Fig. 1 Binding of anti-IL13 mAbs to human IL-13 in ELISA

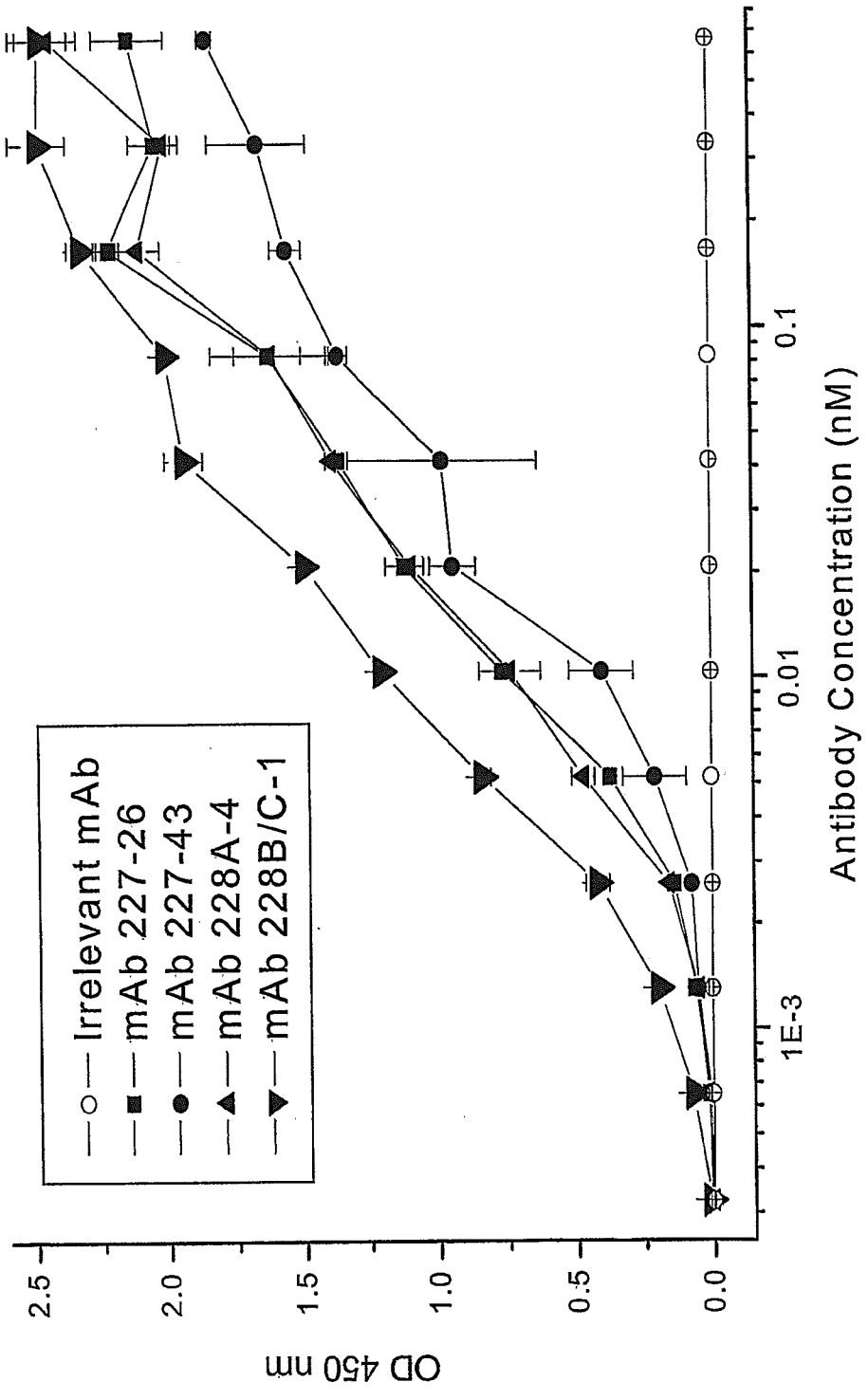


Fig. 2 Binding of anti-IL13 mAbs to MT-IL13/Fc

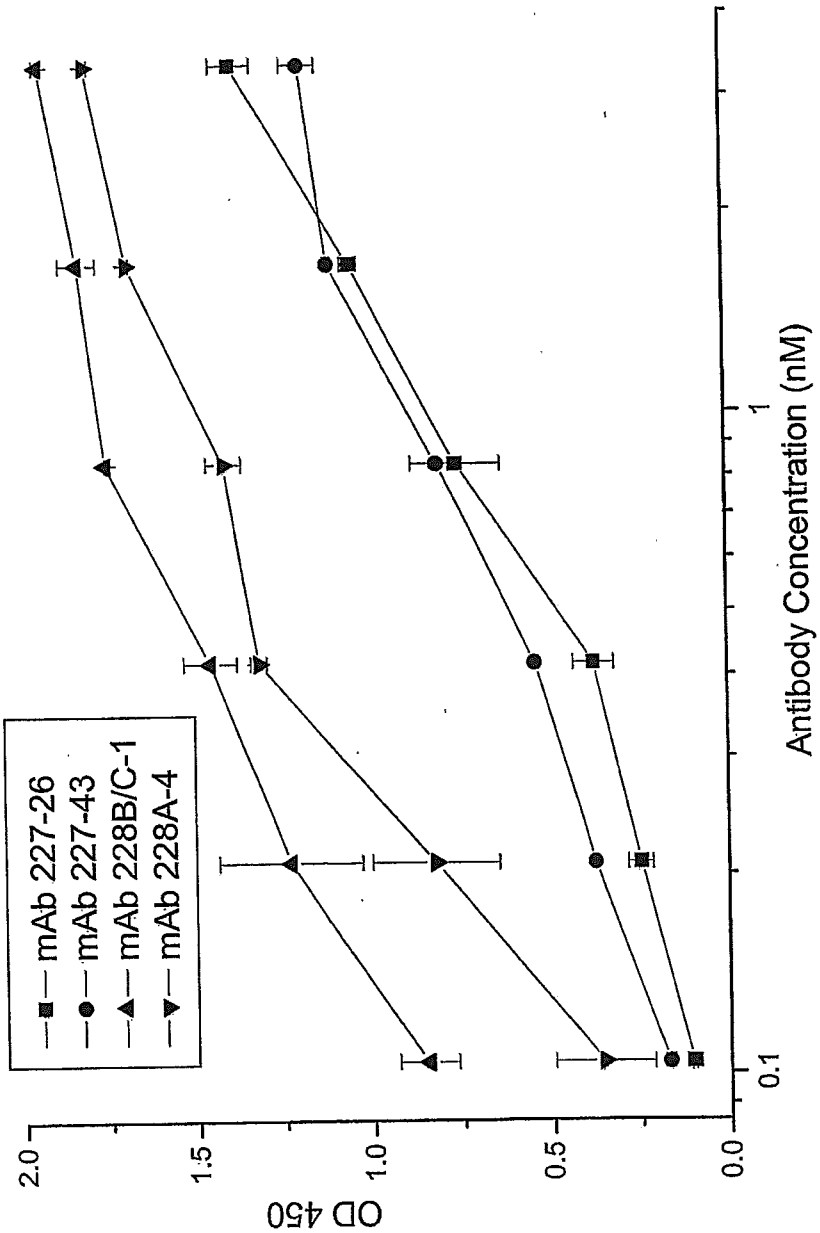


Fig. 3 Anti-IL13 mAb JES10-5A2 does not compete with the binding of mAb 228B/C-1-HRP to Human IL-13 in ELISA

