

VIP	HSDAVFTDNYTRLRKQMAVKKYLNSILN-----	SEQ ID NO 278
PACAP38	HSDGIFTDSYSRYSRKQMAVKKYLAAVLGKRYKQRVKNK	SEQ ID NO 279
PACAP27	HSDGIFTDSYSRYSRKQMAVKKYLAAVL-----	SEQ ID NO 280
	.:.*:* ***** :.*	

FIG. 1

FIG. 2A
VL alignment

	CDR-1	CDR-2
054M	DIVMTQSPDLSAVSLGERATINCKSSQSLDSDGKTYLNWLQQKPGQSPKRLIYLVSKLDSGVPDFRFSG	
919A	DIVMTQSPDLSAVSLGERATINCKSSQSLDSDGKTYLNWLQQKPGQPPKRLIYLVSTRESGVPDFRFSG	
917B	DIVMTQSPDLSAVSLGERATINCKSSQSLDSDGKTYLNWLQQKPGQPPKRLIYLVSTRESGVPDFRFSG	
890C	DIVMTQSPDLSAVSLGERATINCKSSQSLDADGKTYLNWLQQKPGQPPKRLIYWASTRESGVPDFRFSG	
604C	DIVMTQSPDLSAVSLGERATINCKSSQSLDSDGKTYLNWLQQKPGQPPKRLIYWASTRESGVPDFRFSG	
605C	DIVMTQSPDLSAVSLGERATINCKSSQSLDADGKTYLNWLQQKPGQPPKRLIYWASTRESGVPDFRFSG	
608C	DIVMTQSPDLSAVSLGERATINCKSSQSLDSDGKTYLNWLQQKPGQPPKRLIYWASTRESGVPDFRFSG	
609C	DIVMTQSPDLSAVSLGERATINCKSSQSLDADGKTYLNWLQQKPGQPPKRLIYWASTRESGVPDFRFSG	
627C	DIVMTQSPDLSAVSLGERATINCKSSQSLDSDGKTYLNWLQQKPGQPPKRLIYWASTRESGVPDFRFSG	
	CDR-3	
054M	SGSGTDFTLTISSLQAEDVAVYCWQGTGFPLTFGGGTKVEIK	
919A	SGSGTDFTLTISSLQAEDVAVYCWQGTGFPLTFGGGTKVEIK	
917B	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	
890C	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	
604C	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	
605C	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	
608C	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	
609C	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	
627C	SGSGTDFTLTISSLQAEDVAVYCWQGTWFDLTFGGGTKVEIK	

FIG. 2B
VH alignment

*		CDR-1	CDR-2
054M	EVQLVQSGAEVKKPGESVKVS	CKASGFTFTDSYMHVVRQAPGQGLEWMGLIYPFSADTRYAQKFQGRVT	
919A	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDSYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
917B	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDSYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
890C	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDVYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
604C	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDSYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
605C	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDSYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
608C	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDLYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
609C	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDLYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
627C	EVQLVQSGAEVKKPGSSVKVS	CKASGFTSDVYMHVVRQAPGQGLEWMGLIYPIFADTRYAQKFQGRVT	
		CDR-3	
054M	ITADESTAYMELSSLRSEDTAVYYCAIDYDGSFAYWGQGTLLTVVSS		
919A	ITADESTAYMELSSLRSEDTAVYYCAIDYDGSFAYWGQGTLLTVVSS		
917B	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		
890C	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		
604C	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		
605C	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		
608C	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		
609C	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		
627C	ITADESTAYMELSSLRSEDTAVYYCAIDQDGSFAYWGQGTLLTVVSS		

* All CDRs are defined according to Kabat definition, except heavy chain CDR-1, which is defined by AbM

