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

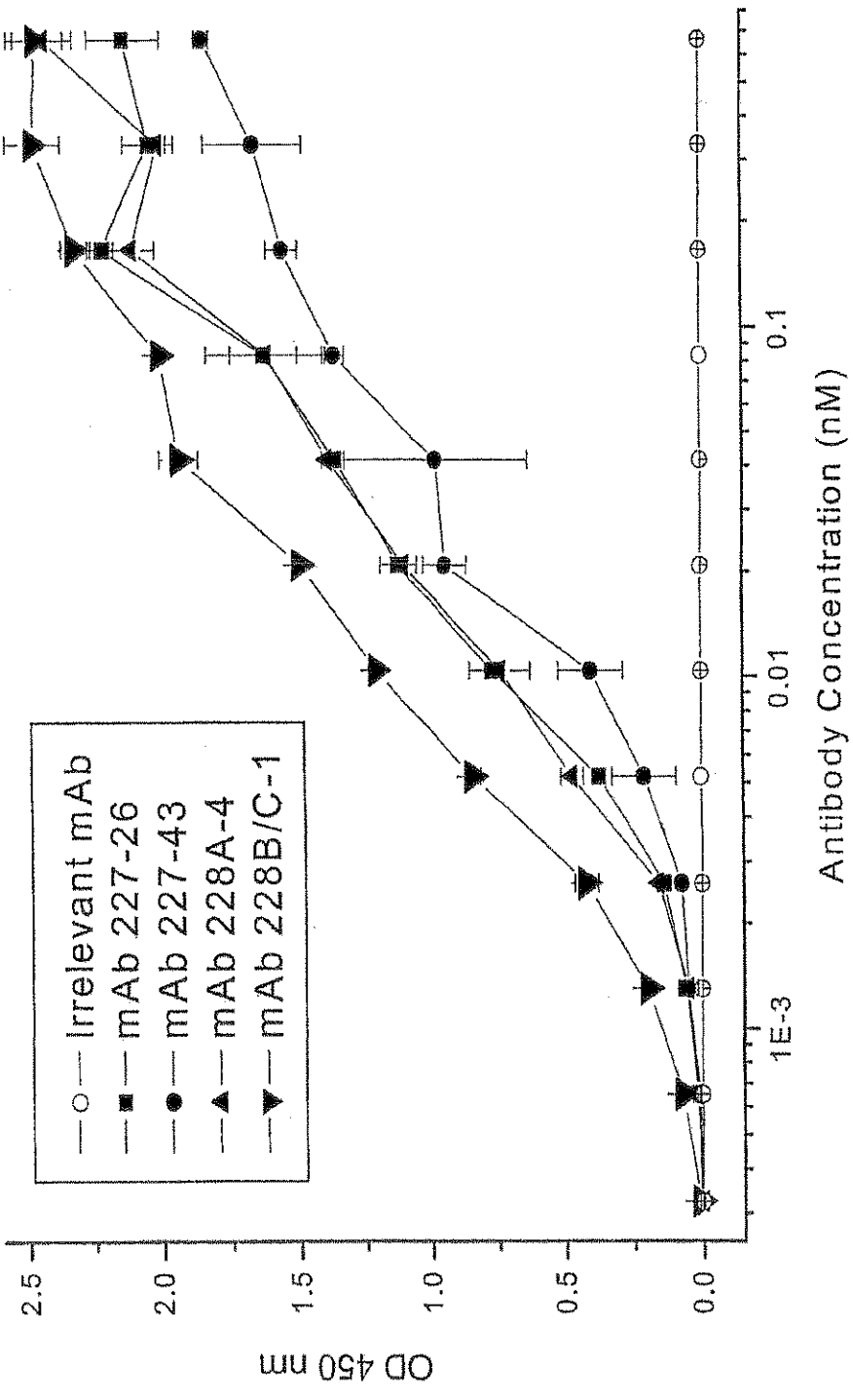


Fig. 2 Binding of anti-IL13 mAbs to MT-IL13/Fc