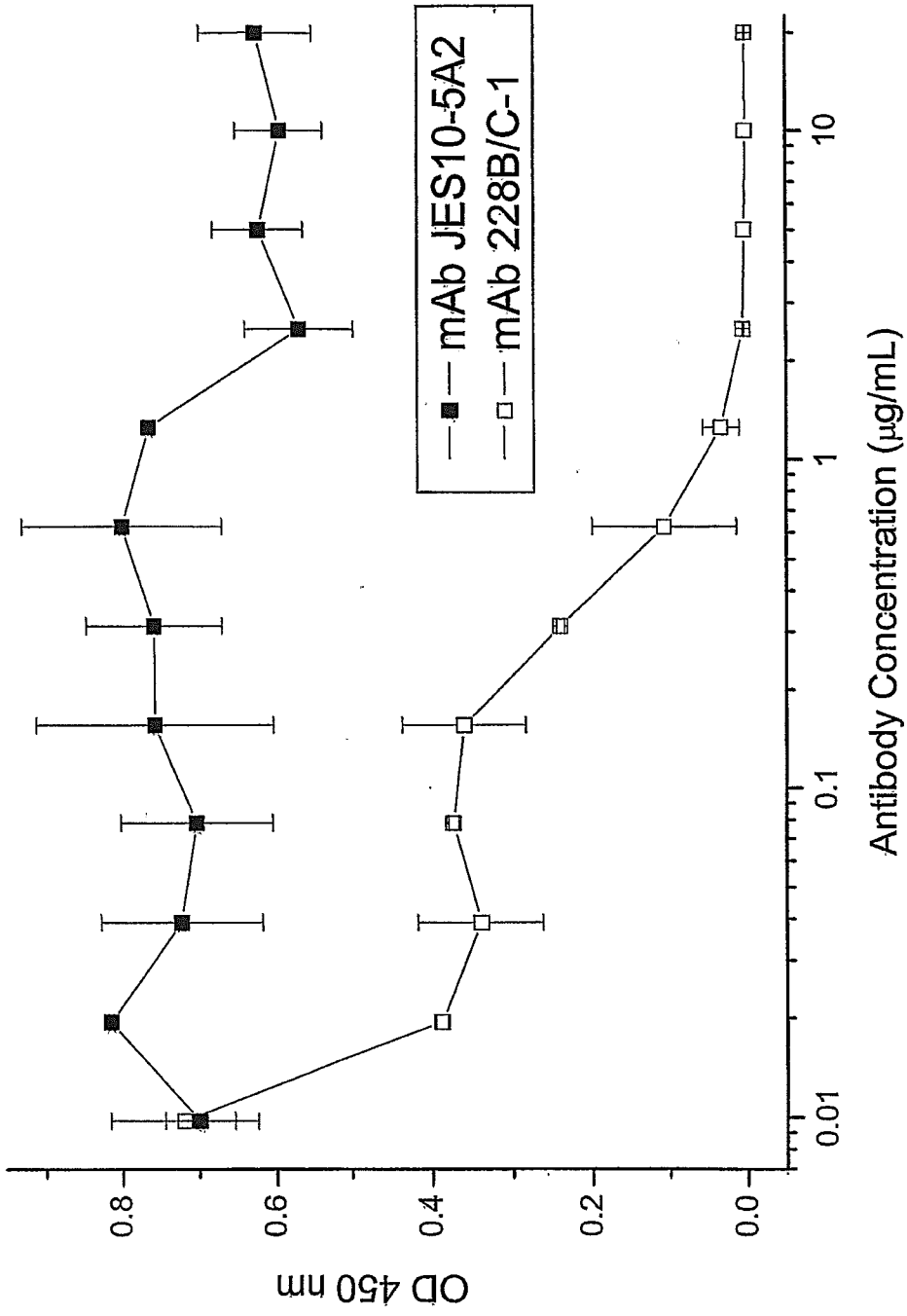


Fig. 4 Effect of anti-IL13 mAbs on the proliferation of L-1236 cells

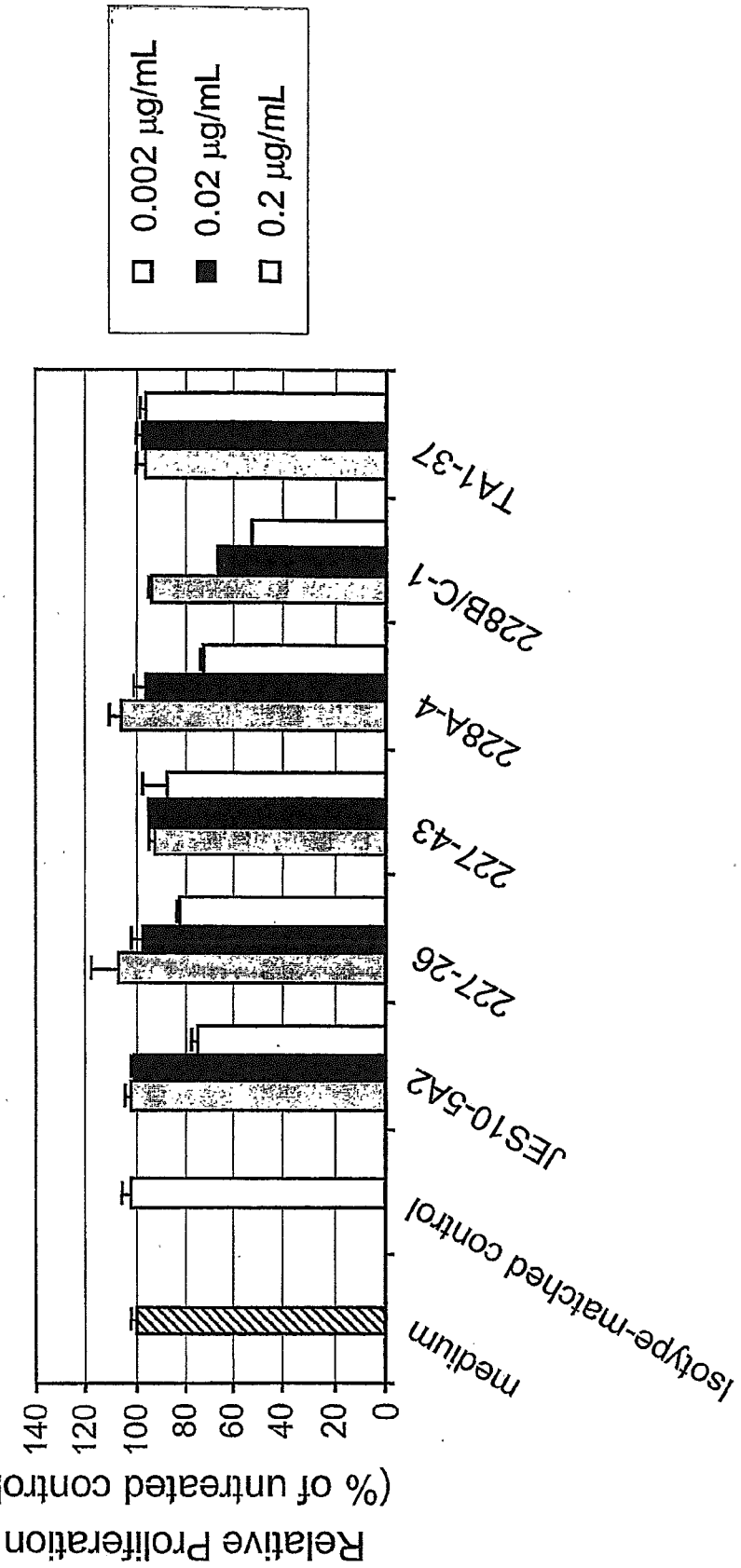


Fig. 5 Effect of anti-IL13 mAbs on IL13-induced suppression of CD14 expression in human monocytes

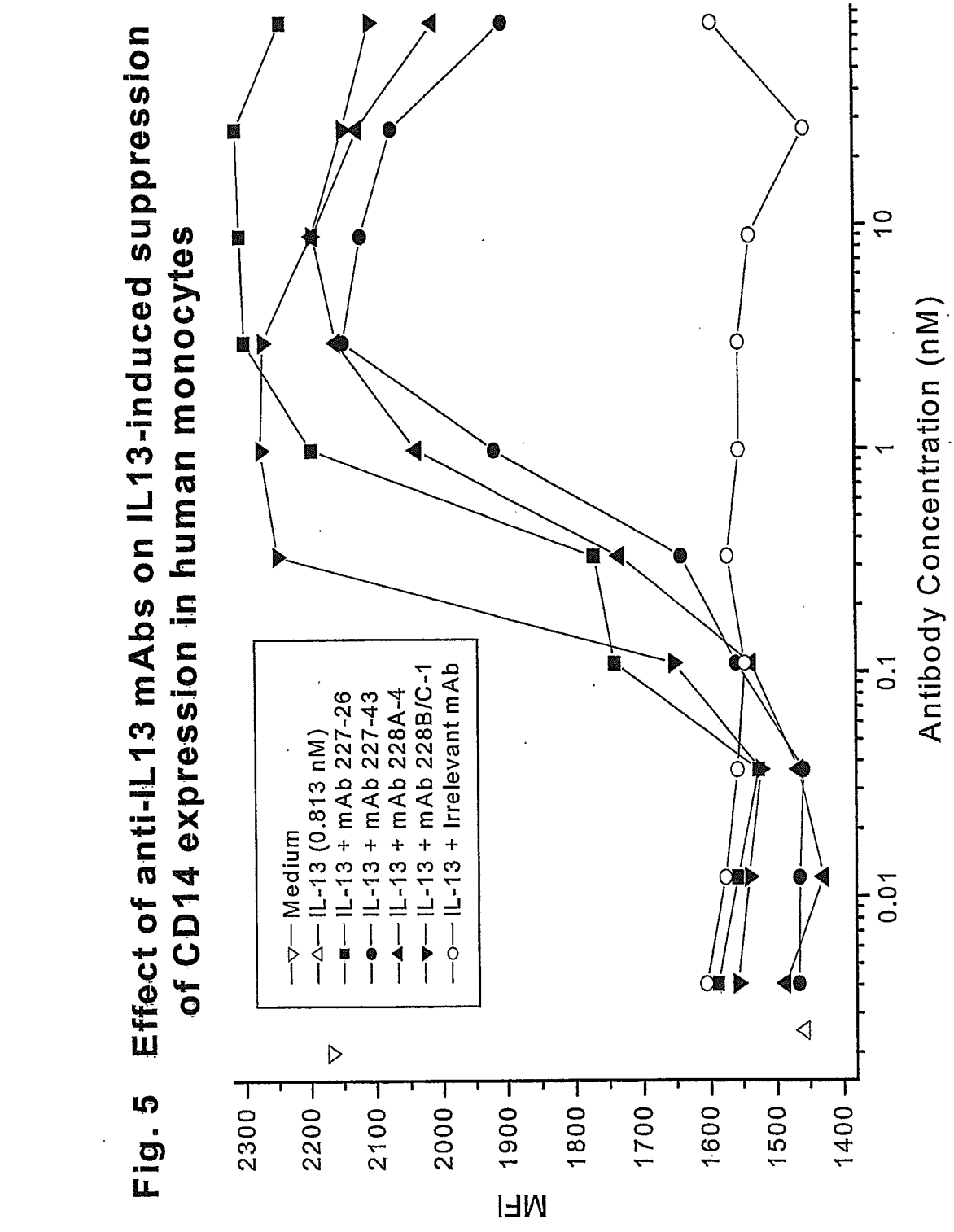


Fig. 6 Effect of anti-IL13 mAbs on IL13-induced upregulation of CD23 expression in human monocytes

