

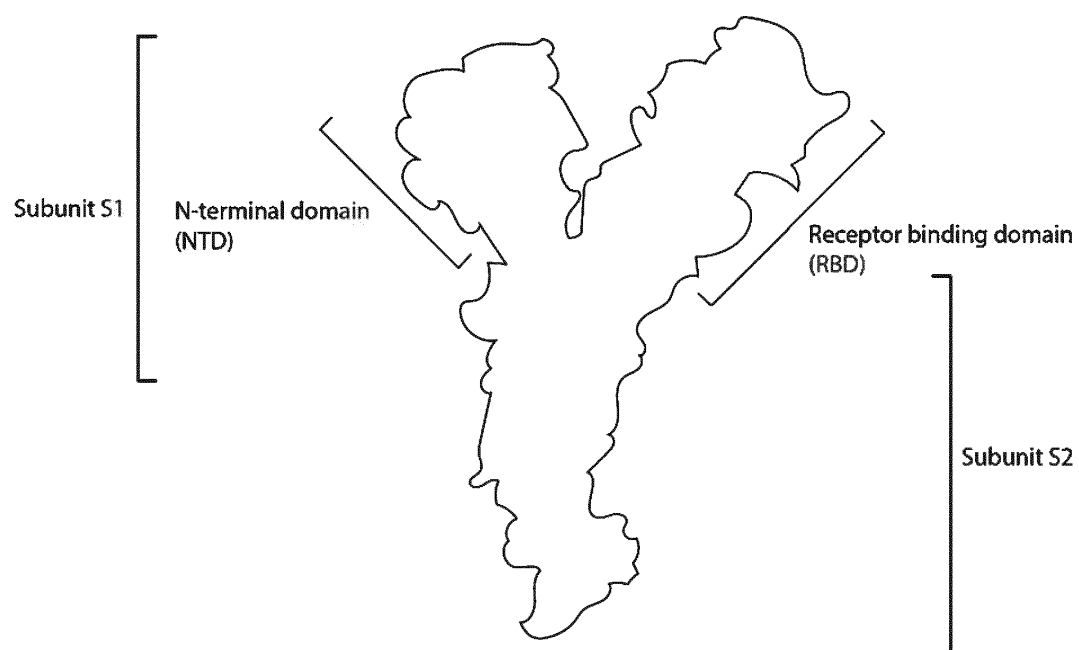


FIGURE 1

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHS 50
 TQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNI 100
 IRGWIFGTTLDSKTQSLIVNNATNVVIKVCEFOFCNDPFLGVYYHKNNK 150
 SWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGY 200
 FKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFOTLLALHRSYLT 250
 PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK 300
 CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASV 350
 YAWNRRKISNCVADYSVLYNASAFSTFKCYGVSPTKLNDLCFTNVYADSF 400
 VIRGDEVROIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYN 450
 YLYRLFRRSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPT 500
 NGVGYPYRVVVLSEFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG 550
 VLTESNKKFLPFQQFGRDIADTTDAVRDPQTEILDITPCSFGGVSVITP 600
 GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCL 650
 IGAEHVNNSYECDIPIGAGICASYQTQTNSEPRRARS**VASQSI**IAYTMSLG 700
 AENSVAYSNNIAIPTNFTISVTTTEILPVSMTKTSVDCTMYICGDSTECS 750
 NLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGF 800
 NFSQILPDPSKPSKRS**F**IEDLLFNKVTLADAGFIKQYGDCLGDLAARDLI 850
 CAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM 900
 QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQD 950
 VVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGR 1000
 LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM 1050
 SFPQSAPHGVVFLHVTYVPAQEKNETTAPAIKCHDGAHFPREGVFVSNGT 1100
 HWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE 1150
 ELDKYFRNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL 1200
 QELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSCCSCLKGCCSC 1250
 GSCCKFDEDDSEPVLKGVKLHYT 1273

FIGURE 2A

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVERSSVLHS 50
TQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNI 100
IRGWIFGTTLDSKTQSLLIVNNATNVVIKVEFQFCNDPFLGVYYHKNNK 150
SWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGY 200
FKIYSKHTPINLVRDLPOGFSALEPLVDLPIGINITRFQTLALHRSYLT 250
PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK 300
CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASV 350
YAWNRRKRI SNCVADYSVLYNSASFSTFKCYGVSPTKLNLDLCFTNVYADSF 400
VIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYN 450
YLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT 500
NGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG 550
VLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITP 600
GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCL 650
IGAHEVNNSYECDIPIGAGICASYQTQTN**PRRARS****VASQSI****IAYTMSLG** 700
AENSVAYSNN**SI****AIPTNFTISVTTEILPVSM****TKTSVDCTMYICGDSTEC** 750
NLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGF 800
NFSQILPDPSKPSKRS**F****IEDLLFNKVT****LADAGFIKQYGDCLG****DI****AARDLI** 850
CAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM 900
QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQD 950
VVNQNAQALNTLVKQLSSNFGAISSVLNDILSR**LD****PP****EA****EVQIDRLITGR** 1000
LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM 1050
SFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAHFPREGVFVSNGT 1100
HWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE 1150
ELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL 1200
QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIML**CCMTSCC****SCLKGCCSC** 1250
GSCCKFDEDDSEPVLKGVKLHYT 1273

FIGURE 2B

Cluster 1 - VH domain

	CDRH1	CDRH2	CDRH3
IMPI-024	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-016	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-034	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-046	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-015	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-043	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-011	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-050	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-009	EVQLVQSGE-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-049	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-058	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-044	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-051	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		
IMPI-026	EVQLVQSGA-EVKKPGESLIKISCKGSGYSF-----TSYWGTVRQMPKPKGLEMMGIIYPG--DSDTRYSPSFQ-GQVTISADKSIStAYLQWMSLKASDPTAMYYQARSYNW--NYFDYWGQGTLLVTVSS		