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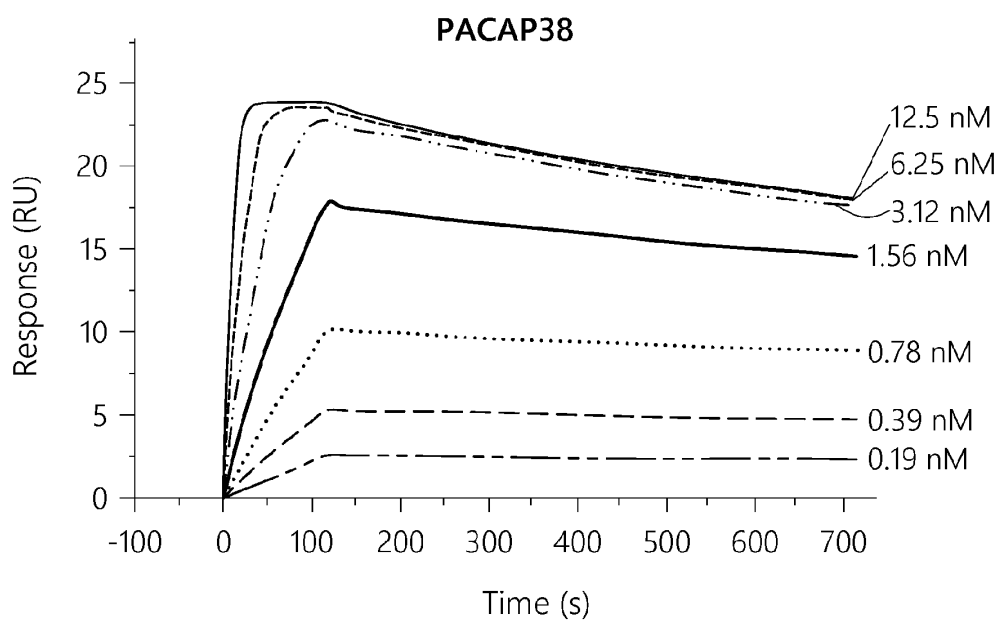