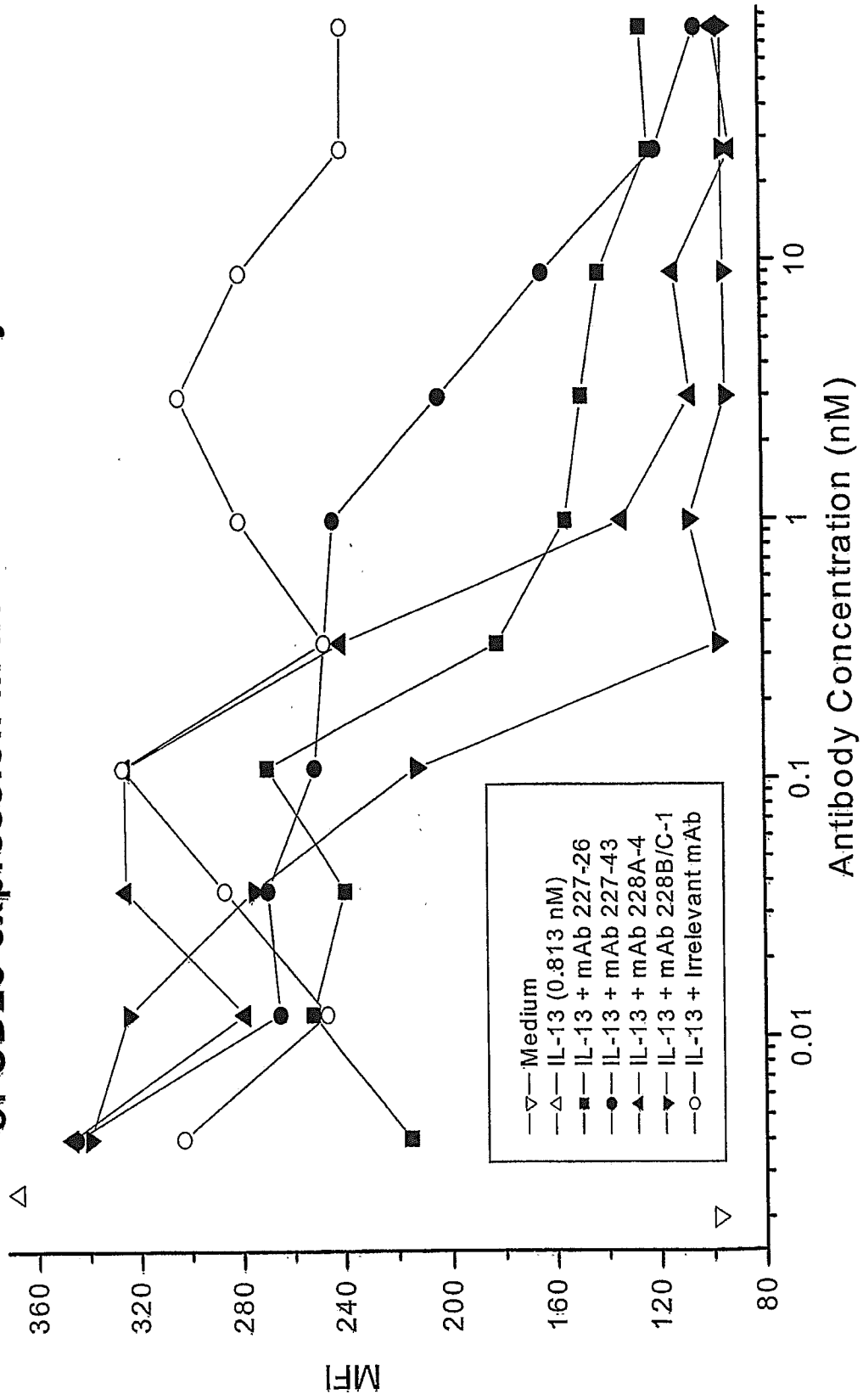


Fig. 7 Anti-IL13 mAbs Inhibit IL13-Induced Stat6 Phosphorylation in THP-1 Cells

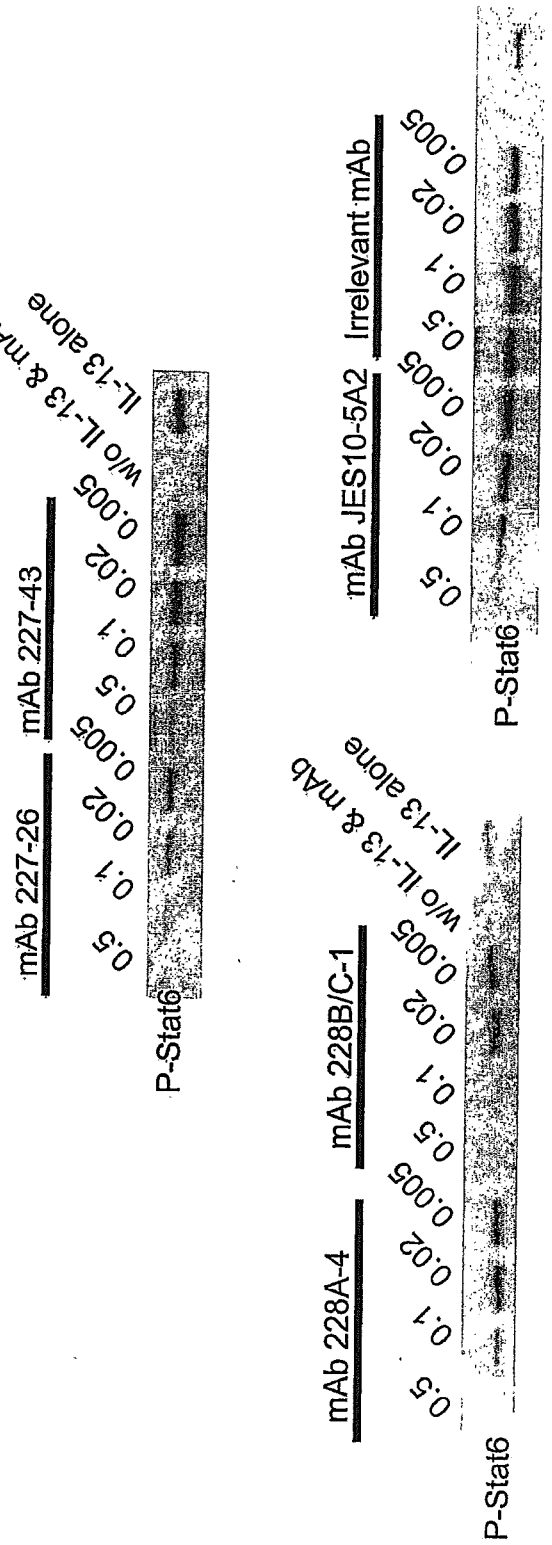


FIGURE 8

228B/C-1 Antibody
Heavy Chain (VH)

```
1                 10                  20                  30
Q V Q L Q E S G P G L V A P S Q S L S I T C T V S G F S L N A Y S V N W V

     40                  50  52a 53          60        65        70
R Q P P G K G L E W L G M I W G D G K I V Y N S A L K S R L N I S K D S S

              80  82              90        95       100 b c d e f 101
K S Q V F L K M S S L Q S D D T A R Y Y C A G D G Y Y P Y A M D N W G H G T

             118
 S V T V S S          (SEQ ID NO 4)
```

Light Chain (VK)

```
                    10                  20                  30
N I V L T Q S P A S L A V S L G Q R A T I S C R A S K S V D S Y G N S F M H W

40                  50                  60                  70
Y Q Q K P G Q P P K L L I Y L A S N L E S G V P A R F S G S G S R T D F T L T I

80                  90                  100                 113
D P V E A D D A A S Y Y C Q Q N N E D P R T F G G G T K L E I K R A     (SEQ ID NO 3)
```

