucleotide segments with total lengths of about 10000, about 5000, about 3000, about 2000, about 1000, about 500, about 200, about 100,

about 50 base pairs in length, and the like, (including all intermediate lengths) are included in many implementations of this invention.

[0115] In some embodiments, the polynucleotide sequences provided herein are used as probes or primers for nucleic acid hybridization, for example, as PCR primers. The ability of such nucleic acid probes to specifically hybridize to a sequence of interest enables them to detect the presence of complementary sequences in a given sample. However, other uses also are encompassed by the described invention, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions. As such, nucleic acid segments of the described invention that include a sequence region of at least about a 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein is particularly useful. Longer contiguous identical or complementary sequences, for example, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) including full length sequences, and all lengths in between, also are used in some embodiments.

[0116] Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, for example, Southern and Northern blotting, and/or primers for use in, for example, PCR. The total size of fragment, as well as the size of the complementary stretch(es), ultimately depends on the intended use or application of the particular nucleic acid segment. Smaller fragments generally are used in hybridization embodiments, wherein the length of the contiguous complementary region can be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches can be used, according to the length complementary sequences one wishes to detect.

[0117] The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 12 bases in length can be utilized, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. Nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired, can be utilized.

[0118] Hybridization probes are selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences is governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

[0119] Further included within the scope of the invention are vectors such as expression vectors, comprising a nucleic acid sequence according to the invention. Cells transformed with such vectors also are included within the scope of the invention.

[0120] The present invention also provides vectors and host cells comprising a nucleic acid of the invention, as well as recombinant techniques for the production of a polypeptide of the invention. Vectors of the invention include those capable of replication in any type of cell or organism, including, for example, plasmids, phage, cosmids, and mini chromosomes. In some embodiments, vectors comprising a polynucleotide of the described invention are vectors suitable for propagation or replication of the polynucleotide, or vectors suitable for expressing a polypeptide of the described invention. Such vectors are known in the art and commercially available.

[0121] "Vector" includes shuttle and expression vectors. Typically, the plasmid construct also will include an origin of replication (for example, the ColE1 origin of replication) and a selectable marker (for example, ampicillin or tetracycline resistance), for replication and selection, respectively, of the plasmids in bacteria. An "expression vector" refers to a vector that contains the necessary control sequences or regulatory elements for expression of the antibodies including antibody fragment of the invention, in bacterial or eukaryotic cells.

[0122] As used herein, the term "cell" can be any cell, including, but not limited to, that of a eukaryotic, multicellular species (for example, as opposed to a unicellular yeast cell), such as, but not limited to, a mammalian cell or a human cell. A cell can be present as a single entity, or can be part of a larger collection of cells. Such a "larger collection of cells" can comprise, for example, a cell culture (either mixed or pure), a tissue (for example, endothelial, epithelial, mucosa or other tissue), an organ (for example, lung, liver, muscle and other organs), an organ system (for example, circulatory system, respiratory system, gastrointestinal system, urinary system, nervous system, integumentary system or other organ system), or an organism (e.g., a bird, mammal, or the like).

[0123] Polynucleotides of the invention may synthesized, whole or in parts that then are combined, and inserted into a vector using routine molecular and cell biology techniques, including, for example, subcloning the polynucleotide into a linearized vector using appropriate restriction sites and restriction enzymes. Polynucleotides of the described invention are amplified by polymerase chain reaction using oligonucleotide primers complementary to each strand of the polynucleotide. These primers also include restriction enzyme cleavage sites to facilitate subcloning into a vector. The replicable vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, and one or more marker or selectable genes.

[0124] In order to express a polypeptide of the invention, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into an appropriate expression vector, i.e., a vector that contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described, for example, in Sambrook, J., et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York. N.Y.

[0125] The present invention also provides kits useful in performing diagnostic and prognostic assays using the anti-

bodies, polypeptides and nucleic acids of the present invention. Kits of the present invention include a suitable container comprising an HIV antibody, a polypeptide or a nucleic acid of the invention in either labeled or unlabeled form. In addition, when the antibody, polypeptide or nucleic acid is supplied in a labeled form suitable for an indirect binding assay, the kit further includes reagents for performing the appropriate indirect assay. For example, the kit may include one or more suitable containers including enzyme substrates or derivatizing agents, depending on the nature of the label. Control samples and/or instructions may also be included. The present invention also provide kits for detecting the presence of the HIV antibodies or the nucleotide sequence of the HIV antibody of the present invention in a biological sample by PCR or mass spectrometry.

[0126] "Label" as used herein refers to a detectable compound or composition that is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. A label can also be conjugated to a polypeptide and/or a nucleic acid sequence disclosed herein. The label can be detectable by itself (for example, radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, can catalyze chemical alteration of a substrate compound or composition that is detectable. Antibodies and polypeptides of the described invention also can be modified to include an epitope tag or label, for example, for use in purification or diagnostic applications. Suitable detection means include the use of labels such as, but not limited to, radionucleotides, enzymes, coenzymes, fluorescers, chemiluminescers, chromogens, enzyme substrates or co-factors, enzyme inhibitors, prosthetic group complexes, free radicals, particles, dyes, and the like.

[0127] According to another embodiment, the present invention provides diagnostic methods. Diagnostic methods generally involve contacting a biological sample obtained from a patient, such as, for example, blood, serum, saliva, urine, sputum, a cell swab sample, or a tissue biopsy, with an HIV antibody and determining whether the antibody preferentially binds to the sample as compared to a control sample or predetermined cut-off value, thereby indicating the presence of the HIV virus.

[0128] According to another embodiment, the present invention provides methods to detect the presence of the HIV antibodies of the present invention in a biological sample from a patient. Detection methods generally involve obtaining a biological sample from a patient, such as, for example, blood, serum, saliva, urine, sputum, a cell swab sample, or a tissue biopsy and isolating HIV antibodies or fragments thereof, or the nucleic acids that encode an HIV antibody, and assaying for the presence of an HIV antibody in the biological sample. Also, the present invention provides methods to detect the nucleotide sequence of an HIV antibody in a cell. The nucleotide sequence of an HIV antibody may also be detected using the primers disclosed herein. The presence of the HIV antibody in a biological sample from a patient may be determined utilizing known recombinant techniques and/or the use of a mass spectrometer.

[0129] In another embodiment, the present invention provides a method for detecting an HIV antibody comprising a heavy chain comprising a highly conserved consensus sequence and a light chain comprising a highly conserved consensus sequence in a biological sample, comprising obtaining an immunoglobulin-containing biological sample from a mammalian subject, isolating an HIV antibody from said sample, and identifying the highly conserved consensus sequences of the heavy chain and the light chain. The biological sample may be blood, serum, saliva, urine, sputum, a cell swab sample, or a tissue biopsy. The amino acid sequences may be determined by methods known in the art including, for example, PCR and mass spectrometry.

[0130] The term "assessing" includes any form of measurement, and includes determining if an element is present or not. The terms "determining", "measuring", "evaluating", "assessing" and "assaying" are used interchangeably and include quantitative and qualitative determinations. Assessing may be relative or absolute. "Assessing the presence of" includes determining the amount of something present, and/or determining whether it is present or absent. As used herein, the terms "determining," "measuring," and "assessing," and "assaying" are used interchangeably and include both quantitative and qualitative determinations.

II. Method of Reducing Viral Replication

[0131] Methods for reducing an increase in HIV virus titer, virus replication, virus proliferation or an amount of an HIV viral protein in a subject are further provided. According to another aspect, a method includes administering to the subject an amount of an HIV antibody effective to reduce an increase in HIV titer, virus replication or an amount of an HIV protein of one or more HIV strains or isolates in the subject.

[0132] According to another embodiment, the present invention provides a method of reducing viral replication or spread of HIV infection to additional host cells or tissues comprising contacting a mammalian cell with the antibody, or a portion thereof, which binds to an antigenic epitope on gp120.

III. Method of Treatment

[0133] According to another embodiment, the present invention provides a method for treating a mammal infected with a virus infection, such as, for example, HIV, comprising administering to said mammal a pharmaceutical composition comprising the HIV antibodies disclosed herein. According to one embodiment, the method for treating a mammal infected with HIV comprises administering to said mammal a pharmaceutical composition that comprises an antibody of the present invention, or a fragment thereof. The compositions of the invention can include more than one antibody having the characteristics disclosed (for example, a plurality or pool of antibodies). It also can include other HIV neutralizing antibodies as are known in the art, for example, but not limited to, VRC01, PG9 and b12.

[0134] Passive immunization has proven to be an effective and safe strategy for the prevention and treatment of viral diseases. (See, for example, Keller et al., Clin. Microbiol. Rev. 13:602-14 (2000); Casadevall, Nat. Biotechnol. 20:114 (2002); Shibata et al., Nat. Med. 5:204-10 (1999); and Igarashi et al., Nat. Med. 5:211-16 (1999), each of which are incorporated herein by reference). Passive immunization using human monoclonal antibodies provides an immediate treatment strategy for emergency prophylaxis and treatment of HIV.

[0135] Subjects at risk for HIV-related diseases or disorders include patients who have come into contact with an infected person or who have been exposed to HIV in some other way. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of HIV-related dis-

ease or disorder, such that a disease or disorder is prevented or, alternatively, delayed in its progression.

[0136] For in vivo treatment of human and non-human patients, the patient is administered or provided a pharmaceutical formulation including an HIV antibody of the invention. When used for in vivo therapy, the antibodies of the invention are administered to the patient in therapeutically effective amounts (i.e., amounts that eliminate or reduce the patient's viral burden). The antibodies are administered to a human patient, in accord with known methods, such as intravenous administration, for example, as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. The antibodies can be administered parenterally, when possible, at the target cell site, or intravenously. In some embodiments, antibody is administered by intravenous or subcutaneous administration. Therapeutic compositions of the invention may be administered to a patient or subject systemically, parenterally, or locally. The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician.

[0137] For parenteral administration, the antibodies may formulated in a unit dosage injectable form (solution, suspension, emulsion) in association with a pharmaceutically acceptable, parenteral vehicle. Examples of such vehicles include, but are not limited, water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Nonaqueous vehicles include, but are not limited to, fixed oils and ethyl oleate. Liposomes can be used as carriers. The vehicle may contain minor amounts of additives such as substances that enhance isotonicity and chemical stability, such as, for example, buffers and preservatives. The antibodies can be formulated in such vehicles at concentrations of about 1 mg/ml to 10 mg/ml.

[0138] The dose and dosage regimen depends upon a variety of factors readily determined by a physician, such as the nature of the infection, for example, its therapeutic index, the patient, and the patient's history. Generally, a therapeutically effective amount of an antibody is administered to a patient. In some embodiments, the amount of antibody administered is in the range of about 0.1 mg/kg to about 50 mg/kg of patient body weight. Depending on the type and severity of the infection, about 0.1 mg/kg to about 50 mg/kg body weight (for example, about 0.1-15 mg/kg/dose) of antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. The progress of this therapy is readily monitored by conventional methods and assays and based on criteria known to the physician or other persons of skill in the art. The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician.

[0139] Other therapeutic regimens may be combined with the administration of the HIV antibody of the present invention. The combined administration includes co-administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. Such combined therapy can result in a synergistic therapeutic effect. The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician.

[0140] The terms "treating" or "treatment" or "alleviation" are used interchangeably and refer to both therapeutic treatment and prophylactic or preventative measures; wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. A subject or mammal is successfully "treated" for an infection if, after receiving a therapeutic amount of an antibody according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of infected cells or absence of the infected cells; reduction in the percent of total cells that are infected; and/or relief to some extent, one or more of the symptoms associated with the specific infection; reduced morbidity and mortality, and improvement in quality of life issues. The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician.

[0141] The term "therapeutically effective amount" refers to an amount of an antibody or a drug effective to treat a disease or disorder in a subject or mammal.

[0142] Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0143] "Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers that are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include, but not limited to, buffers such as phosphate, citrate, and other organic acids; antioxidants including, but not limited to, ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as, but not limited to, serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as, but not limited to, polyvinylpyrrolidone; amino acids such as, but not limited to, glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including, but not limited to, glucose, mannose, or dextrins; chelating agents such as, but not limited to, EDTA; sugar alcohols such as, but not limited to, mannitol or sorbitol; salt-forming counterions such as, but not limited to, sodium; and/or nonionic surfactants such as, but not limited to, TWEEN.; polyethylene glycol (PEG), and PLURONICS.

[0144] Where a value of ranges is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range is encompassed within the invention. The upper and lower limits of these smaller ranges which may independently be included in the smaller ranges is also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either both of those included limits are also included in the invention.

[0145] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials simi-

lar or equivalent to those described herein can also be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference in their entireties.

[0146] As used herein and in the appended claims, the singular forms "a", "and" and "the" include plural references unless the context clearly dictates otherwise

[0147] Publications disclosed herein are provided solely for their disclosure prior to the filing date of the present invention. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

[0148] Each of the applications and patents cited in this text, as well as each document or reference, patient or non-patient literature, cited in each of the applications and patents (including during the prosecution of each issued patent; "application cited documents"), and each of the PCT and foreign applications or patents corresponding to and/or claiming priority from any of these applications and patents, and each of the documents cited or referenced in each of the application cited documents, are hereby expressly incorporated herein by reference in their entirety. More generally, documents or references are cited in this text, either in a Reference List before the claims; or in the text itself; and, each of these documents or references ("herein-cited references"), as well as each document or reference cited in each of the herein-cited references (including any manufacturer's specifications, instructions, etc.), is hereby expressly incorporated herein by reference.

[0149] The following non-limiting examples serve to further illustrate the present invention.

Example 1

Materials, Methods and Instrumentation

[0150] Samples.

[0151] Human samples were collected after signed informed consent in accordance with Institutional Review Board (IRB)-reviewed protocols by all participating institutions. Patient 1 was selected from a cohort of long-term non-progressors followed at the Aaron Diamond Aids Research Center, New York. Patients 3 and 8 were selected from a group of elite controllers that were followed at the Ragon Institute in Boston. Patients 1, 3 and 8 were selected based on their broad neutralizing serum activity against a standard panel of HIV isolates. Patient 12 was selected from the Protocol G Cohort of the "International Aids Vaccine Initiative" based on broad serum neutralizing activity.

[0152] Staining, Single-Cell Sorting and Antibody Cloning.

[0153] Staining and single cell sorting of 2CC-Core and gp140 specific Ig+ memory B cells was performed (J. F. Scheid et al., Nature 458, 636 (Apr. 2, 2009)). Briefly, CD19+B cells were enriched from peripheral blood mononuclear cells using anti human CD19 magnetic MACS beads (Miltenyi Biotec) and subsequently stained with anti human CD20 and anti human IgG antibodies (Becton Dickinson) as well as biotinylated 2CC-Core (B. Dey et al., PLoS Pathog 5, e1000445 (May, 2009)) or YU2-gp140 trimer (R. Diskin, P. M. Marcovecchio, P. J. Bjorkman, Nat Struct Mol Biol 17, 608 (May, 2010)) followed by detection with streptavidin coupled phycoerythrin (PE, Beckton Dickinson). Single cells were sorted on a FACSAria III cell sorter (Becton Dickinson), excluding cell doublets, into 96-well PCR plates (Denville) containing 4 μl/well of ice-cold 0.5× phosphate-buffered saline (PBS) containing 10 mM DTT, 8 U RNAsin® (Promega), 0.4 U 5'-3' Prime RNAse Inhibitor™ (Eppendorf). Plates were sealed with Microseal® 'F' Film (BioRad), immediately frozen on dry ice before storage at −80° C.

[0154] cDNA synthesis and Ig amplification were performed (H. Wardemann et al., Science 301, 1374 (Sep. 5, 2003)) with following modifications:

[0155] Instead of using the original primer sets, first and second immunoglobulin specific PCRs were carried out using the primers described in Table 1 in a semi-nested approach. Cloning of heavy and light chain PCR products into their respective expression vectors was performed and 100% identity of cloned expression plasmids with the original PCR product confirmed by sequencing before expression of the antibodies in HEK 293 cells.

[0156] ELISAs.

[0157] High-binding 96-well ELISA plates (Costar) were coated overnight with 100 ng/well of purified antigens (gp140, gp120, gp41, $gp120^{core}$ and 2CC-core) (B. Dey et al., PLoS Pathog 5, e1000445 (May, 2009)) and mutant proteins (gp120 D368R, gp120 I420R) in PBS. After washing, plates were blocked 2 h with 2% BSA, 1 μM EDTA, 0.05% Tween-PBS (Blocking buffer) and then, incubated 2h with IgG antibodies diluted at 4 μg/ml and several consecutive 1:4 dilutions in PBS. After washing, the plates were developed by incubation for 1 h with goat HRP-conjugated anti-mouse IgG (Jackson ImmunoReseach) (at 0.8 μg/ml in blocking buffer) and by adding 100 μl of HRP chromogenic substrate (ABTS solution, Invitrogen). Optical densities were measured at 405 nm ($OD_{405\ nm}$) using an ELISA microplate reader (Molecular Devices). Background values given by incubation of PBS alone in coated wells were subtracted. IgG Antibodies were tested for polyreactivity (H. Mouquet et al., Nature 467, 591 (Sep. 30, 2010)) and considered polyreactive when they recognized at least two structurally different antigens out of the four tested; ssDNA, dsDNA, insulin, and LPS. Threshold values for reactivity were determined by using control antibodies mGO53 (negative), eiJB40 (low positive), and ED38 (high positive).

[0158] Neutralization Assays:

[0159] Neutralization screens were performed (D. C. Montefiori, *Curr Protoc Immunol Chapter* 12, Unit 12 11 (January, 2005)). In brief, neutralization was detected as reduction in luciferase reporter gene expression after single round infection in Tzm-b1 cells. In order to rule out unspecific antiviral activity in antibody samples MuLV (murine leukemia virus) was used as a negative control.

[0160] Clone Specific Identification of Bone Marrow Plasma Cells.

[0161] Bone marrow plasma cells were stained with anti human CD138 and anti CD19 antibodies (Becton Dickinson) after Ficoll purification of mononuclear cells from bone marrow aspirates using Ficoll-Paque (GE Healthcare). CD138+ CD19+ human plasma cells were bulk sorted on a FACSAriaIII cell sorter (Becton Dickinson) and RNA isolation performed on 100.000 cells using Trizol LS reagent (Invitrogen) according to the manufacturers instructions. RNA was reverse transcribed using Superscript III reverse transcriptase (Invitrogen) according to manufacturers instructions. cDNA was then subjected to Immunoglobulin specific PCR with

following modifications: 1 μl of cDNA was amplified in 2 rounds of nested immunoglobulin heavy chain clone specific PCR using first round forward leader and constant region reverse primers shown in Table 1 followed by clone specific forward and reverse primers designed based on sequencing results from single cell analysis. PCR products were gel purified and cloned into TOPO TA vectors (Invitrogen) according to the manufacturers instructions. Colonies were screened by PCR with clone specific primers and sequenced.

[0162] Surface Plasmon Resonance.

[0163] All experiments were performed with a Biacore T100 (Biacore, Inc) in HBS-EP+ running buffer (Biacore, Inc) at 25° C. as described previously (Mouquet 2010). YU-2 gp140 and 2CC-core proteins at 12.5 μg/mL were immobilized on CM5 chips (Biacore, Inc.) by amine coupling at pH 4.5 resulting in an immobilization level of 100 RUs. For kinetic measurements on the gp140- and 2CC-core-derivatized chips, IgGs were injected through flow cells at 700 nM and 4 successive 1:2-dilutions in HBS-EP+ running buffer (Biacore, Inc.) at flow rates of 40 μL/min with 3 min association and 5 min dissociation. The sensor surface was regenerated between each experiment with a 30 second injection of 10 mM glycine-HCl pH 2.5 at a flow rate of 50 μL/min. Off rate (k_d (s^{-1})), on rate (k_a (M^{-1} s^{-1}) and binding constants (K_D (M) or K_A (M^{-1}) were calculated after subtraction of backgrounds (binding to control flow cells and signal of the HBS-EP+ running buffer) using Biacore T100 Evaluation software using the kinetic analysis and the 1:1 binding model. The sensorgrams showed in FIG. **2** and FIG. **8** are derived from the Biacore data processing using Scrubber 2 sofware (Center for Biomolecular Interaction Analysis, University of Utah).

[0164] CD4i Site Induction.

[0165] 293T cells were transfected with $gp160^{BAL.26}\Delta c$ or $gp160^{YU.2}\Delta c$ in a pMX-IRES-GFP construct (Pietzsch et al. 2010) using Fugene™6 (Roche) at a 1:2 plasmid:Fugene ratio. After 48 hours 293T cells were washed with PBS and detached with Trypsin-free cell dissociation buffer (Gibco) and resuspended at a concentration of 10^7 cells/ml in FACS buffer (1×PBS, 2% FBS, 2 mM EDTA). sCD4 (Progenics Pharmaceuticals, Inc.) and mAbs were added to gp160-expressing 293T cells in a 1:4 dilution series starting with a final concentration of 40 μg/ml. mGO is a negative control antibody that does not bind to gp160Δc (H. Mouquet et al., Nature 467, 591 (Sep. 30, 2010)). After incubation for 15 min on ice cells were split and stained for 25 min on ice with an Alexa647-labeled CD4-induced site mAb (3-67; (J. F. Scheid et al., Nature 458, 636 (Apr. 2, 2009)) or an Alexa647-labeled control mAb (i.e. PG16; L. M. Walker et al., Science 326, 285 (Oct. 9, 2009)) or 2G12 for $gp160^{YU.2}$ and 2G12 for $gp160^{BAL.26}$). Antibody labeling was performed by using Alexa Fluor® 647 Microscale Protein Labeling Kit (Invitrogen). Cells were analyzed on an LSRFortessa cell analyzer (BD Bioscience).

[0166] Crystallization.

[0167] The 3BNC60 IgG was expressed by transient expression in HEK293-6E cells and prepared the Fab fragment was prepared by papain cleavage (R. Diskin, P. M. Marcovecchio, P. J. Bjorkman, Nat Struct Mol Biol 17, 608 (May, 2010). Crystallization screens were conducted at 20° C. by vapor diffusion in nL sitting drops using a Mosquito™ (TTP LabTech) crystallization robot on MRC crystallization plates (Jena Bioscience). We combined 3BNC60 Fab at a concentration of 9.5 mg/ml with reservoir solution in a 1:1 ratio to create 400 nL drops. Initial crystallization hits were obtained using the PEGRx HT™ (Hampton Research) crystallization screen and further optimized manually. Crystals suitable for data collection grew after several weeks in 11.7% polyethylene glycol 20,000, 0.1 M sodium acetate pH 5.0, 100 mM potassium/sodium tartrate, 20 mM lithium sulfate, 10 mM N-Cyclohexyl-2-aminoethanesulfonic acid (CHES) pH 9.5 in the monoclinic space group $P2_1$ with two Fabs in the asymmetric unit. Crystals were soaked in reservoir solution supplemented with 15% glycerol for 2 hours before immersing in reservoir solution supplemented with 30% glycerol and flash cooling in liquid nitrogen. Diffraction data were collected at the Stanford Synchrotron Radiation Lightsource (SSRL) beam-line 12-2 at 100 K using a Pilatus 6M detector. Data were indexed, integrated, and scaled using XDS W. Kabsch, *Acta Crystallogr D Biol Crystallogr* 66, 125 (February, 2010) (Table 8). Molecular replacement was conducted using Phaser with the V_H and C_H1 domains from the anti-tumor antibody CTM01 (PDB code 1AD9) and with the V_L and C_L domains of the anti-gp120 b13 antibody (PDB code 3IDX) as search models. Model building and refinement to 2.65 Å resolution was done iteratively using Phenix P. Emsley, B. Lohkamp, W. G. Scott, K. Cowtan, Acta Crystallogr D Biol Crystallogr 66, 486 (April, 2010) and Coot (P. Emsley, B. Lohkamp, W. G. Scott, K. Cowtan, Acta Crystallogr D Biol Crystallogr 66, 486 (April, 2010)). The structure was refined using a maximum-likelihood target function and non-crystallographic symmetry restraints. The final model (R_{work}=20.7%; R_{free}=25.7%) includes 6478 protein atoms, 146 water molecules and 28 sugar atoms (Table 8). 91.9%, 7.6% and 0.5% of the residues were in the favored, allowed, and disallowed regions, respectively, of the Ramachandran plot. Structural analyses and visualization were done using PyMol (The PyMOL Molecular Graphics System, Version 1.3, Schrodinger, LLC). The 3BNC60 structure consists of residues 3-205 for the light chain (including the first N-acetylglucosamine within an N-linked carbohydrate attached to Asn72) and 2-217 for the heavy-chain. Residues at the termini residues and residues 133-140 within the C_H1 domain are disordered.

[0168] Mass Spectrometry.

[0169] IgG was purified from serum using ProteinG Sepharose (GE Healthcare) according to the manufacturers instructions. IgGs were then digested with immobilized papain (Pierce) and digested Fab-Fc fragment mixes incubated with saturating quantities of biotinylated 2CC-Core protein. Streptavidin coupled Dynabeads (Invitrogen) were added after incubation for 15 minutes at room temperature and subjected to 10 rounds of washing with Phosphate Buffered Saline (Gibco). Bound Fab fragments were eluted with lithium dodecyl sulfate buffer (Invitrogen) at 95 C and sample purity confirmed with SDS-polyacrylamide gel electrophoresis followed by silver stain or coomassie staining before analysis by mass spectrometry.

[0170] Isolated Fab fragments were reduced with dithiothreitol, alkylated using iodoacetamide, resolved by 1D gel electrophoresis on a 4-12% NuPAGE Novex Bis-Tris gel (Invitrogen), and stained with Coomassie Blue (Thermo Fisher). The Fab fragments were excised from the gel, and digested using 200 ng of trypsin (Promega). The resulting peptides were isolated using reverse phase resin (PORS 20 R2, Applied Biosystem) and eluted using an aliquot of 40% acetonitrile in 0.5% acetic acid and a second aliquot of 80% acetonitrile in 0.5% acetic acid. Acetonitrile was removed using a speedvac (Thermo Fisher Scientific) and aliquots of

the remaining solution pressure loaded onto self-packed PicoFrit® column (New Objective, Woburn, Mass.) with integrated emitter tip (360 μm O.D., 50 μm I.D., 10 μm tip), packed with 6 cm of reverse-phase C18 material (ReproSil-Pur C18-AQ, 3 μm beads from Dr. Maisch GmbH) and interfaced to a Agilent 1200 series HPLC system (Agilent) with either a LTQ Orbitrap™ XL mass spectrometer or a LTQ Orbitrap Velos™ mass spectrometer (Thermo Fisher Scientific) using a home-built micro electrospray source. The peptides were eluted into the mass spectrometer with the following gradient: 0 to 5% B in 5 min, 40% B in 125 min, 60% B in 150 min, 100% B in 165 min (A=0.1 M acetic acid, B=70% acetonitrile in 0.1 M acetic acid, flow rate 90 nL/min). Both instruments were operated in the data dependent mode and for both mass spectrometers the target value was set to 5e5 ions and a resolution of 60,000 (at 400 m/z). For analysis on the LTQ Orbitrap™ XL a full scan was followed by 8 MS/MS scans on the 8 most abundant ions from that full scan. The peptides (only charge states>1) were isolated with a 2 Da window, target window of 1e4 ions, dissociated via CAD (normalized collision energy=35, activation Q=0.25, activation time 30 msec) and mass analyzed in the LTQ. For analysis on the LTQ Orbitrap™ Velos a full scan was followed by 10 MS/MS scans at 7,500 resolution on the 10 most abundant ions from the immediate preceding full scan. The peptides (only charge state>2) were isolated with a 3 Da window, target window of 2e5 ions, dissociated via HCD (normalized collision energy=40, activation time 0.100 msec) and mass analyzed in the Orbitrap. For either instrument the ions selected for MS/MS were set on an exclusion list for 30 seconds. The resulting MS/MS spectra were searched against the Human IPI and in-house patient specific IgG database using Xtandem!, peptides were automatically compared to tryptic peptides in the human IPI and our in-house patient specific database. Peptide hits corresponding to patient specific IgG were manually confirmed.

[0171] Multiple Sequence Alignments.

[0172] All multiple sequence alignments were conducted using CLUSTALW2 with default parameters (weight matrix: GONNET for proteins and UIB for DNA, gap open=10, gap extension 0.1). Alignments shading were generated using TeXshade package.

[0173] Alignment Consensus.

[0174] The consensus sequences for multiple alignments were generated based on identity and similarity between residues (>=70%). The amino acids were grouping due similarity as: FYW, ILVM, RK, DE, GA, ST and NQ.

[0175] Phylogenetic Germline Trees.

[0176] The relationship between sequences was generated using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 replicates was taken to represent the relationship. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated sequence clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the number of differences method and are in the units of the number of amino acid differences per sequence. All ambiguous positions were removed for each sequence pair. Evolutionary analyses were conducted in MEGAS.

[0177] R/S Ratio Calculation.

[0178] DNA sequences were superposed over the proteins alignments to replacement/substitution calculation. All gaps positions were removed from the analysis. The R/S ratio analysis was conducted using Perl scripts.

Example 2

Isolating HIV Antibodies

[0179] To determine whether HIV antibody cloning is limited because of somatic mutation, a new series of primers was designed to avert this potential problem (Table 1). The new primer set was tested by sorting B cells that bind to an HIV-gp120 core protein lacking the V1-3 loops and containing a pair of stabilizing disulfide bonds (2CC-core). In contrast to the re-surfaced bait used to clone VRC01, the 2CC-core bait also allows capture of antibodies to the CD4-induced co-receptor binding site (CD4i).

[0180] In side-by-side comparisons, the new primer set increased recovery of IgH chains when compared to the initial primer set (FIG. **4**(*a*)). The antibodies obtained with the new primer set were more mutated (average 35.6 vs. 19.8 p=<0. 0001 and maximum 85 vs. 50 for IgH) and included clones that were not found with the original primer set (FIG. **4**(*a*)). To determine whether the new primers rescue VRC01-like antibodies from cells that had been sorted with YU2 gp140, frozen cDNA samples from that individual which had already been examined exhaustively with the original primer set without producing any VRC01 related clones were examined. In 80 wells, 3 antibodies corresponding to VRC01 variants as determined by the IgH and IgL sequences were found (FIGS. **5**A and B). It was concluded that VRC01-like antibodies were captured by the gp140 trimer, and that primers that were specifically designed to clone highly mutated antibodies captured a larger fraction of anti-HIV antibodies from the memory B cells of patients with high titers of broadly neutralizing antibodies.

[0181] Four unrelated HIV infected individuals, including 2 Caucasians, 1 Hispanic and 1 African donor, showing high titers of broadly neutralizing antibodies were examined using the 2CC-core bait, including 2 individuals whose previously cloned antibodies could not account for their serologic activity (Table 2 and FIGS. **6**A and B). 576 antibodies representing 201 different unique and diversified clones were obtained from a starting population of 1.5×10^5 IgG^+ memory B cells (Table 3).

Example 3

Binding Specificity of HIV Antibodies

[0182] The size of the antibody clones captured by 2CC-core bait differed widely ranging from 2-76 diversified members (Table 3). To determine whether the antibodies captured by the 2CC-core bind to the HIV spike, ELISAs were performed using YU2 gp120 on representative members of each expanded clone. All of the antibodies tested bound to gp120 (Table 3).

