Figure 1 Phage Vector

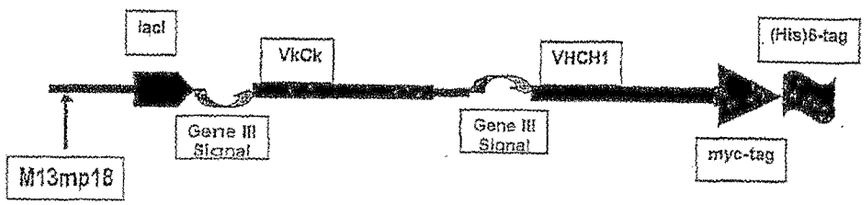


FIGURE 2

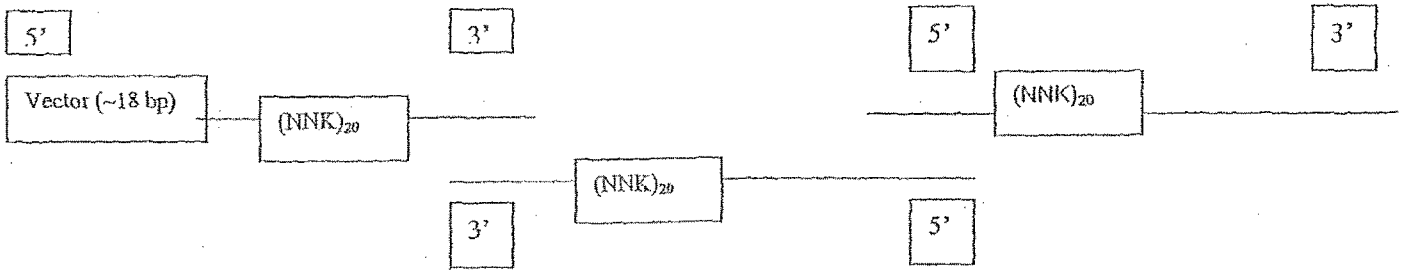


Figure 3 TES-C21 and Template Comparison

A. Light Chain (V_K) (Underlined: Kabat CDR. Bold/Italic: Chothia CDR) (TES-C21 LIGHT CHAIN – SEQ ID NO 1 L16/JK4 – SEQ ID NO2)

```
                                  10                  20                  30
Mu TES-C21    D I L L T Q S P A I L S V S P G E R V S F S C R A S Q S I G T N I H W Y Q Q
L16 VK        E   V M           T                   A T L   R A S Q S V S S N L A

                40                  50                  60                  70
TES-C21       R T D G S P R L L I K Y A S E S I S G I P S R F S G S G S G T E F T L N I N
L16 VK        K P G Q A           Y G A S T R A T       A                       T   S

                80                  90                 100       107
TES-C21       S V E S E D I A D Y Y C Q Q S D S W P T T F G G G T K L E I K
L16 VK-JK4      L Q       F   V       Q Q Y N N W P L T           V
```

B. Heavy Chain (V_H)

TES-C21 HEAVY CHAIN – SEQ ID NO 3 DP88/JH4b – SEQ ID NO 4

```
                1                  10                  20                  30
Murine TES-C21 Q V Q L Q Q S G A E L M K P G A S V K I S C K T T G Y T F S M Y W L E W V
DP88 VH          V           V K       S       V       A S   G       S Y A I S

                   40                  50  52a 53          60        65        70
TES-C21         K Q R P G H G L E W V G E I S P G T F T T N Y N E K F K A K A T F T A D T
DP88 VH         R   A     Q         M   G I I P I F G T A N Y A Q K F Q G R V   I       K
\
                         80  82a b c 83          90        95        100 b c d e f 101
TES-C21         S S N T A Y L Q L S G L T S E D S A V Y F C A R F S H F S G S N Y D Y F D Y
DP88 VH           T S       M E     S   R       T       Y       - - - - - - - - - - Y F D Y

                103           110   113
TES-C21         W G Q G T S L T V S S
DP88-JH4b       L V
```