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

FIGURE 9
228A-4 Antibody
Heavy Chain (VH)

```
1                 10                  20                  30
Q V Q L K E S G P G L V A P S Q S L S I T C T V S G F S L T D Y N I N W I R Q

40                  50 52a53            60        65        70
P P G K G L E W L G M I W G D G S T A Y N S A L K S R L S I S K D N S K S Q I F

80 82ab c 83      90        95        100 b c d e f 101   110
L K M N S L Q T E D T A R Y Y C A R D G Y F P Y A M A Y W G Q G T

         118
S V T V S S          (SEQ ID NO 6)
```

Light Chain (VK)

```
1                 10                  20                  30
N I V L T Q S P T S L A V S L G Q R A T I S C R A S E S V D S Y G N G F I H W

40                  50                  60                  70
Y Q Q K P G Q P P K L L I Y L A S N L E S G V P A R F S G S G S R T D F T L T I

80                  90                  100                 113
D P M E A D D A A T Y Y C Q Q N N E D P R T F G G G T K L E I K R A      (SEQ ID NO 5)
```

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

FIGURE 10
227-26 Antibody
Heavy Chain (VH)

```
1                 10                  20                  30
Q V Q L Q Q S G D D L V L P G A S V K L S C K A S G Y T F T S Y W I N W I

      40                  50  52a 53          60        65        70
K Q R P G Q G L E W I G H I A P G S G S T Y F N E M F K G K A T L T V D T

               80                  90        95       100 b c d e f
S S S T A Y I Q L S S L S S E D S A V Y F C A R S D I F L S Y A M D Y W G Q

              118
G T S V T V S S       (SEQ ID NO 8)
```

Light Chain (VK)

```
1               10                  20                  30

D V L M T Q T P L S L P V S L G D Q A S I S C R S S Q S I V H S N G N T Y L Q

40                  50                  60                  70

W Y L Q K P G Q S P K L L I Y K V S N R F S G V P D R F S G S G S G T D F T L K

80                  90                  100                 114
I S R V E A E D L G V Y Y C F Q G S H V P Y T F G G G T K L E I K R A      (SEQ ID NO 7)
```

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

FIGURE 11 A

VK CHAIN

	FM1																					SEQ ID NO	FR2															SEQ ID NO
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	CDR1	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	CDR2
Murine 22BB/C-1	N	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	Q	R	A	T	I	S	C	20	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	29
Human Template	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	21	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
Clone B	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	22	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
Clone J	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	23	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
Clone L	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	24	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
Clone N	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
Clone P	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
Clone R	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
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HT2-NEW #9	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-NEW #14	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
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HT2-NEW #21	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
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HT2-NEW #65	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
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HT2-NEW #70	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
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HT2-NEW #139	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-NEW #177	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-NEW #313	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C		W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	

FIGURE 11 C

	FM1																							SEQ ID NO
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HT2-dp27 #282	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
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HT2-dp27 #276	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #299	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #301	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #308	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #467	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #530	D	I	V	M	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #580	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #345	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #374	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #443	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #459	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #470	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #471	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #486	D	I	V	M	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #610	D	I	V	M	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #624	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	
HT2-dp27 #634	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	

	FM2															SEQ ID NO
	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	CDR2
HT2-dp27 #7	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	29
HT2-dp27 #13	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #19	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #29	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #34	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #40	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #43	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #50	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #53	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #57	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #66	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #67	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #73	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #74	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #89	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #92	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #100	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #111	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #112	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #118	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #123	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27-#136	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #144	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #146	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #15	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #26	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #83	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #164	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #177	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #195	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #198	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #150	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #268	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #270	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #199	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #273	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #282	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #304	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #155B	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #274	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #275	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #276	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #299	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #301	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #308	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #467	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #530	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #580	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #345	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #374	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #443	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #459	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #470	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #471	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #486	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #610	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #624	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #634	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	

FIGURE 11 B

FM3																																SEQ ID NO	FR4												SEQ ID NO
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	89	90	91	92	93	CDR3	103	104	105	106	107	108	109	110	111	112	113	114	
G	V	P	A	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	P	V	E	A	D	D	A	A	S	Y	Y	C	30	F	G	G	G	T	K	L	E	I	K	R	A	57
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	A	E	D	V	A	V	Y	Y	C	31	F	G	G	G	T	K	V	E	I	K	R		58
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	L	Q	A	E	D	V	A	V	Y	Y	C	32	F	G	G	G	T	K	L	E	I	K	R		59
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	S	L	Q	A	E	D	V	A	V	Y	Y	C	33	F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	P	L	Q	A	E	D	V	A	V	Y	Y	C	34	F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	35	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	S	V	Q	A	E	D	V	A	V	Y	Y	C	36	F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	S	S	V	Q	A	E	D	V	A	V	Y	Y	C	37	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	S	P	V	Q	A	E	D	V	A	V	Y	Y	C	38	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C	38	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	S	P	V	E	A	E	D	V	A	V	Y	Y	C	40	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	S	S	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C	41	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	S	S	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	L	E	A	E	D	V	A	V	Y	Y	C	42	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	S	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	P	V	Q	A	E	D	V	A	V	Y	Y	C	43	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	S	V	E	A	E	D	V	A	V	Y	Y	C	44	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	P	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	S	L	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	S	L	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	P	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	S	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	S	L	E	A	E	D	V	A	V	Y	Y	C	45	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	L	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	R	T	D	F	T	L	T	I	D	S	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	L	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	46	F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	D	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		
G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	V	E	A	E	D	V	A	V	Y	Y	C		F	G	G	G	T	K	V	E	I	K	R		

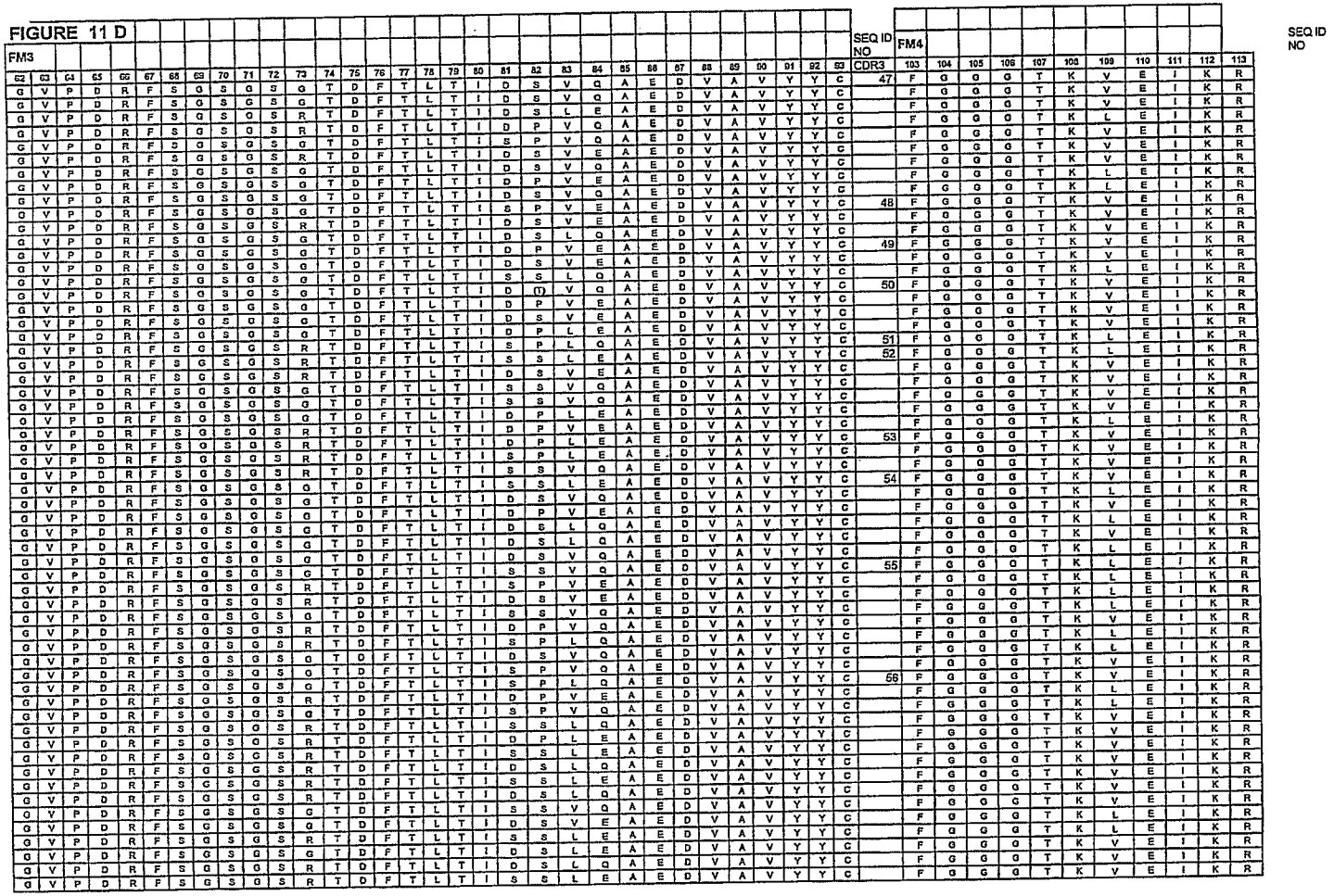

FIGURE 11 D
FM3
SEQ ID NO
FM4
SEQ ID NO
CDR3
47
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56