[0183] The site of antibody binding on the HIV spike was mapped using mutant proteins that interfere with either the CD4bs (gp120(D368R)), or the CD4-induced co-receptor binding site (CD4i, gp120(I420R)). As reported, X. Wu et al., *Science* 329, 856 (Aug. 13, 2010), VRC01 is classified as a CD4bs antibody since it is sensitive to the D368R mutation, but because of the proximity of the CD4i site, it also shows some sensitivity to the 1420R mutation. NIH45-46, which is

a VRC01 variant, and antibodies 3BNC60, 8ANC131, and 12A12 showed ELISA patterns that were similar to VRC01 (These clonal members were selected based on neutralizing activity, Table 3). Other clones, including 1B2530, and 8ANC195, were equally sensitive to both mutations and could not be classified precisely based solely on ELISA.

[0184] To determine whether the antibodies are polyreactive, ELISAs were performed on purified ssDNA, dsDNA, insulin, and LPS. 63% of the anti-2CC Core antibodies tested were polyreactive. It was concluded that the majority of the antibodies captured by the 2CC-bait recognize either the CD4bs or the CD4i site on gp120 and many are also polyreactive.

Example 4

Somatic Hypermutation

[0185] Somatic hypermutation is required for development of high affinity antigen binding and in some cases contributes to polyreactivity of anti-HIV antibodies. To test if this is the case for highly mutated 2CC-core specific antibodies, 4 representative antibodies were reverted to the corresponding germline. Reversion led to complete loss of antigen binding in ELISA for all 4 clones tested and to loss of polyreactivity.

Example 5

HIV Neutralization

[0186] HIV neutralizing activity was measured in standardized in vitro assays using an initial panel of 8 viruses including 3 tier 1 Clade A, B and C, and 5 tier 2 Clade B Env pseudovirus variants (M. S. Seaman et al., J Virol 84, 1439 (February, 2010)). The neutralizing activity of the antibodies was compared to VRC01 and purified serum IgG from the donors (FIG. **1**A, Table 4 and FIG. **6**). Antibodies showing high levels of neutralizing activity were further tested on a panel of 15 additional tier 2 Clade A, B, C, D, G, AG and AE Env pseudovirus variants (FIG. **1**B, Table 5) including 5 viruses that are resistant to VRC01 (FIG. **1**B and Table 5).

[0187] 90% of all of the antibodies tested showed some neutralizing activity and 6 clones contained antibody variants that showed high levels of potency and breadth (FIGS. **1**A, B and C and Tables 4 and 5). These clones were also the most abundant among those captured by the 2CC-bait in each of the four patients studied (Table 3). The most impressive of the new antibodies, 3BNC117 belonging to a clone with 76 members, showed an average IC_{80} on a combined group of 14 tier 2 viruses of 0.5 μg/ml as compared to 1.8 μg/ml for VRC01 (FIG. **1**C, Tables 4 and 5).

[0188] Only 4 of the 20 viruses tested were more sensitive to VRC01 than 3BNC117, whereas 14 were more sensitive to 3BNC117 including DU172.17 which is completely resistant to VRC01 but sensitive to 3BNC117 (FIGS. **1**B and C). NIH45-46, a new variant of VRC01, is more potent than VRC01 on 15 of the 20 viruses tested but still less potent than 3BNC117 (FIGS. **1**B and C and Tables 4, and 5).

[0189] There was substantial variation in neutralizing breadth and potency among the members of the 5 most potent neutralizing antibody clones. For example, 3BNC156, a variant of 3BNC117, neutralized only 2 of the viruses in the initial panel and at much higher concentrations than 3BNC117 (FIG. **1**A and Table 4) and 3BNC55, another variant, was intermediate between the two showing activity against 6 viruses at an average IC_{50} of 4 μg/ml (FIG. **1** and Table 4). Finally, the most active antibodies were highly hypermutated. The average number of mutations for the top 10 antibodies was 72 for V_H and 45 for V_L, and this was associated with their breadth and potency (Tables 4 and 5). Reversion of the mutated residues to germline resulted in a complete loss of neutralizing activity for all of the antibodies tested.

Example 6

Identification of Diagnostic Peptides

[0190] The foregoing cloning strategy captured antibodies produced by antigen binding memory B cells, but circulating antibodies are not produced by these cells, and originate instead from plasma cells in the bone marrow. However, cognate antigen cannot be used as bait to capture plasma cells because they do not express surface Ig A. (Radbruch et al., Nat Rev Immunol 6, 741 (October, 2006)). In addition, the relationship between plasma cells in the bone marrow and circulating memory B cells is not defined precisely. To determine whether the antibodies cloned from memory B cells are also found in the bone marrow plasma cell compartment, CD138-expressing plasma cells were purified from paired bone marrow samples from 2 of the 4 individuals studied and used PCR to specifically amplify IgV_H genes for the more potent antibodies cloned from memory B cells in these individuals. The following were the clone specific primers for RU01:

(FWRD)
(SEQ ID NO. 584)
CTGCAACCGGTGTACATTCTCAAGTGCAACTGGTGC,

(FWRD)
(SEQ ID NO. 585)
CTGCAACCGGTGTACATTCTCAGGTCCATTTGTCACAG,

(REV)
(SEQ ID NO. 586)
TGCGAAGTCGACGCTGACGAGACAGTGACCTGC,

(REV)
(SEQ ID NO. 587)
TGCGAAGTCGACGCTGAAGAGACAATAATTTG,

(REV)
(SEQ ID NO. 588)
TGCGAAGTCGACGCTGACGAGACAATAACT
and for RU10:

(FWRD)
(SEQ ID NO. 589)
CTGCAACCGGTGTACATTTTCAGGGGCACTTGGTG,

(REV)
(SEQ ID NO. 590)
TGCGAAGTCGACGCTGAGGTGACGATGACCGTG.

Members of the selected clones and large numbers of additional variants were readily identified in both patients.

[0191] To verify that these antibodies can also be found in serum, IgG purified from the serum of the same 2 and one additional individual were adsorbed on the 2CC-core bait and mass spectrometry was performed on the eluted IgG (FIG. **1**D, FIG. **7** and FIGS. **10**A-C). Diagnostic peptides were found for the highly active antibody variants in all cases (FIG. **7**, FIG. **10**A-C). It was concluded that broad and potent anti-HIV antibodies cloned from memory B cells were also found

in the bone marrow plasma cell compartment, and in the circulating IgGs of patients with high serum titers of broadly neutralizing antibodies.

Example 7

HIV Antibody Binding Characteristics

[0192] To determine whether antibody affinity to gp120 is related to neutralizing activity, the binding of the highly active antibodies, selected clonal relatives and germline reverted progenitors were compared using Surface Plasmon Resonance (SPR) (FIGS. **2**A and B, FIG. **8** and Table 6).

[0193] The top neutralizing antibodies showed affinities (K_A) ranging from $\cong 10^7$-10^{12} (M^{-1}) on YU2 gp140 trimers and $\cong 10^7$-10^{11} (M^{-1}) on the 2CC-core (FIGS. **2**A and B and Table 6). Consistent with their decreased neutralizing potency and breadth, 3BNC66, 3BNC156 and 3BNC55 displayed lower affinities on YU2 gp140 trimers than 3BNC117, but surprisingly, affinities to 2CC-core did not correlate with neutralizing activity (FIG. **1**, FIG. **8**, Table 4 and Table 6). Binding by SPR was not detected for any of the germline reverted antibodies tested (FIG. **2**B, Table 6). It was concluded that the anti-HIV antibodies captured by the YU2 2CC-core tended to show higher affinity to the corresponding gp140 trimer than to the 2CC-core.

[0194] When VRC01 binds to the HIV spike it produces large conformational changes that mimic CD4 binding and expose the CD4i site. By contrast, b12 and most other known anti-CD4bs antibodies do not.

[0195] To determine whether this is a shared feature of the highly active antibodies, HIV-BAL.26Δc or -YU2 gp160Δc was expressed on the surface of HEK 293T cells and CD4i antibody binding measured in the presence or absence of CD4 or anti-CD4bs antibodies (FIG. **2**C). With one exception, all of the highly active antibodies tested resembled CD4 and VRC01 in that they facilitated anti-CD4i antibody binding to either HIV-BAL.26 or YU2 gp160Δc or both (FIG. **2**C).

[0196] The only highly active antibody that did not share this characteristic, 8ANC195, was not a traditional anti-CD4bs antibody in that it was equally sensitive to the D368R and I420R mutations (Table 3). In addition, it differed from the other highly active antibodies in its neutralization pattern: it did not neutralize any of the tier 1 viruses and showed potent activity against H086.8, a Glade B virus resistant to all other antibodies tested including 3BNC117, VRC01 and b12 (FIGS. **1** A and B and Tables 4 and 5).

Example 8

HIV Antibody Sequence Identity

[0197] To determine whether highly active anti-CD4bs antibodies share common sequence features, the 10 best antibodies: 2 variants each from 5 independently derived antibody clones from 5 different patients were aligned (FIG. **3**). Comparison of the IgV_H regions revealed a highly conserved consensus sequence covering 68 IgV_H residues (FIG. **3**A). The IgV_H consensus included 6 of VRC01-gp120 contact residues, including VRC01-Arg 71, which mimics the key interaction of $Arg59_{CD4}$ and $Asp368_{gp120}$ (FIG. **3**A). Moreover, the consensus, including the 6 contact residues, was entirely conserved in both of the closely related germline IgV_H genes (V_H1-2 and V_H1-46) that give rise to all of the antibodies in this class (FIGS. **3**A and B).

[0198] The codons encoding the consensus residues were highly somatically mutated in the 10 selected antibodies, nevertheless the amino acid sequence was conserved (FIG. **9**). The ratio of replacement to silent mutations in the consensus residues ranged from 0.7-1.7, whereas it was 3.5-22 in the non-consensus residues indicating that conservation of the consensus is strongly selected (Table 7). In contrast to the heavy chain, the light chain of VRC01 made only 8 out of a total of 32 contacts with gp120. Consistent with its more limited role, comparison of the light chain sequences of the same antibodies uncovered a less extensive consensus covering 53 IgV_L residues including 3 VRC01-gp120 contact residues (FIG. **3**B). Finally, like the heavy chains, the light chains arose from a limited set of germline genes: 2 were derived from IgK1D-33, 2 from IgK3-11, and one from IgL1-47 (FIG. **3**B and Table 3). Antibody 8ANC195, which differed from the others in several important respects did not entirely conform to the consensus and did not arise from related heavy or light chains (FIGS. **3**A and B) It was concluded that there is significant sequence convergence among highly active agonistic anti-CD4bs antibodies (HAADs).

Example 9

Crystal Structure of 3BNC60 Fab

[0199] To determine whether the structure of the antibodies in different patients is also conserved, the crystal structure of the 3BNC60 Fab was solved to 2.65 Å resolution and compared it to VRC01. The structure revealed the four domains, V_H, C_H1, V_L, and C_L, of a canonical Fab and the complementarity-determining regions (CDRs) within V_H and V_L that form the antigen binding site. The two Fabs in the 3BNC60 asymmetric unit were almost identical; however, the conformation of residues 74-78 in the loop connecting strands D and E varied slightly due to different chemical environments formed by crystal lattice contacts.

[0200] Superimposition of the V_H domains from 3BNC60 and VRC01 in the VRC01-gp120 co-crystal structure (T. Zhou et al., Science 329, 811 (Aug. 13, 2010)) yielded a root mean square deviation (rmsd) of 1.3 Å (calculated for 111 Cα atoms) with major differences confined to CDR2 residues 58-65 (3BNC60 numbering). Superimposing the structures indicated conservation of the recognition interface with gp120. For example, $Arg72_{3BNC60}$ adopted a similar conformation as $Arg71_{VRC01}$, which mimics an important salt bridge normally formed between $Arg59_{CD4}$ and $Asp368_{gp120}$. In addition, $Trp47_{3BNC60}$ adopted the same conformation as $Trp47_{VRC01}$, a residue that contacts gp120 and is involved with a complex network of interactions of aromatic and aliphatic residues that stabilize the conformations of CDRH3 and CDRL3. $Gln65_{3BNC60}$, which corresponds to $Gln64_{VRC01}$, is within the residue segment (residues 58-65) that differs in structure from VRC01. The conformation of this region of 3BNC60, which is involved in a lattice contact in the crystals, is likely to change upon binding gp120, as it would clash with the CD4-binding loop on gp120.

[0201] Superimposing the 3BNC60 and VRC01 V_L domains yielded an rmsd of 0.9 Å (calculated for 95 Cα atoms) and showed that some of gp120-contacting residues are structurally conserved; $Tyr91_{3BNC60}$ and $Glu91a_{3BNC60}$ adopted similar conformations as $Tyr91_{VRC01}$ and $Glu96_{VRC01}$, which engaged loop D of gp 120 via polar inter-

actions. Overall, these structural comparisons suggested that 3BNC60 binds gp120 with the same architecture as observed for the binding of VRC01.

Example 10

HIV Antibody Consensus Sequence

[0202] The foregoing experiments defined a class of agonistic anti-CD4bs antibodies, HAADs, that shares IgV_H and IgV_L consensus sequences including 8 of the contact residues between VRC01 and the HIV spike (FIGS. **3**A and B). In five different donors, selected for their high level serologic anti-HIV activity, these antibodies originated from only 2 closely related IgV_H and 3 IgV_L germline genes that conform to the HAAD consensus: V_H1-2 and V_H1-46 differ by only 7 amino acids, none of which are part of the consensus (FIG. **3**A). Despite extensive somatic hypermutation, the consensus residues were retained in their germline form.

[0203] The only exception to the consensus, 8ANC195, differed from the others in a number of ways that suggest that it may have a unique mode of antigen recognition: absence of the Arg in the heavy chain that mimics the critical $Arg59_{CD4}$ and $Asp368_{gp120}$ contact site; unique neutralizing pattern; and inability to facilitate anti-CD4i antibody binding. This antibody is one of two distinct highly active antibodies arising in one patient, lending additional support to the idea that serologic neutralizing activity is combinatorial.