FIG. 3A

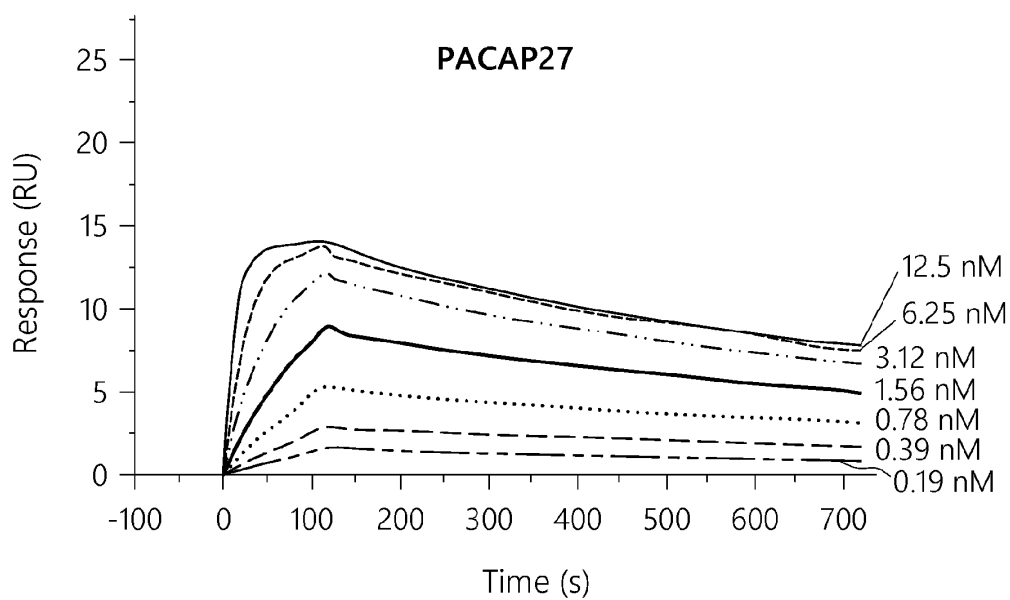


FIG. 3B

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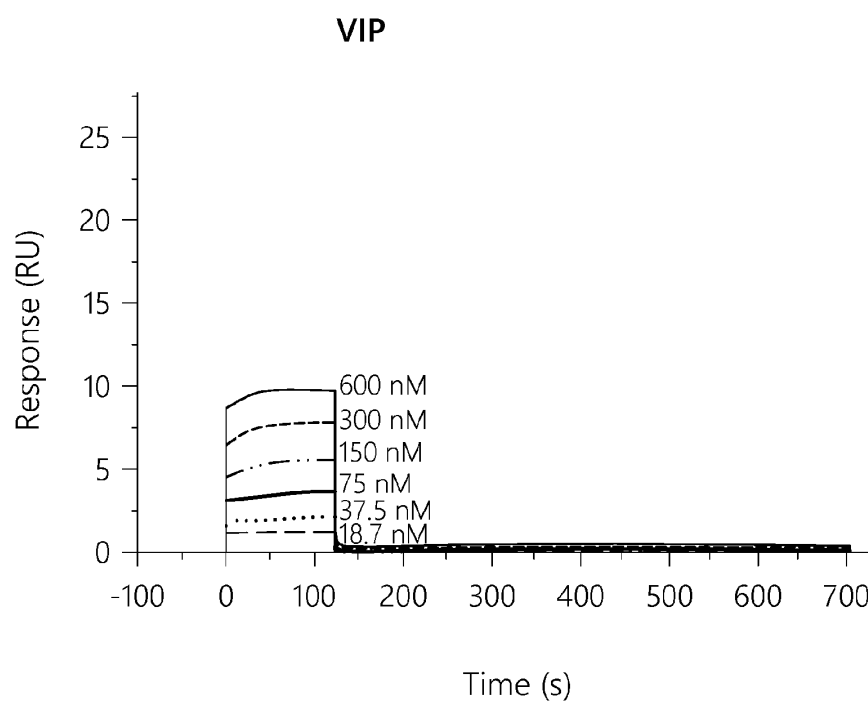