FIGURE 3A

Cluster 1 - VL domain

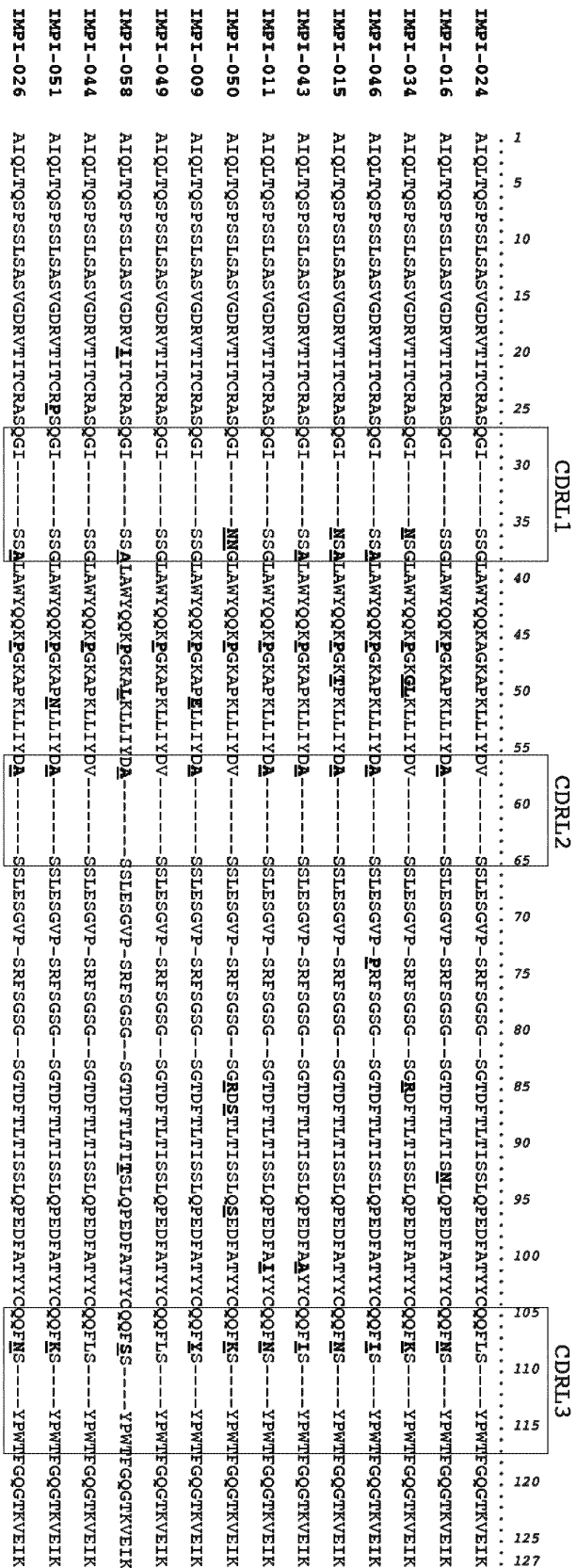


FIGURE 3B

Cluster 2 - VH domain

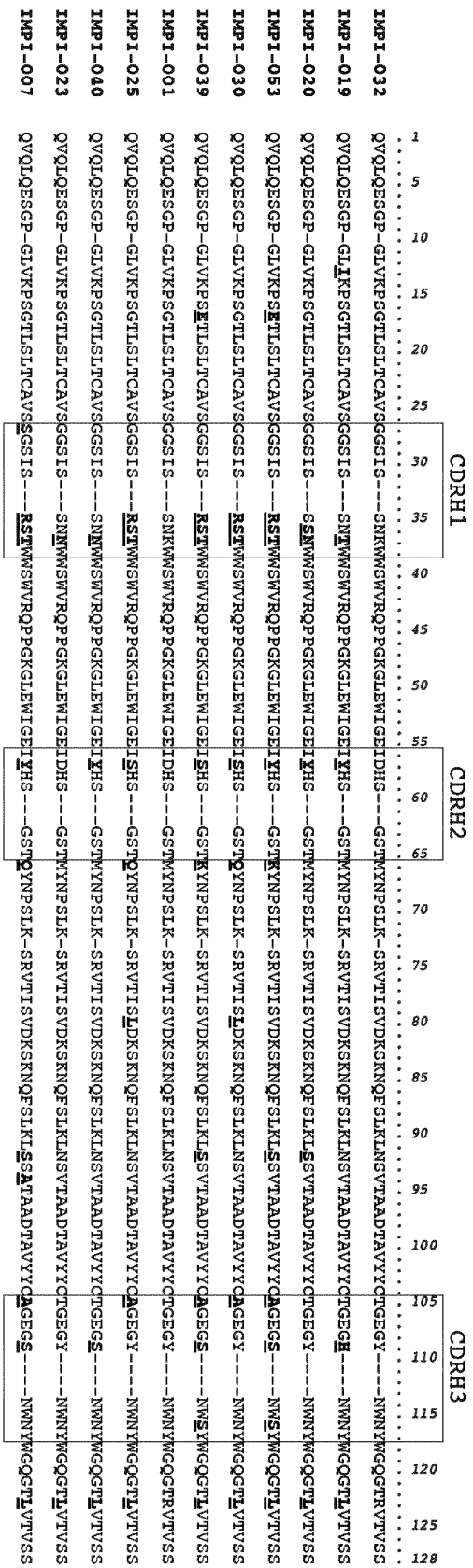


FIGURE 3C

Cluster 2 - VL domain

	CDRL1	CDRL2	CDRL3
IMPI-032	DVVMTQSPPLSLPVTILGQTASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-019	DVVLTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-020	DVVLTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-053	DVVMTQSPYSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-030	DVVMTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-039	DVVMTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-001	DVVLTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-025	DVVMTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-040	DVVMTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-023	YVVMTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK
IMPI-007	DVVMTQSPPLSLPVTILGQEPASISCRSSQSILYTDGNTYLSWFOQRPGQSPRRLIKV-----SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	SKWESGVP-DRESGSG--SGTDFTLKISRVEADVGIYCMQGTHTH-----WPLTFGGGKVEIK	WPLTFGGGKVEIK

FIGURE 3D

Cluster 3 - VH domain

	1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	128																																																																									
	CDRH1												CDRH2												CDRH3																																																																											
IMPI-027	QVQLQESGP	-GLV	KPSQ	TL	SL	TC	TV	S	G	S	I	S	---	S	Y	G	Y	M	N	N	I	R	O	H	P	G	K	G	L	E	N	I	G	T	Y	S	---	G	S	T	Y	N	P	S	L	K	-	S	R	V	T	I	S	V	D	T	S	K	N	Q	L	S	I	R	L	N	S	V	S	A	A	D	T	A	V	Y	Y	Q	A	R	D	F	G	G	N	S	N	Y	F	D	Y	M	G	G	T	L	V	T	V	S
IMPI-033	QVQLQESGP	-GLV	KPSQ	TL	SL	TC	TV	S	G	S	I	S	---	S	Y	G	Y	M	N	N	I	R	O	H	P	G	K	G	L	E	N	I	G	T	Y	S	---	G	S	T	Y	N	P	S	L	K	-	S	R	V	T	I	S	V	D	T	S	K	N	Q	L	S	I	R	L	N	S	V	S	A	A	D	T	A	V	Y	Y	Q	A	R	D	F	G	G	N	S	N	Y	F	D	Y	M	G	G	T	L	V	T	V	S
IMPI-018	QVQLQESGP	-GLV	KPSQ	TL	SL	TC	TV	S	G	S	I	S	---	R	G	E	Y	M	S	W	I	R	O	H	P	G	K	G	L	E	N	I	G	T	Y	S	---	G	S	T	Y	N	P	S	L	K	-	S	R	V	T	I	S	V	D	T	S	K	N	Q	L	S	I	R	L	N	S	V	S	A	A	D	T	A	V	Y	Y	Q	A	R	D	F	G	G	N	S	N	Y	F	D	Y	M	G	G	T	L	V	T	V	S
IMPI-014	QVQLQESGP	-GLV	KPSQ	TL	SL	TC	TV	S	G	S	I	S	---	S	Y	G	Y	M	S	W	I	R	O	H	P	G	K	G	L	E	N	I	G	T	Y	S	---	G	S	T	Y	N	P	S	L	K	-	S	R	V	T	I	S	V	D	T	S	K	N	Q	L	S	I	R	L	N	S	V	S	A	A	D	T	A	V	Y	Y	Q	A	R	D	F	G	G	N	S	N	Y	F	D	Y	M	G	G	T	L	V	T	V	S
IMPI-048	QVQLQESGP	-GLV	KPSQ	TL	SL	TC	TV	S	G	S	I	S	---	S	Y	G	Y	M	S	W	I	R	O	H	P	G	K	G	L	E	N	I	G	T	Y	S	---	G	S	T	Y	N	P	S	L	K	-	S	R	V	T	I	S	V	D	T	S	K	N	Q	L	S	I	R	L	N	S	V	S	A	A	D	T	A	V	Y	Y	Q	A	R	D	F	G	G	N	S	N	Y	F	D	Y	M	G	G	T	L	V	T	V	S
IMPI-045	QVQLQESGP	-GLV	KPSQ	TL	SL	TC	TV	S	G	S	I	S	---	S	Y	G	Y	M	S	W	I	R	O	H	P	G	K	G	L	E	N	I	G	T	Y	S	---	G	S	T	Y	N	P	S	L	K	-	S	R	V	T	I	S	V	D	T	S	K	N	Q	L	S	I	R	L	N	S	V	S	A	A	D	T	A	V	Y	Y	Q	A	R	D	F	G	G	N	S	N	Y	F	D	Y	M	G	G	T	L	V	T	V	S

FIGURE 3E

Cluster 3 - VL domain

	CDRL1	CDRL2	CDRL3
1			
5			
10			
15			
20			
25			
30			
35			
40			
45			
50			
55			
60			
65			
70			
75			
80			
85			
90			
95			
100			
105			
110			
115			
120			
125			
127			

FIGURE 3F

Cluster 4 - VH domain

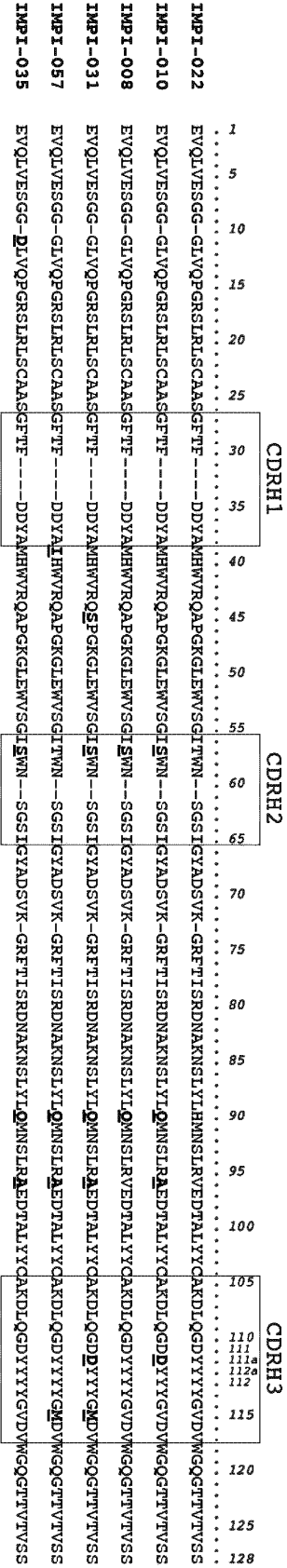


FIGURE 3G

Cluster 4 - VL domain

	CDRL1	CDRL2	CDRL3
IMPI-022	AIQLTQSPSSLSASVGDRTVITTCRASQGI-----SSALAWYQQRPGKAPKLLLYDA-----	SSLVSGVP--SRFGSR--SGNDFTLTISLQPEDFATFYCOQFIS-----YPLTFGGGTVEIK	YPLTFGGGTVEIK
IMPI-010	AIQLTQSPSSLSASVGDRTVITTCRASQGI-----SSALAWYQQRPGKAPKLLLYDA-----	SSLVSGVP--SRFGSR--SGNDFTLTISLQPEDFATFYCOQFIS-----YPLTFGGGTVEIK	YPLTFGGGTVEIK
IMPI-008	AIQLTQSPSSLSASVGDRTVITTCRASQGI-----SSALAWYQQRPGKAPKLLLYDA-----	SSLVSGVP--SRFGSR--SGNDFTLTISLQPEDFATFYCOQFIS-----YPLTFGGGTVEIK	YPLTFGGGTVEIK
IMPI-031	AIQLTQSPSSLSASVGDRTVITTCRASQGI-----SSALAWYQQRPGKAPKLLLYDA-----	SSLVSGVP--SRFGSG--SGNDFTLTISLQPEDFATFYCOQFIS-----YPLTFGGGTVEIK	YPLTFGGGTVEIK
IMPI-057	AIQLTQSPSSLSASVGDRTVITTCRASQGI-----SSALAWYQQRPGKAPKLLLYDA-----	SSLVSGVP--SRFGSR--SGNDFTLTISLQPEDFATFYCOQFIS-----YPLTFGGGTVEIK	YPLTFGGGTVEIK
IMPI-035	AIQLTQSPSSLSASVGDRTVITTCRASQGI-----SSALAWYQQRPGKAPKLLLYDA-----	SSLVSGVP--SRFGSR--SGNDFTLTISLQPEDFATFYCOQFIS-----YPLTFGGGTVEIK	YPLTFGGGTVEIK