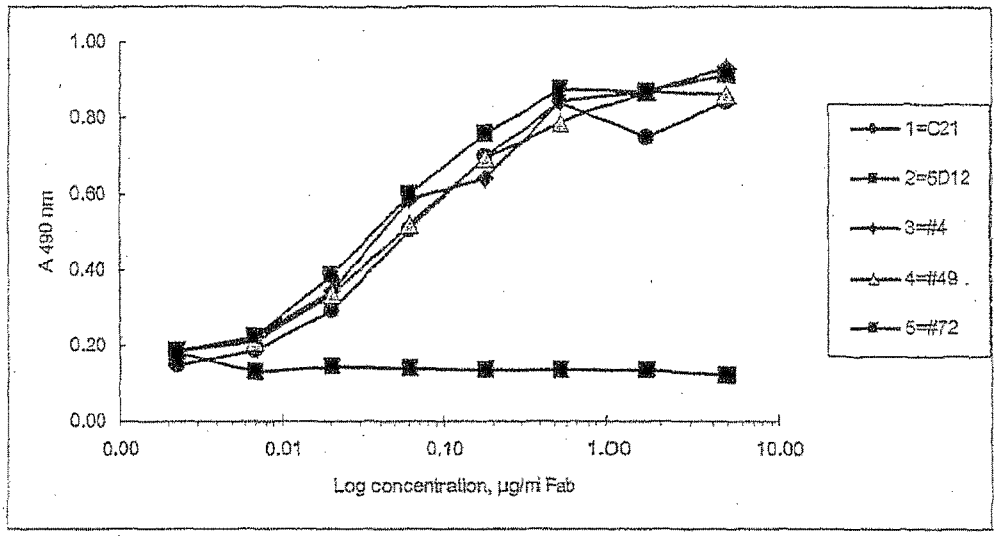
Figure 4 Framework Sequences of High Affinity Candidates*

VK Positions	1	3	4	49	60	85	VH Positions	12	27	43	48	67	69
Mouse	D	L	L	K	S	D	Mouse	M	Y	H	V	A	F
Human	E	V	M	Y	A	V	Human	K	G	Q	M	V	I
1 (clone ID)	D	L	M	K	S	V		M	Y	H	M	A	F
2	D	V	L	K	A	V		K	Y	Q	M	V	F
4	D	L	L	Y	S	V		M	Y	Q	M	V	F
8	D	V	M	Y	S	V		M	Y	Q	V	A	F
13	E	V	L	K	A	D		K	Y	Q	M	A	F
15	D	L	M	Y	A	V		M	Y	Q	V	V	F
16	D	L	M	Y	A	V		M	Y	Q	M	V	F
18	E	L	L	K	S	D		M	Y	Q	M	V	F
21	D	V	L	Y	A	V		M	Y	H	V	V	F
23	E	L	L	K	A	D		M	Y	Q	M	V	F
25	D	V	M	Y	A	V		M	Y	Q	V	A	F
27	E	L	M	Y	S	D		M	Y	Q	V	V	F
30	E	V	L	Y	A	D		K	Y	Q	V	V	F
31	E	V	L	Y	A	V		M	Y	H	V	A	F
33	E	V	L	Y	S	V		K	Y	Q	M	V	F
35	E	V	M	Y	A	D		K	Y	H	M	V	F
38	E	V	M	K	A	D		K	Y	Q	M	V	F
43	E	V	L	Y	S	V		M	Y	H	M	V	I
44	E	V	L	Y	A	D		M	Y	H	V	V	I
45	E	V	M	K	A	V		M	Y	Q	M	V	F
46	E	V	L	K	S	V		M	Y	H	V	V	F
48	E	V	M	Y	A	D		M	Y	H	V	V	F
49	E	V	M	Y	A	V		M	Y	Q	M	V	F
50	D	L	L	Y	A	D		M	Y	H	V	A	F
52	E	L	L	Y	A	D		K	Y	Q	V	V	F
53	D	V	L	Y	S	V		M	Y	H	M	V	F
56	D	L	M	Y	S	V		M	Y	H	M	A	F
58	D	V	M	K	S	V		M	Y	H	M	V	F
61	D	V	M	K	S	V		M	Y	H	M	V	F
63	D	V	L	K	S	V		K	Y	Q	V	V	F
64	E	V	M	K	S	D		M	Y	Q	V	V	F
68	D	V	L	Y	S	V		M	Y	Q	V	V	F
70	D	V	L	Y	A	D		K	Y	Q	M	A	F
72	D	V	L	Y	A	V		M	Y	H	M	V	F
75	E	L	L	K	S	V		K	Y	Q	M	A	F
76	D	V	M	Y	S	V		M	Y	Q	M	V	F
78	D	V	M	Y	S	V		M	Y	Q	M	V	F
81	E	V	L	K	S	D		M	Y	Q	M	A	F
83	E	V	L	K	A	D		M	Y	H	V	V	F
86	E	L	M	K	A	V		M	Y	Q	M	V	F
89	E	L	M	Y	A	V		M	Y	H	V	V	F
90	D	V	M	Y	A	D		K	Y	H	V	V	F
93	E	L	M	K	A	V		M	Y	Q	V	A	F
103	D	V	L	Y	A	V		M	Y	Q	V	A	I
109	D	L	L	K	S	V		M	Y	H	M	A	F
114	D	L	L	Y	A	V		M	Y	Q	V	V	F
124	E	V	L	Y	S	D		K	Y	Q	V	V	F
126	D	V	M	Y	A	V		M	Y	Q	V	V	F
135	D	V	L	K	S	V		M	Y	Q	M	V	F
136	E	V	M	Y	A	V		M	Y	H	M	V	F
152	E	V	L	Y	S	V		M	Y	H	V	V	F
153	D	L	L	Y	S	V		K	Y	Q	M	V	F
157	D	L	M	Y	S	D		K	Y	Q	M	V	F
1136-2C	E	V	M	Y	S	D		K	Y	Q	M	V	F