TABLE A

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
5	8A253HC	QGQLVQSGGGLKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTAYNFQDRLSLRRDRSTGTVFMELRGLRPDDT AVYYCARDGLGEVAPDYRYGIDVWGQGSTVIVTAASTKG
6	8A275HC	QGLLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGPL WLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
7	8ABM11	FQGHLVQSGGGVKKPGTSVTLSCLASEYTFTEFTIHWIRQAPGQG PLWLGLIKRSGRLMTSYRFQDRLSLRRDRSTGTVFMELRSLRTDD TAVYYCARDGLGELAPAYHYGIDAWGQGTTVIVTSASTS
8	8ABM12	QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSAST
9	8ABM13	QGHLVQSGGGVKKLGTSVTISCLASEDTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTS
10	8ABM14	GHLVQSGGGXKKPGTSVTISCLASEYTFTEFTIHRIRQAPGQGPL WLGLIKGSGRLMTSYGFQDRLSLRRDRSTGTVFMELRSLRTDDTA VYYCARDGLGELAPAYHYGIDVWGQGTTVIVTSASTS
11	8ABM20	GVHFQGHLVQSGGGVKKPGSSVTISCLASEYTFTEFTIHWIRQAP GQGPLWLGLIKRSGRLMTSYRFQDRLSLRRDRSTGTVFMELRGL RIDDTAVYYCARDGLGEVAPAYLYGIDVWGQGTTVIVTSASTS
12	8ABM24	FQGQLVQSGGGVKKPGSSVTISCLASEYTFTEFTIHWIRQAPGQG PLWLGLIKRSGRLMTSYGFQDRLSVRRDRSTGTVFMELRSLRTDD TAVYYCARDGLGELAPAYHYGIDVWGQGTTVIVTSASTS
13	8ABM26	QGQLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTS
14	8ABM27	QGHLVQSGXEVKKPGSSVKVSCKASGGTFSXYAIGWVRQAPGQ GLEWMGGIIPILGTTNYAQRFQGGVTITADESTNTAYMDVSSLRSD DTAVYYCAKAPYRPRGSGNYYYAMDVWGQGTTVIVSSASTS
15	8ANC105HC	QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
16	8ANC116HC	QGQLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVSSASTKG
17	8ANC127HC	QGHLVQSGGGVKKLGTSVTISCLVSEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
18	8ANC131HC	QGQLVQSGGGLKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTAYNFQDRLRLRRDRSTGTVFMELRGLRPDDT AVYYCARDGLGEVAPDYRYGIDVWGQGSTVIVTAASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
19	8ANC134HC	QGQLVQSGGGVKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGP VWLGLIKRSGRLMTSYKFQDRLSLRRDRSTGTVFMELRGLRLDDT AVYYCARDGLGEVAPAYLYGIDAWGQGSTVIVTSASTKG
20	8ANC13HC	QGQLVQSGGGVKKPGASVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTAYKFQDRLSLRRDRSTGTVFMELRGLRPEDT AVYYCARDGLGEVAPDYRYGIDVWGQGSTVIVSAASTKG
21	8ANC171HC	QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
22	8ANC18	GVHFQGHLVQSGGGVKKPGSSVTISCLASEYTFTEFTIHWIRQAP GQGPLWLGLIKRSGRLMTSYRFQDRLSLRRDRSTGTVFMELRGL RIDDTAVYYCARDGLGEVAPAYLYGIDVWGQGSTVIVTSASTS
23	8ANC182HC	QGQLVQSGGGVKKPGTSVTISCLASEYTFTEFTIHWIRQAPGQGP LWLGLIKRSGRLMTAYRFQDRLSLRRDRSTGTVFMELRNLRMDDT AVYYCARDGLGELAPAYQYGIDVWGQGTTVIVSSASTKG
24	8ANC192HC	QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
25	8ANC22HC	QGHLVQSGGGVKKLGTSVTISCLASEDTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
26	8ANC26HC	QGQLVQSGGGVKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGP VWLGLIKRSGRLMTSYKFQDRLSLRRDRSTGTVFMELRGLRLDDT AVYYCARDGLGEVAPAYLYGIDAWGQGSKVIVTPASTKG
27	8ANC2HC	QGQLVQSGGGVKKLGTSVTIPCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
28	8ANC30HC	QGQLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
29	8ANC37HC	QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
30	8ANC40HC	QGHLVQSGGGVKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVTSASTKG
31	8ANC41HC	QGQLVQSGGGVKKTGTSVTISCLASEYTFTEFTIHWIRQAPGQGP LWLGLIKRSGRLMTANRFQDRLSLRRDRSTGTVFMELRSLRIDDT AVYYCARDGLGELAPAYHYGIDVWGQGTTIIVTSASTKG
32	8ANC45HC	QGQLVQSGGGVKKTGTSVTISCLASEYTFTEFTIHWIRQAPGQGP LWLGLIKRSGRLMTANRFQDRLSLRRDRSTGTVFMELRSLRIDDT AVYYCARDGLGELAPAYHYGIDVWGQGTTIIVTSASTKG
33	8ANC50HC	QGQLVQSGGGVKKPGTSVTISCLASEYTFTEFTIHWIRQAPGQGP LWLGLIKRSGRLMTAYRFQDRLSLRRDRSTGTVFMELRNLRMDDT AVYYCARDGLGELAPAYQYGIDVWGQGTTVIVSSASTKG
34	8ANC53HC	QGQLVQSGGGGKKLGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYQFQDRLSLRRDRSTGTVFMELRGLRVDDT AVYYCARDGLGEVAPAYLYGIDAWGQGTTVIVSSASTKG
35	8ANC88HC	QGQLVQSGGGVKKPGTSVTISCLASEYTFNEFVIHWIRQAPGQGP LWLGLIKRSGRLMTSYKFQDRLNLRRDRSTGTVFMELRGLRPDDT AVYYCARDGLGEVAPDYRYGIDVWGQGSTVIVTAASTKG
36	8ANC103HC	QVQLQQWGSGLLKPSETLSLTCAVYGGSFRSYYWNWIRQSPGK GLEWIGEVSHSGSTNYNPALKSRVTISVDTSKNQFSLKVKSVTAAD TALYYCSRGRGKRCSGAYCFAGYFDSWGQGGLVVVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
37	8ANC106HC	EVQLVESGGGVVEPGESLRLSCAASGFTFRSYDMFWVRQATGKS LEWVSAIGIAGDTYYSGSVKGRFTISRENARTSLYLQLSGLRVEDS AVYFCVRGSPPRIAATEYNYYYGLDVWGQGTTVSVFSASTKG
38	8ANC107HC	VVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGMIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRS DDTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVS SASTKG
39	8ANC108HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADEPKNTVYLDFNSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
40	8ANC109HC	EVQLVESGGGLVKPGGSLRLSCAASGFSFSEHYMSWIRLAPGKG LEWLSYISSSTRTTYSADSVRGRFTISRDTAKQLLFLHMSSLRAED TAVYYCVRLYGGINGWFDQWGQGTLVSVSSASTKG
41	8ANC10HC	QVQLVQSGAEVKKPGSSVKVSCKTSGGSFSNYAFSWVRQAPGE GLEWMGRIIPIFGTAKYTQKLQGRVTITADKFTSTVYMELSSLRSE DTAIYYCASLHQGPIGYTPWHPPPRAPLGQSVCG
42	8ANC111HC	QVQLVESGAEVKKPGASVKVSCKASGYTFTSHDINWVRQATGQG LEWMGWMNPNSGDTGYAHKFQGRVTMTRNTPISTAYMELSSLR SEDTAVYYCARGRATSRNTPWAHYYDSSGYYGAGDYWGQGTLV TVSSASTKG
43	8ANC112HC	QVQLVESGGGVVQPGRSLRLFCAASGFAFNTYGMHWVRQAPGK GLEWVAVTWHDGSQKYYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAIYYCASDQGGFDDSSGYFAPGGMDVWGRGTTVIVSSAPT KG
44	8ANC113HC	QVQLVESGAELRKPGESLEISCKASGYSFSSHWIGWARQMPGKG LEWMGIIYPGDSNTIYSPSFQGQVTISADKSINTAYLQWSSLKASD TAMYFCASNYHDYFYWGQGTLVTVSSASTKG
45	8ANC114HC	EVQLVESGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQG LEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
46	8ANC115HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADEPKNTVYLDFNSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
47	8ANC117HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQ GLEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSE DTAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
48	8ANC11HC	QVFVQLVQSGGGLVQPGGSVRLSCTASGFLFSTYSMNWVRQAP GKGLEWVSSISTTSNYIYYADSVKGRFTISRSNGQGSLYLQLNSLR VEDTAVYYCARDTKVGAPRQDCYAMDLWGQRDHGHRLLSFHQG PIGLPPGALLQ
49	8ANC121HC	QVQLLESGPGLVTPSGTLSLACAVSGASISSSHWWTWVRQSPGK GLEWIGEIDRRGTTNYNPSLRSRVTILLDNSKNQFSLSLRSVTAAD TAVYYCTKVYAGLFNERTYGMDVWGHGTTVLVSSASTKG
50	8ANC126HC	QVQLVESGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
51	8ANC130HC	QVQLLQSGAEVKKPGASVKVSCKVSGYTLTELSINWVRQAPGKGL EWMGGFDPEDDEAIYEPKFQGRLTMTEDTSTDTAYMELSSLRSE DTAVYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
52	8ANC132HC	QVQLVQSGTEVQKPGASVKVSCKTSGYTFSKYYIHWVRQAPGQG LEWVGRINTDSGGTDYAEKFQGRVTMTRDTSITTVYLEMRGLTSD DTAAFYCARGPPHAGGWTIYYYGLDVWGQGTSVIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
53	8ANC133HC	QVQLVQSGAEVKKPGASVKVSCKVSGHTLSELSINWVRHVPGKG LEWMGGLDPEDGEAIHEPKFQGRLTMTEDTSTDTAYVELSSLRSE DTAMYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
54	8ANC136HC	EVQLVESGGGVVQPGRSLRLSCAASGFTFSHHGIHWVRQAPGEG LEWVAVISEDGTNIHYEDSVRGRFTISRDNSKNTVDLQMNSLRAE DTAVYYCASLISMRDGDAFDLWGQGTRVTVSSASTKG
55	8ANC137HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
56	8ANC139HC	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGK GLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAE DTAVYYCAREGSYYYGMDVWGQGTTVTVSSASTKG
57	8ANC140HC	EVQLVQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGK GLEWVSGISWNSGTIGYADSVRGRFTISRDDAKSSLYLQMNSLRT EDTALYYCAKDGWVGSGSSTLRGSDYWGQGTLVTVSSASTKG
58	8ANC142HC	QIHLVQSGTDVKKPGSSVTVSCKAYGVNTFGLYAVNWVRQAPGQ SLEYIGQIWRWKSSASHHFRGRVLISAVDLTGSSPPISSLEIKNLTS DDTAVYFCTTTSTYDQWSGLHHDGVMAFSSRGQGTLISVSAAST KGPSVFPLAPSSKSTYGLAHVL
59	8ANC143HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADEPKNTVYLDFNSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
60	8ANC144HC	QLQLQESGPGLVKPWETLVLTCSVSGGSISSGDYYWGWIRQSPG KGPEWIGNIFYSSGNTYYNTSLKSRVTISVDVSKNRFSLKLTSMTA ADTAVYYCGRLSNKGWFDPWGQGTLVSVSSASTKG
61	8ANC145HC	QVQLLESGGGLVQRGGSLRLSCTASGFVFNNYWMTWVRQAPGN GLEWVANIDQDGSEKHYLDSVKGRFTISRDNAKNSLYLQMNSLRA EDTAIYYCARVRFKVTAWHRFDSWGQGDLVTVSSTSTKG
62	8ANC146HC	LVQLLQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKGL EWMGGFDPEDDEAIYEPKFQGRLTMTEDTSTDTAYMELSSLRSE DTAVYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
63	8ANC147HC	QVQLVESGGGLGQPGGSLRLSCAASGFTFRNYAMSWVRQAAGK GLEWVSGVSGGGDTTYYGDSVKGRFTISRDNSKNTLYLQMNNLR AEDTAVYYCAKDKGVWGSSDFDYWGQGTLVTVSSASTKG
64	8ANC148HC	QVHLVQSGAEVKKPGASVRVSCKASGYTFTTYGISWVRQAPGQG LEWMGWISAHSGDTNYAQKLQARVTMTTDTSTNTAYMELRSLTS DDTAVYYCARDRPRHYYDRGGYYSPFDYWGQGTLVTVSSASTKG
65	8ANC149HC	QVQLVESGAEVKKPGSSVKVSCKASGGTFNIFAFSWVRQAPGQG LEWMGGIIPIFASPNYAQRFQGRVTITADESTSTVHMELSSLRSED TAIYYCAKDAHMHIEEPRDYDYIWGTSPYYFDYWGQGTLVTVSSA STKG
66	8ANC14HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKG LEWMGGFDSEDGEAFYKQNFQGRVTMTEDTSTDTAYMELRRLR SEDTAVYYCATADRFKVAQDEGLFVIFDYWGQGTLVTVSSASTKG
67	8ANC150HC	QVQLLQSGGEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKG LEWMGGFDPEDDEAIYEPKFQGRLTMTEDTSTDTAYMELSSLRSE DTAVYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
68	8ANC151HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGK GLEWVSYISGSSYTIYYADSVRGRFTISRDNAKNSLYLQMNSLRDE DTAVYFCARATPPNPLNLYNYDSSGSSFDYWGQGTLVTVSSAST KG
69	8ANC153HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGMIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRS DDTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVS SASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
70	8ANC154HC	QVQLVESGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADEPKNTVYLDFNSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
71	8ANC155HC	QVQLVQSGAEIKKPGESLKISCKASGYTFNDYWIGWVRQMPGKG LEWMGIFYPDDSDSNYSPSFQGRVTISADKSITTAYLQWSTLKASD SAMYFCARLLGDSGAFDIWGQGTMVIVSSASTKG
72	8ANC156HC	EVQLVESGAEVRKPGSSLKVSCKSSGGTFSRFVVNWVRQAPGQ GLEWMGGMIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRS DDTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVS SASTKG
73	8ANC157HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQ GLEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSE DTAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
74	8ANC158HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRFVVNWVRQAPGQ GLEWMGGMIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRS DDTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVS SASTKG
75	8ANC160HC	QVQLVQSGGGVVQPGRSLRLSCAASGFTFSHHGIHWVRQAPGE GLEWVAVISEDGTNIHYEDSVRGRFTISRDNSKNTVDLQMNSLRA EDTAVYYCASLISMRDGDAFDLWGQGTRVTVSSASTKG
76	8ANC161HC	EVQLVQSGGGLVKPGGSLRLSCAASGFTFKNAWMSWVRQAPGK GLEWVGHIKSKTDGGTIDYAAPVKGRFTISRDDSKNTLYLQMNSLK IEDTAVYYCTTDIGSGRGWDFHYYDSNDWGQGTLVTVSSASTKG
77	8ANC162HC	EVQLVQSGGGVVQPGRSLRLSCVVSGFTFSSFTFHWVRQAPGK GLEWVAGMSFHATYIYYADSVKGRFTISRDDSQDTLYLEMDSLRS EDTAIYYCARDPGIHDYGDYAPGAFDYWGQGSPVTVSSASTKG
78	8ANC163HC	LVQLVQSGAEVKKPGASVKVSCKVSGHTLSELSINWVRHVPGKGL EWMGGLDPEDGEAIHEPKFQGRLTMTEDTSTDTAYSTLSVWAPV AAAMYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
79	8ANC164HC	EVQLVESGAEVKKPGSSVKVSCKASGGTFSSYSISWVRQAPGQG LEWMGGIIPIFATTHYGQKFQGRIKITADKSTSTAYMELSRLRSEDT AVYYCARDREFYFYGMDVWGQGTTVTVSSASTKG
80	8ANC165HC	QVQLQQWGAGLLKPSETLSLTCAVYAGSFSGYYWTWIRQPPGKG LEWIGEVNHGGSTNYNPSLKSRVTLSVDTSKNQFSLKLTSVTAAD TAVYYCARVSRYDFWSGNYGSYGLDVWGQGTTVTVSSASTKG
81	8ANC166HC	WQLVQSGAEVRKPGSSLKVSCKSSGGTFSRFVVNWVRQAPGQ GLEWMGGMIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRS DDTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVS SASTKG
82	8ANC168HC	LVQLVQSGAEVKKPGASVKVSCKVSGYSLTELSIHWVRQAPGKGL EWMGGFDSEDGEAIYKQNFQGRVTMTEDTSTDTAYMELSRLRSE DTAVYYCATADPFKVAQDEGLFVIFDYWGQGTTGHRLLSLHQGP HRLYSLGTLLSRAPIVQTHMA
83	8ANC169HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQ GLEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSE DTAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
84	8ANC16HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPIEG LEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
85	8ANC173HC	QVQLVQWGAGLLKPLETLSLTCAVYGGSFNGYFWSWIRQTPGKG LEWIGEINHGGSANFNPSLKSRVTMSVDTSKNQFSLKLASVTAAD TAIYYCARGRITMVRGDPQRGGVRMDVWGQGTSVTVSSASTKG
86	8ANC174HC	QVQLMQSGAEVKRPGASVKVSCKAFRHSLNNLGISWIRRAPGRG LEWLGWINVYEGNTKYGRRFQGRVTMTTDRSTNTVSMELRSLTS DDTAVYYCARDNHFWSGSSRYYYFGMDVWGQGTTVIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
87	8ANC175HC	QVQLVQSGGGLVQPGESLRLSCTASGFTFSSYNMNWVRQAPGK GLEWISYISDKSKNKYYADSVRGRFTISRDNAQNSLFLQMSSLRDE DTAVYYCTREGPQRSFYFDYWGQGIQVTVSSASTKG
88	8ANC176HC	QVQLQESGPGLVKPSETLSLTCTVSGGSISNHYWSWIRQPPGKGL EWIGYIYHSGNINYKSSLKSRATISIDTSNNQFSLKLSSVIAADTAVY YCARNFGPGSPNYGMDVWGQGTTVTVSSASTKG
89	8ANC177HC	VVQLVQSGPGLVKPSQTLSLTCTVSGGSISSGDFYWSWIRQPPGK GLEWIGYIYYSGSTYYNPSLKSRLTISVDTSKNQFSLRLSSVTAADT AVYYCARDLNSRIVGALDAFDIWGQGTMVTVSSASTKG
90	8ANC178HC	QVQLVESGGALVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGK GLEWVSAISRSGGSTYYADSVKGRFTISIDNSNNTLYLQMNSLRVE DTAVYYCAKREAFYYGAGGYGMDVWGQGTTVTVSSASTKG
91	8ANC179HC	EVQLVESGGGLVKPGGSLRLSCEASGFTFTNAWMNWVRQAPGK GLEWVGRIKSQTHGGTTRYAAPVKGRFTISRDDSKHTLYLQMDRL TTEDTAVYYCTGTITGSTFYYYGMDVWGQGTTVTVSPASTKG
92	8ANC17HC	EVQLVESGGGLLQPGGSLRLSCAASGFSFNDFEMNWVRQAPGK GLEWVSYISNDGTMIHYADSVKGRFTISRDNAKKSLFLQMNSLRA EDTAVYYCARLAEVPPAIRGSYYYGMDVWGQGTTVTVASASTKG
93	8ANC180HC	QVQLQESGPGLLRPLETLSLTCSVSGGSIRGYFWSWVRQPAGRG LEWIGRIYSSGTTRFNPSLKSRVRLSIDTAKSEVSLNITSVTAADSA SYFCAGTSPVHGGLDLWGLGLRVTVSSASTKG
94	8ANC181HC	HLVQSGTEVKKPGSSVTVSCKAYGVNTFGLYAVNWVRQAPGQSL EYIGQIWRWKSSASHHFRGRVLISAVDLTGSSPPISSLEIKNLTSDD TAVYFCTTTSTYDQWSGLHHDGVMAFSSWGQGTLISVSAASTKG
95	8ANC184HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKGL EWMGGFDPEDDEAIYEPKFQGRLTMTEDTSTDTAYMELSSLRSE DTAVYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
96	8ANC185HC	QVQLVESGGGLVQPGGSLRLSCAASGFTFSTHWMHWVRQAPGK GLVWVSRIHSDGRSTSYADSVKGRFTISRDNAKNTLYLQMNSLRA EDTAVYYCARGAAVFGVVIIGGMDLWGQGTTVTVSSASTKG
97	8ANC186HC	EVQLVESGGGVVQPGGSLRLSCAASGFMFKNYAMHWVRQPPGK GLEWVAVIWYGGRDQNYADSVKGRFTISRDDSDNTLYLQMNSLR AGDTAVYFCARNSQVGRLMPAAGVWGQGTLVTVSSASTKG
98	8ANC187HC	EVQLVESGGGLIQRGGSLRLSCVASGFPVSDNHMSWVRQAPGK GLEWVSIIYSDGGTYYADSVKGRFTISRDNSKNTVYLQMNSLRAT DTAVYYCARDPGFHYGLDVWGQGTTVTVSSASTKG
99	8ANC188HC	VVQLVESGGGLVQPGGSLRLSCAASGFAFRSYWMSWVRQAPGR GLEWVANIKQDGSEKYYADSVKGRFTISRDNTKNSLYLQMNSLRA EDTAVFYCASRGDRYGPIDYWGQGTLVTVSSASTKG
100	8ANC191HC	VVQLVESGTEVKKPGSSVKVSCKASGGTFSGSDISWVRQAPGQG LEWMGGIIPMFDIENHAEKFRGRLTITAVKSTGAAYMELSSLRSED AAVYYCARSSGNYDFAYDIWGQGTRVIVSSASTKG
101	8ANC193HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQ GLEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSE DTAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
102	8ANC194HC	EVQLVQSGGGLVQPGGSLRLSCAASGLTFRNFAMSWVRQAPGK GLEWVSSISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRG EDTAVYFCAKGVGYDILTGLGDAFDIWGQGTVVAVSSASTKG
103	8ANC195HC	QIHLVQSGTEVKKPGSSVTVSCKAYGVNTFGLYAVNWVRQAPGQ SLEYIGQIWRWKSSASHHFRGRVLISAVDLTGSSPPISSLEIKNLTS DDTAVYFCTTTSTYDKWSGLHHDGVMAFSSWGQGTLISVSAAST KG
104	8ANC196HC	VVQLVQSGTEVKKPGSSVKVSCKASGGTFSGSDISWVRQAPGQG LEWMGGIIPMFDIEDHAQKFRGRLTITADKSTGAAYMELSSLRSED AAVYYCARSSGNYDFAFDIWGQGTRLIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
105	8ANC20HC	QVQLGESGGGLVEPGGSLRLSCAASGFLFSDYQMSWIRLAPGKG LEWISFISGFGSVYYADSVEGRFTISRDNARNSLYLQMNNLRAEDT AVYYCARAYGTGNWRGLYYYYYGMDVWGHGTTVTVSSASTKG
106	8ANC21HC	QLQLVESGGGVVQPGRSLRLSCAASGFTFSTYTMHWVRQAPGK GLEWVAVISYDGTNKYYADSVKGRFTISRDNSKNTLYLQMNSLRG EDTAVYYCARSPSYYFDYWGQGTLVTVSAASTKG
107	8ANC24HC	QVQLVQSGAEVKMPGASVKVSCKVSGYSLTELSIHWVRQAPGKR LEWMGGFDPEDDERIYAQKFQDRVTMTEDTSTDTAYMDLNSLRS EDTAVYYCTTGGLYCSSISCIMDVWGQGTTVIVSSASTKG
108	8ANC25HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKR LEWMGGFDPEDGERIYAQKFQGRVTMTEDTSTDTAYMELNSLRS DDTAVYYCATGGLYCSSISCIMDVWGQGTTVTVSSASTKG
109	8ANC27HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKG LEWMGGFDSEDGEAIYKQNFQGRVTMTEDTSTDTAYMELSRLRS EDTAVYYCATADRFKVAQDEGLFVIFDYWGQGNPGHRLLSLHQG PIGLPPGTLPPKATSGHAARR
110	8ANC31HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGK GLEWVAVISYDGSNKYYADSVKGRFTISRDDSKSTVYLQINSLRAA DTAVYFCAREGGLRFLEWLFWGQGTLVTVSSGESSASTKG
111	8ANC33HC	EFQLVQSGGGLVKPGGSLRLSCTGSTFSFSSDDMNWVRQAPGK GLEWVSSMSDSGSHIYYADFVKGRFTISRDNAKKSLYLQMNSLRA EDTAVYYCAQSRPPQRLYGMDVWGQGTTVTVSSASTKG
112	8ANC34HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKG LEWMGGFDPEDGEASFEPKFQGRLTMTEDTSTDTAYMELSSLRS EDTAVYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
113	8ANC36HC	QVQLVESGGGVVQPGKSLRLSCAASGFTFSTHAMHWVRQAPGK GLDWVAVISHDGDNQYYADAVKGRFTISRDDSRDTVFLQMNSLRT EDTGVYYCAADSSGSNWFDYWGQGILVTVSSASTKG
114	8ANC38HC	EPMFQPGQSGGVVVQSGESLHLSCEASGFKFASQMMHWVRHVP GRGLEWVALISWDGSGKLFADSVRGRFTIHRWNDRNSLYLDVKN VRPEDAAIYYCTRNGFDVWGQGILVTVSSASTKG
115	8ANC39HC	QVQLLQSGAEVKKPGASVKVSCKVSGYTLTELSIHWVRQAPGKGL EWMGGFDPEDDEAIYEPKFQGRLTMTEDTSTDTAYMELSSLRSE DTAVYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
116	8ANC3HC	QVHLQESGPRLVRSSETLSLTCSVPGGSIVNPITNYYWSWIRQSP RKGLQWIGDIYYTGTSSRNPSLDSRVSISMDVSRKQISLTLYSVTA ADTAVHYCASQSLSWYRPSGYFESWGQGILVTVSSASTKG
117	8ANC43HC	QVQLVQSGAEVKKPGSSMKVSCKSSGGTFSNHAISWVRQAPGK GLEWMGGIIPMSGTTNYLQKFQGRVTITADEFATTAYMELSSLTSE DTAVYYCARARADSHTPIDAFDIWGPGTRVIVSSASTKG
118	8ANC46HC	QVQLVQSGTEVKKPGSSVKVSCKASGGTFSDSDIAWVRQAPGQG LEWMGGITPMFDMAKSAQKFRGRLIITADKSTGTAYMELSSLRYE DAAVYFCARSSGNFEFAFEIWGQGTKIIVSLASTKG
119	8ANC48HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQG LEWMGWMNPNSGNTGYAQTFQGRVTMTRNTSISTAYMELSSLR SEDTAVYYCARDRWLPQYYYYGMDVWGQGTTVTVSSASTKG
120	8ANC49HC	FVQLVESGGGLVQPGGSLRLSCAASGFNFNTYWMNWVRQAPGK GLEWVANMKEDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLR AEDTAVYYCARNPESRCIVGRNRGWCRYFDLWGRGSLVTVSPAS TKG
121	8ANC51HC	LVQLVESGGGVVQPGRSLRLSCAASGFTFSTYAMHWVRQAPGK GLEWVAVISYDGSNKFYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCARPKFLPGADIVVVVAATPFDYWGQGNPGHRLLSFH QGPIGLPPG
122	8ANC57HC	PMFQPGQSGGVVVQSGESLHLSCEASGFKFASQMMHWVRHVP GRGLEWVALISWDGSGKLFADSVRGRFTIHRWNDRNSLYLDVKN VRPEDAAIYYCTRNGFDVWGQGILVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
123	8ANC58HC	QVQLVQSGAEVKKPGASVKVSCKVSGHTLSELSINWVRHVPGKG LEWMGGLDPEDGEAIHEPKFQGRLTMTEDTSTDTAYVELSSLRSE DTAMYYCATADPFKVAQDEGLYVIFDYWGQGTLVTVSSASTKG
124	8ANC5HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRFWNWVRQAPGQ GLEWMGGMIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRS DDTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVS SASTKG
125	8ANC60HC	LVQLVESGGGVVQPGKSLRLSCATSGFTFSTYGMHWVRQAPGK GLEWVAVIWYDGSYKYYADSVKGRFTISRDNSKNTLFLQMNSLRA EDTAMYYCGREMAVGGTKALDHWGQGTLVTVSSASTKG
126	8ANC63HC	QVQLVQSGAEAKRPGDSVKVSCKASGYTFTEYYIHWVRQTPGQG FEWMGIITPGAGNTTYAQKFQGRITVTRDTSAATVYMELSNLTSED TAVYFCSRGVSFWGQGTLVTVSSASTKG
127	8ANC65HC	QVQMVASGGGLVKPGGSLRLSCEASGFTFSDYYMSWVRQAPGK GLEWISYITSGGNALYYADSVKGRFTISRDNAKNSLYLQMNSLRAE DTAVYYCARDLLHAHDFGRQGTLVTVSSASTKG
128	8ANC67HC	QVQLVESGGGVVQPGRSLRLSCATSGFTSKNYGVHWVRQAPGK GLEWVAVIWYDGSNKFYADSVKGRFTISRDRSKNMVYLQMNSLR VEDTAIYYCARDSVAFVLEGPIDYWGQGTLVTVSSASTKG
129	8ANC69HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYYIHWVRQAPGQG LEWMGWINPSTGGTNFVQKFLGRVTMTSDTSINTAYMELRRLKN DDAAIYYCATYSTRQFFHYYYVTDVWGQGTTVTVSSASTKG
130	8ANC6HC	QVQLVQSGAEVKKPGSSVKVSCRASGGSFGNYAINWVRQAPMQ GLEWMGGIIPIFGTTNYAQNFRGRVTINADTFTNTVNMDLSSLRSE DTAVYYCGRSINAAVPGLEGVYYYYGMAVWGQGTTVTVSSASTKG
131	8ANC70HC	QVQLHQWGAGLLKPSDTLSLTCGILGVSPPGSLTGYYWTWIRQPP GKGLEWIGEVYHSGSTNYNPSLASRVTISMGTTKTQFSLRLTSVTA ADSAVYYCASGKVWGITARPRDAGLDVWGQGTTVTVTSASTKG
132	8ANC71HC	EVQVVESGGGLVQPGGSLRLSCVASGFTFSEYWMSWVRQAPGK GLEWVATIKRDGSEESYVDSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARVRDPNYNLHFDSWGQGTLVTVSSASTKG
133	8ANC72HC	QVQLVESGGGLIQPGGSLRLSCEASGFAVGDINYMSWVRQAPGK GLEWVSVLYSGGSSQYADSVKGRFTISRDNSRNTLYLQMDNLRA EDTAVYYCARGLRVYFDLWGQGILVTVSSASTKG
134	8ANC74HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQ GLEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSE DTAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG
135	8ANC75HC	QVQLQESGPGLVKPSETLSLTCTVSGGSISSRSYYWGWIRQPPG KGLEWVGSIYYTGSTYYSPSLKSRVTISVDTSQNQFSLKLNSVTAA DTAVYYCARQKGSGTSLLYWGQGTLVTVSSASTKG
136	8ANC76HC	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAINWVRQAPGQG LEWMGWINTNTGNPTYAQGFTGRFVFSLETSVSTAYLQINSLKAE DTAVYYCARDLLESRTYYNDIRDCWGQGTLVTVSSASTKG
137	8ANC78HC	QVQLQESGSGLVKPSGTLSLTCAVSNGPISSGNWWSWVRQTPEK GLEWIGEVYHSGSTNHNPSLKSRATILVDKSKNQFSLNLRSVTAAD TAVYYCARVRGSWNFDYWGQGILVTVSSASTKG
138	8ANC79HC	QHQLVPCVAEVRKPGASVKVSCKVSGYTLTEISMHWVRQAPGKG LEWMGGFDREDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRS EDTAVYYCATTYLAVVPDGFDGYSSSWYWFDPWGQGTLVTVSSA SMQGPMLLSPTGTLLPRAPLVQTRPGP
139	8ANC7HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIFGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRSD DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVIVSS ASTKG
140	8ANC80HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAFSWVRQAPGQ GLEWMGGIIPIFGTENYAQKFQGRVTITADKSTSTAYMELSSLRSE DTAVYYCARDRSSAIGYCSSISCYKGSFDIWGQGTMVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
141	8ANC82HC	QVHLEESGPGLVKTSQTLSLTCSVSSYSISRSGYFWTWIRQRPGK GLEWIGYIYFNGRTTYNPSLKSRITISRDTSHSQFSLTLNSLSAADT AVYYCGRCQDGLASRPIDFWGQGTLVTVSSASTKG
142	8ANC83HC	QVQLVESGGGVVQPGKSLRLSCAISGFLFNNYGGQWVRQAPGK GLEWVAAISYDGNNRYYADSAKGRFLISRDTPKNILYLQIYSLRLDD TAVYYCARDSVSKSYSAPPEFWGQGTVVTVSSASTKG
143	8ANC91HC	QLQLQESGPGLVKPSETLSLTCSVSDGSINSNSYYWAWIRQSPGK GLEWIGSVYYFGGTYYSPSLKSRVTMSVDRSKNQFSLNVSSVTAA DTAIYYCARHVRPYDRSGYPERPNWFDPWGRGTLVTVSSASTKG
144	8ANC92HC	RVQLVQSGAEVKKPGSSVTVSCKASGGSFSSYAISWVRQAPGQG LEWVGGVKVMFGTVHYSQKVQGRVTITADDSTGTSYLELSGLRS ADTAVYYCARNAGAYFYPFDIWGQGTLIIVSSASTKG
145	8ANC93HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYHIHWVRHAPGQG LEWMGKINPSRASTKYAKKFQDRVTMTRDTSTSTVYMELSSLRG DDTAVYYCGREMGTFTLLGVVIDHYDFYPMDVWGQGTPVTVSSA STKG
146	8ANC9HC	QVQLVQSGAEVRKPGSSLKVSCKSSGGTFSRYVVNWVRQAPGQ GLEWMGGIIPIPGIAKYAQKFQDRVTMTADESKNTVYLDFSSLRSG DTAVYYCARDRGDTRLLDYGDYEDERYYYGMDVWGQGTTVTVS SASTKG
147	12A10HC	SQHLVQSGTQVKKPGASVRVSCQASGYTFTNYILHWWRQAPGQ GLEWMGLIKPVFGAVNYARQFQGRIQLTRDIYREIAFLDLSGLRSD DTAVYYCARDESGDDLKWHLHPWGQGTQVIVSPASTKG
148	12A12HC	SQQLVQSGTQVKKPGASVRISCQASGYSFTDYVLHWWRQAPGQ GLEWMGWIKPVYGARNYARRFQGRINFDRDIYREIAFMDLSGLRS DDTALYFCARDGSGDDTSWHLDPWGQGTLVIVSAASTKG
149	12A13HC	SQQLVQSGTQVKKPGASVRISCQASGYSFTDYVLHWYRQAPGQ GLEWMGWIKPVYGARNYARRFQGRINFDRDIYREIAFMDLSGLRS DDTALYFCARDGSGDDTSWYLDPWGQGTLVIVSAASTKG
150	12A16HC	SQQLVQSGTQVKKPGASVRISCQASGYTFTDYVLHWWRQAPGQ GLEWMGWIKPVYGARNYARRFQGRINFDRDIYREIAYMDLSGLRS DDTARYFCARDGSGDDTSWHLHPWGQGTLVIVSAASTKG
151	12A17HC	SQQLVQSGTQVKKPGASVRVSCQASGYTFMNYIIHWWRQAPGQ RLEWMGWINPVFGARNYAHRFQGRINFDRDINRETFQMELTGLR SDDTAVYYCARDGSGDARDWHLDPWGQGTLVIVSSASTKG
152	12A1HC	SQHLVQSGTQVKKPGASVRVSCQASGYTFTNYILHWWRQAPGQ GLEWMGLIKPVFGAVNYARQFQGRIQLTRDINREIAFLDLSGLRSD DTAVYYCARDESGDDLKWHLHPWGQGTQVIVSPASTKG
153	12A20HC	SQQLVQSGTQVKKPGASVRVSCQASGYTFMNYIIHWWRQAPGQ RLEWMGWINPVFGARNYAHRFQGRINFDRDINRETFQMDLTGLR SDDTAVYYCARDGSGDARDWHLHPWGQGTLVIVSSASTKG
154	12A21HC	SQHLVQSGTQVKKPGASVRVSCQASGYTFTNYILHWWRQAPGQ GLEWMGLIKPVFGAVNYARQFQGRIQLTRDIYREIAFLDLSGLRSD DTAVYYCARDESGDDLKWHLHPWGQGTQVIVSPASTKG
155	12A22HC	SQQLVQSGTQVKKTGASVRVSCQASGYDFTKYLIHWWRQAPGQ GLEWMGWMKPVYGATNYAHRFQGRISFTRDIYREIAFMDLNGLR SDDTAVYFCARDGGGDDRTWLLDAWGQGTLVIVSSASTKG
156	12A23HC	SQHLVQSGTQVKKPGASVRVSCQASGYTFTNYILHWWRQAPGQ GLEWMGLIKPVFGAVNYARQFQGRIQLTRDINREIAFLDLSGLRSD DTAVYYCARDESGDDLKWHLHPWGQGTQVIVSPASTKG
157	12A27HC	SQQLVQSGTQVKKPGASVRISCQASGYTFTDYVLHWWRQAPGQ GLEWMGWIKPVYGARNYARRFQGRINFDRDIYREIAFLDLSGLRS DDTARYFCARDGSGDDTSWHLHPWGQGTLVIVSAASTKG
158	12A2HC	SQQLVQSGTQVKKPGASVRISCQASGYTFTDYVLHWWRQAPGQ GLEWMGWIKPVYGARNYARRFQGRINFDRDIYREIAYMDLSGLRS DDTARYFCARDGSGDDTSWHLHPWGQGTLVIVSAASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
159	12A30HC	SQQLVQSGTQVKKPGASVRISCQASGYTFTDYVLHWWRQAPGQ GLEWMGWIKPVYGARNYARRFQGRINFDRDIYREIAYMDLSGLRS DDTARYFCARDGSGDDTSWHLHPWGQGTLVIVSAASTKG
160	12A37HC	SQQLVQSGTQVKKTGASVRVSCQASGYDFTKYLIHWWRQAPGQ GLEWMGWMKPVYGATNYAHRFQGRISFTRDIYREIAFMDLNGLR SDDTAVYFCARDGGGDDRTWLLDAWGQGTLVIVSSASTKG
161	12A46HC	SQQLVQSGAQVKKPGASVRVSCQASGYTFTNHFLHWWRQAPRQ GLEWMGWINPVHGGRNYARRFQGRINFGRDVYQETAYMELSGL RNDDTATYFCARGGGDGRNWHLHPWGQGTLVIVSAASTKG
162	12A4HC	SQHLVQSGTQVKKPGASVRVSCQASGYTFTNYILHWWRQAPGQ GLEWMGLIKPVFGAVNYARQFQGRIQLTRDIYREIAFLDLSGLRSD DTAVYYCARDESGDDLKWHLHPWGQGTQVIVSPASTKG
163	12A55HC	SQQLVQSGAQVKKPGASLRVSCQASGYTFMNYLLHWWRQAPGQ GLEWMGWINPVYGAVNYAHRFQGRLTFSRDVYREIAYMDLNGLR SDDTAVYFCARDGSGDDRNWHLDPWGQGTLVIVSSASTKG
164	12A56HC	SQQLVQSGTQVKKPGASVRVSCQASGYTFTNYILHWWRQAPGR GLEWMGLIKPVYGAVNYARQFQGRIQLTRDIYREIAFLDLSGLRPD DTAVYYCARDESGYDLNWHLDSWGQGTQVIVSPASTKG
165	12A6HC	SQQLVQSGTQVKKPGASVRVSCQASGYTFTDYVLHWWRQAPGQ GLEWMGWIKPVYGARNYAHRFQGRINFDRDVYREIAYMDLSGLR SDDTAVYFCARDGSGDATSWHLHPWGQGTLVIVSSASTKG
166	12A7HC	SQQLVQSGTQVKKPGASVRVSCQASGYTFMNYIIHWWRQAPGQ RLEWMGWINPVFGARNYAHRFQGRINFDRDINRETFQMELTGLR SDDTAVYYCARDGSGDARDWHLDPWGQGTLVIVSSASTKG
167	12A9HC	QVTLVQSGAEVKKPGASVRISCRASGFTFDDYSDYSFIPTTYLIHW FRQAPGQGLEWMAWINSVNGGRNIARQFQGRVTVARDRSNSIAF LEFSGLRHDDTAVYFCARDRRDDDRAWLLDPWGQGTRVTVSSA STKG
168	LSSB2339HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIVHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLTSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
169	LSSB2351HC	QVRLEQSGTAVRKPGASVTISCQASGYNFVKFFIHWVRQRPGQG FEWVGMIEPFRGRPWSAGNFQGRLSLSRDVSTETLYMTLNNLRS DDTAVYFCARLEAESDSHSRPIMFDHWGHGSLVTVSSASTKG
170	LSSB2361HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
171	LSSB2364HC	QVRLEQSGAAVRKPGASVTLSCQASGYNFVNYIIHWVRQRPGLDF EWVGMIDPYRGRPWSAHKFQGRLSLSRDVSTEILYMTLSSLRSDD TATYFCARAEAESQSHSRPIMFDFWGQGSRVTVSSASTKG
172	LSSB2367HC	QVRLSQSGAAIKKPGASVTISCETEGYTFINYIIHWVRQPPGRGFE WLGMIDPRNGRPWFGQSVQGRLSLRRDTYTEVVYMTLSGLTSDD AGHYFCARNEPQYHDGNGHSLPGMFDYWGQGTLVAVSSASTKG
173	LSSB2416HC	QVRLSQSGAAVKKPGASVTIVCETEGYNFIDYIIHWVRQPPGRGFE WLGMIDPRNGRPWSGQKVHGRLSLWRDTSTEKVYMTLTGLTSD DTGLYFCGRNEPQYHDDNGHSLPGMIDYWGQGTMVTVSSASTKG
174	LSSB2434HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
175	LSSB2483HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
176	LSSB2490HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
		RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
177	LSSB2503HC	QVRLEQSGAAVRKPGASVTLSCQASGYNFVRYIIHWVRQRPGLDF EWVGMIDPYRGRPWSAHKFGGRLSLTRDVSTEILYMTLTSLRSDD TATYFCARAEAESQSHSRPIMFDSWGQGSRVTVSSASTKG
178	LSSB2525HC	QVRLEQSGNAVRKPGASVTISCQASGYNFVKFFIHWVRQRPGQG FEWVGMIEPFRGRPWSAGNFQGRLSLSRDVSTETLYMTLNNLRS DDTAVYFCARLEAESDSHSRPIMFDHWGHGSLVTVSSASTKG
179	LSSB2530HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIIHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
180	LSSB2538HC	QVRLFQSGAAMRKPGASVTISCEASGYNFLNYFVHWVRQRPGRG FEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGLRS DDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSASTKG
181	LSSB2554HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIIHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
182	LSSB2573HC	QVRLSQSGAAIKKPGASVTISCETEGYTFINYIIHWVRQPPGRGFE WLGMIDPRNGRPWFGQSVQGRLSLRRDTYTEVVYMTLSGLTSDD TGLYFCARNEPQYHDGNGHSLPGMFDSWGQGTLVAVSSASTKG
183	LSSB2578HC	QVQLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
184	LSSB2586HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIVHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
185	LSSB2609HC	QVRLFQSGAAMKKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDISTEMFYMRLDGLR SDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAST KG
186	LSSB2612HC	QVRLEQSGTAMRKPGASVTLSCQASGYNFVKYIVHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
187	LSSB2630HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
188	LSSB2640HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
189	LSSB2644HC	QVRLSQSGAAIKKPGASVTISCETEGYTFINYIIHWVRQPPGRGFE WLGMIDPRNGRPWFGQSVQGRLSLRRDTYTEVVYMTLSGLTSDD TGLYFCARNEPQYHDGNGHSLPGMFDSWGQGTLVAVSSASTKG
190	LSSB2665HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
191	LSSB2666HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIIHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
192	LSSB2669HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIIHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
193	LSSB2680HC	QVRLEQSGVAMRKPGASVTLSCQASGYNFVKYIIHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
		DTATYFCARAEAASDIHSRPIILTGPGEYGLDLEHMDWTWRILCLL AVAPGCHSQ
194	LSSB2683HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIVHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
195	LSSB344HC	QVRLEQSGTAVRKPGASVTISCQASGYNFVKFFIHGVRQRPGQGF EWVGMIEPFRGRPWSAGNFQGRLSLSRDVSTETLYMTLNNLRSD DTAVYFCARLEAESDSHSRPIMFDHWGHGSLVTVSSASTKG
196	LSSNEC107HC	QVRLVQSGPQVKTAGASMRVSCEASGYRFLDYIIVWIRQTHGQHF EYVGMINPRGGTPWPSSKFRDRLTLTRDIYTDTFYLGLNNLGSGD TAIYFCARLEADGDDYSPKMFDYWGQGTRIIVSAASTKG
197	LSSNEC108HC	QVHTFQSGSSMKKSGASVTISCEATGYNIKNYILHWVRQKPGRGF EWVGMIDPINGRPWFGQPFRGRLTLTRDLSTETFYMSLSGLTSDD TATYFCARREADYHDGNGHTLPGMFDFWGPGTLITVSSASTKG
198	LSSNEC109HC	QVSLVQSGPQVKTPGASMRVSCETSGYRFLDYIIVWIRQTHGQHF EYVGMINPRGGTPWPSSKFRDRLTMTRDIHTDTFYLGLNNLRSDD TAIYFCARLEADGDDYSPKMFDYWGQGTRIIVSAASTKG
199	LSSNEC110HC	QVRLVQSGPQMKTPGASLRLSCEVSGYRFLDYFIVWVRQTGGQG FEYVGMINPRGGRPWSSWKFRDRLSLTRDIETDTFYLGLNNLRSD DTAIYFCARLEADGDNYSPKMVDYWGQGTKIIVSPASTKG
200	LSSNEC116HC	QVRLSQSGAAVVKTGASVTISCETEGYNFVNYIIHWVRRPPGRGF EWLGMIDPRNGHPWFAQTVRGRLSLRRDTFKETVYMTLSGLTSD DTGVYFCARNEPQYHSLPGMFDYWGHGTPVTVSSASTKG
201	LSSNEC117HC	QVRLVQSGAQLKKPGASVTVSCEASGYNFVNYIINWVRQTPGRG FEWVGMIDPRRGRPWSAQKFQGRLTLTRDIDSEKLYMHLSGLRG DDTAVYYCARQDSDFHDGHGHTLRGMFDSWGQGSPVTVSSAST KG
202	LSSNEC118HC	QVRLVQSGPQVKTPGASMRISCEASGYRFQDYIIVWIRQTHGQGF EYVGMINPRGGTPWSSSKFRDRLSLTRDIYTDTFYLGLNNLGSDD TAIYFCARLEADGGDYSPKMFDYWGQGTRIIVSAASTKG
203	LSSNEC11HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
204	LSSNEC122HC	QVRLVQSGPQVKRPGASIRLSCETSGYRFQDYIVAWIRQTRGQRF EFVGMVNPRGGRPWPSSKFRDRVTLTRDIESETFHLGLNDLTSDD TATYFCARLEADGADYSPKMFDFWGQGTKIWSPASTKG
205	LSSNEC123HC	QVRLEQSGAAVRKPGASVTLSCQASGYNFVNYIIHWVRQRPGLDF EWVGMIDPYRGRPWSAHKFEGRLSLSRDVSTEVLYMTLSSLRSD DTATYFCARAEAESQSHSRPIMFDYWGQGSRVTVSSASTKG
206	LSSNEC127HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIIHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
207	LSSNEC18HC	QVRLSQSGAAVMKTGASVTISCETEGFNFVNYIIHWVRRPPGRGF EWLGMIDPRNGHPWFAQTVRGRLSLRRDTFNEIVYMTLSGLTTDD TGLYFCARNEPQYHSLPGMFDYWGQGTPVTVSSASTKG
208	LSSNEC24HC	QVRLSQSGAAMKKPGASVTISCETEGYTFINYIIHWVRQPPGRGFE WLGMIDPRNGRPWFGQSVQGRLSLRRDTYTEVVYMTLSGLTSDD AGLYFCARNEPQYHDGNGHSLPGMFDYWGQGTLVAVSSASTKG
209	LSSNEC29HC	QVRLSQSGAAVVKTGASVTISCETEGYTFVNYIIHWVRQSPGRGF EWLGMIDPRNGHPWFGQRLRGRLSLRRDRSTETVFMTLSGLTSD DTAIYFCARNEPQYYDGSGHSLPGMFDYWGQGTRVVVSSASTKG
210	LSSNEC2HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
211	LSSNEC33HC	QVRLVQSGPQVKTPGASIRLSCEASGYRFLDYFIVWVRQTPGQGF EYVGMINPRGGRPWSSWKFRDRLSLTREIDTDTFYLGLSNLRSDD TAIYFCARLEADGDDYSPKMVDYWGQGTKIIVSAASTKG
212	LSSNEC34HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