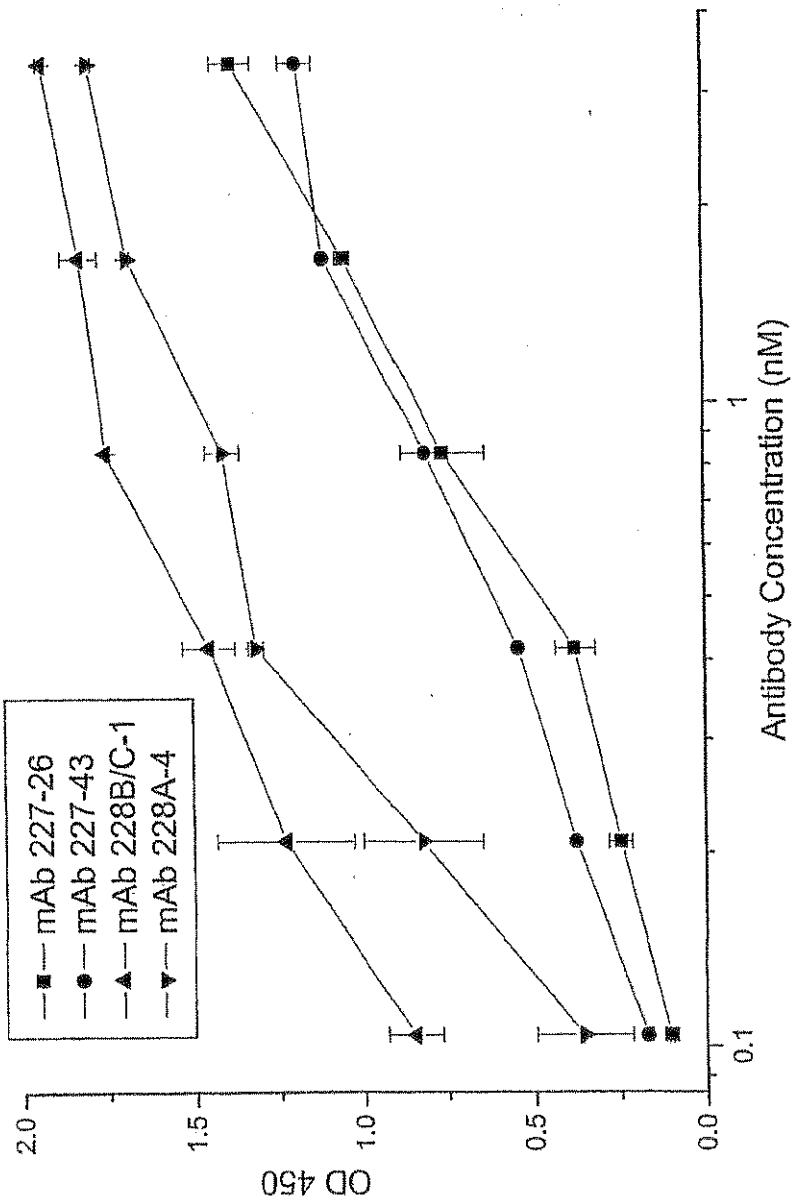


Fig. 3 Anti-IL13 mAb JES10-5A2 does not compete with the binding of mAb 228B/C-1-HRP to Human IL-13 in ELISA