*P=parent sequence; T=human template sequence; amino acids listed in bold are murine residues

Figure 5 ELISA TITRATION CURVE

A



B

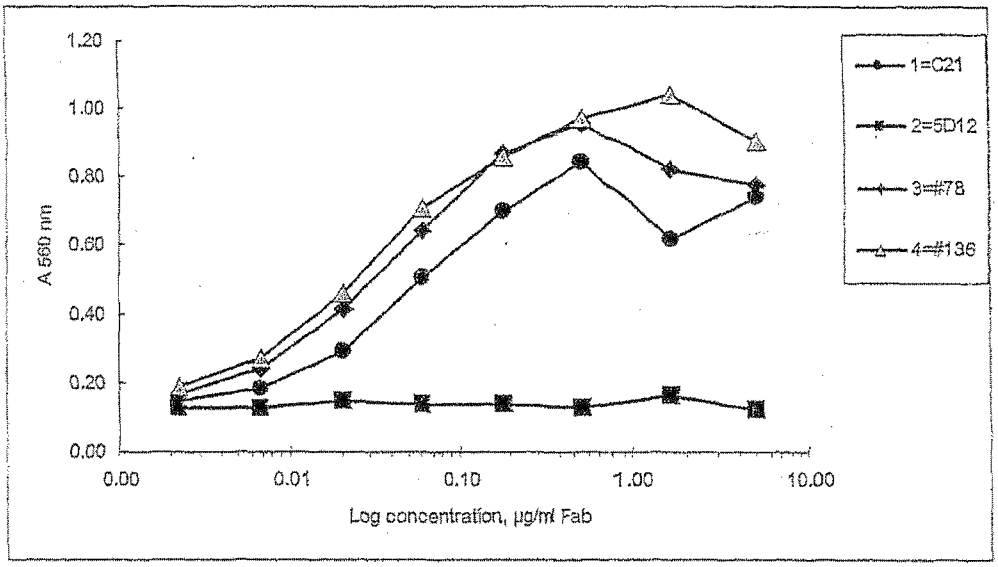


Figure 6 Inhibition Assay

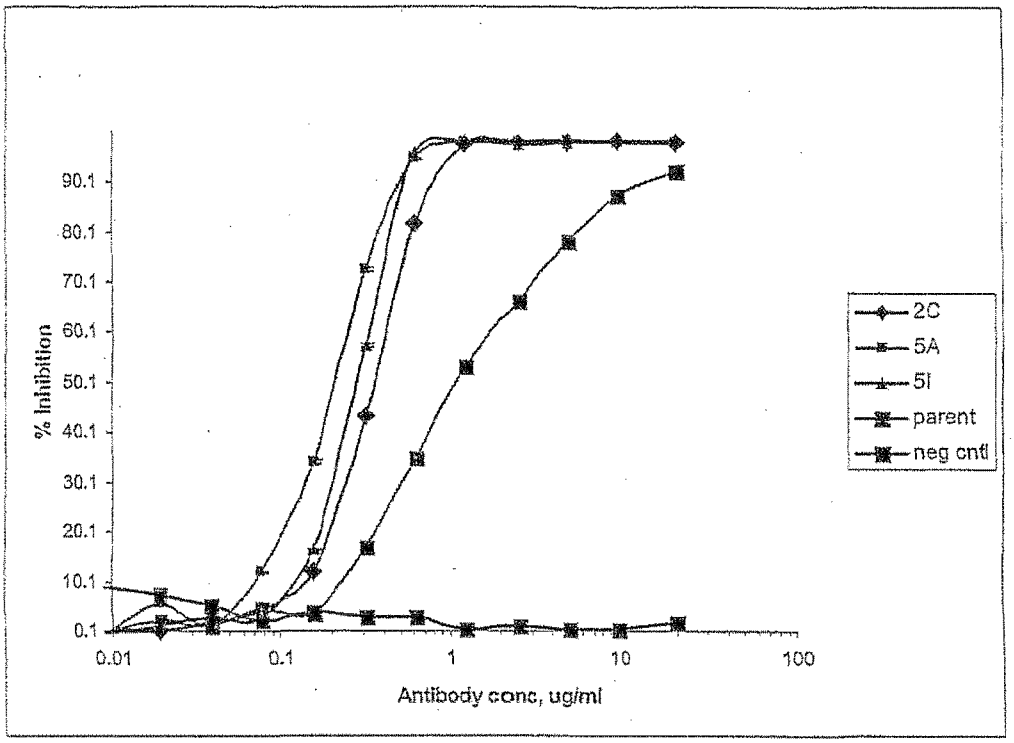


Figure 7: List of High Affinity Candidates from Library

Clone	CDR-L1	CDR-L	CDR-L3	CDR-H1	CDR-H2	CDR-H3
136	RASRSIG	YASE	QQSASW	MYWLE	EISPGTFTTNYNEKF	FSHFSGSNYDY
L3-9	wt	wt	QQSWSW	wt	wt	wt
CL-2	wt	wt	QQSWSV	WYWLE	wt	wt
R5-E	wt	wt	QQSWSW	YYWLE	wt	wt
R87-1	wt	wt	QQSWSV	wt	EIEPGTFTTNYNEKF	wt
CL-2	wt	wt	QQSWSV	wt	EIDPGTFTTNYNEKF	wt
R2-C	wt	wt	QQSWSW	WYWLE	EIEPGTFTTNYNEKF	wt
CL-2	wt	wt	QQSWSW	WYWLE	EIDPGTFTTNYNEKF	wt
CL-2	wt	wt	QQSWSW	YYWLE	EIEPGTFTTNYNEKF	wt