FIGURE 3H

Cluster 5 - VH domain

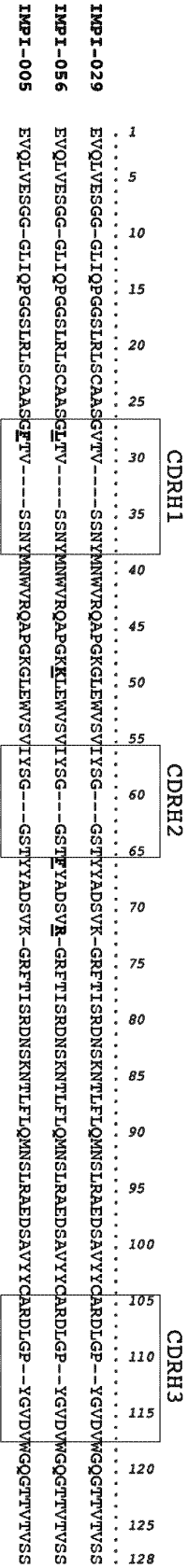


FIGURE 31

Cluster 5 - VL domain

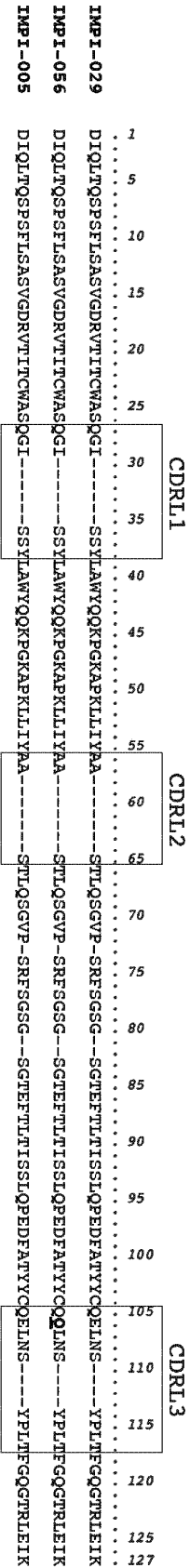


FIGURE 3J

Cluster 6 - VH domain

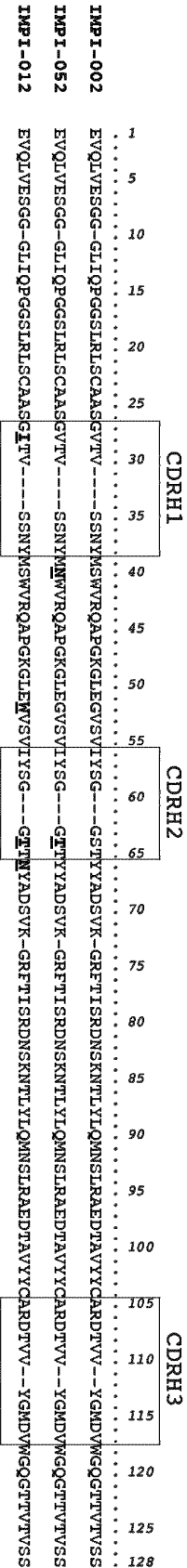


FIGURE 3K

Cluster 6 - VL domain

	1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	127
																											
IMPI-002	DIQLTQSPFSLASVGD	RVTITC	WASQGI	-----	SSYLAWYQOKPKG	AKPILIIYAA	-----	STLQSGVP-SRFS	SGG--SGTEFTLT	ISSLPEDFA	YYCQQLNS	-----	YPLTFGGG	TKVEIK													
IMPI-052	DIQLTQSPFSLASVGD	RVTITC	WASQGI	-----	SSYLAWYQOKPKG	AKPILIIYA	-----	STLQSGVP-SRFS	SGG--SGTEFTLT	ISSLPEDFA	YYCQQLNS	-----	YPLTFGGG	TKVEIK													
IMPI-012	DIQLTQSPFSLASVGD	RVTITC	WASQGI	-----	SSYLAWYQOKPKG	AKPILIIYAA	-----	STLQSGVP-SRFS	SGG--SGTEFTLT	ISSLPEDFA	YYCQQLNS	-----	YPLTFGGG	TKVEIK													