213	LSSNEC3HC	QVRLEQSGAAVRTPGASVTLSCQASGYKFVNYIIHWVRQRPGLAF EWVGMIDPYRGRPWSAHSFEGRLSLSRDVSMEILYMTLTSLRSD DTATYFCARAEAESQSHSRPIISTSGAR
214	LSSNEC46HC	QVQFFQSGSSMKKSGASVTISCEATGYNIKNHILHWVRQKPGRGF EWVGMIDPINGRPWFGQAFRGRLTLTRDLSTETFYMSLSGLTSDD TATYFCARREADYHDGNGHTLPGMFDFWGPGTLVTVSSASTKG
215	LSSNEC48HC	QVRLSQSGAAVVKTGASVTISCETEGYTFVNHIIHWVRQPPGRGF EWLGMIDPRNGHPWFGQRLRGRLSLRRDRSTETVFMTLSGLTSD DIGIYFCARNEPQYFDGSGHSLPGMFDYWGQGTRVWSSASTKG
216	LSSNEC52HC	QVRLSQSGAAVVKTGASVTISCETEGYTFVNYIIHWVRQPPGRGF EWLGMIDPRNGHPWFGQRLQGRLSLRRDRSTETVFMTLSGLTSD DTGIYFCARNEPQYYDGSGHSLPGMFDYWGQGTRVVVSSASTKG
217	LSSNEC56HC	QVRLVQSGPQVKTPGASMRVSCEASGYRFLDYIIVWIRQTHGQHF EYVGMINPRGGTPWPSSKFRDRLSLTRDIHTDTFYLGLNNLGSDD TAIYFCARLEADGDDYSPKMFDHWGQGTRIIVSAASTKG
218	LSSNEC60HC	QVRLEQSGAAVKKPGASVTISCQASGYNFVKFFIHWVRQRPGQG FEWVGMIEPYRGRPWSAGNFQGRLSLSRDVSTETLYMTLNNLRS DDTAVYFCARLEAESDSHSRPIMFDHWGHGSLVTVSSASTKG
219	LSSNEC66HC	QVRLSQSGAAVMKTGASVTISCETEGYNFVNYIIHWVRRPPGRGF EWLGMIDPKNGHPWFAQAVRGRLSLRRDTFNEVVYMTLSGLTSD DTGLYFCARNEPQYHDGNGHSLPGMFDFWGQGTLVTVSSASTKG
220	LSSNEC70HC	QVRLSQSGAAVVKTGASVTISCETEGYTFVNYIIHWVRQPPGRGF EWLGMIDPRNGHPWFGQRFRGRLSLRRDRSTETVFMTLSGLTSD DNGIYFCARNEPQYYDGSGHSLPGMFDYWGQGTRVVVSSASTKG
221	LSSNEC72HC	QVRLEQSGAAVRKPGASVTLSCQASGYNFVNYIIHWVRQRPGLDF EWVGMIDPYRGRPWSAHKFQGRLSLSRDVSTEILYMTLSSLRSDD TATYFCARAEAESQSHSRPIMFDFWGQGSRVTVSSASTKG
222	LSSNEC7HC	QVRLEQSGAAVRKPGASVTLSCQASGYNFVNYIIHWVRQRPGLDF EWVGMIDPYRGRPWSAHKFQGRLSLSRDVSTEILYMTLNSLRSD DTATYFCARAEAESQSHSRPIMFDSWGQGSRVTVSSASTKG
223	LSSNEC82HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
224	LSSNEC89HC	QVRLEQSGGALRKPGASVTLSCQASGYNFVKYIIHWVRQRPGLGF EWVGMIDPYRGRPWYAHSFAGRLSLSRDTSTETLYMTLSSLKSD DTATYFCARAEAASDSHSRPIMDWTWRILCLLAVVPASTKG
225	LSSNEC8HC	QVRLFQSGAAMRKPGASVTISCEASGYNFMNYFVHWVRQRPGR GFEWLGMINPRGGRPWSAQSVQGRLTLTRDTSTEMFYMRLDGL RSDDTATYFCARNEADYHDGNGHSLRGMFDYWGQGSLITVSSAS TKG
226	LSSNEC94HC	QVRLEQSGAAMRKPGASVTLSCQASGYNFVKYIVHWVRQKPGLG FEWVGMIDPYRGRPWSAHKFQGRLSLSRDTSMEILYMTLTSLKSD DTATYFCARAEAASDSHSRPIMFDHWGQGSRVTVSSASTKG
227	LSSNEC95HC	QVRLVQSGPQVKRPGASIRLSCESSGYRFQDYIVAWIRQTRGQGF EFVGMVNPRGGRPWPSSRFRDRVTLTRDIESETFYLGLNDLTSDD TATYFCARLEADGSDYSPKMFDFWGQGTKIVVSPASTKG
228	LSSNEC9HC	QVRLVQSGAQLKKPGASVTVSCEASGYNFVNYIINWVRQTPGRSF EWVGMIDPRRGRPWSAQKFQGRLTLTRDIDSEKLYMHLSGLRGD DTAVYYCARQDSDFHDGHGHTLRGMFDSWGQGSPVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
229	LSSB2055HC	QVQLVQSGPELMKPGSSVKVSCRASGDNFLTSTFNWLRQAPGQ RLEWMGRFIPSLGLITSAPKFSDRLTITADQATLTAYMELTGLTSED TALYYCARGLCRGGNCRLGPSGWLDPWGRGTQVTVSSASTKG
230	LSSB2066HC	QVVLIQSGAEVKRPGSSVKVSCKASGGSFPITWVRQAPGHGLEW MGGINPFFGTTNYAQKFQGRVSITADESTSTTYLHLSDLRSEDTAV YFCARENREKWLVLRSWFAPWGQGTLVTVSSASTKG
231	LSSB2068HC	EESGPGLVKPSQTLSLTCSVSGDSVSSGGYFWSWIRQHPTKGLE CLGYVYYTGNTYYNPSLKSPPTIEVAMANNQVSLKLGSVTAADTA VYYCARIKRFRGGNYFDTWGHGLLVTVSSASTKG
232	LSSB2080HC	LAQLEQSGGGVVKPGGSLRLPCAASGFTFIDYYMAWIRLAPGKGL EWLSYISKNGDYTKYSESLKGRFTISRDNAKNLVILQLNRLRADDT AIYFCARADGLTYFGELLQYIFDLWGQGARVIVSSASTKGPSVFPL APSSKSTSGHASV
233	LSSB2133HC	QVQLVQSGAEVKKPGASVKISCKASGYSFRNYAVHWVRQAPGQ GLEWMGEINGGNGNTEYSQKSQGRLTITRDISATTAYMELSSLRS DDTAVYYCARVAYVHVVTTRSLDNWGQGTLVTVSSASTKG
234	LSSB2182HC	QVQIRQSGPGLVKPLETLSLSCIVFGGSFIAYHWTWIRQAPLKGLE WIGDIDQGGDITYSPSLKSRVTMSVDRSKSQFSLKLSSVTAADAAV YYCVRGPPNRYAVTSFTSGTHRERSSYYFDYWGPGTLVTVSSAS TKG
235	LSSB218HC	KAPATLSLSPGERATLSCRASQSVGSDLAWYQQKPGQAPRLLIYD ASNRATAIPARFSGSGSGTDFTLSISSLEPEDFAVYFCQQRYDKIT FGQGTRLEIQRTVAAPSVFIFPPSDEQ
236	LSSB2277HC	FVQLVESGGGVVQPGTSLRLSCTTSGFIFSDYGMHWVRQAAGKG LEWVAVIWHDGSNRFYADSVKGRFTISRDNSKNAVYLEMNNLRVE DTALYYCARTSMDIDYWGQGTPVTVSSASTKG
237	LSSB2288HC	QVYLVQSGPELKKPGASVKISCKASGYNFPKYAIHWVRQAPGQGL QWMGWINGDNGDARYSQKLQGRVTPSTDTSASVVYMELKRLRS EDTAVYYCARALYPWEIGGVPSTMGDDYWGQGTLITVSSASTKG
238	LSSB331HC	QVHLQQWGAGLLKPSETLSLTCAVSGGSFSGFFWTWIRQSPGKG LEWIGEVNHSGFTHSNPSLESRATISVAASNTQFSLRLASVTAADT AIYFCALRYFDWSPFRRDTYGTDVWGQGTTVIVSSASTKG
239	LSSNEC101HC	QVQLVQSGAELKKPGSSVKVSCKASGGTFNNHTFNWVRQAPGQ GLEWMGRTIPILGSRDYAKTFQDRVTIIADKSTSTVYLELR TGVYYCATSMYYFDSGGYYRNTDLDKWGQGSLVTVSSASTKG
240	LSSNEC106HC	GLDLEHDGHHKEEPRASVTVSCEASGYNFVNYIIHWVRLTPGRGF EWMGMIDPRRGRPWSAQKFQGRLTLTRDIDSERLYMQLSGLRGD DTAVYFCARQEPDFHDGHGHTLRGMFDSWGQGSPVSVSSASTKG
241	LSSNEC112HC	QVQLVQSGAELKKPGSSVKVSCKASGGTFSNYAINWVRQAPGQG FEWMGGIIPLFATPTYAQKFQGRVRITADDSTSTAYMELSSLRSDD TAVYFCARPNVVRSALDYWGQGTLVTVSSASTKG
242	LSSNEC115HC	QARLDQWGTGLLKPSETLSLKCAVFGVLFTDYNWTWVRQSPGKG LEWIGHLDHRGGGNYNPSLESRVTISLDYSKAQFSLHLKSVTVADT ALYYCAGAVKGFWFDEVYNWFGPWSQGTLVTVASASTKG
243	LSSNEC124HC	QVQLQESGPGLVKPSGTLSLTCAVSGASISSRNWWTWVRQPPGK GLEWIGEIYESGATNYNPSLKSRVTISVDKSKNQFSLRLTSVTAAD TAVYFCARLMTPGGLIGTLDYWGQGTLVTVLQPPPRAHRYHPRNL LQEHLCARVMP
244	LSSNEC125HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAISWVRQAPGQG LEWMGGIIPSFSMSNYAQDFQGRLTITADESTSSVYMELNSLRSE DTAVYYCARDFPRFHRLVGNYDFWRGTLDRFSYMDLWGRGTAV TVSSASTKG
245	LSSNEC126HC	QVHLVQSGAEAKRPGSSVRVSCRASGGDFSSYTLSWVRQAPGQ GIEWMGGVVPMLDTVHYAQKFQGRLTLSVDEGTSTAYMELSSLR SEDTAMYYCTRGRQTFRAIWSGPPAVFDIWGQGTLVIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
246	LSSNEC14HC	NGGSLRLSCRVSGFGFHLYEMNWVRQAPGKGLEWISSISGSGES THYSDSITGRFSMSRDEAKDSLYLQMNNLRVEDTAVYYCTRGFS MGDGTGFSFDTWGRGTMVTVSSGLDTVSLASTKGPSVFPLAPCS RSTSDARLS
247	LSSNEC16HC	AARLDQWGTGLVKPSETLSLKCAVFGVDFPDYTWTWARQAPGK GLEWIGHRDHRGGSSYNPSLSGRATISLDTSKAQFSLHIKSVTVAD TATYYCAGAVAGLWFEDAYNWFGPWSQGTLVTVAAASTKGPSVF PLAPSSKSTSGHASVL
248	LSSNEC21HC	QARLDQWGTGLLKPSETLSLKCAVFGVLFTDYNWTWVRQSPGKG LEWIGHLDHRGGGNYNPSLESRVTISLDYSKAQFSLHLKSVTVADT ALYYCAGAVKGLWFDETYTWFGPWSQGTRVTVASASTKGPSVFP LAPSSKSTSGTRDLS
249	LSSNEC30HC	QVQLVQSEAEVKKPGSSVKVSCKASGGTFRGYTISWVRQAPGQG LEWMGRIIPILGKAIYAPSFQGRVTLTADKSTGTAYMELSRLRSDD TAVYYCAKVKMRGSSGYYYLFDDWGQGTLVTVSSASTKG
250	LSSNEC49HC	QVHLVQSGAEVKKPGASVKVSCKVSGYTLSELSIHWVRQGPGRG LEWMANFDPEDGETIYAPQFQGRVTLTEDTSTDTAYMQLTSLRSE DTAVYYCATDRYTDTGRWGPGTLVTVSSASTKG
251	LSSNEC54HC	QARLDQWGTGLLKPSETLSLKCAVFGVLFTDYNWTWVRQSPGKG LEWIGHLDHRGGGSYNPSLESRVSISLDYSKAQFSLHLKSVTVADT ALYYCAGAVKGFWFDEPSTWFGPWSQGTMVTVASASTKG
252	LSSNEC55HC	QARLDQWGTGLLKPSETLSLKCAVFGVLFTDYNWTWVRQSPGKG LEWIGHLDHRGGGNYNPSLESRVTISLDYSKAQFSLHLKSVTVADT ALYYCAGAVKGFWFDEVYNWFGPGVREPWLPSPQPPPRAHRSS PWHPPPRAPLVTATVP
253	LSSNEC57HC	QARLDQWGTGLLKPSETLSLKCAVFGVLFTDYNWTWVRQSPGKE LEWIGHLDHRGGGNYNPSLESRVTISLDYSKAQFSLHLKSVTVADT ARYYCAGAVKGFWFDDPYTWFGPWSQGTLVTVASASTKG
254	LSSNEC5HC	QVHLVQSGAEAKRPGSSVRVSCRASGGDFSSYTLSWVRQAPGQ GLERMGGVVPMLDTVHYAQKFQGRLTLSVDEGTSTAYMELSSLR SEDTAMYYCTRGRQTFRAIWSGPPVVFDIWGQGTLVSVSSASTKG
255	LSSNEC67HC	QFRLVQSGPEVKNPGSSVTVSCKASGGTFSGLGINWVRQAPGQG LEWLGDIKTMYGTTNYAPKFQGRVTITADESTSTSYMELSGLRSE DTAVFYCVRELFGHHPAFGVWGQGTSVIVSSASTKG
256	LSSNEC74HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGVSWVRQAPGQ GLEWMGWISPYSGNTNYAQRLQDRVTMTTDTSTNTAYMELRSLR SDDTAVYYCAARSYYYYSMDVWGQGTTVTVSSASTKG
257	LSSNEC77HC	QVQLVQSGADVKKPGASVKVSCKVSGYTVSELSIHWVRQAPGKG LEWMGGFDPEDGKTVSAQNFQGRVTMTEDKSTGTANMELRSLR SEDTAVYYCATTVQLIVDFCNGGPCYNFDDWGQGTLVTVSSASTKG
258	LSSNEC85HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTLSSYTISWVRQAPGQG LEWMGRLIPLVDITTYAQKFQGRVTITADTSTNTAYMELSNLRSED TAIYHCATSTMIAAVINDAFDLWGQGTTVTVSSASTKG
259	LSSNEC91HC	QVQLVQSGAEVKKPGASVKVSCKASGNTFTSYGITWVRQAPGQG LEWMGWISAYNGNTNYAQKLQDRLTMTTDTSTSTAYMELRSLRS DDTAVYYCAFSRHYGSGNYDYWGQGTLVTVSSASTKG
260	LSSNEC92HC	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGK GLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD TAVYYCARLPIGSGWYGRDYWGQGTLVTVSSASTKG
261	3A124HC	EVQLLESGGGLVRPGGSLXLSCSASGFTFNSYAMSWVRQAPGKG LEWVSSVSASGEMTYYADSVRGRFTISRDNANNALHLQMNSLRA EXTAVYYCAKVGGTVWSGYSNYLDYWGPGTLVTVSSASTKG
262	3A125HC	QVQLVQSGAEVKKPGASVKVSCKPSSNTFTSHYIHWVRQAPGQG LEWMGMINPGGSTRYAPKFQGRVTLTRDTSTRTVYMELSSLRSE DTAVYYCARPQYNLGRDPLDVWGLGTMVTVSSASTKG
263	3A140HC	EVQLVESGGGLVKPGGSLRLSCADSGFTFRSYSMHWVRQAPGK GLAWVSSISSTSNYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAE DTAVYYCARTFITASWFDSWGQGTLVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
264	3A144HC	VSGGRFSNYGLSWVRQAPGQGLEWMGRIVPAINRAKYAQKFQG RVILTADKITDTAYMELRSLRSEDTAIFYCARDPQIElRGNAFDIWG QGTVVTVSSASTKG
265	3A160HC	QVQLQESGPGLVKPSGTLSLTCNVYGGSMISYYWSWIRQPPGKG LEWIGHVYNSGNTKYSPSLKNRVTISMDTSRNLFSLKVTSVTPADT AVYYCARADYDNIWDSRGGFDLWGQGTLVTVSSASTKG
266	3A18HC	QVQLVQLLQSGAEVKKPGSSVKVSCQISGYGFSNYAISWVRQAP GQGLEWLGRIVPAVGMTEYAQKFQGRVTFTADRSTITAYMDLRGL RSDDTAVYYCVRDPQVEVRGNAFDIWGQGTMVTVSSASTKG
267	3A204HC	QVQLVQSGAEMKKPGASVKVSCKASGHTFTNYYMHWVRQAPGQ GLEWMGMINPTGDSTRYAQRFQGRVTMTRDTSTRTVYMELSSLR SDDTAVYYCARAHHDFWRAPVDVWGKGTTVTVSSASTKG
268	3A228HC	EVQLVQSGAEVKKPGESLRISCKTSGYNFNDDWIAWVRQRPDKG PEWMGIFYPGDSQATYSPSFQGHVTFSADTSISTAYLQWTSLKAS DTAIYYCARTRCFGANCFNFMDVWGKGTALTVTVSSASTKG
269	3A233HC	QVQLQESGPGPVKPSETLSLTCTVSGGSMISYYWSWIRQPPGKG LEWIGYIFTNGRTTYSPSLRSRVTISLDTSTNHFSLRLKSVTAADTAI YYCARLDGEAFRYYLDLWGQGNLVTVSSASTKG
270	3A244HC	IRSFYWHWIRQSPGKGLEWLGSVFDNGLTTHNPSLKSRLTISEDP SRNQISLKLRSMTAADTAVYYCARGDYDILTSSYQFDYWGQGTLV AVSSASTKG
271	3A255HC	QVQLQESGPGLVKPSETLSLTCTVFGASIRSFYWHWIRQSPGKGL EWLGSVFDNGLTTYNPSLKNRLSISEDPSRNQISLNLRSMTAADTA VYYCARADYDLLTSSYHFDSWGQGTLVTVSSASTKG
272	3A296HC	QVQLQESGPGLVKPSETLSLTCTVSGGSISYYYWSWIRQPPGKGL EWIGDIYYSGTTDYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTA VYYCARRRGQRLLAYFDYWGQGSLVTVSSASTKG
273	3A334HC	QVQLVQSGAEVKKPGASVKVSCKAPGYTFIGHYMHWIRQAPGQG LEWMGWINPNSGDTNYAQTFQGRVTMTRDTSISTAYMELTRLRS DDTAVYYCARDLRPMRGNWAMHVWGEGTTVTVSSASTKG
274	3A366HC	CTVSGGSISSAGYYWTWIRQHPGKGLEFIGYIYYIGTTYYNPSLKS RLTISIDTSKNQFSLKLSSVTAADTAIYYCARDYTARGRHFFDYWG QGALVTVSSASTKG
275	3A381HC	SSFAISWVRQAPGQGLEWMGGIIPIFEATSYAQKFQDRLTITTDES TTTAYMDLSSLRSEDTAVYYCARAQGDILTEGYFDYWGQGTLVTV SSASTKG
276	3A384HC	QVQLVQSGAEVKKPGSSVKVSCKVSFFSNYGISWVRQRPGQGLE WMGRIIPAIDDMTYAQTFRGRVTFSADKFTTTAYMELTGLTFEDTA TYFCARDPQVNRRGNCFDHWGQGTLVTVSSASTKG
277	3A419HC	LEWMGRIIPAIDDVTYAQTFRGRVTFSADKFTTTAYMDLTGLRSED TATYFCARDPQVNRRGNCFDHWGQGTLVTVSSASTKG
278	3A461HC	QVQLVQSGAEVKKPGAAVKISCKASRFTFSSYYIHWVRQAPGQGL EWMGIINPSGGSTSNAQKFQDRVTLTRDMSTGTVYMELSRLTSED TAVYYCATPEPSSIVAPLYYWGQGTLVTVSSASTKG
279	3A474HC	EVQLLESGGGLVQPGGSLRLSCAVSGFTFGGHAVSWVRQAPGK GLEWLSQISGTGSRTDYADAVKGRFTVSRDNSKKTVYLQMNSLR VEDTALFYCATRSPGGGYAFDIWGQGAMVTVSSASTKG
280	3A518HC	QVQLQESGPGLVKPSETLSLTCTVSGGSISSAGYYWSWIRQHPEK GLEFIGYIYYLGTTYYNPSLKSRVSISIDTSNNQFSLELSSVSAADTA IYYCARDYTASGRHFFDYWGQGTLVTVSSASTKG
281	3A539HC	EVQLLESGGALVQPGGSLRLSCAASGFTFSTSSMSWVRQAPGKG LEWVSAIGSGRGSTFYADSVKGRFTISRDNSKNTLSLQMNSLTAE DTATYYCTKTGGLLRFPEVWGKGTTVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
282	3A576HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNYAISWVRQAPGQG LEWMGGIIPIFEAASYAQKFQDRLTITTDESTTTAYMDLSSLRSEDT AIYYCARAQGDILTEGYFDYWGQGTLVTVSSASTKG
283	3A613HC	QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGL EWIGYISYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTA VYYCARHKSVLLWFRELDYWGQGTLVTVSSASTKG
284	3A64HC	QVQLVQSGAEVKKPGSSVKVSCKTSGVRFSSNAISWVRQAPGQG LEWMGRTTPMLGGANHAPSFKGRVTISADESTRTVYMEMSSLRY EDTAVYYCASGRREGLNFLLDYWGQGTLVTVSSASTKG
285	3A650HC	QVQLVQSGAEVRKPGASVKVSCKTSGYTFTNSYIHWVRQAPGQG LEWMGIINPPGGNTYYAQKFHGRVTLTRDTSTSTVYMELNSLRSE DTAVYFCARPHSPTNIPSRPLDYWGQGTLVTVSSASTKG
286	3A67HC	QVQLVQSGAEVKKPGASVKVSCKVSGYPLAELSVHWVRQVPGK GLEWVGGFDPEEGKTVYAQKFQGRVTMTEDRSTDTVYMELISLR YEDTAVYYCATDNPVLQLGELSSSLDYWGQGTLVTVSSASTKG
287	3A779HC	PSETLSLTCRVSGASISNFYWTWIRQPAGKGLEWIGRLYSSDKTN YNPSLNGRVTMSLDTSKNQFSLRLTSMTDADTAIYYCAREKGQW VTLPPYYFDSWGQGILVTVSSASTKG
288	3A816HC	NTFTSHYVHWVRQAPGQGLEWMGMINPGGTTRYAPKFQDRVTL TRDTSTRTVYMELRSLRSEDTAVYYCARPQYNLGREPLNVWGQG TMVTVSSASTKG
289	3A869HC	QVQLQESGPGLVKPSETLSLTCSVSGASISNFYWTWIRQPAGKGL EWVGRLYSSDRTNYNPSLNGRVTMSLDTSKNQFSLRLTSMTDAD TAIYFCAREKGQWLTVPPYYFDSWGQGILVTVSSASTKG
290	3A93HC	CTVSGGSIISYYWNWIRQSPGKGLEWLGYIFDGGRANYNPSLRSR LTMSVDTSKNQISLKVKSVTAADSAIYYCARLDGEAFRYYFDSWG QGTLVTVSSASTKG
291	3A966HC	QTLSLTCSVSGGSISSAGYYWGWIRQHPGKGLEWIGHIYYSGNTN YNPSLKSRLSMSVETSKNQFSLNLASVTAADTAVYFCARDYSAAG RHLFDSWGQGILVTVSSASTKG
292	3A978HC	KPSQTLSLTCTVSGGSISSAGYYWTWIRHHPGKGLEFIGYIYHIGT PYYNPSLKSRLTISIDTSKNQFSLKLSSVTAADTAIYYCARDYTARG RHFFDYWGQGALVTVSSASTKG
293	3ANC3HC	QVQLVQSGADVKKPGASVTVSCKTDEDEDDFRAHLVQWMRQAP GQRLEWVGWIKPQTGQPSYAQKFQGRVTLTREVSTSTVFLQLRN LRSDDTAVYYCARPRGGRDNWSFHVWGRGTLVTVSSASTKG
294	3ANC42HC	QVQLVQSGAAVKKPGASVKVSCETYGYTFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLK FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
295	3ANC66HC	QVQLVQSGAAVKKPGASVKVSCETYGYKFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLR FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
296	3ANC79HC	QVQLVQSGAAVKKPGASVKVSCEAYGYKFTDHFMHWWRQAPGQ GLEWMGWINPYTSAVNYSPKYQGRVTMTRDTFLETVYMELRGLR VDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
297	3B10HC	QVQLQESGPGLVKPSETLSLTCSVSNGSISSGGYYWSWLRQFPG KGLEWIGSIHYTGRTMYNPSLMGRPALSMDTSNNQFSLKLRSVTA ADTALYFCARDLQWIFVVDPWGQGTLVTVSSASTKG
298	3B120HC	LQQLQVPRLSMWRVFKVAAATGAQTLTVEEPGSSVKVSCKASGG SSTAYGYSWVRQAPGQGFEWMGRIIPFYGIITYAPKFQGRVTITAD RSTSTVYMELTSLTFADTALFFCARDFGDPRNGYYFDSWDQGLW LTVSSASTKG
299	3B126HC	QVHLVQSGAEVKKPGSSVRVSCKASGWTFGDSVNSAITWVRQAP GQGLEWMGRFIPILGLSNYAQKFQDRVTINVDRSTNTAYMELSGL RSEDTAVYYCARLITGMNAPWFYYMDVWGKGTTITVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
300	3B129HC	FICFSVVVRLLEFGGRLVQPGGSLRLSCSASGFTFSNSAMSWVRQ APGKGLEWVSSILSSGVGTFYADSVKGRFTVSRDNSRNTLYLQMK SLRAEDTALYYCAKVQIQQLNFGVITDAGLDVWGKGTTLIVSSAST KG
301	3B142HC	QVQLGQSGTEVKKPGFSVKVSCKASGGSSTAYGYSWVRQAPGQ GFEWMGRIIPFYGIITYAPKFQGRVTITADRSTSTVYMELTSLTFAD TALFFCARDFGDPRNGYYFDSWDQGLWLTVSSASTKG
302	3B154HC	QVQLVQSGGEVRKPGSSVKVPCKISGNAFSNYGVNWVRQAPGQ GLEWVGRIIPVIGVAQHAPKFQGRVTITADKSTTTAYLELSSLRSDD TAVYFCAKDHGDPRTGYYFDYWGQGALVTVSSASTKG
303	3B165HC	QVQLLQSGTEVKKPGSSVKVSCRASGWTLGNSPNSAIGWVRQAP GQGLEWIGRIIPILDVTNYAQKFQGRVTISADKSTNIAYMEISSLGSE DTAFYYCARVITGMTSPWYFYMDVWGEGTTVIVSSASTKG
304	3B171HC	VQSQVYLVQSGGEVKKPGSSVKVSCKASGDSFSSSVITWVRQAP GQGPEWMGRIIPVLGVAAYAQNFYGRVTISADTSSNTAYMELSSL RFEDTAVFYCARETGRGGNLALRQYFFDSWGQGTLVTVSSPSTKG
305	3B17HC	EVQLVESGGGLVQPGGSLRISCSATGFTFSTHAMHWVRQAPGKG LEYVSAINSNGRSAFYADSVKGRVTISRDNSKNTLFLQMTSLRAED TAVYYCVKGPLLRYLDSWGQGTLVTVSSASTKG
306	3B186HC	QVQLVESGGGLVKPGGSLRLSCAASGFSFNEYYMSWIRQAPGQG LEWVANIGSSDAYTIYADSVKGRFTISRDNAENTVYLQMNSLRGE DTAVYYCARIEGYCSNSRCSNYFDPWGQGALVTVSSASTKG
307	3B193HC	MFLFLVAGATGVQSQVYLVPFGPEVKKPGSSVKVSCKASGDSFTS SVITWVRQAPGQGPEWMGRVIPVLGVAAYAQKFYGRVTITADTSS NTAYMEVNSLRFEDTAVYYCARETGRGGNLALRQYFFDSWGQGT LVTVSSPSTKG
308	3B22HC	CQVQLVESGGGVVQPGRSLRLSCVGSGFTFSSSGMHWVRQAPG KGLEWVAVISSDGSDEYYGDSVEGRFTISRDNSKNTLFLQLDSLE AEDSAVYYCAKTPPHYDALTGYPSSVLEFWGLGTLVTVSSASTKG
309	3B27HC	EVQLVESGGGLVQPGGSLRISCSATGFTFSTHAMHWVRQAPGKG LEYVSAINSNGRSAFYADSVKGRVTISRDNSKNTLFLQMTSLRAED TAVYYCVKGPLLRYLDSWGQGTLVTVSSASTKG
310	3B29HC	QVHLVQSGAEVKKPGSSVRVSCKASGWTFGDSVNSAITWVRQAP GQGLEWMGRFIPILGLSNYAQKFQDRVTINVDRSTNTAYMELSGL RSEDTAVYYCARLITGMNAPWFYYMDVWGKGTTITVSSASTKG
311	3B2HC	SGGRLVQPGGSLRLSCSASGFTLSNSAMSWVRQAPGKGLEWVS SILSSGVGTFYADSVKGRFTVSRDNSRNTLYLQMKSLRAEDTALY YCAKVQIQQLNFGVITDAGLDVWGKGTTLIVSSASTKG
312	3B31HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFTTYDISWVRQAPGQG LEWIGGILPDFGAPSYAQKFQDRVTITTDESSRTAYMELNSLRSED TAIYYCARGRGDDFWSGESPSWYFDYWGQGTQVTVSSASTKG
313	3B33HC	PLVQLEPSGVEVKKRGASVKVSCKVSGYSLTELSMHWVRQAPGK GLEWMGSFDPLDGDTIYAQKFQGRVTMTVDTSTDTAYMDLSSLR FEDTAVYYCATPSKAYYYDSPNYEGDFYMDVWGKGTTVIVSSAST KG
314	3B40HC	QVQLVESGGGVVQPGRSLRLSCVGSGFTFSSSGMHWVRQAPGK GLEWVAVISSDGSDEYYGDSVEGRFTISRDNSKNTLFLQLDSLEA EDSAVYYCAKTPPHYDALTGYPSSVLEFWGLGTLVTVSSASTKG
315	3B41HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKG LEWMGVFDPLEGDGVYAEKFRGRVIMTEDTSTDTGYMELTSLRS EDTAIYYCATKAKDYYYESSDYSPYYYYYMDVWGKGTTVTVSSAS TKG
316	3B44HC	EVRLLESGGGLVQPGGSLRLSCSASGFTFSNSALSWVRQAPGKG LEWVSSVVSSGGDTFYADSVKGRFTISRDNSRNTLYLQMKSLRAE DTALYYCAKVQIQQLNFGVITDAGMDVWGKGTTVIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
317	3B45HC	VEEPGSSVKVSCKASGGSSTAYGYSWVRQAPGQGFEWMGRIIPF YGIITYAPKFQGRVTITADRSTSTVYMELTRLTFADTALFFCARDYG DPRNGYYFDSWDQGLWLTVSSASTKG
318	3B48HC	QVQLVESGGGLVQPGGSLRISCSATGFTFSTHAMHWVRQAPGKG LEYVSAINSNGRSAFYADSVKGRVTISRDNSKNTLFLQMTSLRAED TAVYYCVKGPLLRYLDSWGQGTLVTVSSASTKG
319	3B50HC	QVQLVQSGPGLVKPSETLSLTCSVSNGSISSGGYYWSWLRQFPG KGLEWIGSIHYTGRTFYNPSLMGRTALSMDTSNNQFSLKVSSVTA ADTALYYCARELQWMFVVDPWGQGTLVTVSSASTKG
320	3B51HC	QVQLLQSGTEVKKPGSSVKVSCRASGWTLGNSPNSAIGWVRQAP GQGLEWIGRIIPILDVTNYAQKFQGRVTISADKSTNIAYMEISSLGSE DTAFYYCARVITGMTSPWYFYMDVWGEGTTVIVSSASTKG
321	3B56HC	QVQLVQSGGEVKKPGASVKVSCKVSGYSLTELSMHWVRQAPGK GLEWMGVFDPLEGDGVYVQKFRGRVIMTEDTSTDTAYMELTSLR SEDTAIYYCATKAKDYYYESSDYSPYYYYYMDVWGKGTTVTVSSA STKG
322	3B57HC	GSEVQLVESGAEVKKRGASVKVSCKVSGYSLTELSMHWVRQAPG KGLEWMGSFDPLDGDTIYAQKFQGRVTMTVDTSTDTAYMDLSSL RFEDTAVYYCATPSKAYYYDSPNYEGDFYMDVWGKGTTVIVSSA STKG
323	3B5HC	SVVQLVESGPGLVKPSETLSLTCSVSNGSISSGGYYWSWLRQFP GKGLEWIGSIHYTGRTMYNPSLMGRPALSMDTSNNQFSLKLRSVT AADTALYFCARDLQWIFVVDPWGQGTLVTVSSASTKG
324	3B61HC	SVDERLLEFGGRLVQPGGSLRLSCSASGFTFSNSAMSWVRQAPG KGLEWVSSILSSGVGTFYADSVKGRFTVSRDNSRNTLYLQMKSLR AEDTALYYCAKVQIQQLNFGVITDAGLDVWGKGTTLIVSSASTKG
325	3B6HC	QLQLKESGPGMVKPSETLSLTCSVSGASVVSANDYWGWIRQAPG KGLECIGIILYTGSTFYNPSLQSRVTISRDPSKNHVSLTLTSVTAADS AVYYCARIPYHSESYYNVVIGGFDVWGQGTRVTVSSASTKG
326	3B77HC	QVHLVQSGAEVKKPGSSVRVSCKASGWTFGDSVNSAITWVRQAP GQGLEWMGRFIPILGLSNYAQKFQDRVTINVDRSTNTAYMELSGL RSEDTAVYYCARLITGMNAPWFYYMDVWGKGTTITVSSASTKG
327	3B79HC	QVQLGQSGTEVKKPGFSVKVSCKASGGSSTAYGYSWVRQAPGQ GFEWMGRIIPFYGIITYAPKFQGRVTITADRSTSTVYMELTSLTFAD TALFFCARDFGDPRNGYYFDSWDQGLWLTVSSASTKG
328	3B84HC	SQVQLVESGPGLVKPSETLSLTCSVSNGSISSGGYYWSWLRQFP GKGLEWIGSIHYTGRTMYNPSLMGRPALSMDTSNNQFSLKLSSVT AADTALYFCARDLQWIFVVDPWGQGTLVTVSSASTKG
329	3B86HC	RVHSQVQLVESGPGLVKPSQTLSLTCTVSGGSISNGGHYWNWIR QHPGKGLEWIGHIYNIATTYYNPSLKSRVSISVDTSKNQFSLKLSSV TAADTAVYYCARGSGRWTIGARIYFDNWGQGALVAVSSASTKG
330	3B8HC	QVQLVQSGGEVRKPGSSVKVPCKISGNAFSNYGVNWVRQAPGQ GLEWVGRIIPVIGVAQHAPKFQGRVTITADKSTTTAYLELSSLRSDD TAVYFCAKDHGDPRTGYYFDYWGQGALVTVSSASTKG
331	3B93HC	QVHLVQSGAEVKKPGSSVRVSCEASGWTFGSVNSAITWVRQAPG QGLEWMGRTIPFLGISNYAQKFQGRVTITADKSTNIAYVDVTSLTS QDTAVYYCARLITGMTAPWFYYMDVWGKGTTVTVSSASTKG
332	3BNC101HC	EVQLVQSGSDVKKPGTTVTISCKADEDEDDFTAYNYFMHWVRQA PGQGLEWIGWINPRTGQPNHAKQLQGRVTLTRERSTSTVFMKLT NLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLIVSSASTKG
333	3BNC124HC	QSQVHLVQSGAEVKKPGSSVKVSCQASGGTFNTFAINWVRQAPG QGLEWVGGIIPVFGTASYAQKFQGRVTVTTDESRGTAYMELNSLR SEDTAVYYCARGQTDLNDDLWSDYSTPGFDYWGQGTLVTVSSAS TKG
334	3BNC130HC	RVQLGQSGAEVKKPGASVKVSCKVSGNSLTEFSIHWVRQAPGKG LEWMGGFDPEEGETVPAQKFKGRVTMTEDTSTNTAYMELSSLRS EDTAVYYCSTEPREMGTLTAGFEYWGQGTLVIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
335	3BNC149HC	QPQLVQSGSGAEVKKPGASVRISCEASEYNVFDHFMQWVRQAP MEGLEWMGWINPRGGYPSYSPTFQGRLTFTRQPSWDDSTITFHM ELRGLRHDDTAVYYCARPHSPDDAWSLDVWGRGTLVTVSSASTKG
336	3BNC177HC	LQPRVHSEVQLVESGAEVKKPGASVKVSCKVSGYTLSDLSMHWV RQAPGKGLEWMGGFDEEDGEITYAQKFQGRVSMTEDTSRDTAY MELSSLRSEDTAVYYCATAPRLELGELSSGFHYWGLGTLVTVSSA STKG
337	3BNC17HC	RVQLGQSGAEVKKPGASVKVSCKVSGNSLTEFSIHWVRQAPGKG LEWMGGFDPEEGETVPAQKFKGRVTMTEDTSTNTAYMELSSLRS EDTAVYYCSTEPREMGTLTAGFEYWGQGTLVIVSSASTKG
338	3BNC48HC	IWAPLIAVTFLVLHCESLGTCCCCQASGGTFNTFAINWVRQAPGQ GLEWVGGIIPVFGTASYAQKFQGRVTVTTDESRGTAYMELNSLRS EDTAVYYCARGQTDLNDDLWSDYSTPGFDYWGQGTLVTVSSAST KG
339	3BNC58HC	EVQLVESGAEVKKPGASVKVSCKVSGYTLSDLSMHWVRQAPGKG LEWMGGFDEEDGEITYAQKFQGRVSMTEDTSRDTAYMELSSLRS EDTAVYYCATAPRLELGELSSGFHYWGLGTLVTVSSASTKG
340	3BNC78HC	EVQLVESGAEVKKPGASVKVACKVSGKKLSDLSIHWVRQAPGKG LEWMGGFDEEDGKISYERKFQGRVTMTEDTARDTAFMEMSSLRS DDTAVYFCAAAPRLDLGELSSGFHFWGLGTLVSVSSASTKG
341	3BNC82HC	CNPRVHSEVQLVESGAEVKKPGASVKVACKVSGKKLSDLSIHWV RQAPGKGLEWMGGFDEEDGKISYERKFQGRVSMTEDTARDTAF MEMSSLRSDDTAVYFCAAAPRLDLGELSSGFHFWGLGTLVTVSS ASTKG
342	3BNC8HC	EVQLVESGAEVKKPGASVKVSCKVSGNSLTEFSIHWVRQAPGKG LEWMGGFDPEEGETVPAQKFKGRLTMTEDTSTNTAYMELSSLRS EDTAVYYCSTEPREMGTLTAGFEYWGQGTLVTVSSASTKG
343	3a426hc	QVQLQESGPGLVKPSETXSLTCSVSNGSISSGGYYWSWLRQFPG KGLEWIGSIHYTGRTMYNPSLMGRPALSMDTSNNQFSLKLSSVTA ADTALYFCARDLQWIFVVDPWGQGTLVTVSSASTKG
344	3a515hc	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTTYDISWVRQAPGQG LEWMGGILPDFGAPSYAQKFQDRVTITTDESSSTAYMELNSLRSE DTAIYYCARGRGDDFWSGESPSWYFDYWGQGTLVTVSSASTKG
345	3b46HC	GYSEVQLVQSGPGLVKPSQTLSLTCTVSGGSISNGGHYWNWIRQ HPGKGLEWIGHIYNIATTYYNPSLKSRVSISVDTSKNQFSLKLSSVT AADTAVYYCARGSGRWTIGARIYFDNWGQGALVAVSSASTKG
346	3ANC32HC	QVQLVQSGADVKKPGATVTVSCKTDEDEDDFRAHLMQWMRQAP GQRLEWVGWIKPQTGQPSYGQKFQGRVTLTREVSTSTVFLQLRN LRSDDTAVYYCARPRGGRDNWSFHVWGRGTLVTVSSASTKG
347	3ANC3HC	QVQLVQSGADVKKPGASVTVSCKTDEDEDDFRAHLVQWMRQAP GQRLEWVGWIKPQTGQPSYAQKFQGRVTLTREVSTSTVFLQLRN LRSDDTAVYYCARPRGGRDNWSFHVWGRGTLVTVSSASTKG
348	3ANC41HC	QVQLVQSGAAVKKPGASVKVSCETYGYTFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLK FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
349	3ANC42HC	QVQLVQSGAAVKKPGASVKVSCETYGYTFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLK FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
350	3ANC66HC	QVQLVQSGAAVKKPGASVKVSCETYGYKFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLR FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
351	3ANC70HC	QVQLVQSGAAVKKPGASVKVSCETYGYKFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLR FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
352	3ANC75HC	QVQLVQSGAAVKKPGASVKVSCETYGYTFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLK FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
353	3ANC79HC	QVQLVQSGAAVKKPGASVKVSCEAYGYKFTDHFMHWWRQAPGQ GLEWMGWINPYTSAVNYSPKYQGRVTMTRDTFLETVYMELRGLR VDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
354	3ANC87HC	QVQLVQSGGAVKKPGASVKVSCETYGYTFTDHFMHWWRQAPGQ GLEWMGWINPYSSAVSYSPRYQGRVTMTRDTFLETVYMELRGLK FDDTAIYYCATPKSGRDYWSFDLWGQGTLVTVSSASTKG
355	3ANC8HC	QVQLVQSGADVKKPGASVTVSCKTDEDEDDFRAHLVQWMRQAP GQRLEWVGWIKPQTGQPSYAQKFQGRVTLTREVSTSTVFLQLRN LRSDDTAVYYCARPRGGRDNWSFHVWGRGTLVTVSSASTKG
356	3ANC96HC	QVQLVQSGADVKKPGASVTVSCKTDEDEDDFRAHLVQWMRQAP GQRLEWVGWIKPQTGQPSYAQKFQGRVTLTREVSTSTVFLQLRN LRSDDTAVYYCARPRGGRDNWSFHVWGRGTLVTVSSASTKG
357	3B106HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRHASWDFDTFSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGTQVIVSSASTKG
358	3B16HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPCQFQGRVSLTRHASWDFDTFSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTK
359	3B180HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPCQFQGRVSLTRQASWDFDTISFYMDLK ALRLDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
360	3B183HC	QVRLLQSGAAVTKPGASVRVSCEASGYEIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDSYSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGSQVTVSSASTKG
361	3B191HC	QVRLLQSGAAVTKPGASVRVSCEASGYEIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDSYSFYMDL KALRSDDTGVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
362	3B21HC	QVRLLQSGAAVTKPGASVRVSCEASGYEIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDSYSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
363	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG PQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
364	3BBM60	QVHLSQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARQRSDYRDFDVWGSGTQVTVSSASTKG
365	3BBM60	QVHLSQSGAAVTKPGASVRVSCEASGYKIRDYSIHWWRQAPGQG LQWVGWINPQTGQPNIPRPFQGRISLTRQASWDFDTFSFYMDLE ALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
366	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLE ALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
367	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
368	3BBM60	QVHLSQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDTYSFYMGL KAVRSDDTAIYFCARQRSDFWDFDVWGSGTQVTVSSASTKG
369	3BBM60	QVHLSQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
370	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISGHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
371	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNIPRQFQGRISLTRQASGDFDTFSFYMDLKA LRSDDTAVYFCARQRSDYWDFGVWGSGTQVTVSSASTKG
372	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDIDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
373	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
374	3BBM60	QVHLSHSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
375	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
376	3BBM60	QVHLSQSGAVVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
377	3BBM60	QVHLSQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARHRSDYWDFDVWGSGTQVTVSSASTKG
378	3BNC101HC	EVQLVQSGSDVKKPGTTVTISCKADEDEDDFTAYNYFMHWVRQA PGQGLEWIGWINPRTGQPNHAKQLQGRVTLTRERSTSTVFMKLT NLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLIVSSASTKG
379	3BNC102HC	QPQLVQSGSGAEVKKPGASVRISCEASEYNVFDHFMQWVRQAP GQGLEWMGWINPRGGYPSYSPRFQGRLTFTRQPSWDDSSVTFH MELRGLRHDDTAVYYCARPHSPDDAWSLDVWGRGTLVTVSSAST KG
380	3BNC104HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
381	3BNC105HC	HVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDTFSFYMDL KALRLDDTAIYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
382	3BNC106HC	VVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
383	3BNC107HC	QVQLVQSGAALKKPGASLRISCQAYGYKFTDYLIHWWRQAPGQG LEWIGWIKPETGQPSYSYKFQGRVSLTRDTFEEILFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGGGSQVLVSSASTKG
384	3BNC108HC	QVQLVQSGTAVKKPGASVRVSCQASGYTFTDYFIYWWRQAPGQ GLEWLGWINPRTSQPSYPYRFQGRVTLTRDIFEEMLYMDLRGLRS DDTGIYFCARRHSDYCDFDIWGSGTQIIVSSASTKG
385	3BNC10HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
386	3BNC114HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
387	3BNC117HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRHASWDFDTFSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
388	3BNC126HC	QPQLVQSGSGAEVKKPGASVRISCEASEYNVFDHFMQWVRQAP GQGLEWMGWINPRGGYPSYSPTFQGRLTFTRQPSWDDSTITFH MELRGLGHDDTAVYYCARPHSPDDAWSLDVWGRGTLVTVSSAS TKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
389	3BNC127HC	EVQLVESGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQA PGQGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKLT NLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
390	3BNC134HC	QVQLVQSGAALKKPGASLRISCQAYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYKFQGRVSLTRDTFQEILFMNLRGLRSD DTAIYFCARRHSDYCDFDVWGSGSQILVSSASTKG
391	3BNC140HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
392	3BNC141HC	VVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
393	3BNC142HC	QVQLVQSGAALKKPGASVRISCQAYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYKFQGRVTLTRDTFEEIHFMDLRGLRYD DTATYFCARRHSDYCDFDVWGSGSQVSVSSASTKG
394	3BNC148HC	QVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSRGRGTSLTVSSASTKG
395	3BNC149HC	QPQLVQSGSGAEVKKPGASVRISCEASEYNVFDHFMQWVRQAP MEGLEWMGWINPRGGYPSYSPTFQGRLTFTRQPSWDDSTITFHM ELRGLRHDDTAVYYCARPHSPDDAWSLDVWGRGTLVTVSSASTKG
396	3BNC151HC	QVQLVQSGATLKKPGASVRISCQAYGYKFTDHLIHWWRQAPGQG LEWIGWIKPETGQPSYAYKFQGRVSLTRDTFEEILFMDLRGLRSD DTAIYFCARRHSDYCDLDVWGGGTQLLVSSASTKG
397	3BNC153HC	QVQLVQSGAALKKPGASLRISCLTYGYKFTDHLIYWWRQAPGQGL EWIGWIKPETGQPSYSYRFQGRVSLTRDTFEEIVFMDLRGLRSDD TAIYFCARRHSDYCDFDVWGSGSQVIVSSASTKG
398	3BNC156HC	QVQLVQSGAALKKPGASLRISCQTYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYRFQGRVSLTRDTFEEIVFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGGGSQVIVSSASTKG
399	3BNC158HC	QVQLVQSGAALKKPGASLRISCQTYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYRFQGRVSLTRDTFEEIVFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGSGSQVIVSSASTKG
400	3BNC159HC	QVQLVQSGAALKKPGASVRISCQTYGYKFTDHLIHWWRQAPGQG LEWIGWIKPDTGQPSYSSRFQGRVSLTRDTFEEIVFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGSGSQVLVSSASTKG
401	3BNC15HC	QVQLVQSGAALKKPGASLRISCQTYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYRFQGRVSLTRDTFEEIVFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGSGSQVLVSSASTKG
402	3BNC173HC	QVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
403	3BNC175HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
404	3BNC176HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRHASWDFDTFSFYMDL KGLRSDDTAIYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
405	3BNC181HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYDYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
406	3BNC186HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
407	3BNC18HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
408	3BNC193HC	QVQLVQSGTAVKKPGASVRVSCQASGYTFTDYFIYWWRQAPGQ GLEWLGWINPRTSQPSYPYRFQGRVTLTRDIFEEMLYMDLRGLRS DDTGIYFCARRHSDYCDFDIWGSGTQIIVSSASTKG
409	3BNC196HC	QVQLLQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRISLTRQASWDFDTFSFYMDLK ALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
410	3BNC20HC	QVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
411	3BNC29HC	WQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
412	3BNC31HC	QVQLVQSGAALKKPGASVRISCQTYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYRFQGRVSLTRDTFEEIVFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGSGSQVLVSSASTKG
413	3BNC33HC	WQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
414	3BNC42HC	QVQLVQSGAALKKPGASVRISCQAYGYKFTDYLIHWWRQAPGQG LEWIGWIKPETGQPSYSYKFQGRVTLTRDTFEEILFMDLRGLRSDD TAIYFCARRHSDYCDFDVWGSGSQVIVSSASTKGA
415	3BNC44HC	EVQLVESGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQA PGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKLT NLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
416	3BNC45HC	VVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
417	3BNC53HC	QVQLVQSGAALKKPGASVRISCQAYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYAYKFQGRVTLTRDTFEEIHFMDLRGVRND DTATYFCARRHSDYCDFDVWGSGSQVIVSSASTKG
418	3BNC54HC	EVQLVESGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQA PGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKLT NLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
419	3BNC55HC	QVQLVQSGTAVKRPGASVRVSCQASGYTFTDYFIYWWRQAPGQ GLEWLGWINPLTSQPSYPSRFQGRLTLTRDTFDEMLYMDLRGLR SDDTGIYFCARRHSDYCDFDIWGSGTQIIVSSASTKG
420	3BNC59HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
421	3BNC60HC	QVHLSQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDTYSFYMDL KAVRSDDTAIYFCARQRSDFWDFDVWGSGTQVTVSSASTKG
422	3BNC62HC	QVRLLQSGAAVTKPGASVRVSCEASGYEIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDSYSFYMDL KALRSDDTGVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
423	3BNC64HC	QVHLSQSGAAVTKPGASVRVSCEASGYKISDHFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDTYSFYMDL KALRSDDTAIYFCARQRSDFWDFDVWGSGTQVTVSSASTKG
424	3BNC65HC	QVQLLPFGGAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPCQFQGRVSLTRPASWDFDTISFYMDLK ALRLDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
425	3BNC66HC	QVQLVQSGAALKKPGASLRISCQTYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYRFQGRVSLTRDTFEEIAFMDLRGLRSD DTAIYFCARRHTDYCVFDVWGSGSQIIVSSASTKG