CL-2	wt	wt	QQSWSW	YYWLE	EIDPGTFTTNYNEKF	wt
CL-3	wt	wt	QQSWSW	wt	EISPETFTTNYNEKF	wt
R47-1	wt	wt	QQSWSW	wt	EISPDTFTTNYNEKF	wt
CL-3	wt	wt	QQSWSW	YYWLE	EISPETFTTNYNEKF	wt
R3-A	wt	wt	QQSWSW	YYWLE	EISPDTFTTNYNEKF	wt
CL-3	wt	wt	QQSWSW	WYWLE	EISPETFTTNYNEKF	wt
CL-3	wt	wt	QQSWSW	WYWLE	EISPDTFTTNYNEKF	wt
R5-K	wt	wt	QQSWSW	wt	EISPGTFETNYNEKF	wt
CL-4	wt	wt	QQSWSW	WYWLE	EISPGTFETNYNEKF	wt
R5-D	wt	wt	QQSWSW	YYWLE	EISPGTFETNYNEKF	wt
CL-5	wt	wt	QQSWSW	wt	EIEPGTFETNYNEKF	wt
CL-5	wt	wt	QQSWSW	wt	EIDPGTFETNYNEKF	wt
CL-5	wt	wt	QQSWSW	WYWLE	EIEPGTFETNYNEKF	wt
CL-5	wt	wt	QQSWSW	WYWLE	EIDPGTFETNYNEKF	wt
R5-H	wt	wt	QQSWSW	YYWLE	EIEPGTFETNYNEKF	wt
R5-N	wt	wt	QQSWSW	YYWLE	EIDPGTFETNYNEKF	wt