FIGURE 3L

Cluster 7 - VH domain

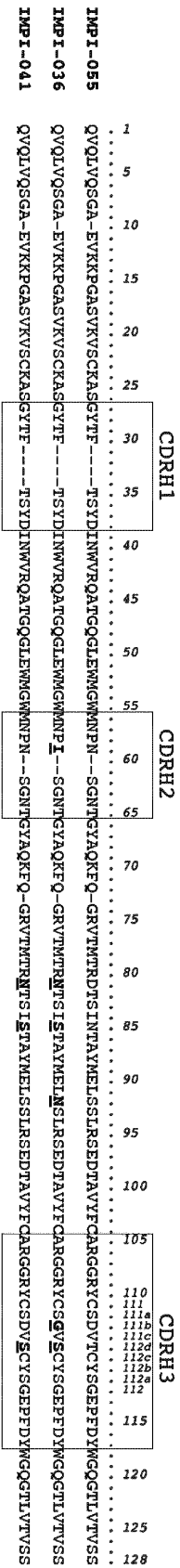


FIGURE 3M

Cluster 7 - VL domain

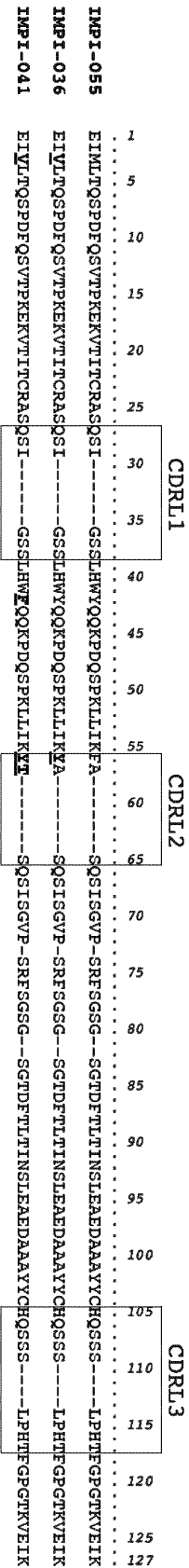


FIGURE 3N

Cluster 8 - VH domain

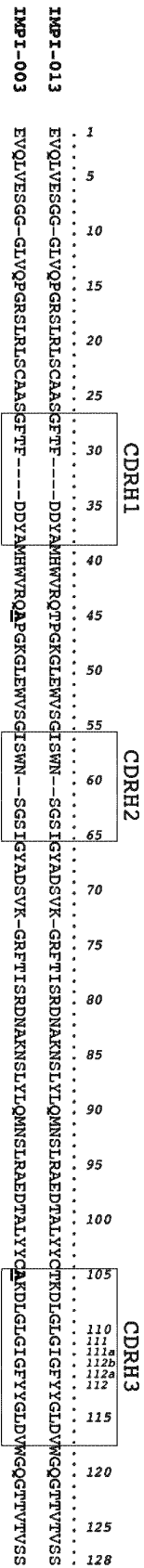


FIGURE 30

Cluster 8 - VL domain

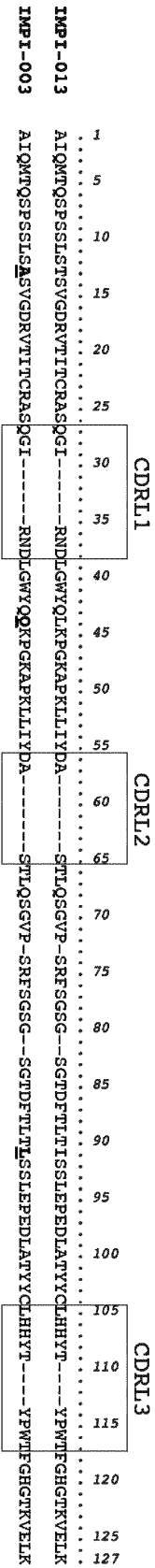


FIGURE 3P

Cluster 9 - VH domain

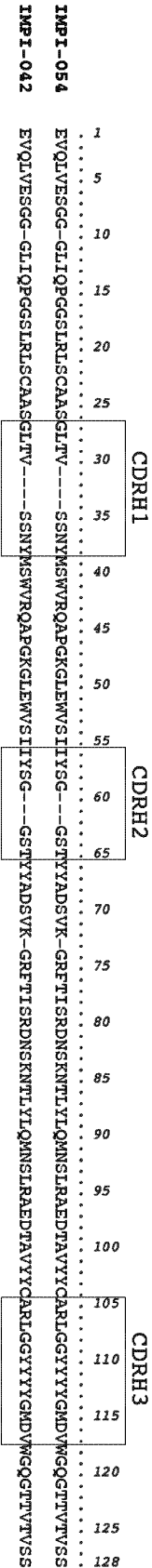


FIGURE 3Q

Cluster 9 - VL domain

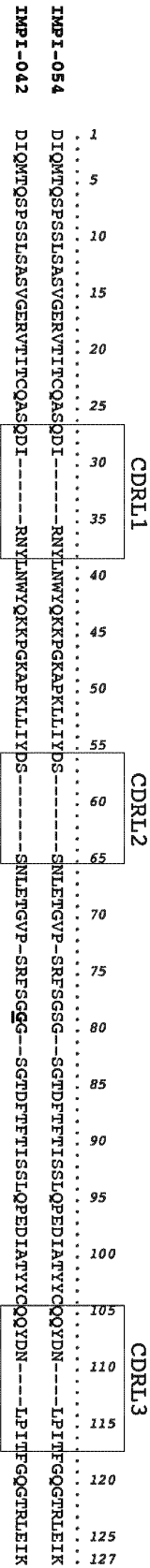


FIGURE 3R

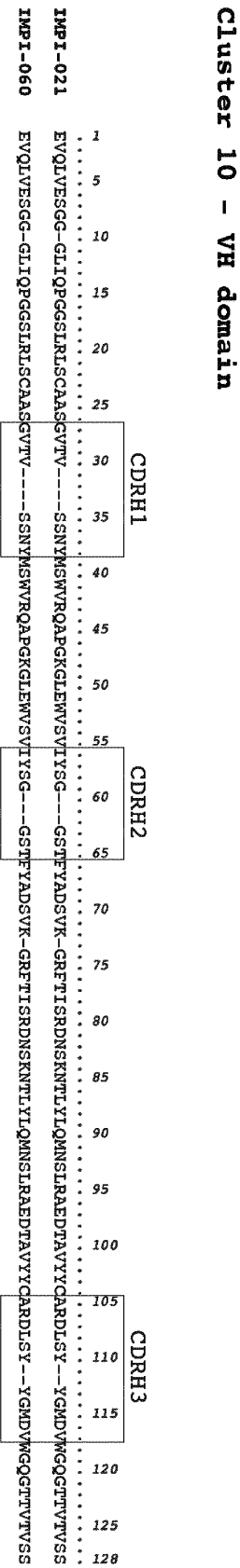


FIGURE 3S

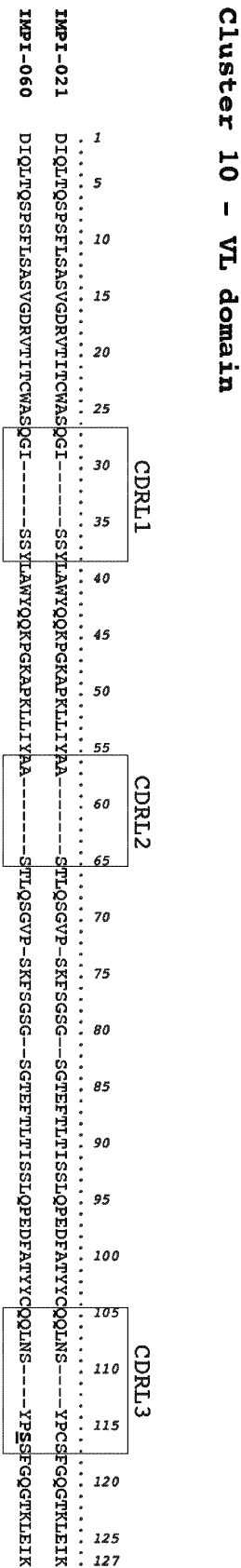


FIGURE 3T

Cluster 11 - VH domain

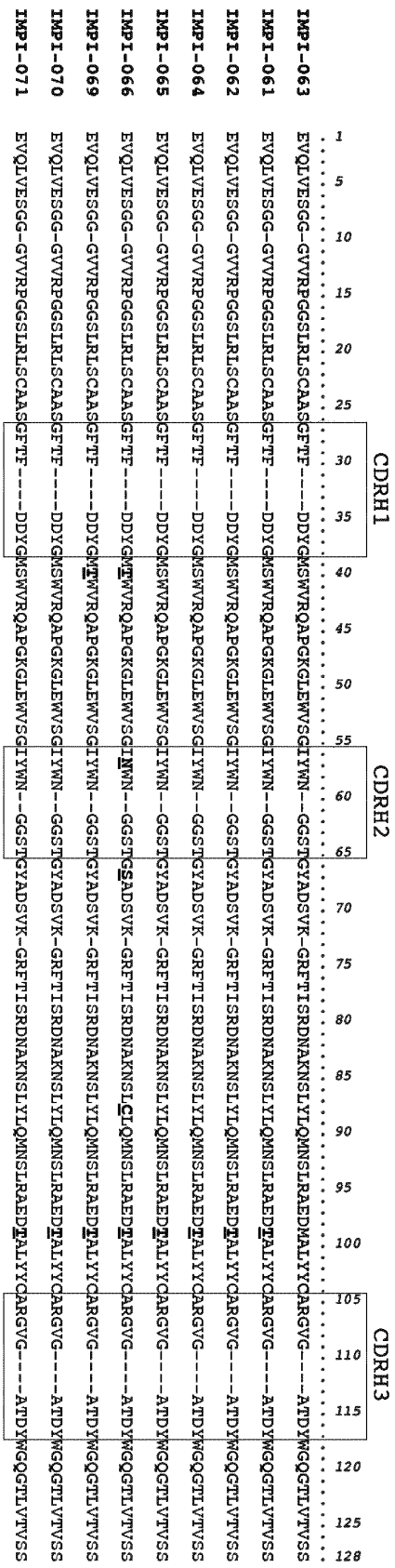


FIGURE 3U

Cluster 11 - VL domain

	CDRL1	CDRL2	CDRL3
1			
5			
10			
15			
20			
25			
30			
35			
40			
45			
50			
55			
60			
65			
70			
75			
80			
85			
90			
95			
100			
105			
110			
115			
120			
125			
127			
IMPI-063	EIVLTQSPGTLSSSGERATLACRASESVR-----GSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGN---SPMCSFGGQGTKLEIK		
IMPI-061	EIVLTQSPGTLSSSGERATLSCRASSVS-----GSLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGN---SPMCSFGGQGTKLESK		
IMPI-062	EIVLTQSPGTLSSSGERATLSCRASSSVR-----GSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGN---SPMCSFGGQGTKLEIK		
IMPI-064	EIVLTQSPGTLSSSGERATLSCRASSSVR-----GSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGH---SPMCSFGGQGTKLEIK		
IMPI-065	EIVLTQSPGTLSSSGERATLSCRASSSVR-----GSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGH---SPMCSFGGQGTKLEIK		
IMPI-066	EIVLTQSPGTLSSSGERATLSCRASSVS-----SSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGS---SPMSFGGQGTKLEIK		
IMPI-069	EIVLTQSPGTLSSSGERATLSCRTSQNIS-----GSFLAWYQOKSGQYPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGN---SPMCSFGGQGTKLEIK		
IMPI-070	ENVLTQSPGTLSSSGERATLSCRASSVS-----GSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--AGTDFTLTISRLEPEDFAVYYCQOYNN---SPMCSFGGQGTKLEIK		
IMPI-071	EIVLTQSPGTLSSSGERATLSCRASSSVR-----GSFLAWYQOKPGQAPRLLIYGA-----SRRATGIP-DRESGSG--SGTDFTLTISRLEPEDFAVYYCQOYGN---SPMCSFGGQGTKLEIK		