FIG. 3C

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FIG. 4

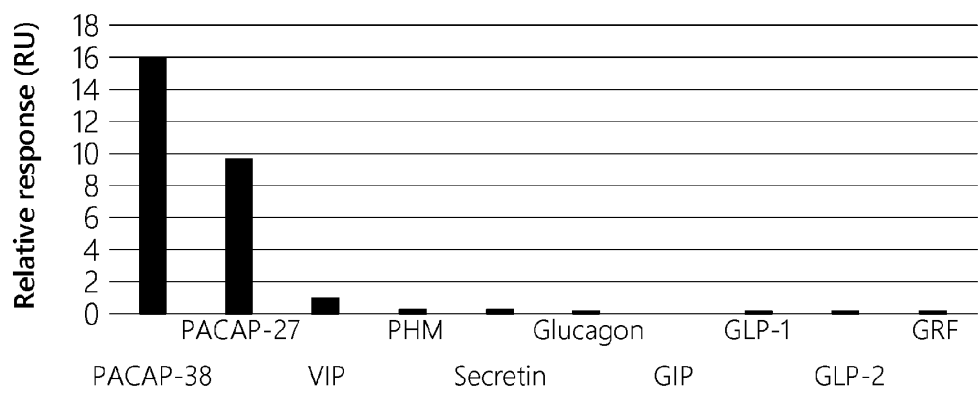
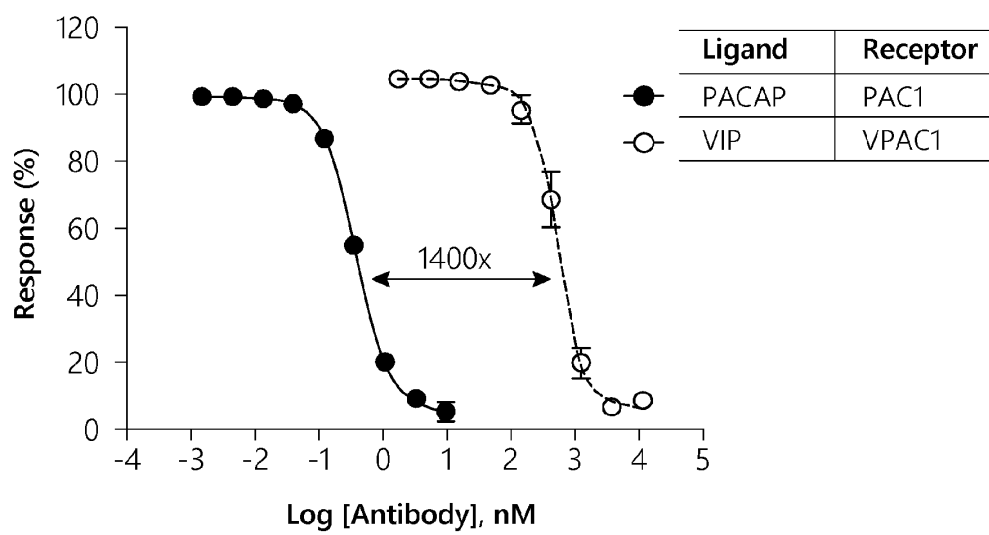