Changes from parent amino acid sequence are listed in **BOLD.**

FIGURE 8A

VK Alignment

	1	2	3	4	5	6	7	8	9	#	#	#	#	#	#	#	#	#	20	21	22	23	SEQ ID	24-34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	SEQ ID	50-56
136	E	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	30	CDR-L1	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	38	CDR-L2
1	D	I	L	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	31		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K	39	
2	D	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	32		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
4	D	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	33		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
13	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	34		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
15	D	I	L	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
18	E	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	35		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
23	E	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
25	D	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	36		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
27	E	I	L	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	37		W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
30	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
31	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
33	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
35	E	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
38	E	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
45	E	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
46	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
50	D	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
52	E	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
53	D	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
56	D	I	L	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
58	D	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
63	D	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
64	E	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
70	D	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
72	D	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
75	E	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
78	D	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
81	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
86	E	I	L	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
89	E	I	L	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
90	D	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
109	D	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	K		
114	D	I	L	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		
124	E	I	V	L	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C			W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y		

FIGURE 8B

57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	SEQ ID	89-97	98	99	##	##	##	103	##	##	##	##	SEQ ID
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C	40	CDR-L3	F	G	G	G	T	K	V	E	I	K	44
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C	41		F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C	42		F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C	43		F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C			F	G	G	G	T	K	V	E	I	K	
G	I	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	D	Y	Y	C			F	G	G	G	T	K	V	E	I	K	

FIGURE 9A

VH alignments

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	SEQ ID 45	CDR-H1 31-35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	SEQ ID 47	CDR-H2 50-66
136	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	S	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G		
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S	46		W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	48		
2	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
4	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
8	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	49		
13	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
15	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	V	G			
21	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	V	G	50		
30	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	V	G			
31	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
35	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
43	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
44	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	V	G			
53	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
81	Q	V	Q	L	V	Q	S	G	A	E	V	M	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	M	G			
90	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	V	G			
103	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S			W	V	R	Q	A	P	G	Q	G	L	E	W	V	G			

FIGURE 9B

67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	SEQ ID	99-112	113	114	115	116	##	118	119	120	121	122	123	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R	51	CDR-H3	W	G	Q	G	T	L	V	T	V	S	S	55
R	A	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R	52		W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	A	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	A	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	A	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	I	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R	53		W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	I	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	A	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	V	T	F	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R			W	G	Q	G	T	L	V	T	V	S	S	
R	A	T	I	T	A	D	T	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R	54		W	G	Q	G	T	L	V	T	V	S	S	

Figure 10A Polypeptide sequence of Mab 136

LIGHT CHAIN

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION Vk

EIVMTQSPAT LSVSPGERAT LSCRASQSIG TNIHWYQQKP GQAPRLLIYY
ASESISGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ SDSWPTTFGG
GTKVEIK (SEQ ID NO 57)

CONSTANT REGION Ck

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS
FNRGEC (SEQ ID NO 58)

HEAVY CHAIN (IgG1)

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION VH

QVQLVQSGAE VMKPGSSVKV SCKASGYTFS MYWLEWVRQA PGHGLEWMGE
ISPGTFTTNY NEKFKARVTF TADTSTSTAY MELSSLRSED TAVYYCARFS
HFSGSNYDYF DYWGQGTLVT VSS (SEQ ID NO 59)

CONSTANT REGION CH1-3(IgG1) (SEQ ID NO 60)

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

Figure 10B Polypeptide Sequence of MAb CL-2C

LIGHT CHAIN

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION Vk

EIVMTQSPAT LSVSPGERAT LSCRASQSIG TNIHWYQQKP GQAPRLLIYY
ASESISGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ SWSWPTTFGG
GTKVEIK (SEQ ID NO 61)

CONSTANT REGION Ck

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS
FNRGEC (SEQ ID NO 58)

HEAVY CHAIN (IgG1)

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION VH (2C)

QVQLVQSGAE VMKPGSSVKV SCKASGYTFS WYWLEWVRQA PGHGLEWMGE
IDPGTFTTNY NEKFKARVTF TADTSTSTAY MELSSLRSED TAVYYCARFS
HFSGSNYDYF DYWGQGTLVT VSS (SEQ ID NO 62)

CONSTANT REGION CH1-3(IgG1) (SEQ ID NO 60)

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

Figure 10C Polypeptide Sequence of MAb CL-5I

LIGHT CHAIN

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION Vk

EIVMTQSPAT LSVSPGERAT LSCRASQSIG TNIHWYQQKP GQAPRLLIYY
ASESISGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ SWSWPTTFGG
GTKVEIK (SEQ ID NO 63)