FIGURE 3V

Cluster 12 - VH domain

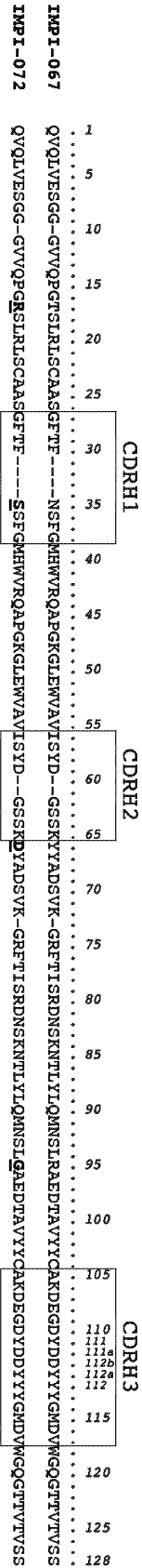


FIGURE 3W

Cluster 12 - VL domain

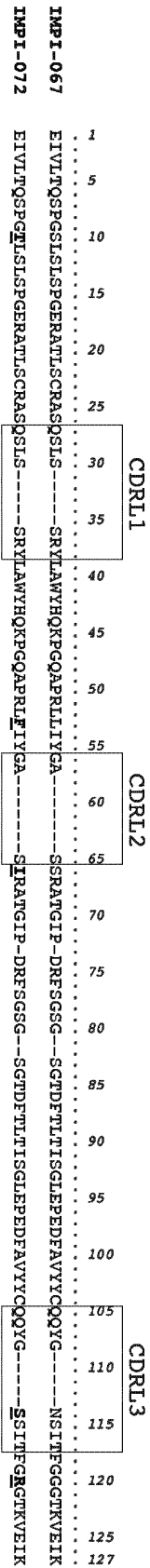


FIGURE 3X

Singletons - VH domain

	CDRH1	CDRH2	CDRH3
IMPI-004	QVQLVESGG-GVVQPGKSLRLSCAASGFTF-----SSYGMHWVRQAPGKGLEWVAIVTWD--GKNKYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA RYVNL M-----GYGMDVWGQGSTTIVTSS	1	110 111 111a 111b 112 112a 112b
IMPI-047	EVQLVESGG-GLIQPGGSLRLSCAASGFTV-----SSNMNMWVRQAPGKGLEWVSVIYSG--GSTYYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA RDLVA-----YGGDVMWGQGSTTIVTSS	5	115
IMPI-017	EVQLVESGG-GLIQPGGSLRLSCAASGLTV-----SSNMNMWVRQAPGKGLEWVSVIYSG--GSTYYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA RDLGT-----LGGDVMWGQGSTTIVTSS	10	
IMPI-028	EVQLVESGG-GLIQPGGSLRLSCAASGFTV-----SSNMNMWVRQAPGKGLEWVSVIYSG--GSTYYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA RYGD-----LYPDVMWGQGLVTVSS	15	
IMPI-006	QLQLQESGP-GLVKPSETLSLTCTVSGGIS--NSNYMGWIRQPPGKLEWIGSIYYS--GRYYNP SLK-SRVTISVDTSKNQFSIKLSVTAADTA VVYCA R MGLIMFG EFGMDVMWGQGSTTIVTSS	20	
IMPI-037	EVQLVESGG-GLVKPGGSLRLSCAASGFTF-----SNAMMSWVRQAPGKGLEWVGRIKKNADGTDIYAPVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCTTEELIMF-GESEFD CWGQGLVTVSS	25	
IMPI-059	EVQLVESGG-GLIQPGGSLRLSCAASGFTV-----SSIYMSWVRQAPGKGLEWVSIIYSR--GSTDYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA R DGTWVR-GVHAFDIWGQGMVTVSS	30	
IMPI-038	QVQLVESGG-GVVQPGKSLRLSCAASGFTF-----SSYGMHWVRQAPGKGLEWVAIVSYD--GSDKYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA KTVAGY YYY YGGMDVMWGQGSTTIVTSS	35	
IMPI-068	QVQLVESGG-DVVQPGKSLRLSCAASGFTF-----SRYGHWVRQAPGKGLEWVAIVSYD--GSDKYADSVK-GRFTISRDN SKNTLYIQMNSLR AEDTA VVYCA KQLPLIY-YYGMDVMWGQGSTTIVTSS	40	

Singletons - VL domain

	CDRL1	CDRL2	CDRL3
IMPI-004	EIVLTQSPGTLSPGDKATLSCRASQSI-----SSHLAWYQQRKGAPRLIYGA-----SSRATGIP-DKFSGSG--SGTDFTLTISRLEPEDEFAVYQQQYG-----SSLTFGGKVEIK		
IMPI-047	DIQLTQSPSFLSASVGDRTITTCWASQGI-----SSYLAWYQQRKGAPKVLIIYAA-----STLQSGVP-SRFSGSG--SGTEFTLTISLQPEDEFAITYYQQLINS-----NPLTFGGKVEIK		
IMPI-017	DIQLTQSPSFLSASVGDRTITTCWASQGI-----STYLAWYQQRKGAPKRLIIYAA-----STLQSGVP-SRFSGSG--SGTEFTLTISLQPEDEFAITYYQQLINS-----YLPITFGGKVEIK		
IMPI-028	EIVLTQSPGTLSPGERATLSCRASQSI-----SSYLAWYQQRKGAPRLIYGA-----SSRATGIP-DKFSGSG--SGTDFTLTISRLEPEDEFAVYQQQYGS-----SPRTFGGKVEIK		
IMPI-006	DIQMTQSPSSLASVGDRTITTCRASQGI-----SSWLAWYQQRKEKAPKSLIYDA-----SSLQRGVP-SRFSGSG--SGTDFTLTISLQPEDEFAHYQQQYNS-----YPLTFGGKTRVEIK		
IMPI-037	DIQLTQSPSFLSASVGDRTITTCWASQGI-----NSYLAWYQQRKGAPKRLIIYAA-----STLQSGVP-SRFSGSG--SGTEFTLTISLQPEDEFTYYQQQFND-----YPRITFGGKTRVEIK		
IMPI-059	DIQMTQSPSSLASISGDRVTITTCASQDI-----SNYLAWYQQRKGAPKRLIYDA-----SNIETGVP-SRFSGSG--SGTDFTLTISNLQPEDEIVTYQQQYDN-----LPSSFGGKTRVEIK		
IMPI-038	DIQMTQSPSSVSASVGDRTVITCRASQDI-----SSWLAWYQQRKGAPKFLIYDA-----SNIENGVP-SRFSGSG--SGTDFTLTISLQPEDEFAITYYQQQAKS-----FWITFGGKTRVEIN		
IMPI-068	AIQLTQSPSSLASVGDRTITTCRASQGI-----SSALAWYQQRKGAPNLLIYDA-----SNIENGVP-SRFSGSG--SGTDFTLTISLQPEDEFAITYYQQQFNI-----YPHITFGGKTRVDIK		