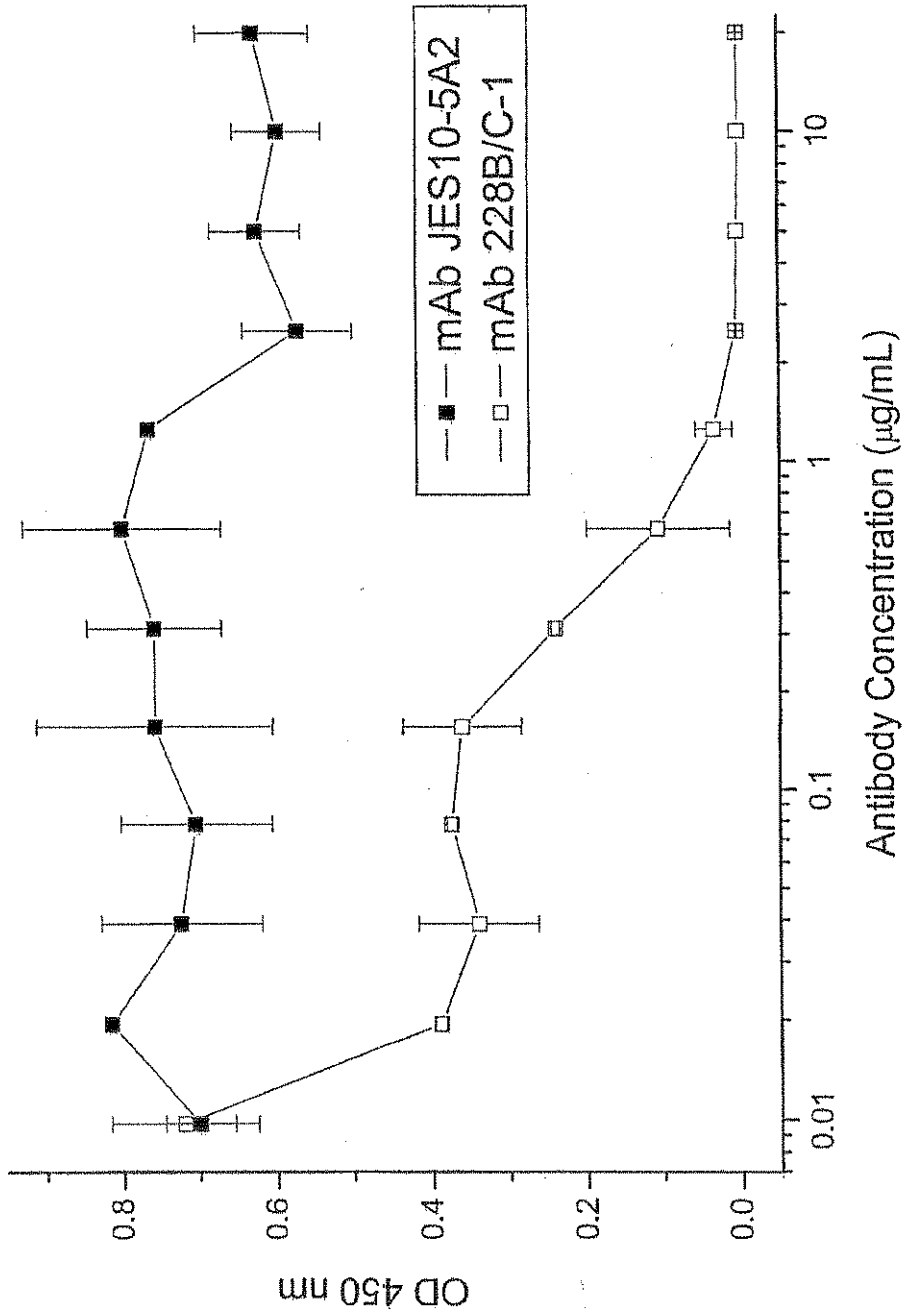


Fig. 4 Effect of anti-IL13 mAbs on the proliferation of L-1236 cells