FIGURE 12A

VH CHAIN

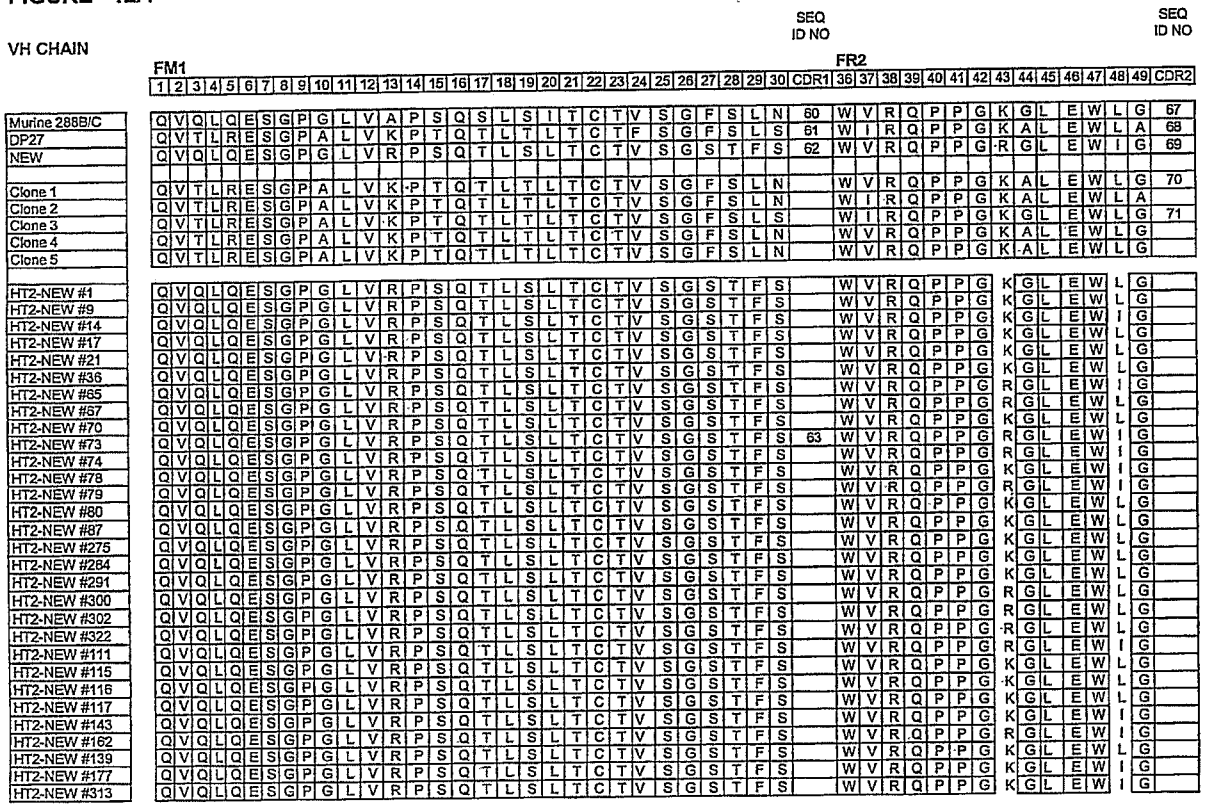


FIGURE 12C

FM1 · SEQ ID NO (CDR1) · FR2 · SEQ ID NO (CDR2)

	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	CDR1	36	37	38	39	40	41	42	43	44	45	46	47	48	49	CDR2
HT2-dp27 #7	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N	64	W	I	R	Q	P	P	G	K	A	L	E	W	L	G	72
HT2-dp27 #13	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #19	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #29	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #34	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #40	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S	65	W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #43	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	I	R	Q	P	P	G	K	G	L	E	W	L	A	73
HT2-dp27 #50	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	74
HT2-dp27 #53	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #57	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #66	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #67	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #73	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #74	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #89	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #92	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	I	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #100	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	A	L	E	W	L	A	75
HT2-dp27 #111	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #112	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #118	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #123	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	A	L	E	W	L	A	
HT2-dp27 #136	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #144	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #146	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #15	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #26	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #83	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #164	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #177	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #195	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #198	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #150	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #268	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	F	S	G	F	S	L	N	66	W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #270	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #199	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #273	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #282	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	A	L	E	W	L	A	
HT2-dp27 #304	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #155B	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #274	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #275	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #276	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	I	R	Q	P	P	G	K	A	L	E	W	L	A	
HT2-dp27 #299	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #301	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #308	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #467	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #530	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #580	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #345	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #374	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #443	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #459	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #470	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	A	L	E	W	L	A	
HT2-dp27 #471	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	G	
HT2-dp27 #486	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	A	L	E	W	L	G	
HT2-dp27 #610	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	S		W	V	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #624	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	I	R	Q	P	P	G	K	G	L	E	W	L	A	
HT2-dp27 #634	Q	V	T	L	R	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	V	S	G	F	S	L	N		W	V	R	Q	P	P	G	K	G	L	E	W	L	G	

FIGURE 12 B

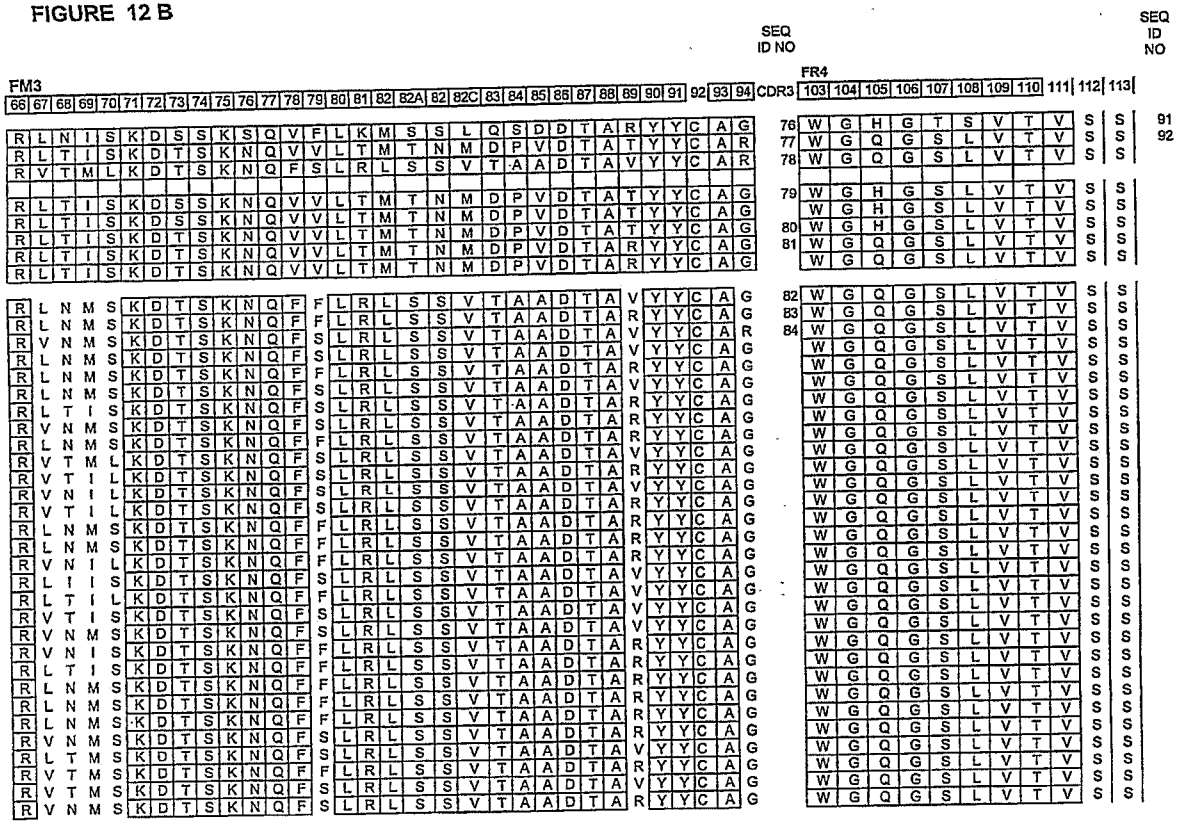

SEQ ID NO
SEQ ID NO
FM3
FR4
66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 82A 82 82C 83 84 85 86 87 88 89 90 91 92 93 94 CDR3 103 104 105 106 107 108 109 110 111 112 113