FIGURE 3Z

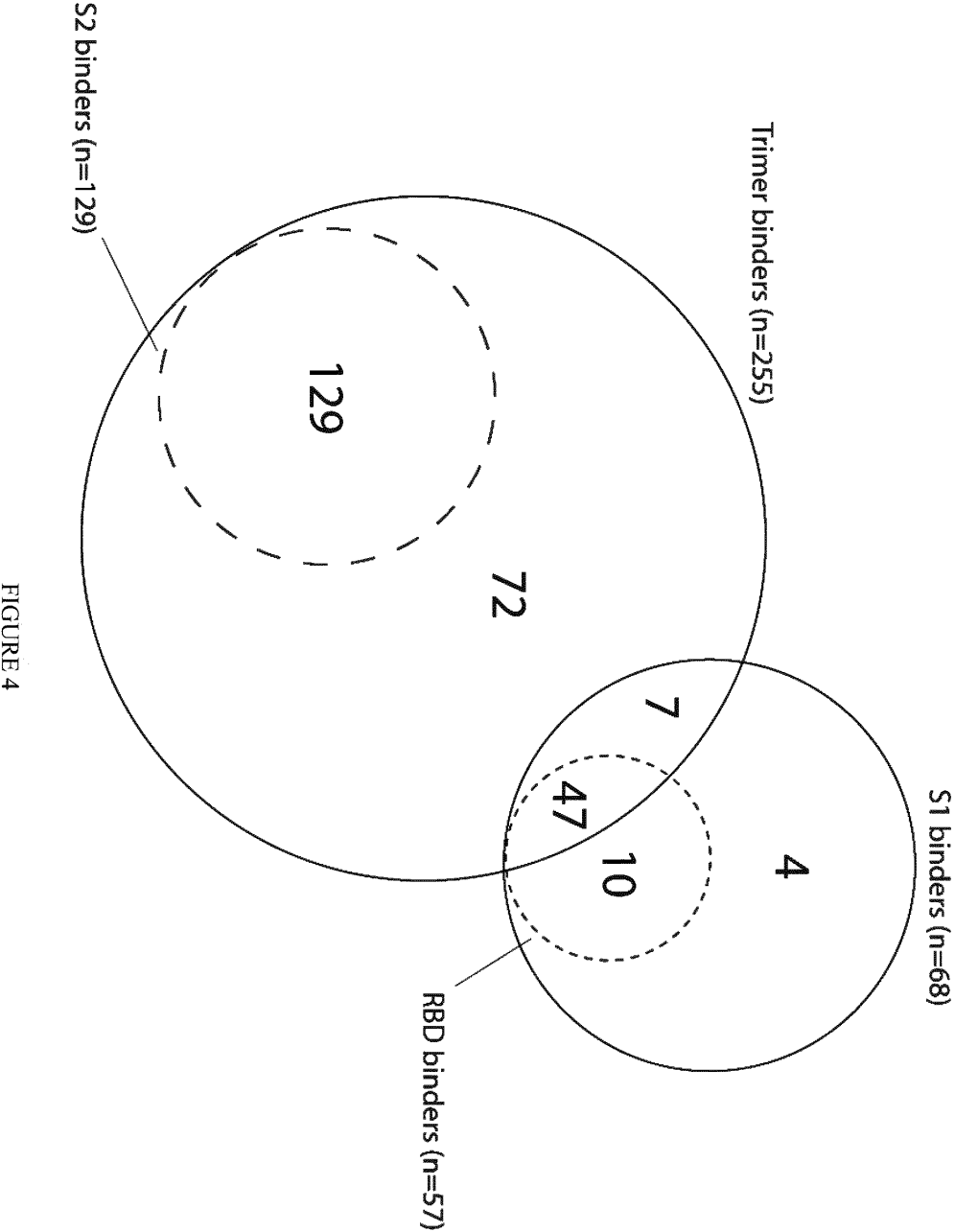


FIGURE 4

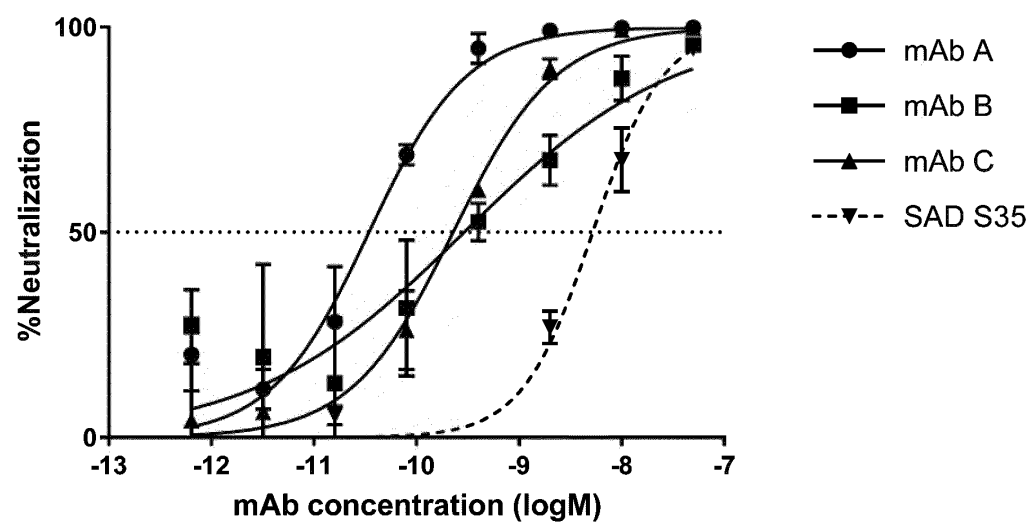


FIGURE 5

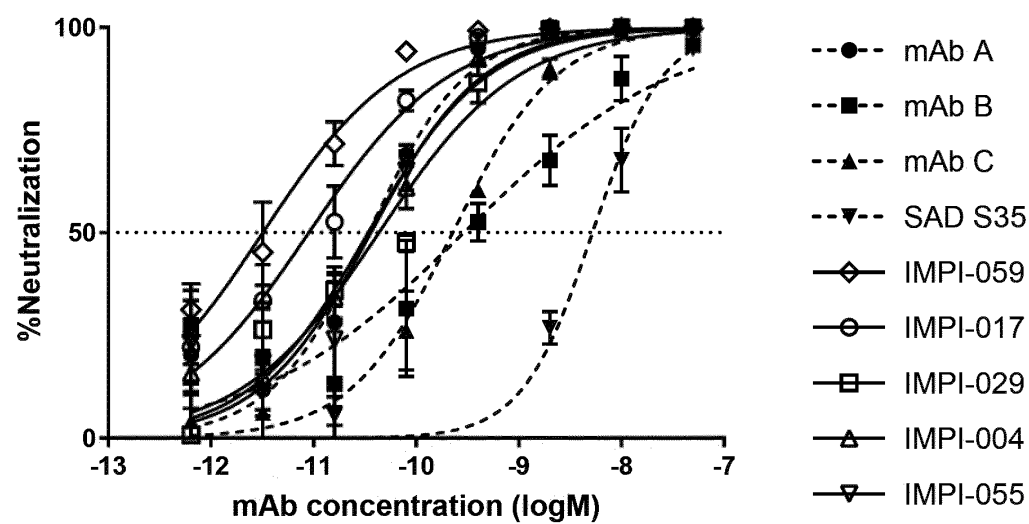


FIGURE 6

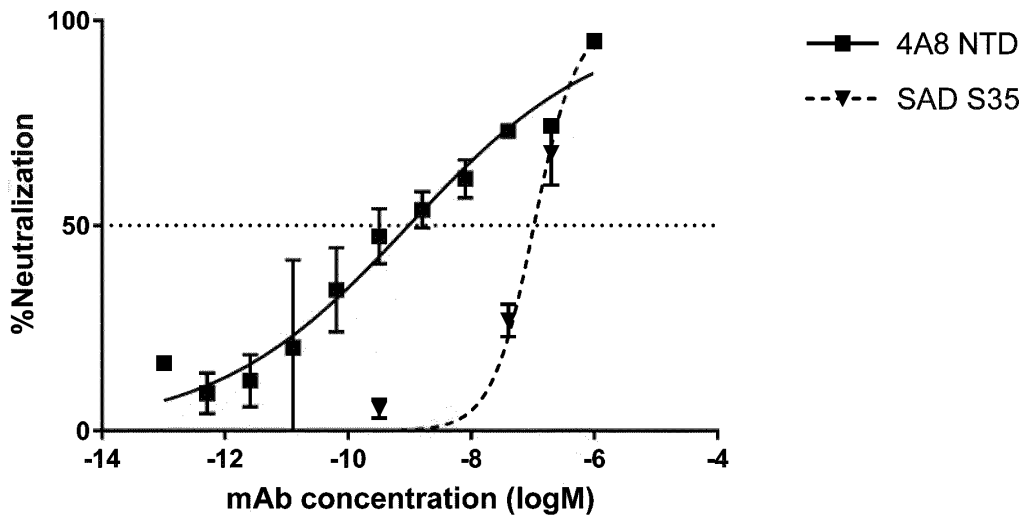


FIGURE 7

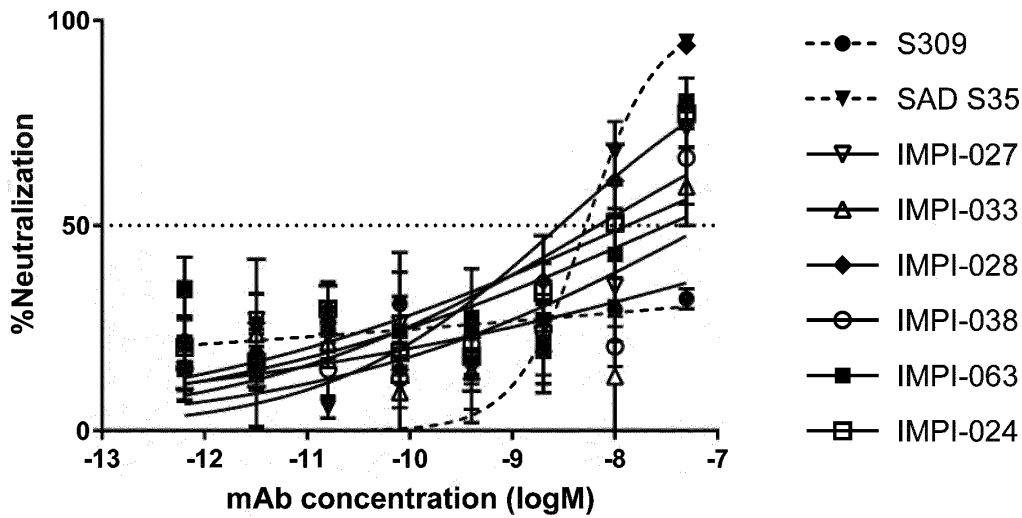


FIGURE 8

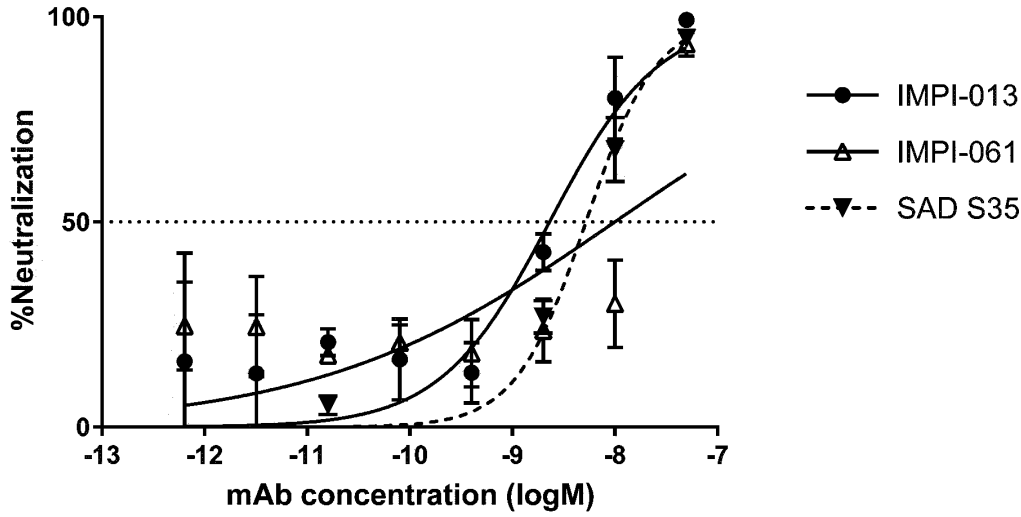


FIGURE 9

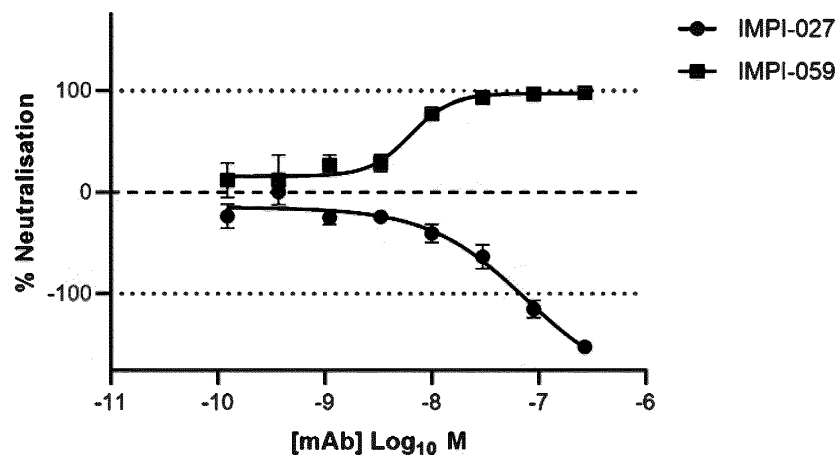


FIGURE 10

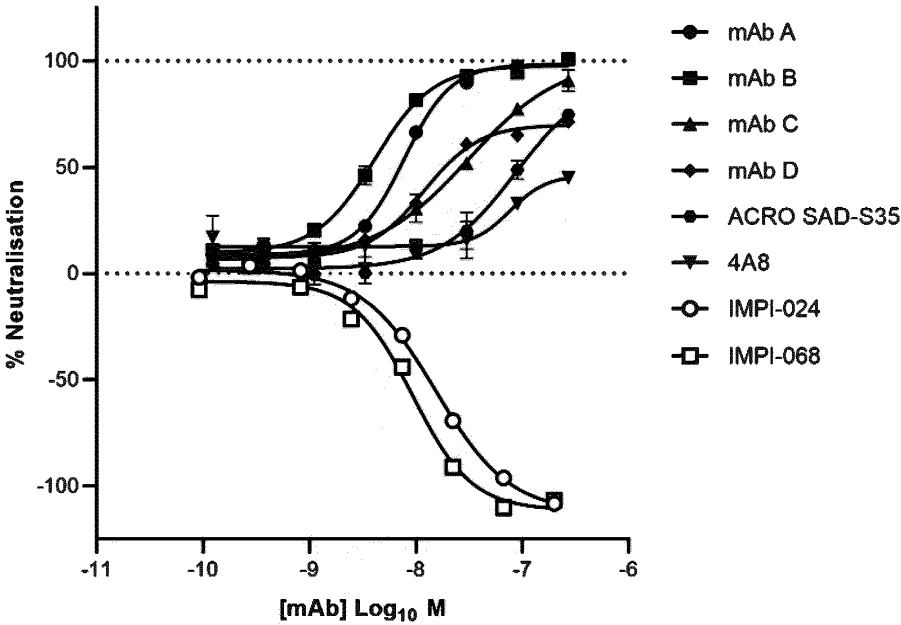


FIGURE 11

	IMPI-006	IMPI-047	IMPI-056	IMPI-005	IMPI-028	IMPI-054	IMPI-017	IMPI-004	IMPI-055	IMPI-059	SAD S35	IMPI-060	IMPI-037
IMPI-006													
IMPI-047													
IMPI-056													
IMPI-005													
IMPI-028													
IMPI-054													
IMPI-017													
IMPI-004													
IMPI-055													
IMPI-059													
SAD S35													
IMPI-060													
IMPI-037													