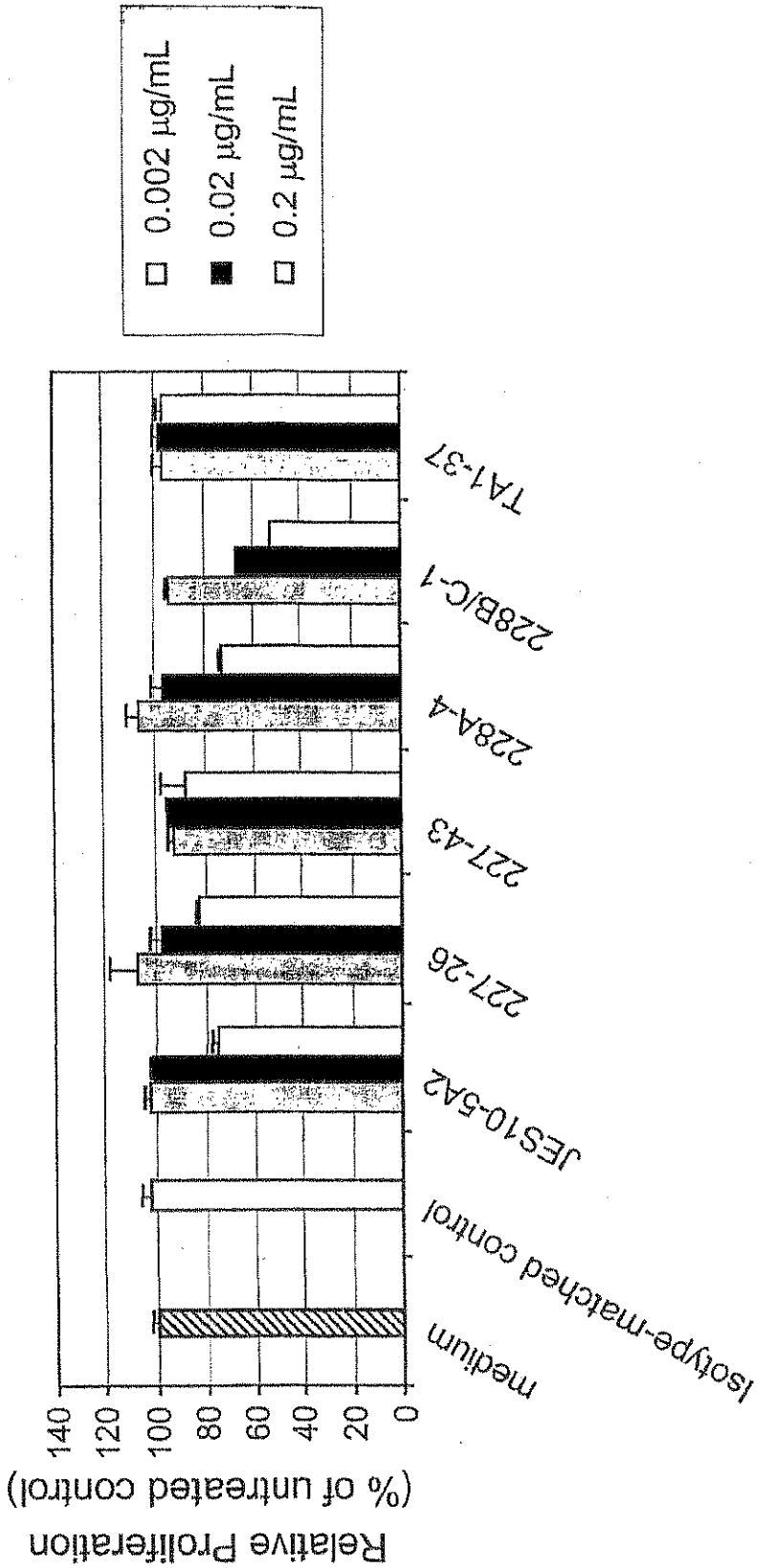


Fig. 5 Effect of anti-IL13 mAbs on IL13-induced suppression of CD14 expression in human monocytes