TABLE A-continued

Seq ID No.	Antibody	Heavy Chain Amino Acid Sequence
426	3BNC6HC	QVQLVESGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
427	3BNC72HC	QVQLVQSGAALKKPGASLRISCQTYGYKFTDHLIYWWRQAPGQG LEWMGWIKPETGQPSYSYRFQGRVSLTRDTFEEIVFMDLRGLRS DDTAIYFCARRHSDYCDFDVWGSGSQVIVSSASTKG
428	3BNC75HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRHASWDFDTFSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVYSASTKG
429	3BNC79HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRQASWDFDTISFYMDLK ALRLDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
430	3BNC81HC	RQVQLVQSGAALKKPGASLRISCQAYGYKFTDHLIYWWRQAPGQ GLEWIGWIKPETGQPSYSYKFQGRVSLTRDTFQEILFMDLRGLRS DDTAIYFCARRHSDYCDFDVWGSGSQILVSSASTKG
431	3BNC84HC	QVQLVQSGAALKKPGASLRISCQAYGYKFTDHLIYWWRQAPGQG LEWIGWIKPETGQPSYSYKFQGRVSLTRDTFQEILFMDLRGLRSD DTAIYFCARRHSDYCDFDVWGSGSQVIVSSASTKG
432	3BNC86HC	QVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
433	3BNC87HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRQFQGRVSLTRHASWDFDTFSFYMDL KALRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG
434	3BNC89HC	QVQLVQSGTAVKRPGASVRVSCQASGYTFIDHFIYWWRQAPGQG LEWLGWINPLTSQPSYPSRFQGRLTLTRDTFDEMLYMDLRGLRSD DTGIYFCARRHSDYCDFDIWGSGTQIIVSSASTKG
435	3BNC91HC	QVQLLQSGAVVTKPGASVRVSCEASGYKIRDYFIHWWRQAPGQG LQWVGWINPQTGQPNIPRPFQGRVTLTRHASWDFDTFSFYMDLK ALRSDDTAIYFCARRRSDYCDFDVWGSGTHVTVSSASTKG
436	3BNC92HC	EVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
437	3BNC94HC	QVQLVQSGSDVRKPGATVTVSCKADEDEDDFTAYNYFMHWVRQ APGHGLEWIGWINPRTGQPNHAKQFQGRVTLTRERSTSTVFMKL TNLRLDDTAVYFCARPLRGGDTWHYHSWGRGTSLTVSSASTKG
438	3BNC95HC	QVQLLQSGAAVTKPGASVRVSCEASGYNIRDYFIHWWRQAPGQG LQWVGWINPKTGQPNNPRLFQGRVSLTRHASWDFDTFSFYMDLK AVRSDDTAVYFCARQRSDYWDFDVWGSGTQVTVSSASTKG

TABLE B

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
439	8ANC131KC	EIVLTQSPATLSLSPGERATLSCRASQGLNFVVWYQQKRGQAPR LLIHAPSGRAPGVPDRFSARGSGTEFSLVISSVEPDDFAIYYCQEY SSTPYNFGPGTRVDRKRTVAAPSVFIFPPSDEQ
440	8ANC134KC	EIVLTQSPATLSLSPGERATLSCRASQGLNFVVWYQQKGGQAPR LLIHGPTDRAPGVPDRFSARGSGTEFSLVISSVEPDDFALYYCQE YSSTPYNFGPGTRVDRKRTVAAPSVFIFPPSDEQ
441	8ANC13KC	EIVLTQSPATLSLSPGERATLSCRASQGLNFVVWYQQKRGQAPR LLIHGPSHRAPGVPDRFSARGSGTEFSLVISSVEPDDFAIYYCQE YSSTPYNFGPGTRVDRKRTVAAPSVFIFPPSDEQ
442	8ANC45KC	EIVLTQSPATLSLSPGERATLSCRASQGVNFVVWYQQKRGQAPR LLIYGPSNRAPGVPDRFSARGSGTEFSLVISSVEPDDFALYYCQE YSSTPYNFGPGTRVDRKRTVAAPSVFIFPPSDEQ

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
443	8ANC50KC	EIVLTQSPTTLSLSPGERATLSCRASQGVNLVVWYQQKRGQAPR LLIYGPSDRAPGVPDRFSARGSGTEFSLVISSVEPDDFALYYCQE YSSTPYNFGTGTRVDRKRTVAAPSVFIFPPSDEQ
444	8ANC88KC	EIVLTQSPATLSLSPGERATLSCRASQGLNFVVWYQQKRGQAPR LLIHAPSDRAPGVPDRFSARGSGTDFSLVISSVEPDDFAIYYCQEY SSTPYNFGPGTRVDRKRTVAAPSVFIFPPSDEQ
445	8anc182kc	EIVLTQSPATLSLSPGERATLSCRASQGVNFVVWYQQKRGQAPR LLIYGPSDRAPGVPDRFSARGSGTEFSLVISSVEPDDFALYYCQE YSSTPYNFGTGTRVDRKRTVAAP
446	8anc192kc	EIVLTQSPATLSLSPGERATLSCRASQGVNFVVWYQQKRGQAPR LLIYGNSDRVPGVPDRFSARGSGTEFSLVISSVEPDDFALYYCQE YSSTPYNFGPGTRVDRKRTVAA
447	8ANC14KC	SEIVLTQSPATLSLSPGERATLSCRASQSINNYLAWYQQKPGQAP RLLIYDASNRATGIPARFSGGGSGTDFTLTISSLEPEDFAVYYCQQ RANWRLLTFGGGTKVEIKRTVAAPSVFIFPPSDEQ
448	8ANC16KC	EIVMTQSPDTLSVSPGERATLSCRASQSVNSNLAWYQQKPGQA PRLLIYGASTRATAVPARFSGSGSGTEFTLTISSLQSEDSAVYYC QQYYQWLSYTFGQGTKLEIKRTVAAPSVFIFPPSDEQ
449	8ANC195KC	DIQMTQSPSTLAASIGGTVRVSCRASQSITGNWVAWYQQRPGKA PRLLIYRGAALLGGVPSRFSGSAAGTDFTLTIGNLQAEDFGTFYC QQYDTYPGTFGQGTKVEVKRTVAAPSVFIFPPSDEQ
450	8ANC24KC	SEIVMTQSPATLSMSPGERATLSCRASLSVNTNLAWYQQKPGQA PRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFALYYCQ QYNHWPQTFGQGTKVEIKRTVAAPSVFIFPPSDEQK
451	8ANC5KC	DIQMTQSPPSLSASVGDRVTITCQASQDINNFLNWYQQKPGKAP RLLIYDASNLESGVSSRFSGSRSGTDFTLTISSLLPEDIATYSCQQ YSNLPYTFSQGTKLEIKRTVAAPSVFIFPPSDEQ
452	12a12kc	DIQMTQSPSSLSASVGDRVTITCQAGQGIGSSLQWYQQKPGKAP KLLVHGASNLHRGVPSRFSGSGFHTTFSLTISGLQRDDFATYFCA VLEFFGPGTKVEIKRTVAAPSVFIFPPSDEQLKS
453	12a13kc	DIQMTQSPSSLSASVGDRVTITCQAGQGIGSSLQWYQQKPGKAP KLLVHGASNLHRGVPSRFSGSGFHTTFSLTISGLQRDDFATYFCA VVEFFGPGTKVDIKRTVAAPSVFIFPPSDEQL
454	12a16kc	DIQMTQSPSSLSASVGDRVTITCQASQGIGSSLQWYQQKPGRAP NLLVHGASKLHRGVPSRFSGSGFHTTFSLTISGLQRDDFATYFCA VLEFFGPGTKVEIKRTVAAPSVFIFPPSDEQLK
455	12a1kc	DIQMTQSPSSLSASVGDRVSINCQAGQGLGSSLNWYQQKPGRA PKLLVHGASNLQRGVPSRFSGSGFHTTFTLTISSLQPDDVATYFC AAFQWFGPGTKVEIKRT
456	12a20kc	DIQMTQSPSSLSASVGDRVSIHCQAGQGIGSSLNWYQQKPGRAP RLLVHGASNLQRGVPSRFSGSGFHTTFTLTISSLQPDDVATYWC AALEFFGPGTKVEI
457	12a21kc	DIQMTQSPSSLSASVGDRVTINCQAGQGIGSSLNWYQKKPGRAP KLLVHGASNLQRGVPSRFSGSGFHTTFTLTISSLQPDDVATYFCA VFQWFGPGTKVDIKRTVAAPSVFIFPPSDEQLK
458	12a22kc	DIQMTQSPSSLSASVGDRVTITCQAGQGIGSSLNWYQQKPGRAP KLLVYGASNLQRGVPSRFSGSGFHTTFTLTISSLQPEDFATYFCS VYEFLGPGTKVEIKRTVAAPSVFIFPPSDEQ
459	12a23kc	DIQMTQSPSSLSVSVGDRVSITCRATQGIGNSLNWYQQKPGKAP KVLIYGTTKLHGGVPSRFSGGGSGSTGTLTIDSLQPEDIATYFCQL FEFFGPGTKVEIKRTVAAPSVFIFPPSDEQ
460	12a27kc	DIQMTQSPSSLSASVGDRVTITCQASQGIGSSLQWYQQKPGRAP NLLVHGASNLHRGVPSRFSGSGFHTTFSLTISGLQRDDFATYFCA VLEFFGPGTKVDIKRTVAAPSVFIFPPSDEQ

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
461	12a46kc	DIQMTQSPSSLPASVGDTVTITCQAGQGIGSSLQWYQQRPGRAP NLLVYDASNLQRGVPSRFTGTGFHTTFTLTIRGLRPEDFGTYFCA SLEFFGPGTKVDIKRTVAAPSVFIFPPSDEQ
462	12a55kc	YIQMTQSPSSLSASIGDRVTITCQAGQGIGSSLNWYQQKPGKAPK LLVHGASNLQRGVSSRFSGSGFHTTFTLTISSLRPEDVGTYFCEV YEFIGPGTKVDIKRTVAAPSVFIFPPSDEQ
463	12a56kc	DIQMTQSPSSLSASVGDRVSINCQAGQGIGSSLNWYQQKRGKAP KLLVHGASTLQRGVPSRFSGSGFHTTFTLTISSLQPDDVATYFCE SFQWFGPGTKVEIKRTVAAPSVFIFPPSDEQ
464	12a6kc	DIQMTQSPSSLSASVGDRVTITCQASQGIGSSLQWYQQKPGRAP KLLVHGASNLHRGVPSRFSGSGFHTSFTLTISSLQPDDVATYFCA VLEFFGPGTKVEIKRTVAAPSVFIFPPSDEQ
465	12a7kc	DIQMTQSPSSLSASVGDRVSIHCQAGQGIGSSLKWYQQKSGRAP RLLVHGASNLQRGVPSRFSGSGFHTTFTLTISSLQPDDVATYWC AVLEFFGPGTKVEIKRTVAAPSVFIFPPSDEQ
466	LSSB2339LC	QSVLTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APNLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEAFYF CATYDSDGSVRLFGGGTTLTVLSQPKAAPSVTLFPPSNGGR
467	LSSB2351LC	QSALTQTPSVSGAPGQRVTISCSGGPSNVGGNYVYWYQQFPGA APKLLIRRDDQRPSGVPDRFSGSKSGNSASLAISGLRLDDEAYYF CATYDSGWSIRLFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
468	LSSB2364LC	SQAVVTQPPSVSGAPGQRVTISCSGGPSNVGGNLVYWYKQFPG TAPKLLIRRDDQRPSGVPDRFSGSKSGNSASLAISGLRPDDEAFY FCATYDSHGSIRLFGGGTLLTVLSQPKAAPSVTLFPP
469	LSSB2367LC	QTVVTQPPSASGTPGQRVTISCSGGGSNIGGNLVSWYQHFPGA APKLLIYRNDQRPSGVPDRFSGSKSGTSASLTISGLRSDDEATYF CAAYDCTLSLRLFGGGTTLNVLSQPKAAPSVTLFPPSSEEL
470	LSSB2490LC	QSALTQPPSVSGTPGQNVTISCSGGGSNVGGNLVSWYQHFPGA APKLLIHRDNQRPSGVPDRFSVLKSGNSASLAISGPRSDDEAFYF CAVYDSSLSLGLFGGGTKLTVLSQPKAAPSVTLFPPSSEEL
471	LSSB2530LC	QSALTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APTLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEGFYF CATYDSDGSIRLFGGGTALTVLSQPKAAPSVTLFPPSSEELK
472	LSSB2554LC	NFMLTQAPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQYPGT APKLLILRDDQRPSGVPDRFSASKSGNSASLAISELRPDDEAFYF CATYDSDGSIRLFGGGTALTVLSQPKAAPSV
473	LSSB2586LC	NFMLTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APNLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEAFYF CATYDSDGSIRLFGGGTTLTVLSQPKAAPSVTLFPP
474	LSSB2612LC	QSVLTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APKLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEAFYF CATYDSDGSIRLFGGGTALTVLSQPKAAPS
475	LSSB2640LC	QLVLTQPPSVSGTPGQNVTISCSGGGSHVGGNLVSWYQHFPGA APKLLIHRDNQRPSGVPDRFSALKSGNSASLAISGLRSDDEAFYF CAVYDSSLSLGLFGGGTKLTVLSQPKAAPSVT
476	LSSB2644LC	RTVVTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGT APKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYY CQSYDSSLSGSGVFGTGTKVTVLGQPKANPTVTLFPPSSEEL
477	LSSB2666LC	QSALTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APKLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEALYF CATYDSDGSIRLFGGGTALTVLSQPKAAPSVTLFPPGWEE
478	LSSB2680LC	QPVLTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APNLLILRDDQRPSGVPDRFSASKSGNSASLAITGLRPDDEAFYF CATYDSDGSIRLFGGGTALTVLSQPKAAPSVTLFPP