FIGURE 12

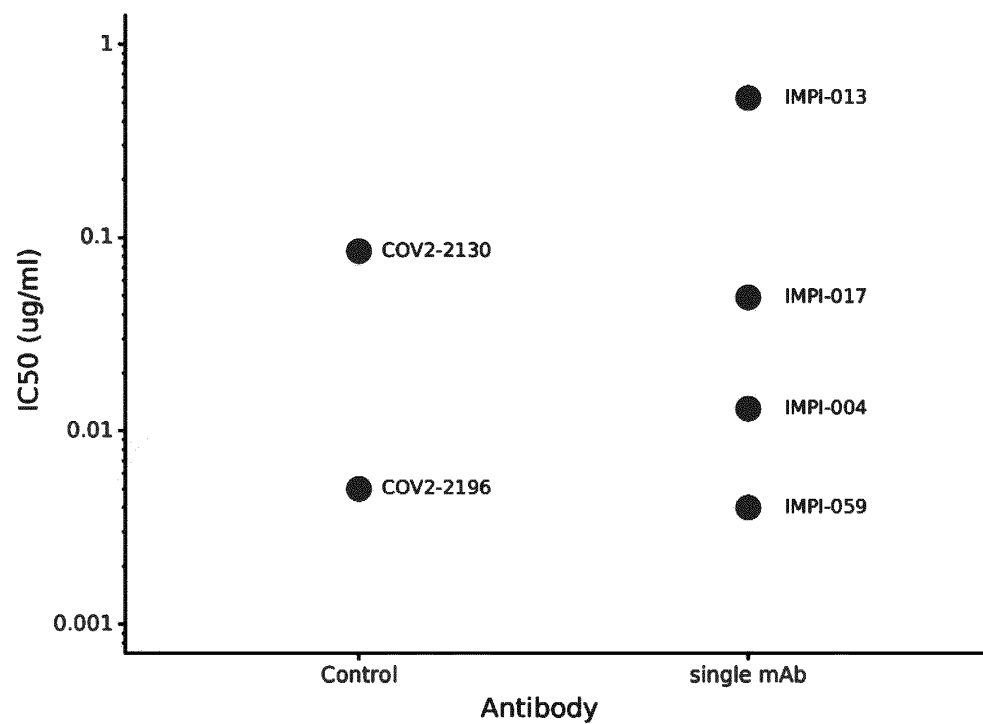


FIGURE 13

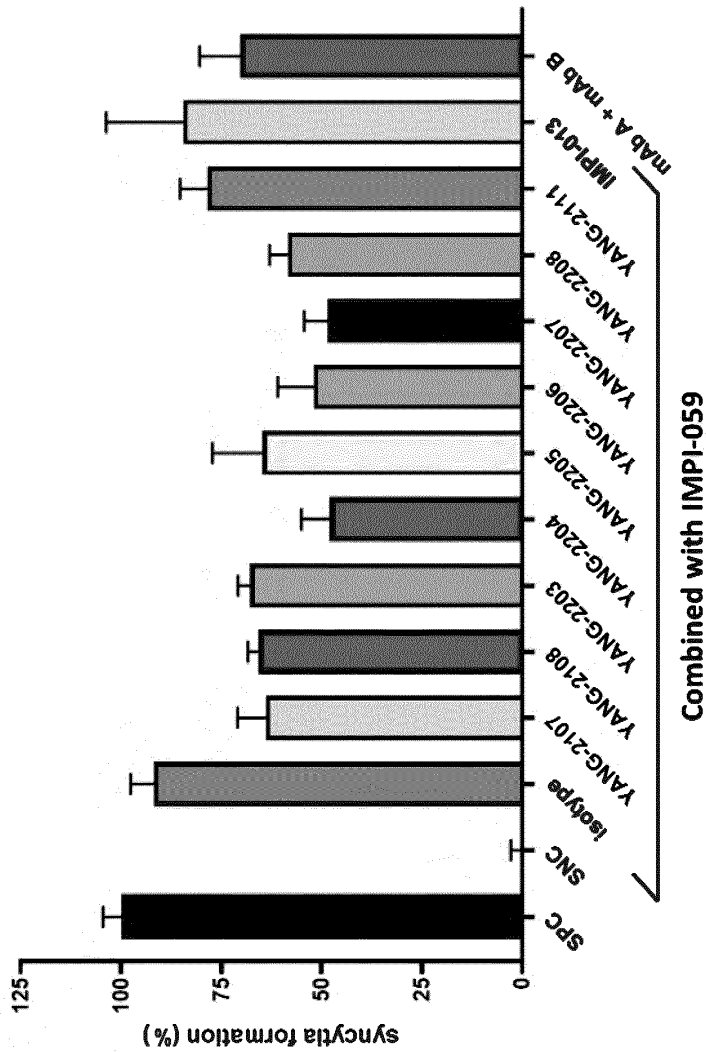


Figure 14

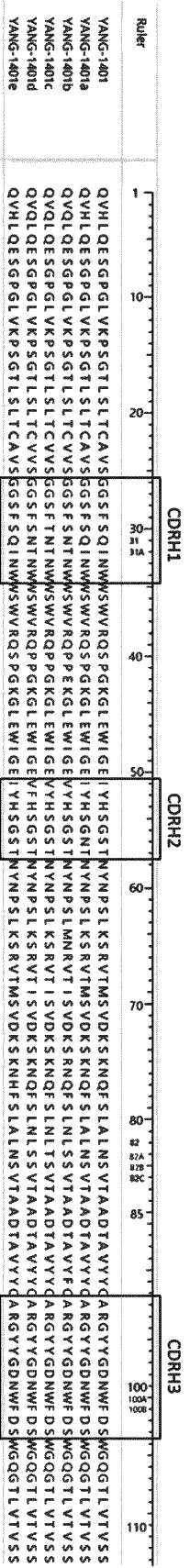


Figure 15

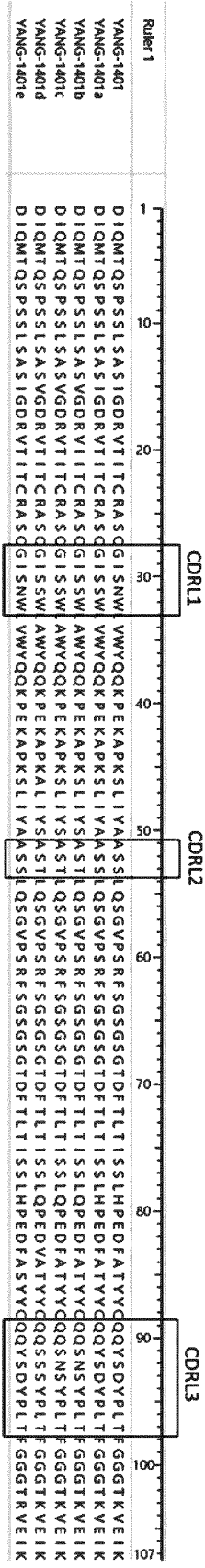


Figure 16

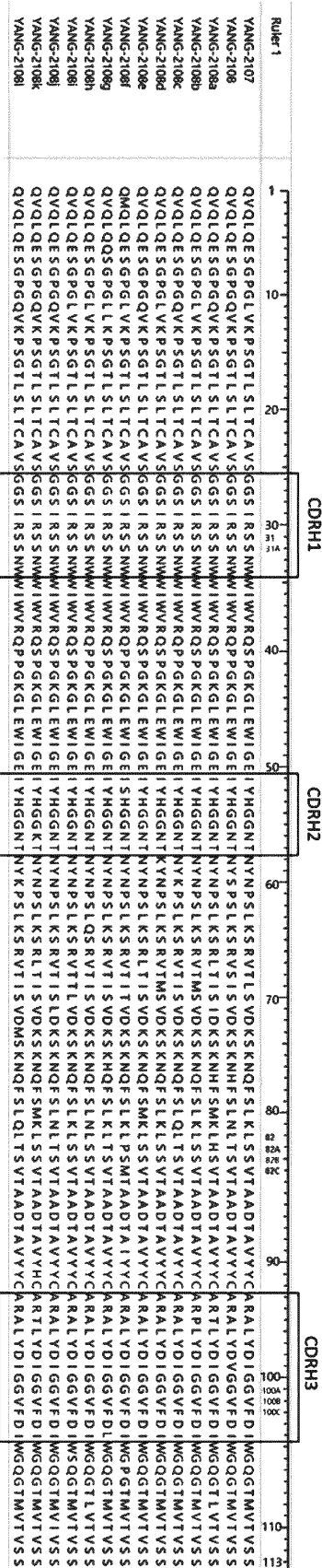


Figure 17

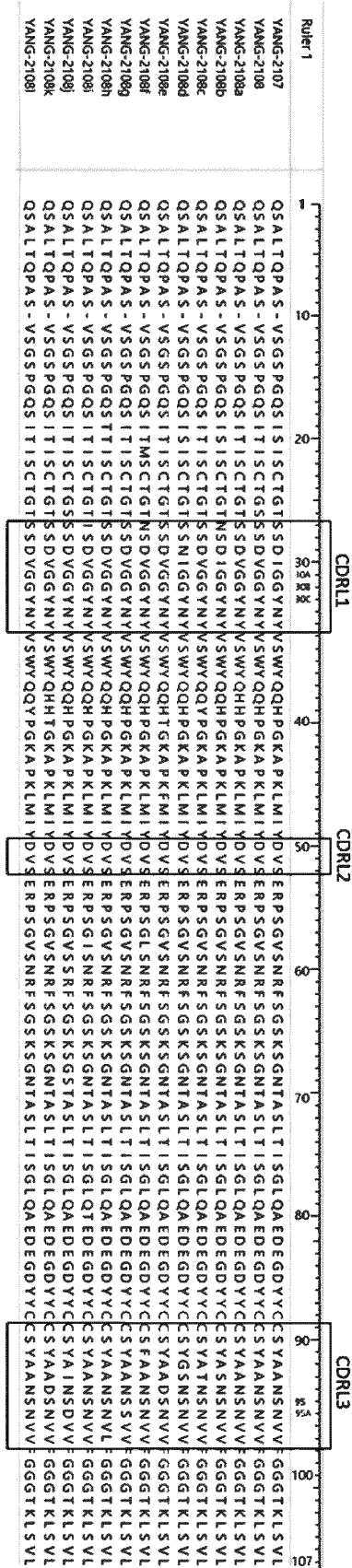


Figure 18

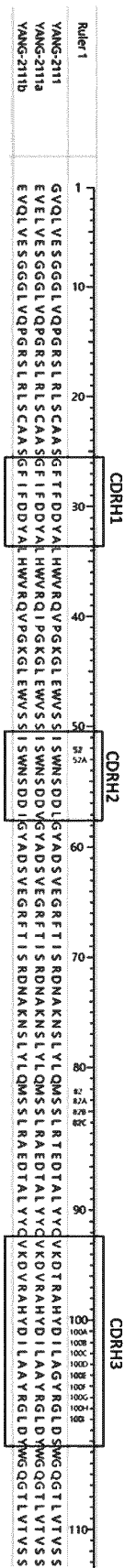


Figure 19