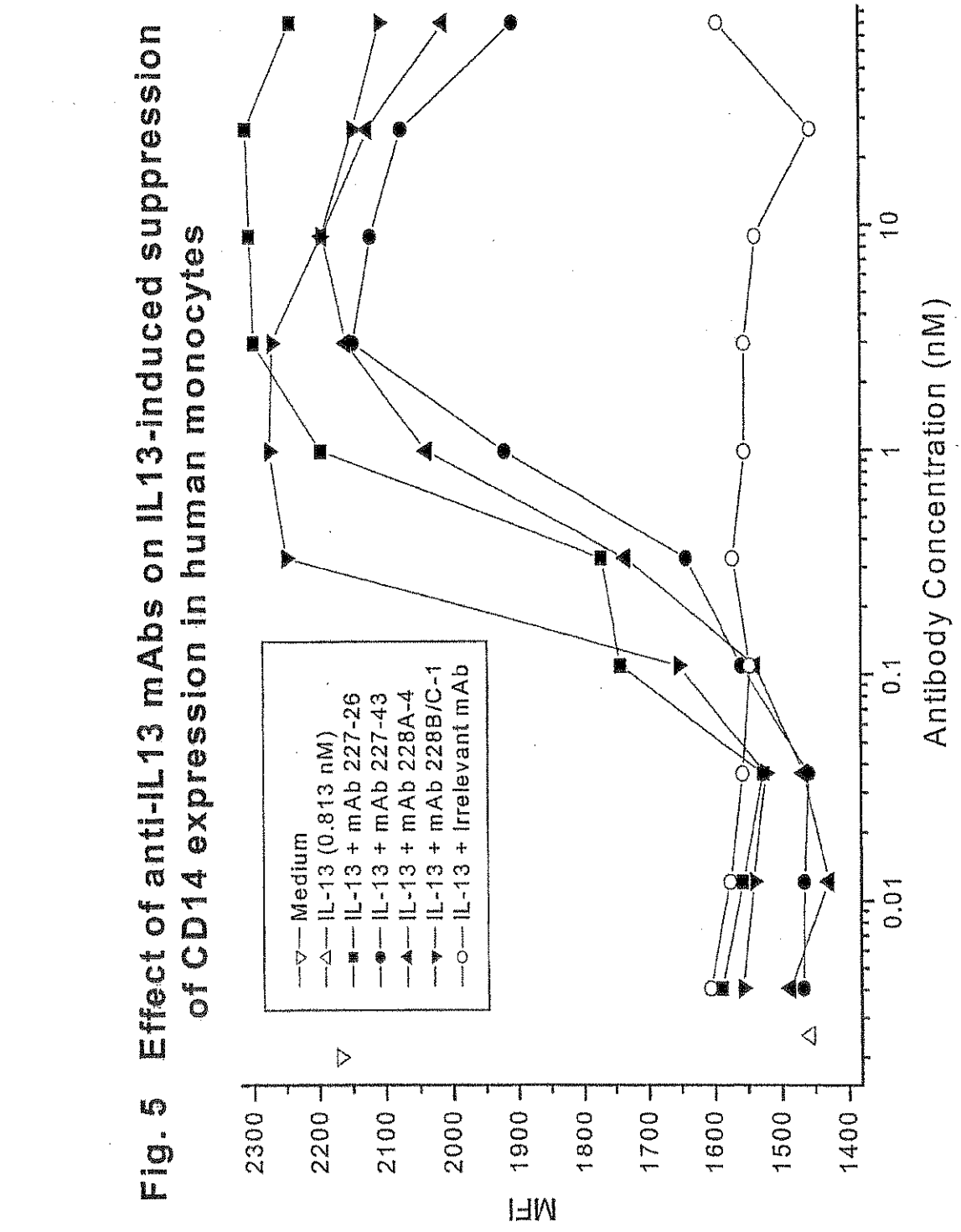


Fig. 6 Effect of anti-IL13 mAbs on IL13-induced upregulation of CD23 expression in human monocytes