FIGURE 12D

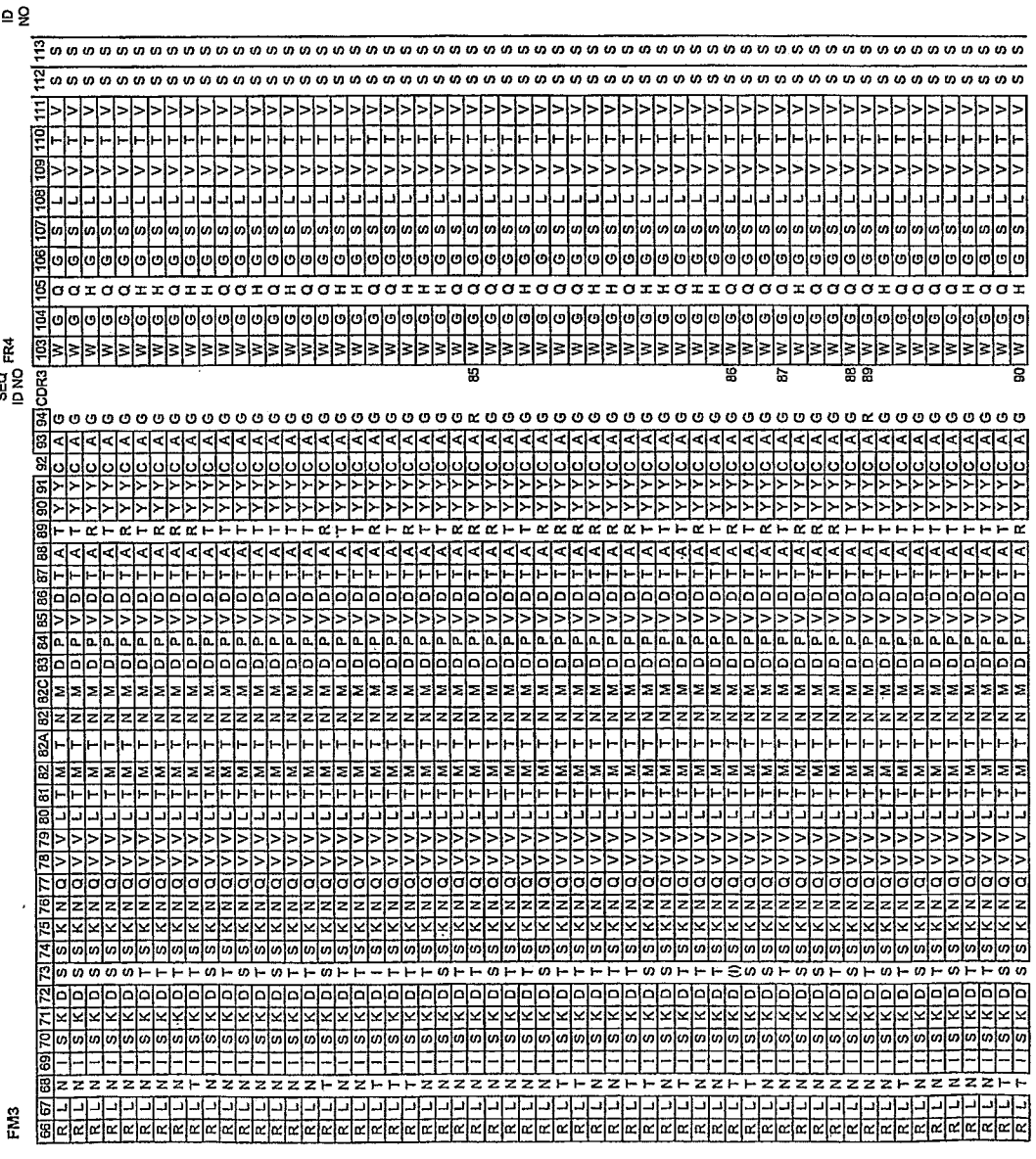


FIGURE 13 A

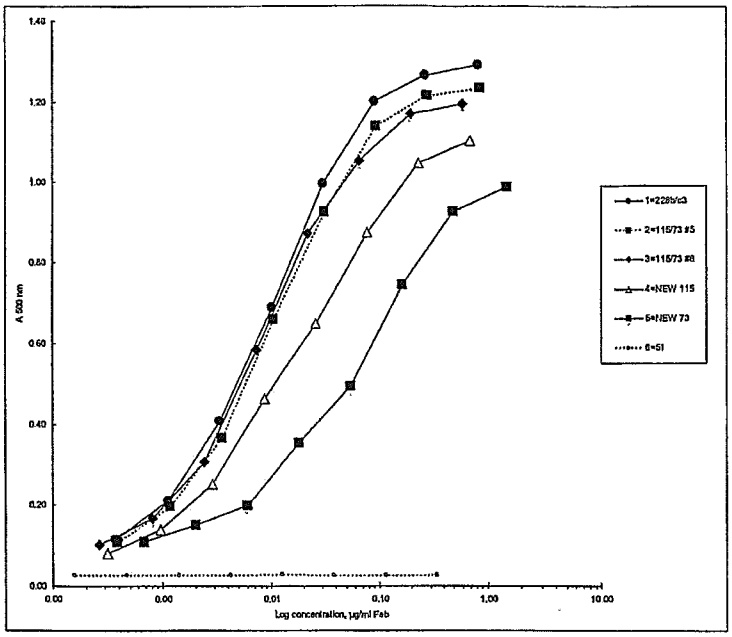


FIGURE 13 B

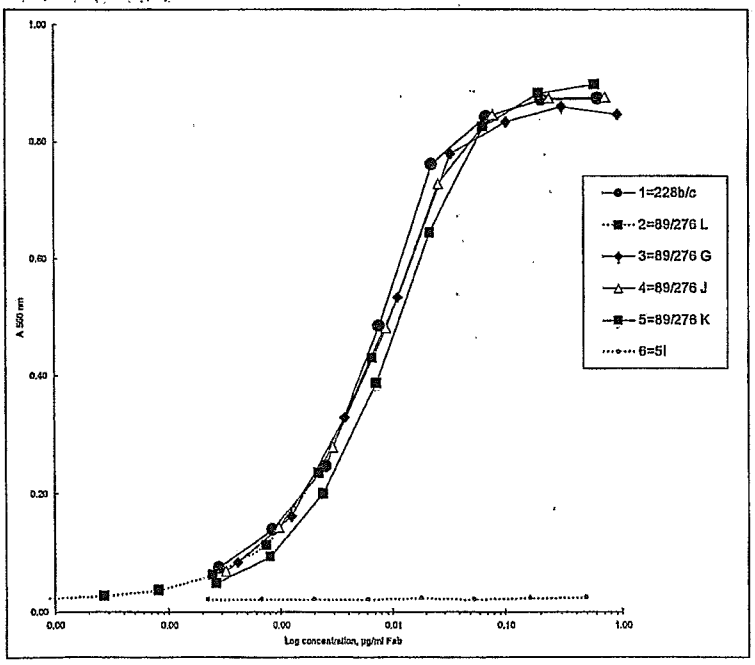


FIGURE 13 C

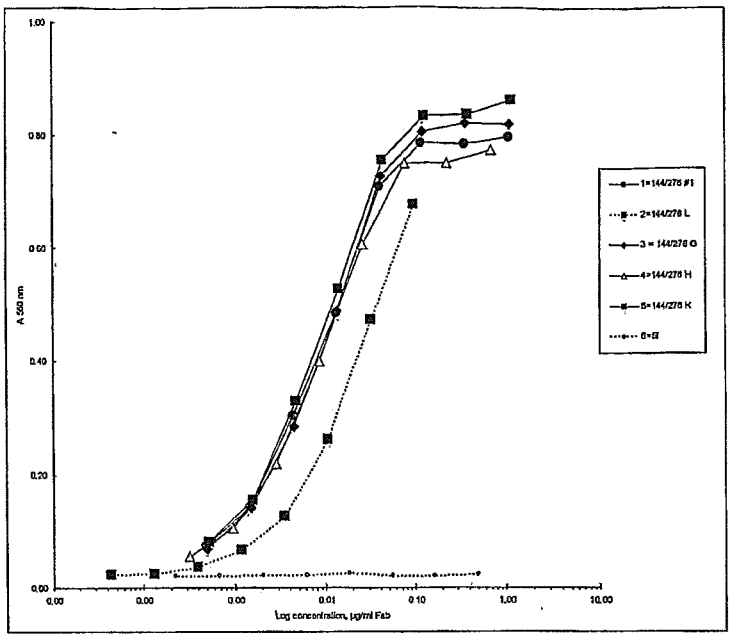


FIGURE 13 D

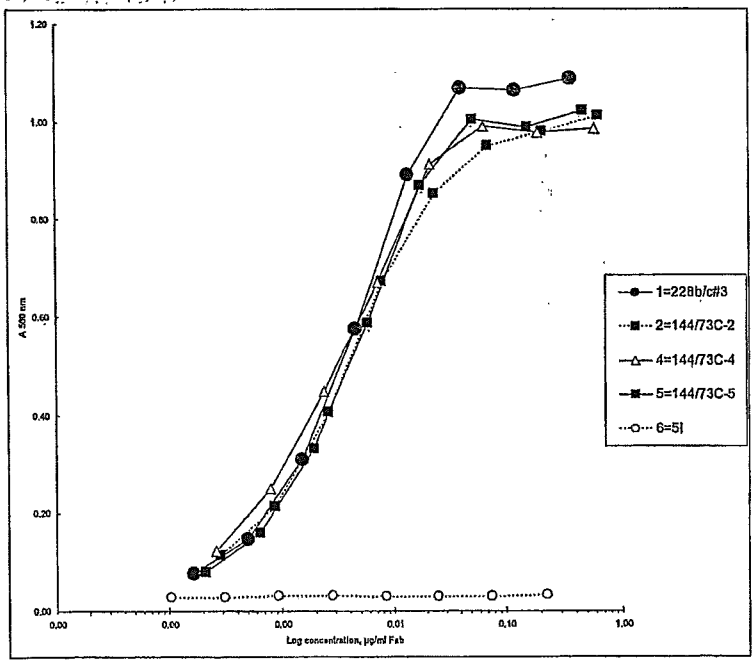


FIGURE 14 A

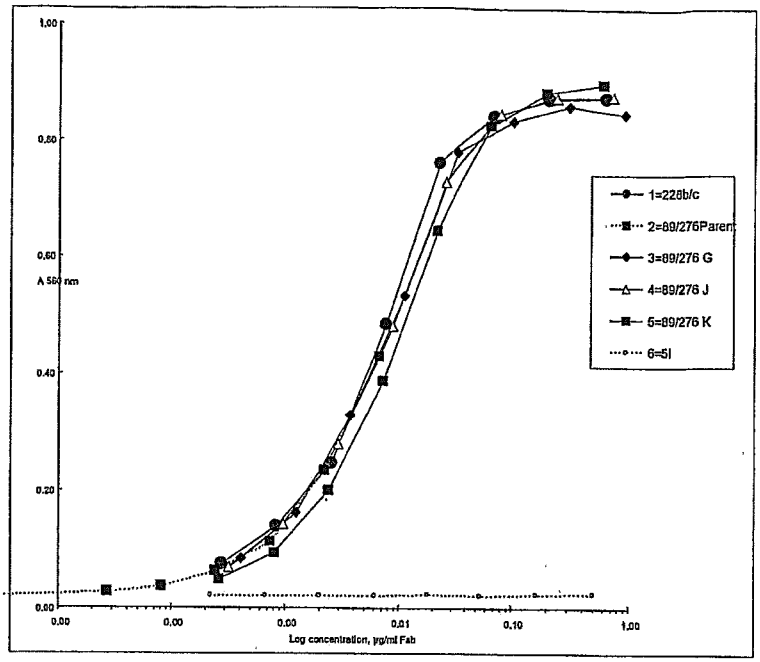


FIGURE 14B

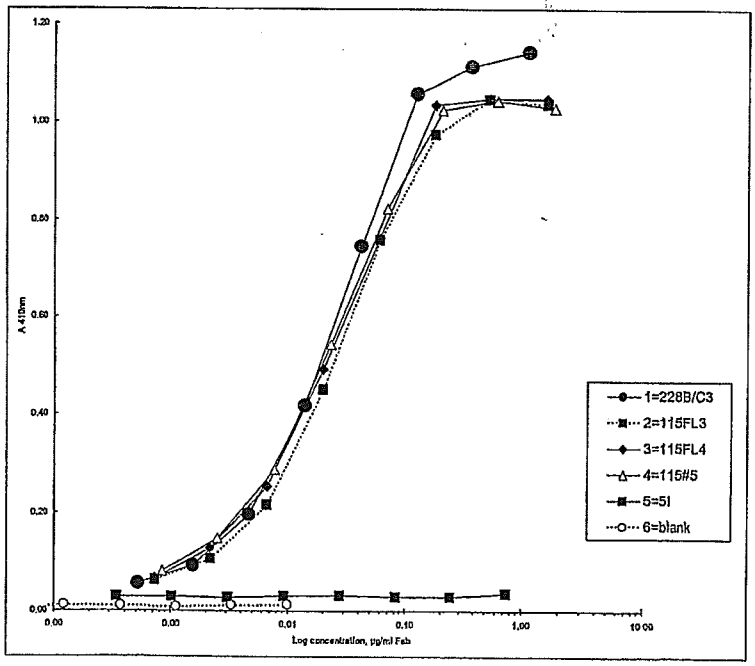


FIGURE 15

L1-59 (parent) CDR-L1	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-5	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-13	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-42	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-48	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-50	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-56	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-65	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-69	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-82	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-94	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H

L1-59 (parent) CDR-L3	Q	Q	N	N	E	D	P	R	T
CL-5	Q	Q	N	A	E	D	P	R	T
CL-13	Q	Q	N	N	E	D	P	R	T
CL-42	Q	Q	N	A	E	D	P	R	T
CL-48	Q	Q	N	N	E	D	P	R	T
CL-50	Q	Q	N	A	E	D	P	R	T
CL-56	Q	Q	N	A	E	D	P	R	T