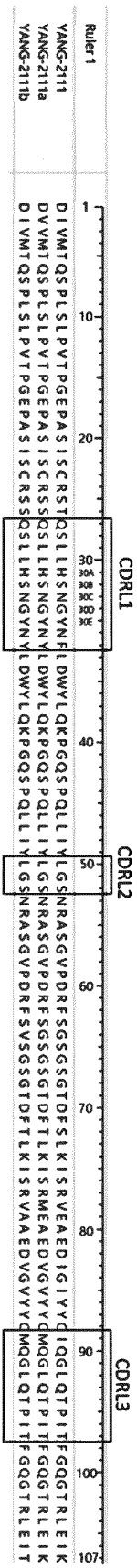


Figure 20

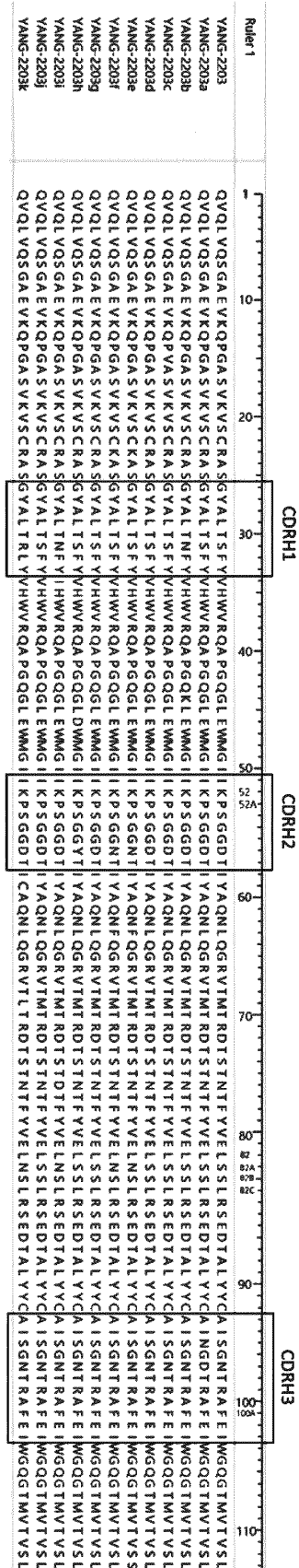


Figure 21

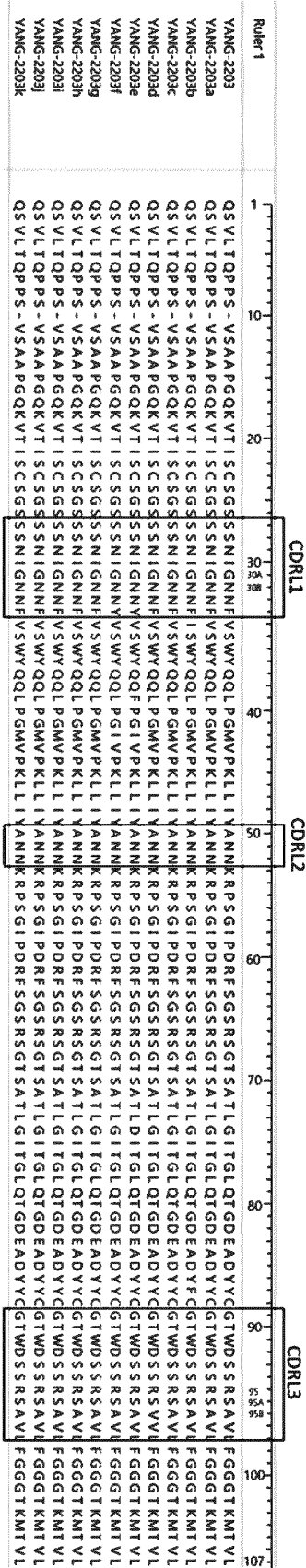
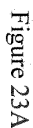


Figure 22



[illegible]

Figure 23B

[illegible]

Figure 23C



Figure 24A

50/51

Figure 24C

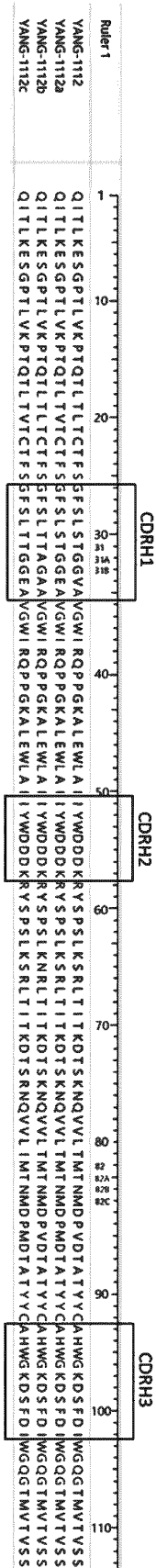


Figure 25

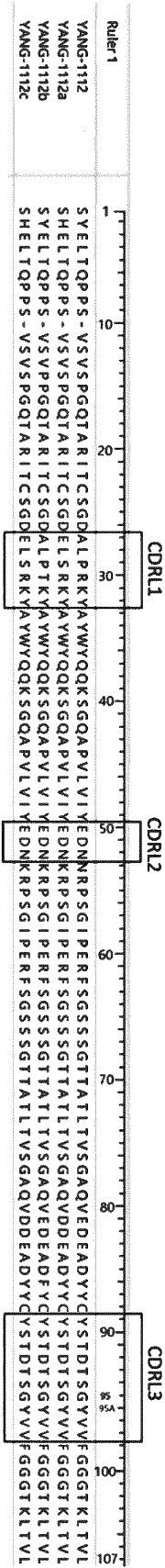


Figure 26