FIG. 5



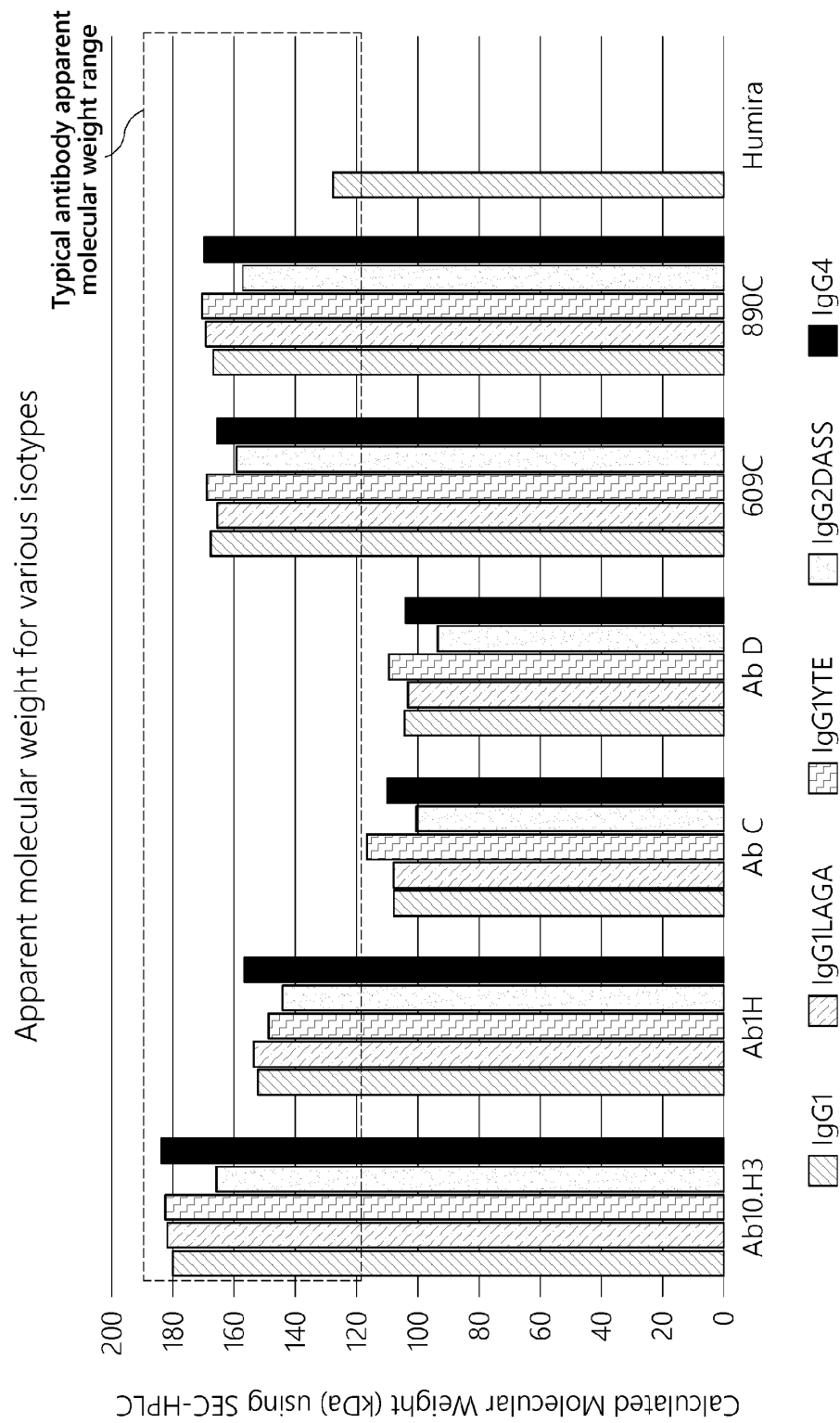


FIG. 6

Summary of predicted immunogenicity profile of V regions of 608C, 609C, 627C, 890C and other anti-PACAP antibodies

Tabulated number of immunogenic epitopes across all tested alleles based on stability index of the MHC class II-peptide complex

	DRB1 *01:01	DRB1 *15:01	DRB1 *03:01	DRB1 *04:01	DRB1 *11:01	DRB1 *13:01	DRB1 *07:01	DRB1 *04:04	DRB1 *04:05	DRB1 *09:01	DRB1 *10:01	DRB1 *11:04	DRB1 *15:02	DRB1 *15:03	DRB1 *16:01
608C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
609C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
627C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
890C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ab10.H3	4	1	0	2	1	0	3	1	3	2	2	0	1	2	0
Ab1.H	1	1	0	2	0	0	3	0	1	4	1	0	0	0	0
Ab B	1	0	0	1	1	0	1	0	0	2	4	0	0	0	0
Ab C	1	0	0	1	1	0	1	0	0	1	3	0	0	0	0
Ab D	1	0	0	1	2	0	1	0	0	1	3	0	0	0	0

FIG. 7

Heavy Chain (890C) ^a						
1	EVQLVQSGAE	VKKPGSSVKV	SCKASGGTFS	DVYMHVVRQA	PGQGLEWMGL	50
51	TYPIFADTRY	AQKFQGRVTI	TADESTSTAY	MELSSLRSED	TAVYYCAIDQ	100
101	DGSFAYWGQG	TLVTVSSAST	KGPSVFPLAP	CSRSTSESTA	ALGCLVKDYF	150
151	PEPTVTSWNS	GALTSGVHTF	PAVLQSSGLY	SLSSVVTVPS	SNFGTQTYTC	200
201	NVDHKPSNTK	VDKTVERKCC	VECPPCPAPP	VAGPSVFLFP	PKPKDTLMIS	250
251	RTPEVTCVVV	DVSHEDPEVQ	FNWYVDGVEV	HNAKTKPREE	QFNSTFRVVS	300
301	VLTVVHODWL	NGKEYKCKVS	NKGLPSSIEK	TISKTKGQPR	EPQVYTLPPS	350
351	REEMTKNQVS	LTCLVKGFYP	SDIAVEWESN	GQPENNYKTT	PPMLDSDGSF	400
401	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	HYTQKSLSLS	PG*	442
Light Chain (890C) ^a						
1	DIVMTQSPDS	LAVSLGERAT	INCKSSQSLL	DADGKTYLNW	LQOKPGQPPK	50
51	RLIYWASTRE	SGVPDRFSGS	GS GT DFTLTI	SSLQAE D VAV	YYCWQGTW FD	100
101	LTFGGG TKVE	IKRTVAAPSV	FIFPPSDEQL	KSGTASVVCL	LNNFY P REAK	150
151	VQWKVDNALQ	SGNSQESVTE	QDSKDS T YSL	SSTLTLSKAD	YEKHKVYACE	200
201	VTHQGLSSPV	TKSFNRGEC				219