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
479	LSSB2683LC	QSALTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APNLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEAFYF CATYDSDGSIRLFGGGTTLTVLSQPKAAPSVTLF
480	LSSB344LC	QSALTQTPSVSGAPGQRVTISCSGGPSNVGGNYVYWYQQFPGA APKLLIRRDDQRPSGVPDRFSGSKSGNSASLAISGLRLDDEAYYF CATYDSGWSIRLFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
481	LSSNEC107LC	QLVLTQPPSVSATPGQTVTISCSGSGSNVGGNHVYWYRQLPGA APTLVISKTDHRPSRVPDRFSGSKSGNSASLAISGLRPDDEAAYF CATYDTGLSLRLFGGGTRLAVLSQPKAAPSVTLFPPSSEEL
482	LSSNEC108LC	QSALTQPPATSGTPGQRVTISCSGGGSNVGGNLVSWYQQFPGA APKLILHRDGQRPSGVPDRFSASKSGTSASLTISGLRSDDEATYF CAAFDSALSLPLFGGGTKLTVLSQPKAAPSVTLFPPSSEEL
483	LSSNEC117LC	QSVLTQVLSVSGTPGQRVIISCSGTSSNVGGNLVSWYQHLPGAA PRLLIHRDDQRPSGVPDRFSGSKSGNSASLVISGLRSDDEADYF CGAYDSTFSLPVFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
484	LSSNEC118LC	NFMLTQPPSVSATPGQTVTISCSGSGSNVGGNHVYWYRQLPGA APTLVISKTDHRPSRVPDRFSGSKSGNSASLAISGLRPDDEAVYF CATYDTGLSLRLFGGGTRLTVLSQPKAAPSVTQFPPSSEE
485	LSSNEC122LC	QSALTQPPSVSATPGQTVTISCSGSGSNVGGNHVYWYRQLPGA APTLLISKTNHRPSQVPDRFSASKSGNSASLAISGLRPDDEADYF CGTYDTSLSLRLFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
486	LSSNEC24LC	QSALTQPPSASGTPGQRVTISCSGGGSNIGGNLVSWYQHFPGTA PKLLIYRNDQRPSGVPDRFSGSKSGTSASLTISGLRSDDEATYFC AAYDSSLSLRLFGGGTTLNVLSQPKAAPSVTLFPPSSEEL
487	LSSNEC2LC	QSALTQPPSVSGTPGQNVTISCSGGGSDVGGNLVSWYQHFPGA APKLLIHRDNQRPSGVPDRFSALKSGNSASLAISGLRSDDEAFYF CAVYDSSLSLGLFGGGTKLTVLSQPKAAPSVTLFPPSSEEL
488	LSSNEC33LC	QAVVTQPPSVSATPGQTVTISCSGSGSNVGGNHVYWYRQLPGA APTLLISKTNRRPSQVPDRFSGSKSGNSASLAISGLRPDDEADYF CATYDTDLSLRLFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
489	LSSNEC46LC	QSALTQPPAASGAPGQRVTISCSGGGSNVGGNLVSWYQQFPGA APKLILHRDGQRPSGVPDRFSASKSGTSASLTISGLRSDDEATYF CAAYDSAVSLPVFGGGTKLTVLSQPKAAPLVT
490	LSSNEC48LC	NFMLTQPPSASGTPGQRVTISCSGGGSNIGGNLVSWYQHFPGA APKLLIYRNDQRPSGVPDRFSGSKSGTSASLAISGLRSDDKATYF CAAYDSTLSLRLFGGGTTLTVLSQPKAAPSVTLFPPSSEE
491	LSSNEC52LC	QSVLTQVLSVSGTPGQRVIISCSGTSSNVGGNLVSWYQHLPGAA PRLLIHRDDQRPSGVPDRFSGSKSGNSASLVISGLRSDDEADYF CAAYDSTFSLPVFGGGTRLTVLSQPKAAPSVTLFPPSSE
492	LSSNEC56LC	QSALTQPPSVSATPGQTVTISCSGSGSNVGGNHVYWYRQLPGA APTLLISKTDHRPSRVPDRFSASKSGNSASLAISGLRPDDEAIYFC ATYDTGLSLRLFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
493	LSSNEC60LC	QSALTRTPSVSGAPGQRVTISCSGGPSNVGGNYVYWYQQFPGA APKLLIRRDDQRPSGVPDRFSGSKSGNSASLAISGLRLDDEAYYF CATYDSGWSIRLFGGGTRLTVLSQPKAAPSVTLFPPSSEEL
494	LSSNEC70LC	QSALTQAPSASGTPGQRVTISCSGGGSNIGGNLVSWYQHFPGA APKLLIYRNDQRPSGVPDRFSASKSGTSASLAISGLRSDDEATYF CAAYDSTLSLRLFGGGTTLAVLSQPKA
495	LSSNEC72LC	NFMLTQPPSVSGAPGQRVTISCSGGPSNVGGNLVYWYKQFPGT APKLLIRRDDQRPSGVPDRFSGSKSGNSASLAISGLRPDDEAFYF CATYDSHGSIRLFGGGTLLTVLSQPKAAPSVTLFPPSSEEL
496	LSSNEC7LC	QLVLTQPPSVSGAPGQRVTISCSGGPSNVGGNLVYWYKQFPGT APKLLIRRDDQRPSGVPDRFSGSKSGNSASLTISGLRPDDEAFYF CATYDSQGSTRLFGGGTVLTVLSQPKAAPSVTLFPPSSEEL

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
497	LSSNEC89LC	QSALTQPPSVSGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APKLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEAFYF CATYDSQGSFRVFGGGTALTVLSQPKAAPSVTLYPPSSEE
498	LSSNEC94LC	NFMLTQPPSASGAPGQRVTISCSGGPSNVGGNYVYWYRQFPGT APNLLILRDDQRPSGVPDRFSASKSGNSASLAISGLRPDDEAFYF CATYDSDGSIRLFGGGTTLTVLSQPKAAPSVTLFPPSSEEL
499	LSSNEC9LC	QVLSVSGTPGQRVIISCSGTSSNVGGNLVSWYQHLPGAAPRLLIH RDDQRPSGVPDRFSGSKSGNSASLVISGLRSDDEADYFCAAYDS TFSLPVFGGGTRLTVLSQPKAAPSVTLYAPSSEE
500	LSSB2066KC	PVTLSASVGDRVTITCRASEDISKYLNWYQHKPGKAPKLLIYTASS LETGVPSRFSGSGSGTDFSLTISSLQPDDFATYYCQQSYTSSVTF GQGTRVEVKRTVAAPSVFIFPPSDEQ
501	LSSB2080KC	PATLAVSPGERATISCKSSQNLLYSANNQHSLAWYQQRPGQPPK LLLYWASTRLSGVPDRFSGSGSGTDFTLTISNLQAEDVAVYYCQ QYYSPPPTFGQGTKVEIRRTVAAPSVFIFPPSDEQL
502	LSSB2133KC	TLSASVGDRVTITCRASQSINNYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFVTYYCQQTYSNPRMF GQGTKVEIKRTVAAPSVFIFPPSDEQ
503	LSSB2182KC	KAPATLSLSPGERATLSCRASQSVGSDLAWYQQKPGQAPRLLIY DASNRATAIPARFSGSGSGTDFTLSISSLEPEDFAVYFCQQRYDKI TFGQGTRLEIQRTVAAPSVFIFPPSDEQ
504	LSSB331KC	RGPVTLAVSLGERATITCKSSQSVLVHSNNKNYLSWYQQKPGQP PKLLIYWASTRESGVPERFSGSGSGTDFTLSISSLQAEDVAVYYC HQYFSTPRTFGQGTKVEIKGTVAAPSVFIFPPSDEQL
505	3A124KC	SEIVLTQSPATLSLSPGESATLSCRASQSLSSSLAWYQQKPGQAP RLLIYDTSDRATGIPARFSGRGSGTDFTLTISSLEPEDFAVYYCQQ RSNWAITFGQGTRLEIKRTVAAPSVFIFPPSD
506	3A125KC	EIVLTQSPGTLSLSPGEXATLSCRASQTISNNYLXWYQQKAGQAP RLLIYGASSGATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGLSPWTFGRGTKVEIKRTVAAPSVFIFPPSD
507	3A140LC	QSALTQPRSVSGSPGQSVTISCTGTSSDVGAYNYVSWYRQHPG KAPKLMINDVSKRPSGVPDRFSGSKSGNTASLTISGLQAEDEADY YCCSYAGTYSYVFGTGTKVTVLGQPKANPTVTLFPPSSEEL
508	3A144KC	APVTLSASVGDTVTITCRASQPIATFLNWYQHKPGQAPKLLIYAAS TFQRGAPSRYSGSGSGTDFTLTINSLQPEDLATYYCQQTFTDPVT FGQGTRLEIKRTVAAPSVFIFPPSD
509	3A160KC	DIQMTQSPASLSASVGDRVTITCRASQGISHYLAWYQQKPGKVP RLLIYAASRLQSGVTSRFSGSGSGTEFTLTISSLLPEDAAVYFCQK YDTDPMTFGQGTRLEIKRTVAAPSVFIFPPSD
510	3A18KC	DIQMTQSPSSLSASIGDRVTITCRANQHIRSFLNWYQQTPGKAPK LLIYAASTLQRGVPSRFSGSGSGTDFTLTITSLEREDLATYYCQQT YTSPITFGQGTRLEIKRTVAAPSVFIFPPSDE
511	3A204KC	EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQA PRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQ QYATSSLYTFGQGTKLEIKRTVAAPSVFIFPPSD
512	3A228KC	LSVSLGERATINCKSSQSILYSSDKKNYLAWYQQKIGQPPKLLLY WASTRESGIPDRFSGSGSGSDFTLTISSLQPEDVAVYYCQQYYIS PFTFGPGTKVDLKRTVAAPSVFIFPPSD
513	3A233LC	NFMLTQPASVSGSPGQSITLSCTGTTSDVRDSNFVSWYQQVPG KAPKLIIYDVSARPSGVSFRFSGSKSGNTASLTISGLQAEDEALYY CSSFTPTNTLVFGGGTKLTVLGQPKAAPSVT
514	3A244LC	SQSVVTQEPSLTVSPGGTVTLTCGPSTGAVTSGFYPHWFQQKP GQAPRALIYSTSNKYSWTPARFSGSLLGGKAVLTLSDVQPDDEA EYYCLLLLYYGGPWIFGGGTKLTVLVS

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
515	3A255LC	QAVVTQEPSLTVSPGGTVTLTCASSTGAVTSGFYPHWFQQKPG QAPRALIYSTSNRYSWTPARFSGSLLGGKAALTLSGVQPEDEAE YYCLLLPYYGGPWIFGGGTKLTVLGQPKAAPSVTLFPPSSEEL
516	3A296KC	EIVMTQSPATLSVSPGDRATLSCRASQSVSTNLAWYQQKPGQAP RLLIYGASTRATGIPATFSGSGFATEFTLTISSLQSEDFAVYYCQQ YNNWPPAFGQGTKVEIKRTVAAPSVFIFPPSD
517	3A334LC	QSVLTQPPSASGSPGQSITISCTGTSSDVGGYNYVSWYQQPPGK APKVIIYEVSKRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYY CSSYAGSNNFVFGTGTEVTVVGQPKANPTVTLFPPSSEELL
518	3A366KC	SLSASVGDRVTITCRASESISFYLNWYQQKPGKAPELLIFATSTLH SGVPSRFSGSGSGTDFTLTISSLQLEDFATYYCQQSSSTPFTFGG GTKVEIKRTVAAPSVFIFPPSD
519	3A384KC	DIQMTQSPSSLSAYVGDRVTITCRASQNINTYLNWYQQRPGKAP KLLIYAASTLQSGVPSRFSGSGSGTDFTLTISNLETEDFAVYYCQQ TYRSVTFGQGTKLEIKRTVAAPSVFIFPPSD
520	3A419KC	LSAYVGDRVTITCRASQNINTYLNWYQQRPGKAPKLLIYAASTLQ SGVPSRFSGSGSGTDFTLTISNLETEDFAVYYCQQTYSSVTFGQ GTKLETRRTVAAPSVFIFPPSD
521	3A461KC	SEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPVQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC QQYGTLHPRTFGQGTKVEIKRTVAAPSVFIFPPSD
522	3A474KC	EIVLTQSPGTLSLSPGERATLSCRASQSISSNYLAWYQQKPGQAP RLLIYGASTRATGIPDRFSGSGSGTDFTLSISRLEPEDIAVYYCHQ YGSSQRFGQGTKVEIKRTVAAPSVFIFPPSD
523	3A518KC	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAP KLLIYAASSLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ QSSSKPFTFGGGTKVEIKRTVAAPSVFIFPPSD
524	3A539LC	NFMLTQPASVSGSPGQSITISCSGTGSDIGVYNYVSWYQQHPGK APRLMIYDVTNRPSGVSNRFSGSKSGFTASLTISGLQGDDEADYY CSSYSSTNTYVFGTGTHVTVLGQPKANPTVTLFPPSSEEL
525	3A576LC	QSALTQPPSASGTPGQRVTISCSGSYHNIGSNAVNWYQQLPGTA PKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYC AAWDDSLHVFGTGTKVTVLGQPKANPTVTLFPPSSEEL
526	3A613LC	QSALTQPPSASGTPGQRVTISCSGSYHNIGSNAVNWYQQLPGTA PKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYC AAWDDSLHVFGTGTKVTVLGQPKANPTVTLFPPSSEEL
527	3A64KC	DIQMTQSPSSLSASVGDRVTITCRASQDITTYLAWLQQKPGKAPK SLIYSASTVQSGVPSRFSGSGSGTEFTLTISGLQPEDFATYYCQQ YNYYPITFGLGTRLEIKRTVAAPSVFIFPPSDE
528	3A650KC	IILFLVATATGSWAQSALTQPRSVSGSLGQSVTISCTGSSSDVGR YNYVSWYQHHPGKAPKLMISDVNKRPSGVPDRFSGSKSGNTAS LTISGLQAEDETDYYCCSYAGSYIWVFGG
529	3A67KC	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGSDTDFTLTISSLEPEDFAVYYCQQ RGIWPLQITFGQGTRLEIKRTVAAPSVFIFPPSDE
530	3A779KC	LSASVGDRVTITCRASQSIDRYLNWYQQKPGKAPKLLIYAASSLH TDVPSRFSGSGAGTYFTLTITSLQPEDFATYYCQQSHSPSFGQE SYSITFGQGTRLEIKRTVAAPSVFIFPPSD
531	3A816KC	VTLSLSPGERATLSCRASQTISNNYLAWYQQKPGQAPRLLIYGAS SGATGLPDRFSGSGSGTDFTLTISRLEPEDFAVYYCHQYALSPW TFGRGTKVEIKRTVAAPSVFIFPPSD
532	3A869KC	IILFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCRASQSIDRYL NWYQHKPGKAPKLLIYAASNLHTDVPSRFSGSGAGTYFTLTITSL QPEDFATYYCQQSHSPSFGQESYSIAFGQGTRLEIKRTVAAPSVF IFPPSDE

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
533	3A93LC	QSVLTQPASVSGSPGQSITISCTGTNSDVGYSYVSWFQQHPGKV PKLLIYDVSRRSSGVSNRFSGSRSGNTASLTISGLRAEDEADYYC GSFTTSLTLVFGGGTKLAVLVSPS
534	3a426kc	EIVLTQSPGTLSLSPGERATLSCRASQSVSSRYLAWYQQKPGQA PRLIIYDASSRASGIPDRFSGSGSETDFTLTITRLEPEDFAVYYCQL YGTSPKFTFGQGTKLEIKRTVAAPSVFIFPPSD
535	3a515kc	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSHGDTYLKCFQQR PGQSPRRPIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDV GV
536	3b129kc	GPATLSVSPGERATLSCRASQSLRNNLAWYQQKTGQSPRLLIYA VSTRATGIPPRFSGGGSGTEFTLTIDSLQSEDFAVYFCQQYDSPQ WTFGQGTKVEIKRTVAAPSVFIFPPSD
537	3b171lc	QSVLTQPASVSGSPGQSITISCTGTSNDVGGQNFVSWYQQHPG TAPQLLIYDVTNRPAGVSSRFSGSKSGNTASLTISGLRTEDEADY YCASFTILNGVDYVFGTGTKVTVLLSPSQPYL
538	3b27kc	EIVLTQSPATLSVSPGERATLSCRAGQSVSSDLAWYQHKPGQAP RLLIYDASKRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQH RTNWPPSITFGQGTRLEIKRTVAAPSVFIFPPSD
539	3b41kc	EIVLTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQKPGQA PRLLIYGASSRATGIPDRFSGSGSGTDFTLSISRLEPEDFAVYYCQ QYGTSSCTFGQGTKLEIKRTVAAPSVFIF
540	3b5kc	EIVLTQSPGTLSLSPGDRAALSCRASETLSGNSLAWYQQKRGQP PRLLIFAASSRATGIPERFSGGGSGTDFTLTITRLEPEDFAVYFCQ QYVDAPITFGQGTRLEIKRTVAAPSVFIFPPSD
541	3b46kc	EIVLTQSPGTLSLSPGERATLSCRASQSVSSNNLAWYQQKPGQA PRLLMSGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHC QQYGSSPPTFGQGTKVEIKRTVAAPSVFIFPP
542	3b57lc	QSVLTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPG KAPKTMIFDVTKRPSGVPDRFSGSKSGNTASLTISGLQAEDEADY YCSSYAGRNTFYVFGTGTTVTVQVSPSQPPP
543	3b8kc	EIVLTQSPGTLSLSPGERATLSCRASQSVSSNLAWYAQKPGQAP RLIIYGASSRASAIPDRFRGSGSGTDFTLTISRLEPEDFAVYYCQQ YDDAPITFGHGTRLEIKRTVAAPSVFIFPPSDE
544	3BNC55KC	DIQMTQSPSSLSASVGDKVTITCQTSAGYLNWYQQRRGRAPKLL MYDGSRLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKSTVAA
545	3BNC60KC	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPARFSGRRWGQEYNLTINNLQPEDVATYFCQVYEF IVPGTRLDLKRTVAA
546	3anc3kc	DIQMTQSPSSVSASVGDRVTITCQASRDTDNSLTWYQQKPGRPP KLLIYHVVNLGPGVPSRFSGSASSATQSTLIISDFQPDDVATYFCQ NYEFFGPGTKVEIKRTVAAPSVFIFPPSDEQ
547	3b106kc	DIQMTQSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEF VVPGTRLDLKRTVAAPSVFIFPPSD
548	3b16kc	DIQMTQSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEF VVPGTRLDLKRTVAAPSVFIFPPSD
549	3b180kc	DIQMTQSPSSLSARVGDTVTFTCQANGYLNWYQQRRGKAPKLLI YDGSKLERGVPSRFSGRGWGQEYNLTINNLQPEDIATYFCQVYE FAVPGTRLDLKRTVAAPSVFIFPPSD
550	3b183kc	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLETGVPSRFTGRRWGQEYNLTINNLQPEDIATYFCQVYEFI VPGTRLDLKRTVAAPSVFIFPPSD

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
551	3b191kc	DIQMTHSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLETGVPSRFTGRRWGQEYNLTINNLQPEDIATYFCQVYEFI VPGTRLDLKRTVAAPSVFIFPPSD
552	3b21kc	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLETGVPSRFTGRRWGQEYNLTINNLQPEDIATYFCQVYEFI VPGTRLDLKRTVAAPSVFIFPPSD
553	3bnc102kc	DIQMTQSPSSLSASVGDRVTITCQASQGISNSLNWYQQKPGKAP RLLIYGTSTLQRGVPSRFSGSGSGTRFTVTINSLQPEDIATYFCQH NEFFGRGTKVDIKRTVAAPSVFIFPPSDEQL
554	3bnc104kc	DIQMTQSPSSLSASIGDRVNITCQASRDTGSALNWYQQKVGRPP RLLISAVSNLGAGVPSRFSGRRSGTQSTLTINTLQPEDIATYFCQH YEFFGPGTKVDIKRTVAAPSVFIFPPSDEQ
555	3bnc105kc	DIQMTQSPSSLSASVGDTVTFTCQANGYLNWYQQRRGKAPKLLI YDGSRLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYE FAVPGTRLDLKRTVAAPSVFIFPPSD
556	3bnc107kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
557	3bnc108kc	DIQMTQSPSSLSARVGDKVTITYQTSAGYLNWYQQRRGRAPKLL MYDGSRLVTGAPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
558	3bnc117kc	DIQMTQSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEF VVPGTRLDLKRTVAAPSVFIFPPSD
559	3bnc134kc	DIQMTQSPSSLSASVGDTVTINCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
560	3bnc142kc	DIQMTQSPSSLSASVGDTVTITCHTNKGYLNWYQQRRGRAPKLL MFDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EVFGPGTRLDLKRTVAAPSVFIFPPSD
561	3bnc151kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
562	3bnc153kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRLSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
563	3bnc156kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQKRGRAPKLL MYDGSKLVTGVPSRLSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
564	3bnc158kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRLSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
565	3bnc159kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
566	3bnc15kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRLSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
567	3bnc176kc	DIQMTQSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQAEDIATYFCQVYEF AVPGTRLDLKRTVAAPSVFIFPPSD
568	3bnc193kc	DIQMTQSPSSLSARVGDKVTITCQTSAGYLNWYQQRRGRAPKLL MYDGSRLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD

TABLE B-continued

Seq ID No.	Antibody	Light Chain Amino Acid Sequence
569	3bnc196kc	DIQMTQSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLM YDGSTLERGVPARFSGRRWGQEYNLTINNLQPEDVATYFCQVYE FIVPGTRLDLKRTVAAPSVFIFPPSD
570	3bnc31kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MCDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
571	3bnc42kc	DIQMTQSPSSLSASVGDTVTITCQTTKGYLNWYQQRRGRAPKLL MFDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDLATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
572	3bnc53kc	DIQMTQSPSSLSASVGDTVTITCHTNKGYLNWYQQRRGRAPKLL MFDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EVFGPGTRLDLKRTVAAPSVFIFPPSD
573	3bnc62kc	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLETGVPSRFTGRRWGQEYNLTINNLQPEDIATYFCQVYEFI VPGTRLDLKRTVAAPSVFIFPPSD
574	3bnc65kc	DIQMTQSPSSLSARVGDTVTFTCQANGYLNWYQQRRGKAPKLLI YDGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYE FAVPGTRLDLKRTVAAPSVFIFPPSD
575	3bnc66kc	DIQMTQSPSSLSASVGDTVTITCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRLSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
576	3bnc75kc	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEF VVPGTRLDLKRTVAAPSVFIFPPSD
577	3bnc79kc	DIQMTQSPSSLSARVGDTVTFTCQANGYLNWYQQRRGKAPKLLI YDGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYE FAVPGTRLDLKRTVAAPSVFIFPPSD
578	3bnc81kc	DIQMTQSPSSLSASVGDTVTINCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSD
579	3bnc84kc	DIQMTQSPSSLSASVGDTVTINCQTNKGYLNWYQQRRGRAPKLL MYDGSKLVTGVPSRFSGRRWGTQYNLTIGSLQPEDIATYYCQVY EFFGPGTRLDLKRTVAAPSVFIFPPSD
580	3bnc87kc	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEF VVPGTRLDLKRTVAAPSVFIFPPSD
581	3bnc89kc	DIQMTQSPSSLSASVGDKVTITCQTSAGYLNWYQQRRGRAPKLL MYDGSRLVTGVPSRFSGRRWGTQYNLTIGSLQPEDVATYYCQV YEFFGPGTRLDLKRTVAAPSVFIFPPSD
582	3bnc91kc	DIQMTQSPSSLSARVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEF AVPGTRLDLKRTVAAPSVFIFPPSD
583	3bnc95kc	DIQMTQSPSSLSASVGDTVTITCQANGYLNWYQQRRGKAPKLLIY DGSKLERGVPSRFSGRRWGQEYNLTINNLQPEDIATYFCQVYEFI VPGTRLDLKRTVAAPSVFIFPPSD

TABLE 1

Forward Leader Sequence Primers

VH1 LEADER-A	ATGGACTGGACCTGGAGGAT	SEQ ID NO 591
VH1 LEADER-B	ATGGACTGGACCTGGAGCAT	SEQ ID NO 592
VH1 LEADER-C	ATGGACTGGACCTGGACAAT	SEQ ID NO 593
VH1 LEADER-D	GGCCTTCTCTTTGTGGTGGC	SEQ ID NO 594
VH1 LEADER-E	ATGGACTGGACCTGGAGGGT	SEQ ID NO 595
VH1 LEADER-F	ATGGACTGGATTTGGAGGAT	SEQ ID NO 596
VH1 LEADER-G	AGGTTCCTCTTTGTGGTGGCAG	SEQ ID NO 597

TABLE 1-continued

VH3 LEADER-A	TAAAAGGTGTCCAGTGT	SEQ ID NO 598
VH3 LEADER-B	TAAGAGGTGTCCAGTGT	SEQ ID NO 599
VH3 LEADER-C	TAGAAGGTGTCCAGTGT	SEQ ID NO 600
VH3 LEADER-D	GCTATTTTTAAAGGTGTCCAGTGT	SEQ ID NO 601
VH3 LEADER-E	TACAAGGTGTCCAGTGT	SEQ ID NO 602
VH3 LEADER-F	TTAAAGCTGTCCAGTGT	SEQ ID NO 603
VH4 LEADER-A	ATGAAACACCTGTGGTTCTTCC	SEQ ID NO 604

TABLE 1-continued

VH4 LEADER-B	ATGAAACACCTGTTTCTT	SEQ ID NO 605
VH4 LEADER-C	ATGAAGCACCTGTGGTTCTT	SEQ ID NO 606
VH4 LEADER-D	ATGAAACATCTGTGGTTCTT	SEQ ID NO 607
VH5 LEADER-A	TTCTCCAAGGAGTCTGT	SEQ ID NO 608
VH5 LEADER-B	CCTCCACAGTGAGAGTCTG	SEQ ID NO 609
VH6 LEADER-A	ATGTCTGTCTCCTTCCTCATC	SEQ ID NO 610
VH7 LEADER-A	GGCAGCAGCAACAGGTGCCCA	SEQ ID NO 611
Reverse Constant Region Primers		
3' Cg CH1 (gamma)	GGAAGGTGTGCACGCCGCTGGTC	SEQ ID NO 612
3' IgG (internal)	GTTCGGGGAAGTAGTCCTTGAC	SEQ ID NO 613

TABLE 2

	gender	clade	year of birth	year of diagnosis	CD4+ T cells/ul	Virus copies/ml	clinical status
pt1	male	B	1948	1985	354	4722	non progressor
pt3	male	B	1965	2002	427	880	non progressor
pt8	male	B	1962	1989	580	<50	elite controller
pt12	male	ND	ND	ND	ND	ND	ND

TABLE 3

A

Ab Name	VH	D	JH	(-)	CDR3 (aa)	SEQ ID NO
3BNC4	1-2	7-27	2/6	3	R H S D Y C D F D V	614
3BNC23	1-2	6-25/3-3	2/6	3	Q R S D F W D F D V	615
3BNC42	1-2	7-27	2/6	3	R H S D Y C D F D V	616
3BNC53	1-2	3-3	2/6	3	R H S D Y C D F D V	617
3BNC55	1-2	3-3/6-19/5-12	2/6	3	R H S D Y C D F D I	618
3BNC62	1-2	6-25/6-13/6-6	2/6	3	Q R S D Y W D F D V	619
3BNC65	1-2	6-25/6-6	2/6	3	Q R S D Y W D F D V	620
3BNC66	1-2	7-27	2/6	3	R H T D Y C D F D V	621
3BNC72	1-2	7-27	2/6	3	R H S D Y C D F D V	622
3BNC79	1-2	6-25/6-6	2/6	3	Q R S D Y W D F D V	623
3BNC81	1-2	7-27	2/6	3	R H S D Y C D F D V	624
3BNC89	1-2	3-3/6-19/5-12	2/6	3	R H S D Y C D F D I	625
3BNC91	1-2	2-21/6-25	2/6	3	R R S D Y C D F D V	626
3BNC95	1-2	6-25/2-8	2/6	3	Q R S D Y W D F D V	627
3BNC105	1-2	6-6/6-25	2/6	3	Q R S D Y W D F D V	628
3BNC107	1-2	7-27/3-3	2/6	3	R H S D Y C D F D V	629
3BNC108	1-2	3-3/6-19/6-25	2/6	3	R H S D Y C D F D I	630
3BNC117	1-2	6-25/2-8	2/6	3	Q R S D Y W D F D V	631
3BNC134	1-2	7-27	2/6	3	R H S D Y C D F D V	632
3BNC142	1-2	3-3	2/6	3	R H S D Y C D F D V	633
3BNC151	1-2	7-27/4-17/3-3	2/6	3	R H S D Y C D L D V	634
3BNC156	1-2	3-3/7-27	2/6	3	R H S D Y C D F D V	635
3BNC159	1-2	7-27	2/6	3	R H S D Y C D F D V	636
3BNC176	1-2	6-25/6-6	2/6	3	Q R S D Y W D F D V	637
3BNC196	1-2	6-25/6-6/6-13	2/6	3	Q R S D Y W D F D V	638