CL-65	Q	Q	N	N	E	D	P	R	T
CL-69	Q	Q	N	A	E	D	P	R	T
CL-82	Q	Q	N	N	E	D	P	R	T
CL-94	Q	Q	N	A	E	D	P	R	T

L1-59 (parent) CDR-H1	A	Y	S	V	N
CL-5	A	Y	S	V	N
CL-13	A	K	S	V	N
CL-42	A	N	S	V	N
CL-48	A	N	S	V	N
CL-50	A	K	S	V	N
CL-56	A	K	S	V	N
CL-65	A	S	S	V	N
CL-69	A	N	S	V	N
CL-82	A	N	S	V	N
CL-94	A	N	S	V	N

L1-59 (parent) CDR-H3	D	G	Y	Y	P	Y	A	M	D	N
CL-5	D	G	Y	Y	P	Y	A	M	K	N
CL-13	D	G	Y	Y	P	Y	A	M	S	N
CL-42	D	G	Y	Y	P	Y	A	M	K	N
CL-48	D	G	Y	Y	P	Y	A	M	K	N
CL-50	D	G	Y	Y	P	Y	A	M	K	N
CL-56	D	G	Y	Y	P	Y	A	M	S	N
CL-65	D	G	R	Y	P	Y	A	M	K	N
CL-69	D	G	Y	Y	P	Y	A	M	D	N
CL-82	D	G	Y	Y	P	Y	A	M	K	N
CL-94	D	G	Y	Y	P	Y	A	M	K	N

FIGURE 16

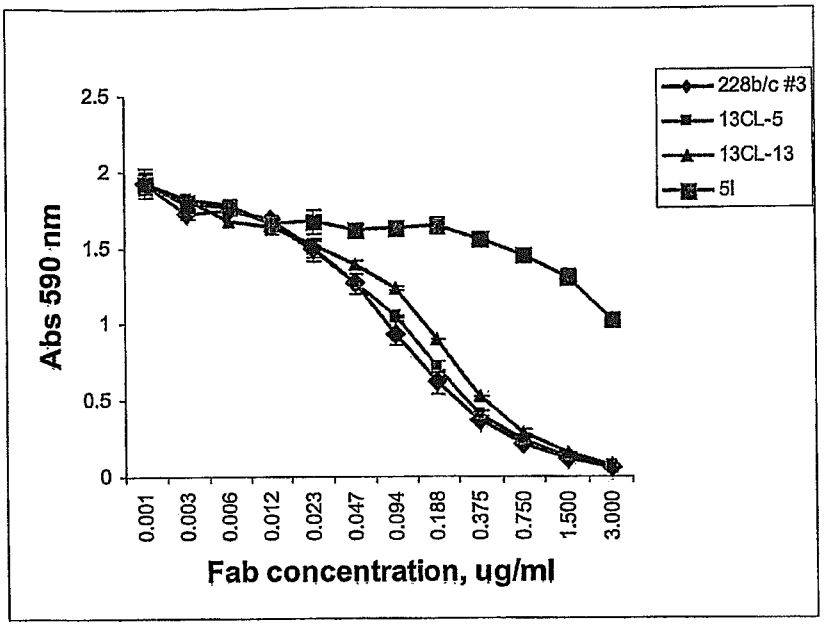

2.5
2
1.5
1
0.5
0
Abs 590 nm
0.001
0.003
0.006
0.012
0.023
0.047
0.094
0.188
0.375
0.750
1.500
3.000
Fab concentration, ug/ml
228b/c #3
13CL-5
13CL-13
5I

Figure 17 Variable Region Amino Acid Sequences for anti-IL13 Candidates

CL-5 (Affinity Matured Candidate) Vk:

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFT
LTISSLQAEDVAVYYCQQNAEDPRTFGGGTKVEIKR (SEQ ID NO 93)

CL-5 (Affinity Matured Candidate) Vh:

QVTLRESGPALVKPTQTLTLTCTGSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKN
QVVLTMTNMDPVDTATYYCAVDGYYPYAMKNWGQGSLVTVSS (SEQ ID NO 94)

CL-13 (Affinity Matured Candidate) Vk:

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFT
LTISSLQAEDVAVYYCQQNNEDPRTFGGGTKVEIKR (SEQ ID NO 95)

CL-13 (Affinity Matured Candidate) Vh:

QVTLRESGPALVKPTQTLTLTCTGSGFSLSAKSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKN
QVVLTMTNMDPVDTATYYCAVDGYYPYAMSNWGQGSLVTVSS (SEQ ID NO 96)

CL-50 (Affinity Matured Candidate) Vk:

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFT
LTISSLQAEDVAVYYCQQNAEDPRTFGGGTKVEIKR (SEQ ID NO 97)

CL-50 (Affinity Matured Candidate) Vh:

QVTLRESGPALVKPTQTLTLTCTGSGFSLSAKSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKN
QVVLTMTNMDPVDTATYYCAVDGYYPYAMKNWGQGSLVTVSS (SEQ ID NO 98)

FIGURE 18

Alignment of IL13 protein sequences



Figure 19 IL13 and the Binding Epitope of 228B/C MAb

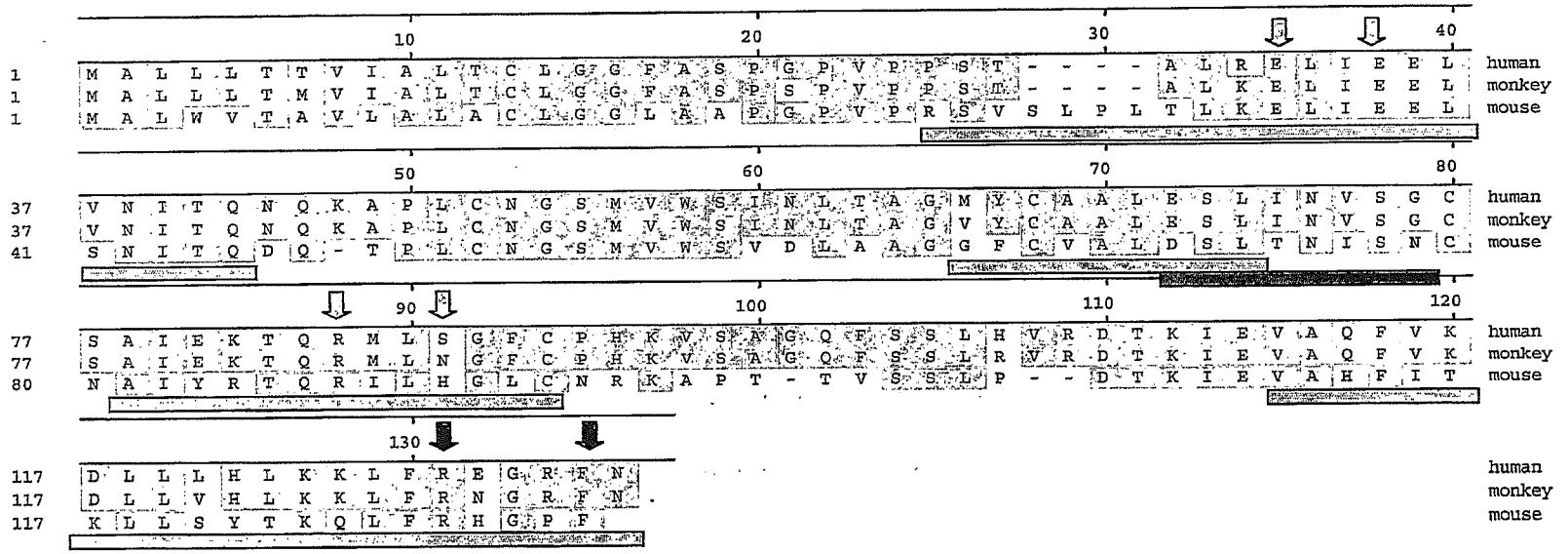


FIGURE 20

	CDR-L1			CDR-H1	
P	RASKSVDSYGNSFMH	SEQ ID NO 99	P	AYSVN	SEQ ID NO 117
V1	RASKSVDSYGQSFMH	SEQ ID NO 100	V1	AKSVN	SEQ ID NO 118
V2	RASKSVDSYGQSFLH	SEQ ID NO 101	V2	ANSVN	SEQ ID NO 119
V3	RASKSVDSYGNSYMH	SEQ ID NO 102	V3	GYSVN	SEQ ID NO 120
V4	RASKSVDSYGNSFLH	SEQ ID NO 103	V4	AHSVN	SEQ ID NO 121
			V5	ARSVN	SEQ ID NO 122
	CDR-L2			CDR-H2	
P	LASNLES	SEQ ID NO 104	P	MIWGDGKIVYNSALKS	SEQ ID NO 123
V1	LASNLNS	SEQ ID NO 105	V1	MIWGDGKISYNSALKS	SEQ ID NO 124
V2	LASNLQS	SEQ ID NO 106	V2	MIWGDGKIVYNSALES	SEQ ID NO 125
V3	LATNLES	SEQ ID NO 107	V3	MIWGDGKIVYNSALKS	SEQ ID NO 126
V4	LASNLKS	SEQ ID NO 108	V4	MIWGDGKIVYNSDLKS	SEQ ID NO 127
V5	LASNLEK	SEQ ID NO 109	V5	MIWGDGKVVYNSALKS	SEQ ID NO 128
V6	LASRLES	SEQ ID NO 110	V6	MIWGDGKIVYNSELKS	SEQ ID NO 129
V7	LASNLHS	SEQ ID NO 111	V7	MIWGDGKIAYNSALKS	SEQ ID NO 130
V8	LASNLSS	SEQ ID NO 112	V8	MIWGDGKIVYNSALKE	SEQ ID NO 131
V9	LASFLES	SEQ ID NO 113	V9	MVWGDGKIVYNSALKS	SEQ ID NO 132
V10	LANNLES	SEQ ID NO 114	V10	MIWGDGKIVYNSALAS	SEQ ID NO 133
			V11	MIWGDGKKVYNSALKS	SEQ ID NO 134
	CDR-L3			CDR-H3	
P	QQNNEDPRT	SEQ ID NO 115	P	DGYYPYAMDN	SEQ ID NO 135
V1	QQNAEDPRT	SEQ ID NO 116	V1	DGRYPYAMDN	SEQ ID NO 136
			V2	DGYYPYAMKN	SEQ ID NO 137
			V3	DGRYPYAMKN	SEQ ID NO 138
			V4	DGYYPYAMSN	SEQ ID NO 139
			V5	DGYYPYAMAN	SEQ ID NO 140
			V6	DGYYPYALDN	SEQ ID NO 141

FIGURE 21A: Variable Region Amino Acid Sequences for certain anti-IL13 Candidates:

CL-89 Vk (SEQ ID NO: 142):

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGT
DFTLTISSLQAEDVAVYYCQQNNEDPRTFGGGTKVEIKR

CL-276G Vh (SEQ ID NO 143):

QVTLRESGPALVKPTQTLTLTCTVSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCAGDGYYPYAMDNWGQGSLVTVSS

RL-36 (Random Library Candidate) Vk (SEQ ID NO 144):

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGT
DFTLTISSLQAEDVAVYYCQQNNEDPRTFGGGTKVEIKR

RL-36 (Random Library Candidate) Vh (SEQ ID NO 145):

QVTLRESGPALVKPTQTLTLTCTGSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCAVDGYYPYAMDNWGQGSLVTV
SS

RL-19 (Random Library Candidate) Vh (SEQ ID NO 146):

QVTLRESGPALVKPTQTLTLTCTSSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCALDGYYPYAMDNWGQGSLVTV
SS

FIGURE 21B: Variable Region Amino Acid Sequences for certain anti-IL13 Candidates:

RL-11 (Random Library Candidate) Vh (SEQ ID NO 147):

QVTLRESGPALVKPTQTLTLTCTTSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCAVDGYYPYAMDNWGQGSLVTV
SS

RL-8 (Random Library Candidate) Vh (SEQ ID NO 148):

QVTLRESGPALVKPTQTLTLTCTLSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTSK
NQVVLTMTNMDPVDTATYYCASDGYYPYAMDNWGQGSLVTV
SS

RL-45 (Random Library Candidate) Vh(SEQ ID NO 149):

QVTLRESGPALVKPTQTLTLTCTTSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCATDGYYPYAMDNWGQGSLVTV
SS

RL36-L1,59 (L1 Affinity Matured Candidate) Vk (SEQ ID NO 150):

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGT
DFTLTISSLQAEDVAVYYCQQNNEDPRTFGGGTKVEIKR

RL36-L1,59 (L1 Affinity Matured Candidate) Vh (SEQ ID NO 151):

QVTLRESGPALVKPTQTLTLTCTGSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCAVDGYYPYAMDNWGQGSLVTVSS

scFV Candidate #212 (SEQ ID NO 152):

QVTLRESGPALVKPTQTLTLTCTVSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCAGDGYYPYAMDNWGQGSLVTV
*SSGGSSRSSSSGGGGSGGGG*DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWYQQKPGQPPKLLI
YLASNLESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQQN
NEDPRTFGGGTKVEIKR