FIG. 8

Heavy Chain (608C) ¹							
1	EVQLVQSGAE	VKKPGSSVKV	SCKASGGTFS	DLYMHWVRQA	PGQGLEWMGL		50
51	IYPIFADTRY	AQKFQGRVTI	TADESTSTAY	MELSSLRSED	TAVYYCAIDQ		100
101	DGSFAYWGQG	TLVTVSSAST	KGPSVFPLAP	CSRSTSESTA	ALGCLVKDYF		150
151	PEPTVSWNS	GALTSGVHTF	PAVLQSSGLY	SLSSVTVPS	SNFGTQTYTC		200
201	NVDHKPSNTK	VDKTVERKCC	VECPPCPAPP	VAGPSVFLFP	PKPKDTLMIS		250
251	RTPEVTCVVV	DVSHEDPEVQ	FNWYVDGVEV	HNAKTKPREE	QFNSTFRVVS		300
301	VLTVVHQDWL	NGKEYKCKVS	NKGLPSSIEK	TISKTKGQPR	EPQVYTLPPS		350
351	REEMTKNOVS	LTCLVKGFYP	SDIAVEWESN	GQPENNYKIT	PPMLDSDGSF		400
401	FLYSKLTVDK	SRWQQGNVFS	CVMHEALHN	HYTQKSLSLS	PG*		442
Light Chain (608C) ^a							
1	DIVMTQSPDS	LAVSLGERAT	INCKSSQSLL	DSDGKTYLNW	LQKPGQP PK		50
51	RLIYWASTRE	SGVPDRFSGS	GS GT DFTLTI	SSLQAE D VAV	YYCWQGTW F D		100
101	LT F GGG T KVE	IKRTVAAPSV	FIFPPSDEQL	KSGTASVVCL	LNNFYPREAK		150
151	VQWKVDNALQ	SGNSQESVTE	QDSKDSTYSL	SSTLTLSKAD	YEKHKVYACE		200
201	VTHQGLSSPV	TKSFNRGEC					219

FIG. 9

Heavy Chain (627C) ^a							
1	<u>EVQLVQSGAE</u>	<u>VKKPGSSVKV</u>	<u>SKKASGGTFS</u>	<u>DVYMHVVRQA</u>	<u>PGQGLEWMGL</u>		50
51	<u>IYPIFADTRY</u>	<u>AQKFQGRVTI</u>	<u>TADESTSTAY</u>	<u>MELSSLRSED</u>	<u>TAVYYCAIDQ</u>		100
101	<u>DGSFAYWGQG</u>	<u>TLVTVSSAST</u>	<u>KGPSVFPLAP</u>	<u>CSRSTSESTA</u>	<u>ALGCLVKDYF</u>		150
151	<u>PEPTVSWNS</u>	<u>GALTSGVHTF</u>	<u>PAVLQSSGLY</u>	<u>SLSSVTVTPS</u>	<u>SNFGTQTYTC</u>		200
201	<u>NVDHKPSNTK</u>	<u>VDKTVERKCC</u>	<u>VECPPCPAPP</u>	<u>VAGPSVFLFP</u>	<u>PKPKDTLMIS</u>		250
251	<u>RTPEVTCVVV</u>	<u>DVSHEDPEVQ</u>	<u>FNWYVDGVEV</u>	<u>HNAKTKPREE</u>	<u>QFNSTFRVVS</u>		300
301	<u>VLTVVHQDWL</u>	<u>NGKEYKCKVS</u>	<u>NKGLPSSIEK</u>	<u>TISKTKGQPR</u>	<u>EPQVYTLPPS</u>		350
351	<u>REEMTKNOVS</u>	<u>LTCLVKGFYP</u>	<u>SDIAVEWESN</u>	<u>GQPENNYKIT</u>	<u>PPMLDSDGSF</u>		400
401	<u>FLYSKLTVDK</u>	<u>SRWQQGNVFS</u>	<u>CVMHEALHN</u>	<u>HYTQKSLSLS</u>	<u>PG*</u>		442
Light Chain (627C) ^a							
1	<u>DIVMTQSPDS</u>	<u>LAVSLGERAT</u>	<u>INCKSSQSLL</u>	<u>DSDGKTYLNW</u>	<u>LQKPGQPPK</u>		50
51	<u>RLIYWASTRE</u>	<u>SGVPDRFSGS</u>	<u>GSGTDFTLTI</u>	<u>SSLQAEDVAV</u>	<u>YYCWQGTWFD</u>		100
101	<u>LTFGGGTKVE</u>	<u>IKRTVAAPSV</u>	<u>FIFPPSDEQL</u>	<u>KSGTASVVCL</u>	<u>LNNFYPREAK</u>		150
151	<u>VQWKVDNALQ</u>	<u>SGNSQESVTE</u>	<u>QDSKDSTYSL</u>	<u>SSTLTLSKAD</u>	<u>YEKHKVYACE</u>		200
201	<u>VTHQGLSSPV</u>	<u>TKSFNRGEC</u>					219