CONSTANT REGION Ck (SEQ ID NO 58)

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS
FNRGEC

HEAVY CHAIN (IgG1)

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION VH (5I)
QVQLVQSGAE VMKPGSSVKV SCKASGYTFS MYWLEWVRQA PGHGLEWMGE
IDPGTFETNY NEKFKARVTF TADTSTSTAY MELSSLRSED TAVYYCARFS
HFSGSNYDYF DYWGQGTLVT VSS (SEQ ID NO 64)

CONSTANT REGION CH1-3(IgG1) (SEQ ID NO 60)

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

Figure 10D Polypeptide Sequence of MAb CL-5A

LIGHT CHAIN

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION Vk

EIVMTQSPAT LSVSPGERAT LSCRASQSIG TNIHWYQQKP GQAPRLLIYY
ASESISGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ SWSWPTTFGG
GTKVEIK (SEQ ID NO 65)

CONSTANT REGION Ck (SEQ ID NO 58)

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS
FNRGEC

HEAVY CHAIN (IgG1)

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION VH (5A)

QVQLVQSGAE VMKPGSSVKV SCKASGYTFS WYWLEWVRQA PGHGLEWMGE
IEPGTFETNY NEKFKARVTF TADTSTSTAY MELSSLRSED TAVYYCARFS
HFSGSNYDYF DYWGQGTLVT VSS (SEQ ID NO 66)

CONSTANT REGION CH1-3(IgG1) (SEQ ID NO 60)

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

Figure 10E Polypeptide Sequence of MAb CL-2B

LIGHT CHAIN

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION Vk

EIVMTQSPAT LSVSPGERAT LSCRASQSIG TNIHWYQQKP GQAPRLLIYY
ASESISGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ SWSWPTTFGG
GTKVEIK (SEQ ID NO 67)

CONSTANT REGION Ck (SEQ ID NO 58)

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS
FNRGEC

HEAVY CHAIN (IgG1)

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION VH (2B)

QVQLVQSGAE VMKPGSSVKV SCKASGYTFS YYWLEWVRQA PGHGLEWMGE
IDPGTFTTNY NEKFKARVTF TADTSTSTAY MELSSLRSED TAVYYCARFS
HFSGSNYDYF DYWGQGTLVT VSS (SEQ ID NO 68)

CONSTANT REGION CH1-3(IgG1) (SEQ ID NO 60)

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

Figure 10F Polypeptide Sequence of MAb CL-1136-2C

LIGHT CHAIN

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION Vk

EIVMTQSPAT LSVSPGERAT LSCRASQSIG TNIHWYQQKP GQAPRLLIYY
ASESISGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ SWSWPTTFGG
GTKVEIK (SEQ ID NO 69)

CONSTANT REGION Ck (SEQ ID NO 58)

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS
FNRGEC

HEAVY CHAIN (IgG1)

SIGNAL PEPTIDE

MEWSGVFMFLLSVTAGVHS (SEQ ID NO 56)

VARIABLE REGION (VH)

QVQLVQSGAE VKKPGSSVKV SCKASGYTFS WYWLEWVRQA PGQGLEWMGE
ISPGTFTTNY NEKFKARVTF TADTSTSTAY MELSSLRSED TAVYYCARFS
HFSGSNYDYF DYWGQGTLVT VSS (SEQ ID NO 70)

CONSTANT REGION CH1-3(IgG1) (SEQ ID NO 60)

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

Figure 11 – Amino Acid Sequence of the CH3 Domain of Human IgE

Nterminal - Asp Ser **Asn** ***Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro*** Ser Pro Phe Asp Leu

Epitope A

Phe Ile Arg Lys Ser Pro Thr IleThr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu

Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg Asn Gly Thr

Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val

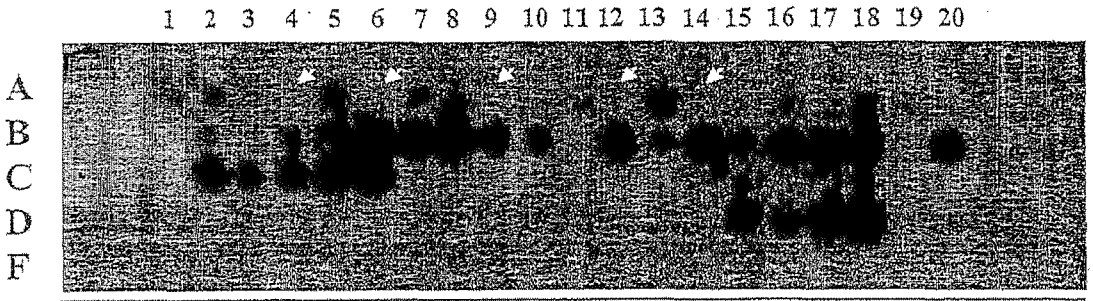
Thr His Pro His ***Leu Pro Arg Ala Leu Met Arg Ser Thr*** Thr Lys Thr Ser (SEQ ID NO 71)