TABLE 3-continued

3BNC6	1-2	3-16/1-7	2	1	P L R G G D T W H Y H S	639
3BNC101	1-2	1-7/3-16	2	1	P L R G G D T W H Y H S	640
3BNC102	1-2	3-22/1-26/1-20	2	3	P H S P D D A W S L D V	641
3BNC126	1-2	3-22/1-26/1-20	2	3	P H S P D D A W S L D V	642
3BNC149	1-2	3-22/1-26/1-20	2	3	P H S P D D A W S L D V	643
3ANC3	1-2	2-21/2-15	1/2	1	P R G G R D N W S F H V	644
3ANC42	1-2	ND	2	2	P K S G R D Y W S F D L	645
3BNC3	1-69	5-5/5-18/5-24	3	2	A T G Y S Y G Y L D A F D I	646
3BNC8	1-24	5-24/4-17	4	3	E P R E M G T L T A G F E Y	647
3BNC48	1-69	3-3	4	5	G Q T D L N D D L W S D Y S T P G F D Y	648
3ANC38	1-69	3-3	4	5	G Q T D L N D D F W S E Y S T P G F D Y	649
3BNC49	1-69	3-22/6-19/5-12	6	3	G E F D S S G F D Y E S W Y P Y Y M D V	650
3BNC58	1-24	3-16/3-10	4/5	2	A P R L E L G E L S S G F H Y	651
3BNC78	1-24		4/5	2	A P R L D L G E L S S G F H F	652
3BNC78	1-24		4/5	2	A P R L D L G E L S S G F H F	653
3BNC71	1-24	1-24	4/5	3	D N P L L Q S G E F S S S L D N	654
3BNC71	1-24	1-24	4/5	3	D N P L L Q S G E F S S S L E N	655
3BNC144	1-69	3-9/5-5	4	3	A Q G D I L T E G Y F D Y	656

Ab Name	(+)	Length	Mutations HC	Primer Set	k/l	Vk/l	Jk/l	(-)
3BNC4	1	10	72	new	k	1D-33	3	1
3BNC23	1	10	79	new	k	1D-33	3	1
3BNC42	2	10	69	new	k	1D-33	3	1
3BNC53	2	10	74	new	k	1D-33	3	1
3BNC55	2	10	64	new	k	1D-33	1/3	1
3BNC62	1	10	81	new	k	1D-33	3	1
3BNC65	1	10	82	new	k	1D-33	3	1
3BNC66	2	10	69	new	k	1D-33	3	1
3BNC72	1	10	72	new	k	1D-33	3	1
3BNC79	1	10	76	new	k	1D-33	3	1
3BNC81	2	10	71	new	k	1D-33	3	1
3BNC89	2	10	68	new	k	1D-33	3	1
3BNC91	2	10	76	new	k	1D-33	3	1
3BNC95	1	10	72	new	k	1D-33	3	1
3BNC105	1	10	77	new	k	1D-33	3	1
3BNC107	2	10	69	new				
3BNC108	2	10	62	new	k	1D-33	3	1
3BNC117	1	10	72	new	k	1D-33	3	1

TABLE 3-continued

3BNC134	2	10	71	new	k	1D-33	3	1
3BNC142	2	10	72	new	k	1D-33	3	1
3BNC151	2	10	69	new	k	1D-33	3	1
3BNC156	2	10	72	new	k	1D-33	3	1
3BNC159	2	10	71	new	k	1D-33	3	1
3BNC176	1	10	72	new	k	1D-33	3	1
3BNC196	1	10	78	new	k	1D-33	3	1
3BNC6	3	12	55	new	k	1D-33	1/3	1
3BNC101	3	12	54	new				
3BNC102	1	12	63	new	k	1D-33	1/3	1
3BNC126	1	12	65	new				
3BNC149	1	2	68	new				
3ANC3	3	12	59	new	k	1D-33	3	1
3ANC42	2	12	53	new	k	1D-33	3	1
3BNC3	0	14	22	new	L	1-44	1	2
3BNC8	1	14	21	old	k	3-11	2	0
3BNC48	0	20	18	new				
3ANC38	0	20	12	new	1	1-47	1/6	2
3BNC49	0	20	23	old	k	3-20	3	
3BNC58	1	15	16	old	k	3-11	2	0
3BNC78	2	15	38	old				
3BNC78	2	15	39	old				
3BNC71	0	16	22	old	k	3-11	5	
3BNC71	0	16	17	old	k	3-11	5	
3BNC144	0	13	15	old	k/l	1-44/1-47	1	2

Ab Name	CDR3 (aa)	SEQ ID NO	(+)	Length	Mutations LC	Binding	NEUT	# of Relatives
3BNC4	Q V Y E F	657	0	5	38		+	7
3BNC23	Q V Y E F	658	0	4	50	CD4BS	+	5
3BNC42	Q V Y E F	659	0	5	42		-	1
3BNC53	Q V Y E V	660	0	5	42		+	1
3BNC55	Q V Y E F	661	0	5	32		+	1
3BNC62	Q V Y E F	662	0	5	43		+	4
3BNC65	Q V Y E F	663	0	5	44		ND	1
3BNC66	Q V Y E F	664	0	5	38		+	1
3BNC72	Q V Y E F	665	0	5	38		+	1
3BNC79	Q V Y E F	666	0	5	44		ND	2
3BNC81	Q V Y E F	667	0	5	38		ND	2

TABLE 3-continued

3BNC89	Q V Y E F	668	0	5	35		+	1
3BNC91	Q V Y E F	669	0	5	42		+	1
3BNC95	Q V Y E F	670	0	5	39		+	9
3BNC105	Q V Y E F	671	0	5	43		ND	1
3BNC107	ND						ND	1
3BNC108	Q V Y E F	672	0	5	38		+	2
3BNC117	Q V Y E F	673	0	5	39	CD4BS	+	9
3BNC134	Q V Y E F	674	0	5	38		ND	1
3BNC142	Q V Y E V	675	0	5	42		+	1
3BNC151	Q V Y E F	676	0	5	40		ND	1
3BNC156	Q V Y E F	677	0	5	37		+	1
3BNC159	Q V Y E F	678	0	5	39		ND	1
3BNC176	Q V Y E F	679	0	5	41		+	3
3BNC196	Q V Y E F	680	0	5	43		ND	1
3BNC6	Q H Y E F	681	1	5	44		+	24
3BNC101	ND						ND	1
3BNC102	Q H Y E F	682	1	5	34		-	1
3BNC126	ND						ND	1
3BNC149	ND						ND	1
3ANC3	Q H Y E F	683	0	5	47		+	1
3ANC42	Q Q Y E F	684	1	5	41		ND	4
3BNC3	A A W D D T L Y V	685	0	9	19	CD4i	+	7
3BNC8	Q H R S I W P L M C T	686	2	11	10	CD4i	+	3
3BNC48	ND						ND	
3ANC38	G A W D D T L Y V	687	0	9	8	CD4i	-	2
3BNC49	ND					CD4i	ND	2
3BNC58	Q Q R T I W P P G C S	880	1	11	10	CD4i	ND	2
3BNC78	ND						ND	1
3BNC78	ND						ND	2
3BNC71	ND					CD4i	ND	1
3BNC71						CD4i	ND	1
3BNC144	ND		1	9		CD4i	ND	1

b

Ab Name	VH	D	JH	(-)	CDR3 (aa)	SEQ ID NO
1NC2	1-46	3-22/5-5	4/5	4	N E A D Y H D G N G H S L R G M F D Y	881
1NC3	1-46	6-19	4/5	3	A E A E S Q S H S R P I M F D F	688

TABLE 3-continued

1NC7	1-46	6-19/1-14	4/5	3	A E A E S Q S H S R P I M F D S	689
1NC9	1-46	5-12/2-8	4/5	4	Q D S D F H D G H G H T L R G M F D S	690
1NC18	1-46	1-14/2-21	4/5	2	N E P Q Y H S L P G M F D Y	691
1NC24	1-46	3-16	4/5	3	N E P Q Y H D G N G H S L P G M F D Y	692
1NC29	1-46	3-16/6-19	4/5	3	N E P Q Y Y D G S G H S L P G M F D Y	693
1NC33	1-46	5-12	4/5	5	L E A D G D D Y S P K M V D Y	694
1NC46	1-46	3-9/3-16	4/5	3	R E A D Y H D G N G H T L P G M F D F	695
1NC48	1-46	3-9/6-19	4/5	2	N E P Q Y F D G S G H S L P G M F D Y	696
1NC52	1-46	3-16/6-19	4/5	3	N E P Q Y Y D G S G H S L P G M F D Y	697
1NC56	1-46	5-12/3-9	4/5	5	L E A D G D D Y S P K M F D H	698
1NC60	1-46	3-22/1-26	1/5	4	L E A E S D S H S R P I M F D H	699
1NC66	1-46	3-16	4/5	2	N E P Q Y H D G N G H S L P G M F D F	700
1NC70	1-46	3-16/6-19	4/5	3	N E P Q Y Y D G S G H S L P G M F D Y	701
1NC72	1-46	6-19/1-14	4/5	3	A E A E S Q S H S R P I M F D F	702
1NC94	1-46	6-13/6-19	4/5	3	A E A A S D S H S R P I M F D H	703
1NC95	1-46	3-16/6-19	4/5	4	L E A D G S D Y S P K M F D F	704
1NC107	1-46	3-3/5-12	4/5	5	L E A D G D D Y S P K M F D Y	705
1NC108	1-46	3-9/3-16	4/5	4	R E A D Y H D G N G H T L P G M F D F	706
1NC109	1-46	5-1/6-19	4/5	5	L E A D G D D Y S P K M F D Y	707
1NC110	1-46	5-24/6-19	4/5	4	L E A D G D N Y S P K M V D Y	708
1NC116	1-46	2-21	4	2	N E P Q Y H S L P G M F D Y	709
1NC118	1-46	3-9/5-12	4	3	L E A D G G D Y S P K M F D Y	710
1NC122	1-46	3-16/3-3	4	4	L E A D G A D Y S P K M F D F	711
1NC123	1-46	6-19	4	3	A E A E S Q S H S R P I M F D Y	712
1NC127	1-46	6-13/6-19	4/5	3	A E A A S D S H S R P I M F D H	713
1B344	1-46	3-22/1-26	1/5	4	L E A E S D S H S R P I M F D H	714
1B2416	1-46	1-14/3-16	4	4	N E P Q Y H D D N G H S L P G M I D Y	715
1B2503	1-46	6-19	5	3	A E A E S Q S H S R P I M F D S	716
1B2573	1-46	3-22	4/5	2	N E P Q Y H D G N G H S L P G M F D S	717
1NC5	1-69	3-3	3	1	G R Q T F R A I W S G P P V V F D I	718
1NC126	1-69	3-3	3	1	G R Q T F R A I W S G P P A V F D I	719
1NC16	4-34	3-10	5	2	A V A G L W F E D A Y N W F G P	720
1NC21	4-34	3-10	5	2	A V K G L W F D E T Y T W F G P	721
1NC54	4-34	3-10	5	2	A V K G F W F D E P S T W F G P	722
1NC57	4-34	3-10	5	2	A V K G F W F D D P Y T W F G P	723
1NC115	4-34	3-10	5	2	A V K G F W F D E V Y N W F G P	724

TABLE 3-continued

Ab Name	(+)	Length	Mutations HC	Primer Set	k/l	Vk/l	Jk/l	(-)
1NC2	2	19	74	new	l	1-47	3	1
1NC3	2	16	86	NEW	l	1-47	6/7	1
1NC7	2	16	77	new	l	1-47	6/7	1
1NC9	4	19	67	new	l	1-47	3	1
1NC18	1	14	85	new				
1NC24	2	19	79	new	l	1-47	3	1
1NC29	1	19	87	new				
1NC33	0	15	84	new	l	1-47	3	2
1NC46	3	19	85	new	l	1-47	3	1
1NC48	1	19	88	new	l	1-47	3	1
1NC52	1	19	82	new	l	1-47	3	1
1NC56	2	15	91	new	l	1-47	3	1
1NC60	3	16	72	new	l	1-47	3	1
1NC66	2	19	91	new	l	1-47	3	1
1NC70	1	19	85	new	l	1-47	3	1
1NC72	2	16	77	new	l	1-47	6/7	1
1NC94	3	16	81	new	l	1-47	3	2
1NC95	0	15	93	new				
1NC107	1	15	90	new	l	1-47	3	1
1NC108	3	19	85	new	l	1-47	3	1
1NC109	1	15	85	new				
1NC110	1	15	88	new				
1NC116	1	14	83	new				
1NC118	0	15	86	new	l	1-47	3	1
1NC122	1	15	94	new	l	1-47	3	1
1NC123	2	16	78	new	l	1-47	3	1
1NC127	3	16	81	new	l	1-47	3	2
1B344	3	16	72	new	l	1-47	3	1
1B2416	2	19	81	new				
1B2503	1	16	78	new	l	1-47	3	1
1B2573	2	19	81	new				
1NC5	2	18	47	new	k	3-11	2	0
1NC126	2	18	47	new				
1NC16	0	16	75	new	k	1D-39	2/3	0
1NC21	1	16	58	new				
1NC54	1	16	59	new				
1NC57	1	16	61	new				

TABLE 3-continued

1NC115	1	16	58	new				
Ab Name	CDR3 (aa)	SEQ ID NO	(+)	Mutations Length	LC	Binding	NEUT	# of Relatives
1NC2	A V Y D S S L S L G L	725	0	11	47		+	15
1NC3	A T Y D S Q R S I R L	726	2	11	55		+	1
1NC7	A T Y D S Q G S T R L	727	1	11	51		+	1
1NC9	A A Y D S T F S L P V	728	0	11	53	?	+	2
1NC18	ND						ND	1
1NC24	A A Y D S S L S L R L	729	0	11	30		+	2
1NC29	ND						ND	1
1NC33	A T Y D T D L S L R L	730	1	11	49		+	1
1NC46	A A Y D S A V S L P V	731	0	11	52		ND	1
1NC48	A A Y D S T L S L R L	732	1	11	37		ND	1
1NC52	A A Y D S T F S L P V	733	0	11	54		ND	1
1NC56	A T Y D T G L S L R L	734	1	11	58		ND	1
1NC60	A T Y D S G W S I R L	735	1	11	46		+	3
1NC66	A A Y D S T L S L R L	736	1	11	33		ND	1
1NC70	A A Y D S T L S L R L	737	1	11	40		ND	1
1NC72	A T Y D S Q G S T R L	738	1	11	51		+	2
1NC94	A T Y D S D G S I R L	739	1	11	41		-	5
1NC95	ND						ND	1
1NC107	A T Y D T G L S L R L	740	1	11	58		ND	1
1NC108	A A F D S A L S L P L	741	0	11	51		+	1
1NC109	ND						ND	1
1NC110	ND						ND	1
1NC116	ND						ND	1
1NC118	A T Y D T G L S L R L	742	1	11	54		ND	1
1NC122	G T Y D T S L S L R L	743	1	11	57		ND	1
1NC123	A T Y D S H G S I R L	744	2	11	48		-	1
1NC127	A T Y D S D G S I R L	745	1	11	41	?	+	5
1B344	A T Y D S G W S I R L	746	1	11	46		+	1
1B2416	ND						ND	1
1B2503	G T Y D S Q G S T R L	882	1	11	49		ND	1
1B2573	ND						-	2
1NC5	Q H R S N W P W T	883	2	9		CD4BS	+	1
1NC126	ND						ND	1
1NC16	Q Q S F A V P Y T	884	0	9	35	ND	ND	1
1NC21	ND					ND	ND	1
1NC54	ND					ND	ND	1

TABLE 3-continued

1NC57		ND				ND	ND	1
1NC115		ND				ND	ND	1

c

Ab Name	VH	D	JH	(-)	CDR3 (aa)	SEQ ID NO
8ANC13	1-46	3-16	6	4	D G L G E V A P D Y R Y G I D V	885
8ANC22	1-46	3-16	6	3	D G L G E V A P A Y L Y G I D A	747
8ANC26	1-46	3-16	6	3	D G L G E V A P A Y L Y G I D A	748
8ANC37	1-46	3-16	6	3	D G L G E V A P A Y L Y G I D A	749
8ANC41	1-46	3-16	6	3	D G L G E L A P A Y H Y G I D V	750
8ANC50	1-46	3-16	6	3	D G L G E L A P A Y Q Y G I D V	751
8ANC88	1-46	3-16	6	4	D G L G E V A P D Y R Y G I D V	752
8ANC127	1-46	3-16	6	3	D G L G E V A P A Y L Y G I D A	753
8ANC131	1-46	3-16	6	3	D G L G E V A P D Y R Y G I D V	754
8ANC142	1-69	3-3	ND	2	T S T Y D Q W S G L H H D G V M A F S S	755
8ANC46	1-69	3-22/2-15	3	2	S S G N F E F A F E I	756
8ANC191	1-69	3-22/2-15	3	2	S S G N Y D F A Y D I	757
8ANC196	1-69	3-22/2-15	3	2	S S G N Y D F A F D I	758
8ANC14	1-24	6-13/5-5	4	4	A D R F K V A Q D E G L F V I F D Y	759
8ANC34	1-24	6-13/5-5	4	4	A D P F K V A Q D E G L Y V I F D Y	760
8ANC58	1-24	6-13/5-5	4	4	A D P F K V A Q D E G L Y V I F D Y	761
8ANC168	1-24	6-13/5-5	4	4	A D P F K V A Q D E G L F V I F D Y	762
8ANC5	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	763
8ANC7	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	764
8ANC9	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	765
8ANC77	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	766
8ANC107	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	767
8ANC108	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	768
8ANC137	1-69	4-17/3-10	6	8	D R G D T R L L D Y G D Y E D E R Y Y Y G M D V	769
8ANC16	1-69	2-2	3	2	D R S S A I G Y C S S I S C Y K G S F D I	770
8ANC24	1-24	2-2	6	1	G G L Y C S S I S C I M D V	771
8ANC25	1-24	2-2	6	1	G G L Y C S S I S C I M D V	772
8ANC38	3-43	3-16	5	1	N G F D V	773

Ab Name	(+)	Length	Mutations HC	Primer Set	k/l	Vk/l	Jk/l	(-)
8ANC13	1	16	75	new	k	3-11	2/3	1
8ANC22	0	16	85	new				
8ANC26	0	16	76	new	k	3-11	2/3	1
8ANC37	0	16	82	new	k	3-11	2/3	1
8ANC41	1	16	71	new	k	3-11	2/3	1

TABLE 3-continued

8ANC50	0	16	71	new	k	3-11	2/3	1
8ANC88	0	16	73	new	k	3-11	2/3	1
8ANC127	0	16	86	new				
8ANC131	1	16	75	new	k	3-11	2/3	1
8ANC142	2	20	72	new	k	1-5	1/5	1
8ANC46	0	11	30	old	l	1-40	3	1
8ANC191	0	11	28	old				
8ANC196	0	11	25	old				
8ANC14	1	18	11	old	k	3-11	4	0
8ANC34	0	18	10	new				
8ANC58	0	18	18	new				
8ANC168	1	18	11	new				
8ANC5	3	24	40	old	k	1D-33	2	0
8ANC7	3	24	37	new				
8ANC9	3	24	35	old				
8ANC77	3	24	50	old				
8ANC107	3	24	38	old				
8ANC108	3	24	37	old				
8ANC137	3	24	37	new				
8ANC16	1	21	12	old	k	3-15	2	0
8ANC24	0	14	12	old	k	3-15	1	0
8ANC25	0	14	6	old				
8ANC38	0	5	70	new	l	2-11	3	0

Ab Name	CDR3 (aa)	SEQ ID NO	Mutations (+)	Length	LC	Binding	NEUT	# of Relatives
8ANC13	Q E Y S S T P Y N	774	0	9	50		+	1
8ANC22	ND						ND	1
8ANC26	Q E Y S S T P Y N	775	0	9	55	CD4BS	+	2
8ANC37	Q E Y S S T P Y N	776	0	9	50	CD4BS	+	8
8ANC41	Q E Y S S T P Y N	777	0	9	42		+	2
8ANC50	Q E Y S S T P Y N	778	0	9	46	CD4BS	+	2
8ANC88	Q E Y S S T P Y N	779	0	9	46		ND	1
8ANC127	ND						ND	1
8ANC131	Q E Y S S T P Y N	780	0	9	45	CD4BS	+	1
8ANC142	Q Q Y D T Y P G T	781	0	9	43	?	+	2
8ANC46	Q S Y D R S L R G S V	782	1	11	30	ND	ND	1
8ANC191	ND						ND	1
8ANC196	ND						ND	1

TABLE 3-continued

8ANC14	Q Q R A N W R L L T	783	2	10	9	CD4i	+	2
8ANC34	ND						ND	5
8ANC58	ND						ND	3
8ANC168	ND						ND	1
8ANC5	Q Q Y S N L P Y T	784	0	9	17	CD4i	-	2
8ANC7	ND						ND	2
8ANC9	ND						ND	1
8ANC77	ND						ND	3
8ANC107	ND						ND	2
8ANC108	ND						ND	4
8ANC137	ND						ND	1
8ANC16	Q Q Y Y Q W L S Y T	785	0	10	13	ND	ND	8
8ANC24	Q Q Y N H W P Q T	786	0	9	7	CD4i	+	1
8ANC25	ND						ND	1
8ANC38	C L K K T S S Y V	787	2	9	41	CORE	+	2

d

Ab Name	VH	D	JH	(-)	CDR3 (aa)	SEQ ID NO
12A1	1-2	5-12/3-10	4/5	4	D E S G D D L K W H L H P	886
12A2	1-2	4-17	4/5	3	D G S G D D T S W H L H P	788
12A4	1-2	5-12/3-10	4/5	4	D E S G D D L K W H L H P	789
12A6	1-2	1-26/3-10	4/5	2	D G S G D A T S W H L H P	790
12A7	1-2	1-26	4/5	4	D G S G D A R D W H L D P	791
12A9	1-2	3-3	4/5	5	D R R D D D R A W L L D P	792
12A12	1-2	1-26/3-10	4/5	4	D G S G D D T S W H L D P	793
12A13	1-2	1-26	4/5	4	D G S G D D T S W Y L D P	794
12A20	1-2	1-26	4/5	3	D G S G D A R D W H L H P	795
12A22	1-2	3-16	4/5	4	D G G G D D R T W L L D A	796
12A23	1-2	3-3	4/5	5	D R R D D G L D W L L D P	797
12A27	1-2	1-26/3-10	4/5	3	D G S G D D T S W H L H P	798
12A46	1-2	3-10	4/5	1	G G G D G R N W H L H P	799
12A55	1-2	1-26	4/5	4	D G S G D D R N W H L D P	800
12A56	1-2	1-26	4/5	4	D E S G Y D L N W H L D S	801

TABLE 3-continued

Ab Name	(+)	Length	# Mutations HC	Primer Set	k/l	Vk/l	Jk/l	(-)
12A1	2	13	60	new	k	1D-33	3	0
12A2	2	13	67	new	k	1D-33	3	10
12A4	2	13	59	new	k	1D-33	3	0
12A6	2	13	61	new	k	1D-33	3	1
12A7	1	13	62	new	k	1D-33	3	1
12A9	3	13	62	new	k	1D-33	3	1
12A12	1	13	60	new	k	1D-33	3	1
12A13	0	13	61	new	k	1D-33	3	1
12A20	3	13	61	new	k	1D-33	3	1
12A22	1	13	61	new	k	1D-33	3	1
12A23	2	13	51	new	k	1D-33	3	1
12A27	2	13	68	new	k	1D-33	3	1
12A46	3	13	62	new	k	1D-33	3	1
12A55	1	13	63	new	k	1D-33	3	2
12A56	1	13	66	new	k	1D-33	3	1

Ab Name	CDR3 (aa)	SEQ ID NO	(+)	Length	Mutations LC	Binding	NEUT	# of Relatives
12A1	A A F Q W	887	0	5	39		ND	1
12A2	A V L E F	802	0	5	44		+	3
12A4	A V F Q W	803	0	5	36	CD4BS	+	3
12A6	A V L E F	804	0	5	39		+	1
12A7	A V L E F	805	0	5	41		ND	2
12A9	Q L F E F	806	0	5	39		ND	1
12A12	A V L E F	807	0	5	41	CD4BS	+	1
12A13	A V V E F	808	0	5	41		ND	1
12A20	A A L E F	809	0	5	40		+	1
12A22	S V Y E F	810	0	5	39		+	2
12A23	Q L F E F	811	0	5	39		+	1
12A27	A V L E F	812	0	5	40		ND	1
12A46	A S L E F	813	0	5	43		+	1
12A55	E V Y E F	814	0	5	37		+	1
12A56	E S F Q W	815	0	5	37		ND	1

e

Ab Name	VH	D	JH	(-)	CDR3 (aa)	SEQ ID NO
3B191	1-2	6-25/6-13/6-6	2/6	3	Q R S D Y W D F D V	816
3B6	4-39	3-9/3-10	3	2	I P Y H S E S Y Y K V V I G G F D V	817
3B8	1-69	4-17/3-22	4	3	D H G D P R T G Y Y F D Y	818

TABLE 3-continued

3B27	3-64	3-9/1-26/4-17	5	1	G P L L R Y L D S	819
3B41	1-24	3-16	6	4	K A K D Y Y Y E S S D Y S P Y Y Y Y Y M D V	820
3B46	4-31	3-3/2-8	4/5	0	G S G R W T I G A R I Y F D N	821
3B144	3-30	3-3/3-10/3-16	4/5	2	T P P H Y D V L T G Y P S S V L E F	822
3B117	1-69	5-5/5-18/5-24	3	2	A T G Y S Y G Y L D A F D I	823
3A869	4-4/4-59	6-19/5-12/1-26	4	2	E K G Q W L T V P P Y Y F D S	824
3A228	5-51	3-3/2-2	6	1	T R C F G A N C F N F M D V	825
3A461	1-46	2-2	4	1	P E P S S I V A P L Y Y	826
3A18	1-69	3-10/5-24	3	3	D P Q V E V R G N A F D I	827
3A125	1-46	1-20/1-7/3-10	3	2	P Q Y N L G R D P L D V	828
3A255	4-59	3-3/3-9	4	3	A D Y D L L T S S Y H F D S	829
3A233	4-59/4-61	3-3/4-17	4/5	3	L D G E A F R Y Y L D L	830

Ab Name	(+)	Length	# Mutations HC	Primer Set	k/l	Vk/l	Jk/l	(-)
3B191	1	10	81	new	k	1D-33	3	1
3B6	1	18	50	new	k	1-9	1/3	0
3B8	2	13	50	new	k	3-20	1/5	2
3B27	0	9	18	old	k	3-11	1/5	0
3B41	2	22	17	old	k	3-20	2	0
3B46	2	15	22	old	k	3-20	1/4	0
3B144	1	18	23	old	k	3-15	1/5	0
3B117	0	14	22	new	l	1-44	1	2
3A869	1	1	33	old	k	1D-39	5	0
3A228	1	1	34	old	k	4-1	3	0
3A461	0	1	15	old	k	3-20	1	0
3A18	1	1	40	old	k	1D-39	5	0
3A125	1	1	22	old	k	3-20	1	0
3A255	1	1	35	old	l	7-43	3	0
3A233	1	1	32	old	l	2-14	2/3	0

Ab Name	CDR3 (aa)	SEQ ID NO	(+)	Length	Binding	NEUT	# of Relatives
3B191	Q V Y E F	831	0	5	CD4BS	+	7
3B6	Q Q L A T	832	0	5	GP41	+	11
3B8	Q Q Y D D A P I T	833	0	9	GP41	-	9
3B27	Q H R T N W P P S I T	834	2	11	CD4i	-	3
3B41	Q Q Y G T S S C T	835	0	9	CD4i	-	2
3B46	Q Q Y G S S P P T	836	0	9	GP41	ND	2
3B144	Q Q Y N N W P P I T	837	0	10	ND	ND	4

TABLE 3-continued

3B117	A A W D D T L Y V	838	0	9	ND	ND	1
3A869	Q Q S H S P S	839	1	7	CD4BS	+	1
3A228	Q Q Y Y I S P	840	0	7	VAR	+	4
3A461	Q Q Y G T L H P R T	841	2	10	GP41	-	3
3A18	Q Q T Y T S P I T	842	0	9	GP41	-	2
3A125	Q Q Y G L S P W T	843	0	9	GP41	-	4
3A255	L L L P Y Y G G P W I	844	0	11	GP41	-	2
3A233	S S F T P T N T L V	845	0	10	GP41	-	2

f

Ab Name	VH	D	JH	(-)	CDR3 (aa)	SEQ ID NO
1B2434	15341	3-22/5-5	1	4	N E A D Y H D G N G H S L R G M F D Y	846
1B218	1-69	3-3	3	1	G R Q T F R A I W S G P P V V F D I	847
1B331	4-34	3-9/3-3	6	3	R Y F D W S P F R R D T Y G T D V	848
1B2174	4-34	3-9/3-3	6	3	R Y L D W S P I G R D T Y G T D V	849
1B2055	1-69	2-21	2/5	1	G L C R G G N C R L G P S G W L D P	850
1B2133	1-3	4-17/2-21	4	1	V A Y V H V V T T R S L D N	851
1A64	4-59	5-5/5-18	6	2	H E A P R Y S Y A F R R Y Y H Y G L D V	852
1A621	4-59	3-3/3-9	6	1	V I S G R I T I F Y Y N Y I D V	853
1A577	3-48	3-10/3-16	1	3	G T L W F G E S G L R L D H	854
1A732	3-7/3-73	3-22/3-10	6	2	N R R V A M P E A M I L S F Y M D V	855
1A74	4-34	3-3/3-9	4	1	V V P M F S I F G V V K A N Y F D Y	856
1A695	4-59	3-3/3-9	3	2	A G L D Y N F W N G K G R K G A F D V	857
1A479	1-69	3-22	4	1	G F R G S P F S S G S L Y F D S	858
1A182	1-69	4-17/1-26	6	6	A V I T D L H T F G D Y E L E D P S Y Y Y M D V	859
1A 693	3-23	7-27/3-22	4	1	R G R R Q I G D Y	860
1A 79	5-51	3-9/3-3	3	4	S Y Y D F S I G D G N D A F D V	861
1A 27	3-11	3-6/5-5	5	2	D T T T F T T F G G G P N M G G F D P	862

Ab Name	(+)	Length	# Mutations HC	Primer Set	k/l	Vk/l	Jk/l	(-)
1B2434	2	19	74	new	l	1-47	3	1
1B218	2	18	47	new	k	3-11	2	0
1B331	3	17	40	new	k	4-1	1/4	0
1B2174	2	17	41	new	k	4-1	1/4	0
1B2055	2	18	62	new	k	3-15	1	2
1B2133	1	14	22	new	k	1D-39	1	0
1A64	5	20	20	old	l	1-44	3	2
1A621	1	16	30	old	l	1-47	3	1

TABLE 3-continued

1A577	1	14	15	old	k	1-16	2	0
1A732	2	18	9	old	k	3-20	3	0
1A74	1	18	23	old	l	1-51	3	1
1A695	3	19	9	old	k	1-5	1	1
1A479	1	16	25	old	k	3-20	1	0
1A182	1	24	28	old	k	1-5	1	0
1A693	3	9	17	old	k	1D-39	2	0
1A79	0	16	30	old	l	1-47	1	3
1A27	0	19	50	old		1-9	1	0