FIG. 10

Heavy Chain (609C) ^a						
1	<u>EVQLVQSGAE</u>	<u>VKKPGSSVKV</u>	<u>SKKASGGTFS</u>	<u>DLYMHWRQA</u>	<u>PGQGLEWMGL</u>	50
51	<u>IYPIFADTRY</u>	<u>AQKFQGRVTI</u>	<u>TADESTTAY</u>	<u>MELSSLRSED</u>	<u>TAVVYCAIDQ</u>	100
101	<u>DGSFAYWGQG</u>	<u>TLVTVSSAST</u>	<u>KGPSVFPLAP</u>	<u>CSRSTSESTA</u>	<u>ALGCLVKDYF</u>	150
151	<u>PEPVTVSWNS</u>	<u>GALTSGVHTF</u>	<u>PAVLQSSGLY</u>	<u>SLSSVVTVPS</u>	<u>SNFGTQTYTC</u>	200
201	<u>NVDHKPSNTK</u>	<u>VDKTVRKCC</u>	<u>VECPPCPAPP</u>	<u>VAGPSVFLFP</u>	<u>PKPKDTLMIS</u>	250
251	<u>RTPEVTCVVV</u>	<u>DVSHEDPEVQ</u>	<u>FNWYVDGVEV</u>	<u>HNAKTKPREE</u>	<u>QFNSTFRVVS</u>	300
301	<u>VLTVVHQDWL</u>	<u>NGKEYKCKVS</u>	<u>NKGLPSSIEK</u>	<u>TISKTKGQPR</u>	<u>EPQVYTLPPS</u>	350
351	<u>REEMTKNQVS</u>	<u>LTCLVKGFYP</u>	<u>SDIAVEWESN</u>	<u>GOPENNYKTT</u>	<u>PPMLDSDGSF</u>	400
401	<u>FLYSKLTVDK</u>	<u>SRWQQGNVFS</u>	<u>CSVMHEALHN</u>	<u>HYTQKSLSLS</u>	<u>PG*</u>	442
Light Chain (609C) ^a						
1	<u>DIVMTQSPDS</u>	<u>LAVSLGERAT</u>	<u>INCKSSQSLL</u>	<u>DADGKTYLNW</u>	<u>LQQKPGQPPK</u>	50
51	<u>RLIYWASTRE</u>	<u>SGVPDRFSGS</u>	<u>GSGETDFTLTI</u>	<u>SSLQAEDVAV</u>	<u>YYCWQGTWFD</u>	100
101	<u>LTFGGGTKVE</u>	<u>IKRTVAAPSV</u>	<u>FIFPPSDEQL</u>	<u>KSGTASVVCL</u>	<u>LNNFYPREAK</u>	150
151	<u>VQWKVDNALQ</u>	<u>SGNSQESVTE</u>	<u>QDSKDSITYSL</u>	<u>SSTLTLSKAD</u>	<u>YEKHKVYACE</u>	200
201	<u>VTHQGLSSPV</u>	<u>TKSFNRGEC</u>				219

FIG. 11