Epitope B

Figure 12: Peptide Scan of Epitope B

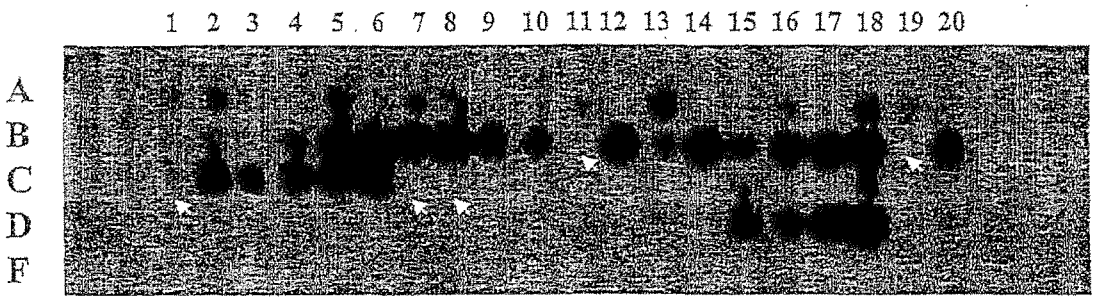
	Peptide sequence	Ab binding
53	YQCRVTHPHLPR	-
54	RVTHPHLPRALM	++
55	HPHLPRALMRST	+++
56	LPRALMRSTTKT	+++
57	ALMRSTTKTSGP	-
Consensus	LPRALMRST	

FIGURE 13 : ALANINE SCAN OF EPITOPE A



Position of peptide in membrane	Peptide sequence	Residue substitution	Anti-IgE Ab Binding signal
A1	NPRGVSAYLSRP	WT	++
A2	aPRGVSAYLSRP	1N→A	++
A3	NaRGVSAYLSRP	2P→A	++
A4	NPaGVSAYLSRP	3R→A	-
A5	NPRaVSAYLSRP	4G→A	+++
A6	NPRGaSAYLSRP	5V→A	-
A7	NPRGVaAYLSRP	6S→A	++
A8	NPRGVSAYLSRP	WT	++
A9	NPRGVSAaLSRP	8Y→A	-
A10	NPRGVSAYaSRP	9L→A	+
A11	NPRGVSAYLaRP	10S→A	++
A12	NPRGVSAYLSaP	11R→A	-
A13	NPRGVSAYLSRa	12P→A	+++
A14	NaeGaSAYLSRP	2P→A,3R→E,5V→A	-
A15	NPeGVSAYLSRP	3R→E	-
A16	NPRGVSAYLSRP	WT	++
A17	11gGpSvfLfRP	IgG1	-
A18	1PRGVSAYLSRP	1N→L	+++
A19	N1RGVSAYLSRP	2P→L	++
A20	NPgGVSAYLSRP	3R→G	-
B1	NPRGpSAYLSRP	5V→P	+
B2	NPRGVSvYLSRP	7A→V	++
B3	NPRGVSAfLSRP	8Y→F	+
B4	NPRGVSAYLfRP	10S→F	++