Ab Name	CDR3 (aa)	SEQ ID NO	(+)	Length	Binding	NEUT	# of Relatives
1B2434	A V Y D S S L S L G L	863	0	11	CD4BS	+	7
1B218	Q H R S N W P W T	864	2	9	CD4BS	+	10
1B331	H Q Y F S T P R T	865	2	9	CORE	+	4
1B2174	H Q Y F N T P R T	866	2	9		ND	1
1B2055	Q Q Y E D P P W T	867	0	9	ND	ND	3
1B2133	Q Q T Y S N P R M	868	1	9	CD4i	-	2
1A64	A S W D D S L S G W V	869	0	11	CD4BS	+	24
1A621	A S W D N S L S G P V	870	0	11	CD4BS	+	3
1A577	Q Q Y N S F P PT	871	0	9	CD4BS	+	8
1A732	Q Q Y G R S P	872	1	7	CD4BS	+	1
1A74	G T W D S S L S A V L	873	0	11	CORE	+	2
1A695	Q Q Y D S	874	0	5	CORE	+	2
1A479	H Q Y A Y S P R T	875	2	9	CORE	+	11
1A182	Q Q Y K S Y S G T	876	0	9	CD4i	+	3
1A693	Q H S F G S P P W T	877	1	11	CD4i	-	1
1A79	A A W D D S F D Y V	878	0	10	V3	+	27
1A27	Q Q L R T	879	1	5	GP41	-	8

TABLE 4

[a]
Patient 3, Clone RU01

	3BNC62	3BNC176	3BNC60	3BNC117	3BNC95	3BNC104
MW965.26	<0.09	<0.10	<0.04	<0.09	<0.07	>50
BaL.26	<0.09	<0.10	<0.04	<0.09	<0.07	0.025
DJ263.8	<0.09	<0.10	<0.04	<0.09	<0.07	0.054
6535.3	0.68	0.46	0.54	0.55	1.0	>50
RHPA4259.7	<0.09	<0.10	<0.05	0.041	<0.07	0.0252
TRO.11	<0.09	<0.10	<0.05	0.077	<0.07	3.791
PVO.4	<0.09	<0.10	0.09	<0.09	<0.07	0.348
YU2.DG	<0.09	<0.10	<0.05	0.054	<0.07	0.034

TABLE 4-continued

Patient 3, Clone RU01						
	3BNC91	3BNC55	3BNC89	3ANC3	3BNC53	3BNC72
MW965.26	<0.08	0.04	>0.05	0.18	0.09	<0.06
BaL.26	>178	>30	>110	>50	>30	>139
DJ263.8	>178	>30	>110	>50	>30	>139
6535.3	1	2.6	1.7	>50	13.6	8.49
RHPA4259.7	<0.08	2.2	12.4	7.66	100.6	>139
TRO.11	3.06	18.4	52.4	10.76	>155	>139
PVO.4	0.44	3.9	2.7	36.77	>155	>139
YU2.DG	<0.08	0.9	0.39	35.01	>155	>139

Patient 3, Clone RU01				
	3BNC156	3BNC158	3BNC153	3BNC108
MW965.26	0.08	0.11	0.15	ND
BaL.26	>111	>109	>100	20.6
DJ263.8	>111	>109	>100	>55
6535.3	11.1	9.9	28.9	>55
RHPA4259.7	>111	>109	>100	45.91
TRO.11	>111	>109	>100	>55
PVO.4	>111	>109	>100	>55
YU2.DG	>111	>109	>100	25.5

Patient 3, Clone RU01				
	3BNC142	3BNC66	3BNC42	3BNC102
MW965.26	0.14	1.24	ND	>50
BaL.26	>172	>189	>26	>50
DJ263.8	>172	>189	>26	>50
6535.3	>172	>189	>26	>50
RHPA4259.7	>172	>189	>26	>50
TRO.11	>172	>189	>26	>50
PVO.4	>172	>189	NF	>50
YU2.DG	>172	>189	>26	>50

Patient 3 Clones RU02-07						
	3A67	3A383	3BNC8	3ANC44	3A576	3ANC38
MW965.26	0.1	0.5	0.74	25.49	>50	>50
BaL.26	19.2	5.3	>50	27.91	27	>50
DJ263.8	>50	>50	>50	>50	>50	>50
6535.3	>50	ND	>50	>50	>50	>50
RHPA4259.7	>50	ND	>50	>50	>50	>50
TRO.11	>50	ND	>50	>50	>50	>50
PVO.4	>50	ND	>50	>50	>50	>50
YU2.DG	>50	ND	>50	>50	>50	>50

B12 and NIH 45 Clone			
	B12	VRC01	NIH45-46
MW965.26	0.2	<0.08	0.04
BaL.26	0.2	0.1	<0.04
DJ263.8	>50	0.08	<0.04
6535.3	1.4	0.539	0.14
RHPA4259.7	0.1	0.06	0.034
TRO.11	>50	0.2	1.9
PVO.4	>50	0.2	0.17
YU2.DG	2.2	0.12	<0.05

b

Patient 1, Clone RU08						
	1B2640	1B2530	1B2364	1NC2	1NC9	1B2490
MW965.26	41.76	0.762	1.85	>50	>50	>50
BaL.26	0.08	>50	>25	0.11	1.37	0.058
DJ263.8	>50	2.71	3.75	>50	>50	>50
6535.3	>50	>50	>25	>50	>50	>50
RHPA4259.7	0.04	3.6	2.18	0.59	0.09	0.414
TRO.11	0.23	0.516	0.27	0.17	0.2	1.06

TABLE 4-continued

PVO.4	1.05	0.275	0.161	0.37	0.34	2.97
YU2.DG	0.2	0.209	2.46	0.12	0.13	0.125

Patient 1, Clone RU08

	1B2351	1B344	1NC24	1NC3	1NC7	1NC33
MW965.26	>50	>50	>50	>25	>50	>50
BaL.26	>50	>50	>50	>25	>50	>50
DJ263.8	8.46	12.62	>50	>25	>50	>50
6535.3	>50	>50	>50	>25	>50	22.04
RHPA4259.7	36.48	29.98	>50	>25	34.27	>50
TRO.11	0.331	0.27	0.2	3.37	16.57	>50
PVO.4	0.25	0.27	0.19	6.68	1.39	1.84
YU2.DG	0.058	0.25	0.16	18.26	>50	>50

Patient 1, Clone RU08

	1NC108	1B2644	1B2339	1NC123
MW965.26	>50	>25	>25	>50
BaL.26	>50	>25	>25	>50
DJ263.8	>50	>25	>25	>50
6535.3	>50	>25	>25	>50
RHPA4259.7	>50	>25	>25	>50
TRO.11	19.37	>25	>25	>50
PVO.4	3.13	>25	>25	>50
YU2.DG	>50	>25	>25	>50

Patient 1, Clone RU09

	1B218
MW965.26	>119
BaL.26	1.1
DJ263.8	>119
6535.3	3.6
RHPA4259.7	>100
TRO.11	>100
PVO.4	>100
YU2.DG	>100

c

Patient 8, Clone RU10

	8ANC192	8ANC134	8ANC13	8ANC131	8ANC182	8ANC50	8ANC45
MW965.26	>73	>50	>50	>50	>115	>50	>50
BaL.26	0.08	0.02	0.04	0.06	0.08	0.17	0.296
DJ263.8	<0.03	0.003	0.008	0.004	<0.05	0.04	0.041
6535.3	0.34	0.06	0.27	0.2	0.89	2.27	0.813
RHPA4259.7	>50	>50	>50	>50	>100	>50	>50
TRO.11	>100	>50	>50	>50	>100	>50	>50
PVO.4	0.89	0.46	0.63	0.81	1.2	3.89	4.259
YU2.DG	0.09	0.15	0.21	0.18	0.22	0.42	0.499

Patient 8, Clones RU11-15

	8ANC57	8ANC195	8ANC24	8ANC14	8ACN5
MW965.26	24.1	>50	0.29	2.01	>50
BaL.26	4.35	>50	47.53	>50	>50
DJ263.8	30.19	>50	>50	>50	>50
6535.3	>103	0.2	>50	>50	>50
RHPA4259.7	1.65	0.34	>50	>50	>50
TRO.11	32.07	0.18	>50	>50	>50
PVO.4	101.15	0.52	>50	>50	>50
YU2.DG	27.52	0.79	>50	>50	>50

d

Patient 12, Clone RU16

	12A12	12A21	12A4	12A37	12A22	12A16
MW965.26	0.042	0.075	0.098	0.056	0.06	0.167
BaL.26	0.017	<0.001	<0.001	0.005	0.04	0.042
DJ263.8	0.002	0.035	0.017	0.013	0.08	0.012

TABLE 4-continued

6535.3	21.97	>50	>50	>50	>25	15.44
RHPA4259.7	0.086	0.038	0.041	0.042	0.04	0.207
TRO.11	0.288	0.164	0.257	0.827	0.56	0.751
PVO.4	0.928	0.584	0.819	0.516	0.45	2.44
YU2.DG	0.084	0.015	0.018	0.019	0.11	0.234

Patient 12, Clone RU16

	12A20	12A6	12A23	12A46	12A55
MW965.26	0.192	0.112	5.1	>50	0.58
BaL.26	0.035	0.072	0.57	0.013	2.87
DJ263.8	0.05	0.004	0.63	5.79	>50
6535.3	48.73	>24	14.73	48.85	>50
RHPA4259.7	0.109	0.227	0.496	>50	>50
TRO.11	0.689	1.52	2.88	>50	21.45
PVO.4	3.04	3.32	2.24	2.18	0.99
YU2.DG	0.142	0.222	0.053	0.49	0.1

B12 and NIH45 Clone

	B12	VRC01	NIH45-46
MW965.26	0.2	<0.08	0.04
BaL.26	0.2	0.1	<0.04
DJ263.8	>50	0.08	<0.04
6535.3	1.4	0.539	0.14
RHPA4259.7	0.1	0.06	<0.05
TRO.11	>50	0.2	1.9
PVO.4	>50	0.2	0.17
YU2.DG	2.2	0.12	<0.05

e

Patient 3, clone RU01

	3BNC62	3BNC176	3BNC60	3BNC117	3BNC95	3BNC104
MW965.26	<0.09	<0.10	0.09	<0.09	<0.07	>50
BaL.26	<0.09	<0.10	<0.04	<0.09	<0.07	0.09
DJ263.8	0.1	<0.10	0.1	0.1	0.1	0.187
6535.3	2.24	1.7	1.77	2.44	4.5	>50
RHPA4259.7	<0.09	<0.10	0.07	0.137	<0.07	0.06
TRO.11	<0.09	<0.10	0.12	0.077	<0.07	30.847
PVO.4	0.23	0.16	0.27	0.19	0.23	0.901
YU2.DG	<0.09	<0.10	0.07	0.054	<0.07	0.097

Patient 3, clone RU01

	3BNC91	3BNC55	3BNC89	3ANC3	3BNC53	3BNC72	3BNC156
MW965.26	<0.08	0.15	0.16	0.64	0.61	0.37	0.47
BaL.26	>178	>30	>110	>50	>30	>139	>111
DJ263.8	>178	>30	>110	>50	>30	>139	>111
6535.3	6.7	5.53	5.92	>50	73.38	133.665	69.66
RHPA4259.7	0.52	8.03	>110	>50	>155	>139	>111
TRO.11	32.31	41.67	>110	>50	>155	>139	>111
PVO.4	2.65	6.5	10.18	>50	>155	>139	>111
YU2.DG	<0.08	1.07	1.49	>50	>155	>139	>111

Patient 3, clone RU01

	3BNC158	3BNC153	3BNC108	3BNC142	3BNC66	3BNC42	3BNC102
MW965.26	0.6	0.63	ND	0.8	29.98	ND	>50
BaL.26	>109	>100	>55	>172	>189	>26	>50
DJ263.8	>109	>100	>55	>172	>189	>26	>50
6535.3	97.75	>100	>55	>172	>189	>26	>50
RHPA4259.7	>109	>100	>55	>172	>189	>26	>50
TRO.11	>109	>100	>55	>172	>189	>26	>50
PVO.4	>109	>100	>55	>172	>189	ND	>50
YU2.DG	>109	>100	>55	>172	>189	>26	>50

TABLE 4-continued

Patient 3, Clones RU02-07						
	3A67	3A383	3BNC8	3ANC44	3A576	3ANC38
MW965.26	16	>25	0.74	>50	>50	>50
BaL.26	>50	>25	>50	>50	>50	>50
DJ263.8	>50	>25	>50	>50	>50	>50
6535.3	>50	ND	>50	>50	>50	>50
RHPA4259.7	>50	ND	>50	>50	>50	>50
TRO.11	>50	ND	>50	>50	>50	>50
PVO.4	>50	ND	>50	>50	>50	>50
YU2.DG	>50	ND	>50	>50	>50	>50

B12 and NIH 45 Clone			
	B12	VRC01	45-46
MW965.26	ND	<0.08	0.21
BaL.26	ND	0.1	0.06
DJ263.8	ND	0.553	0.06
6535.3	ND	2.7	0.28
RHPA4259.7	0.39	0.185	0.146
TRO.11	>50	0.832	9.56
PVO.4	>50	1.2	0.47
YU2.DG	7.8	0.372	0.08

f

Patient 1, Clone RU08							
	1B2640	1B2530	1B2364	1NC2	1NC9	1B2490	1B2351
MW965.26	>50	>50	>25	>50	>50	>50	>50
BaL.26	0.32	>50	>25	0.51	19.92	0.3	>50
DJ263.8	>50	>50	>25	>50	>50	>50	>50
6535.3	>50	>50	>25	>50	>50	>50	>50
RHPA4259.7	0.25	>50	>25	4.33	0.4	1.97	>50
TRO.11	1.62	2.46	1.77	0.55	0.65	3.58	1.13
PVO.4	2.97	1.25	0.65	1.08	1.32	10.57	0.88
YU2.DG	0.7	7.74	>25	0.39	0.56	0.59	0.48

Patient 1, Clone RU08							
	1B344	1NC24	1NC3	1NC7	1NC33	1NC108	1B2644
MW965.26	>50	>50	>25	>50	>50	>50	>25
BaL.26	>50	>50	>25	>50	>50	>50	>25
DJ263.8	>50	>50	>25	>50	>50	>50	>25
6535.3	>50	>50	>25	>50	>50	>50	>25
RHPA4259.7	>50	>50	>25	>50	>50	>50	>25
TRO.11	0.89	0.66	>25	>50	>50	>50	>25
PVO.4	0.94	0.6	>25	7.17	10.12	25.08	>25
YU2.DG	1.29	0.55	>25	>50	>50	>50	>25

Patient 1, Clone RU08		
	1B2339	1NC123
MW965.26	>25	>50
BaL.26	>25	>50
DJ263.8	>25	>50
6535.3	>25	>50
RHPA4259.7	>25	>50
TRO.11	>25	>50
PVO.4	>25	>50
YU2.DG	>25	>50

Patient 1, Clone RU09	
	1B218
MW965.26	>119
BaL.26	5.61
DJ263.8	>119
6535.3	35.12
RHPA4259.7	>100
TRO.11	>100

TABLE 4-continued

PVO.4	>100
YU2.DG	>100

g

Patient 8, Clone RU 10

	8ANC192	8ANC134	8ANC13	8ANC131	8ANC182	8ANC50	8ANC45
TRO.11	>73	>50	>50	>50	>115	>50	>50
BaL.26	0.43	0.11	0.18	0.31	0.73	0.77	7.45
DJ263.8	0.1	0.044	0.069	0.046	0.11	0.15	0.166
6535.3	1.43	2	2.3	1.9	3.93	13.65	10.473
RHPA4259.7	>100	>50	>50	>50	>100	>50	>50
TRO.11	>100	>50	>50	>50	>100	>50	>50
PVO.4	3.94	2.5	3.7	4.9	4.43	14.99	17.315
YU2.DG	0.51	0.616	1.07	0.92	1.46	1.59	2.942

Patient 8, Clones RU11-15

	8AN57	8AN195	8AN24	8AN14	8AN5
TRO.11	>103	>50	0.76	6.64	>50
BaL.26	24.76	>50	>50	>50	>50
DJ263.8	>103	>50	>50	>50	>50
6535.3	>103	0.91	>50	>50	>50
RHPA4259.7	14.44	1.56	>50	>50	>50
TRO.11	>103	0.89	>50	>50	>50
PVO.4	>103	1.87	>50	>50	>50
YU2.DG	91.49	2.77	>50	>50	>50

h

Patient 12, Clone RU16

	12A12	12A21	12A4	12A37	12A22	12A16
MW965.26	0.2	0.85	1.24	0.3	0.21	0.58
BaL.26	0.08	0.004	0.007	0.03	0.14	0.25
DJ263.8	0.31	0.42	1.06	0.57	1.86	0.12
6535.3	>50	>50	>50	>50	>25	>42
RHPA4259.7	0.4	0.13	0.19	0.19	0.13	0.93
TRO.11	0.98	0.57	1.12	3.81	1.94	2.57
PVO.4	3.15	2.09	2.95	1.8	1.49	8.72
YU2.DG	0.31	0.06	0.1	0.07	0.36	1.13

Patient 12, Clone RU16

	12A20	12A6	12A23	12A46	12A55
MW965.26	2.2	0.52	>50	>50	4.49
BaL.26	0.23	0.47	3.47	0.08	>50
DJ263.8	ND	0.08	30.81	>50	>50
6535.3	ND	>24	>50	>50	>50
RHPA4259.7	0.49	1.02	1.69	>50	>50
TRO.11	2.41	5.15	10.11	>50	>50
PVO.4	11.2	17.34	7.81	797	4.3
YU2.DG	0.67	1.2	0.19	0.25	0.29

B12 and NIH45 Clone

	B12	VRC01	NIH45-46
MW965.26	0.2	<0.08	0.04
BaL.26	0.2	0.1	<0.04
DJ263.8	>50	0.08	<0.04
6535.3	1.4	0.539	0.14
RHPA4259.7	0.1	0.06	<0.05
TRO.11	>50	0.2	1.9
PVO.4	>50	0.2	0.17
YU2.DG	2.2	0.12	<0.05

TABLE 5

a

In vitro Tzm-bl neutralization assay, extended panel IC50 values

	B12	VRC01	NIH45-46	3BNC60	3BNC62	3BNC117	3BNC55
Q842.d12	>50	0.03	0.008	0.01	<0.01	<0.01	0.011
3415.v1.c1	2.5	0.06	0.017	0.1	0.17	0.17	0.11
3365.v2.c20	>50	0.03	0.029	0.02	0.03	0.03	0.221
H086.8*	>50	>50	>30	>15	>15	>15	>30
ZM53M.PB12	>50	1.3	0.187	0.22	0.3	0.21	12.549
Du172.17*	0.3	>50	>30	3.81	1.72	1.19	3.518
ZM109F.PB4	>50	0.128	0.059	0.22	0.14	0.14	0.083
3016.v5.c45	1.1	0.16	>30	1.4	0.42	1.38	>30
231965.c1	0.07	0.34	0.021	0.07	0.05	0.05	0.505
X1254_c3	>50	0.07	0.027	0.09	0.08	0.08	0.138
250-4*	>50	>50	>30	>15	>15	>15	0.236
251-18	>50	2.5	1.445	0.35	0.32	0.26	>30
278-50*	>50	>50	>30	>15	>15	>15	>30
620345.c1*	>50	>50	>30	>15	>15	>15	>30
R1166.c1	>50	1.7	0.445	0.14	0.32	0.17	0.298

In vitro Tzm-bl neutralization assay, extended panel IC50 values

	1NC9	1B2530	8ANC131	8ANC134	8ANC195	12A12	12A21
Q842.d12	0.02	0.249	0.053	0.061	>30	0.014	0.015
3415.v1.c1	0.266	0.065	0.299	0.323	2.404	0.121	0.82
3365.v2.c20	0.329	4.357	>30	>30	>30	0.068	0.045
H086.8*	>30	>30	>50	>50	0.095	>30	>30
ZM53M.PB12	0.705	0.912	>30	>30	9.626	0.593	0.42
Du172.17*	>30	>30	>30	>30	10.797	0.196	0.126
ZM109F.PB4	0.023	>30	>30	>30	>30	0.148	2.104
3016.v5.c45	>30	>30	>30	>30	0.195	1.163	0.097
231965.c1	0.393	0.168	6.346	>30	0.514	2.217	>30
X1254_c3	>30	>30	>30	>30	1.524	1.032	26.793
250-4*	>30	>30	>50	>50	>50	>30	>30
251-18	1.234	9.847	0.968	1.56	0.284	2.622	1.713
278-50*	>30	>30	>50	>50	>50	>30	>30
620345.c1*	>30	>30	>50	>50	>50	>30	>30
R1166.c1	0.651	0.119	>30	>30	0.986	0.342	0.292

b

In vitro Tzm-bl neutralization assay, extended panel IC80 values

	B12	VRC01	45-46	3BNC60	3BNC62	3BNC117	3BNC55
Q842.d12	>50	0.096	0.026	0.03	0.03	0.01	0.062
3415.v1.c1	14.1	0.15	0.069	0.37	0.4	0.47	0.388
3365.v2.c20	>50	0.17	0.114	0.08	0.09	0.1	2.341
H086.8*	>50	>50	>30	>15	>15	>15	>30
ZM53M.PB12	>50	4	0.652	0.76	1.1	0.85	>30
Du172.17*	2.6	>50	>30	>15	12.18	8.9	>30
ZM109F.PB4	>50	0.754	0.22	1.23	0.78	0.88	0.396
3016.v5.c45	4	0.42	>30	7.38	2.35	>15	>30
231965.c1	0.16	1.2	0.1	0.25	0.22	0.22	2.78
X1254_c3	>50	0.19	0.078	0.29	0.27	0.27	0.571
250-4*	>50	>50	>30	>15	>15	>15	1.922
251-18	>50	11.2	5.255	0.96	1	0.82	>30
278-50*	>50	>50	>30	>15	>15	>15	>30
620345.c1*	>50	>50	>30	>15	>15	>15	>30
R1166.c1	>50	4.6	1.679	0.51	0.89	0.64	2.351

In vitro Tzm-bl neutralization assay, extended panel IC80 values

	1NC9	1B2530	8ANC131	8ANC134	8ANC195	12A12	12A21
Q842.d12	0.133	2.191	0.179	0.205	>30	0.06	0.066
3415.v1.c1	1.002	0.35	1.555	2.643	17.743	0.418	0.296
3365.v2.c20	2.163	>30	>30	>30	>30	0.192	0.166
H086.8*	>30	>30	>50	>50	5.328	>30	>30
ZM53M.PB12	2.771	4.022	>30	>30	>30	2.069	1.458
Du172.17*	>30	>30	>30	>30	>30	0.992	0.037
ZM109F.PB4	0.146	>30	>30	>30	>30	0.698	13.686
3016.v5.c45	>30	>30	>30	>30	0.872	11.864	0.358
231965.c1	2.276	0.963	>30	>30	2.355	15.102	>30
X1254_c3	>30	>30	>30	>30	6.949	5.777	>30
250-4*	>30	>30	>50	>50	>50	>30	>30

TABLE 5-continued

251-18	6.291	>30	5.55	6.281	1.511	9.39	6.063
278-50*	>30	>30	>50	>50	>50	>30	>30
620345.c1*	>30	>30	>50	>50	>50	>30	>30
R1166.c1	2.669	0.684	>30	>30	4.83	1.85	2.137

TABLE 6

Affinity of IgG Antibodies to YU-2 gp140 and 2CC-core Ligands Measured by Surface Plasmon Resonance

	gp140			2CC-Core		
	k_a ($M^{-1}s^{-1}$)	k_d (s^{-1})	K_D (M)	ka ($M^{-1}s^{-1}$)	k_d (s^{-1})	K_D (M)
12A12	4.59E+04	1.44E−05	3.15E−10	6.33E+04	1.70E−06	2.69E−11
12A21	9.18E+04	3.44E−07	3.75E12	1.82E+05	3.30E−04	1.81E−09
12AGL	/	/	/	/	/	/
3BNC60	2.73E+04	1.86E−04	6.81E−09	3.02E+04	1.64E−03	5.45E−08
3BNC117	3.04E+04	1.99E−04	6.54E−09	1.49E−03	4.05E+04	3.68E−08
3BNC55	1.31E+04	7.55E−04	5.78E−08	8.15E−04	3.16E+04	2.57E−08
3BNC66	1.60E+04	1.41E−03	8.81E−08	3.96E+04	1.33E−03	3.36E−08
3BNC156	1.13E+04	1.98E−03	1.75E−07	1.88E+04	1.53E−03	8.12E−08
3BNC108	/	/	/	/	/	/
3BNC60GL	/	/	/	/	/	/
8ANC131	6.59E+04	1.09E−03	1.65E−08	4.88E+04	3.23E−03	6.61E−08
8ANC134	1.55E+04	1.74E−03	1.13E−07	2.08E+04	9.57E−04	4.61E−08
8AGL	/	/	/	/	/	/
8ANC195	4.88E+04	1.67E−03	3.43E−08	2.41E+04	1.32E−03	5.47E−08
1NC9	4.83E+04	5.81E−04	1.20E−08	5.11E+04	2.36E−04	4.61E−09
1B2530	4.74E+04	1.62E−03	3.42E−08	6.83E+04	4.02E−04	5.90E−09
1GL	/	/	/	/	/	/
4546	4.26E+04	2.87E−04	6.75E−09	1.12E+05	4.94E−04	4.40E−09
VRC01	1.83E+04	8.08E−06	4.41E−10	2.84E+04	3.25E−05	1.15E−09

TABLE 7

	All Nucleotides	Consensus Nucleotides	Non Consensus Nucleotides
	a		
	Replacement/Silent mutation ratios for heavy chain sequences of 10 selected antibodies		
3BNC117HC	1.8	1.0	3.5
3BNC60HC	2.0	1.1	4.4
12A12HC	2.8	1.7	6.3
12A21HC	2.6	1.5	4.8
NIH4546HC	1.7	0.9	5.5
VRCO1HC	2.2	1.1	22.0
8ANC131HC	2.7	1.3	8.0
8ANC134HC	2.2	1.5	3.7
1B2530HC	2.0	0.9	11.0
1NC9HC	1.9	0.7	12.0
	b		
	Replacement/Silent mutation ratios for light chain sequences of 10 selected antibodies		
3BNC117KC	1.7	0.8	2.8
3BNC60KC	1.7	0.7	4.0
12A12KC	1.7	0.6	4.0
12A21KC	2.5	1.4	4.3
NIH4546KC	1.7	0.9	3.0
VRCO1KC	1.8	0.8	4.0
8ANC131KC	1.5	0.5	4.2
8ANC134KC	1.5	0.5	4.2
1B2530LC	1.9	2.0	1.8
1NC9LC	1.2	0.9	1.8

TABLE 8

Crystallization data collection and refinement statistics

Crystal	3BN60 Fab
Data collection*	
Wavelength (Å)	0.9537
Space group	P21
Unit Cell dimensions	
a (Å)	63.6
b (Å)	155.7
c (Å)	74.8
α, β, γ (Y)	90.0, 110.4, 90.0
Resolution, (Å)	39.172.65
R_{mrgd}-F (%)§	8.3 (55.5)
R_{meas} (%)§	7.7 (53.4)
I/σI	15.7 (2.5)
Completeness (%)	96.0 (68.1)
Multiplicity	5.0 (3.6)
Reflections	192709
Unique reflections	38111
Refinement	
Resolution (Å)	39.172.65
No. reflections	37086
R_{work}/R_{free} (%)†	20.7/25.7
RMSD Bond lengths (Å)	0.01
RMSD Bond angles (Y)	1.3
Average B-factor Å^2	64.9
Ramachandran analysis	
Favored (%)	91.9
Allowed (%)	7.6
Outlier (%)	0.5

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20140328862A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. An isolated HIV antibody comprising one or both of a heavy chain comprising the consensus amino acid sequence of SEQ ID NO:1 and a light chain comprising the consensus amino acid sequence of SEQ ID NO:2.

2. The isolated HIV antibody of claim **1** wherein the antibody neutralizes HIV virus ZM53M.PB12 at an IC_{50} concentration of less than 1.0 μg/ml, or HIV virus R1166.c1 at an IC_{50} concentration of less than 1.0 μg/ml, or DU172.17 at an IC_{50} concentration of less than 30 μg/ml.

3. The isolated HIV antibody of claim **1** wherein the antibody neutralizes a VRC01-resistant HIV virus at an IC_{50} concentration of less than 30 μg/ml.

4. An isolated HIV antibody selected from the group consisting of 3BNC117, 3BNC60, 12A12, 12A21, NIH45-46, bANC131, 8ANC134, IB2530, INC9 and 8ANC196

5. An isolated HIV antibody comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-583.

6. An isolated HIV antibody comprising at least one of insertion sequence SEQ ID No: 3 in the FR3 region of the heavy chain and insertion sequence SEQ ID No: 4 in the CDR3 region of the heavy chain.

7. A method to improve the neutralization potency of an isolated HIV antibody comprising making an isolated HIV antibody comprising at least one of insertion sequence SEQ ID No: 3 in the FR3 region of the heavy chain and insertion sequence SEQ ID No: 4 in the CDR3 region of the heavy chain

8. A composition comprising an isolated HIV antibody of any one of claims **1-6**.

9. A nucleic acid molecule encoding the isolated HIV antibody of any one of claims **1-6**.

10. A vector comprising the nucleic acid molecule of claim **9**.

11. A cell comprising the vector of claim **10**.

12. A pharmaceutical composition comprising at least one antibody of any one of claims **1-6** or a fragment thereof and a pharmaceutically acceptable carrier.

13. A method of preventing or treating an HIV infection or an HIV-related disease comprising the steps of:

a) identifying a patient in need of such prevention or treatment, and

b) administering to said patient a therapeutically effective amount of at least one HIV antibody of any one of claims **1-6**.

14. The method of claim **13**, additionally comprising the administration of a second therapeutic agent.

15. The method of claim **14**, wherein said second therapeutic agent is an antiviral agent.

16. A method for making an HIV antibody or fragment thereof according to claims **1-6**, said method comprising culturing a cell comprising a vector comprising a nucleic acid encoding the heavy and light chains of said antibody under conditions whereby the nucleic acid is expressed, and isolating said HIV antibody or fragment thereof.

17. A method to detect the HIV antibody of any one of claims **1-6** in a patient said method comprising isolating a biological sample from the patient and assaying the biological sample for the presence of the HIV antibody or a cell that contains at least one of the DNA or mRNA encoding the antibody.

18. A method for preventing or treating HIV infection or an HIV-related disease comprising steps: (a) identifying a patient in need of such prevention or treatment, (b) administering to said patient a therapeutically effective amount of at least one HIV antibody, or fragment thereof, made by the method of claim **16**.

19. An isolated nucleic acid molecule for amplifying at least one nucleic acid molecule according to claim **9**.

20. The method according to claim **16**, wherein the nucleic acid is amplified with at least one isolated nucleic acid molecule according to claim **19**.

21. An isolated oligonucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 584 to 613.

22. A kit comprising a pharmaceutically acceptable dose unit of a pharmaceutically effective amount of at least one isolated HIV antibody according to claim **1**, and a pharmaceutically acceptable dose unit of a pharmaceutically effective amount of an HIV agent selected from the group consisting of a non-nucleoside reverse transcriptase inhibitor, a protease inhibitor, a entry or fusion inhibitor and an integrase inhibitors, wherein the two pharmaceutically acceptable dose units can optionally take the form of a single pharmaceutically acceptable dose unit.

23. A kit for the diagnosis, prognosis or monitoring the treatment of HIV in a subject comprising one or more detection reagents which specifically bind to anti-HIV neutralizing antibodies in a biological sample from a subject.

24. The kit of claim **23**, further comprising reagents for performing PCR.

25. The kit of claim **23**, further comprising reagents for performing mass spectrometry.

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