FIGURE 14 : ALANINE SCAN OF EPITOPE B



Position of Peptide in membrane	Peptide Sequence	Residue Substitution	Anti-IgE Ab Binding Signal
B5	HPHLPRALMRST	WT	+++
B6	aPHLPRALMRST	1H→A	+++
B7	HaHLPRALMRST	2P→A	+++
B8	HPaLPRALMRST	3H→A	+++
B9	HPHaPRALMRST	4L→A	++
B10	HPHLaRALMRST	5P→A	+
B11	HPHLPaALMRST	6R→A	-
B12	HPHLPRALMRST	WT	+++
B13	HPHLPRAaMRST	8L→A	+
B14	HPHLPRALaRST	9M→A	+++
B15	HPHLPRALMaST	10R→A	+
B16	HPHLPRALMRaT	11S→A	+++
B17	HPHLPRALMRSa	12T→A	+++
B18	HPHLPRALMRST	WT	+++
B19	HkaLPapiekti	IgG1	-
B20	HkHLPRALMRST	2P→K	+++
C1	HPHLPRpLMRST	7A→P	-
C2	HPHLPRAiMRST	8L→I	+++
C3	HPHLPRALeRST	9M→E	+
C4	HPHLPRALMkST	10R→K	++
C5	HPHLPRALMRtT	11S→T	+++
C6	HPHLPRALMRSi	12T→I	+++
C7	HPaLaeALMRST	3H→A, 5P→A, 6R→E	-
C8	HPHLPeALMRST	6R→E	-

Figure 15: WESTERN BLOT ANALYSIS

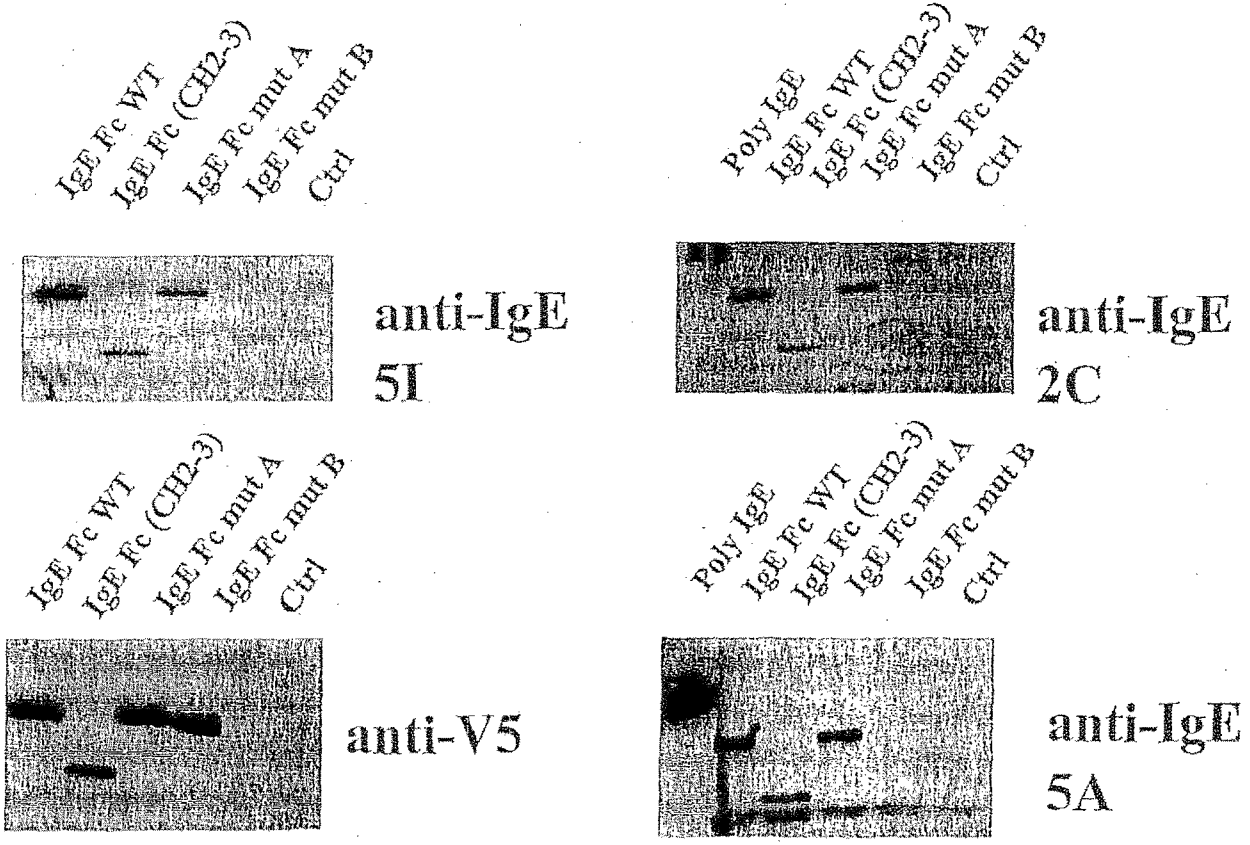


FIGURE 16 Anti-IgE Response in Transgenic mice