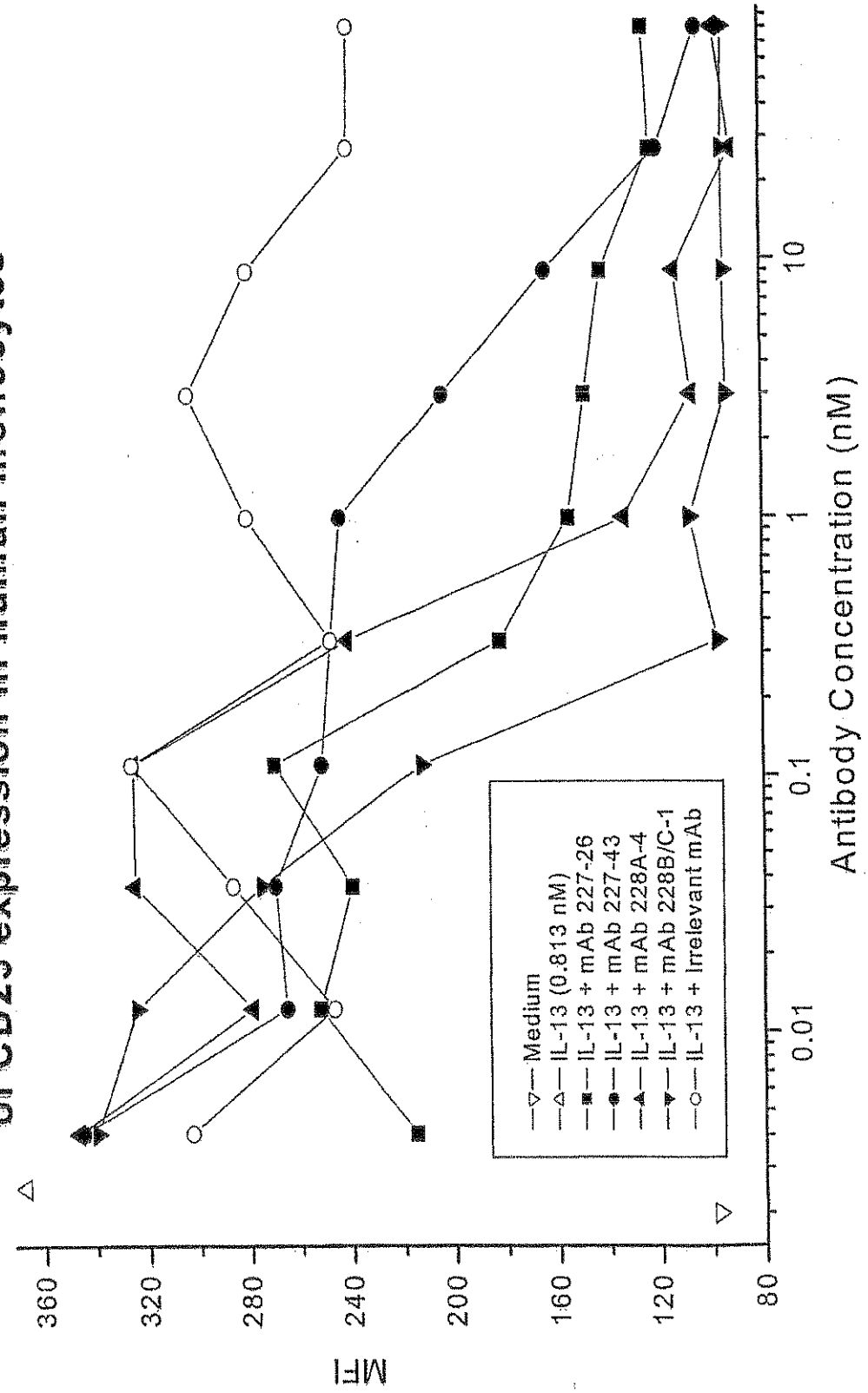


Fig. 7 Anti-IL13 mAbs Inhibit IL13-Induced Stat6 Phosphorylation in THP-1 Cells

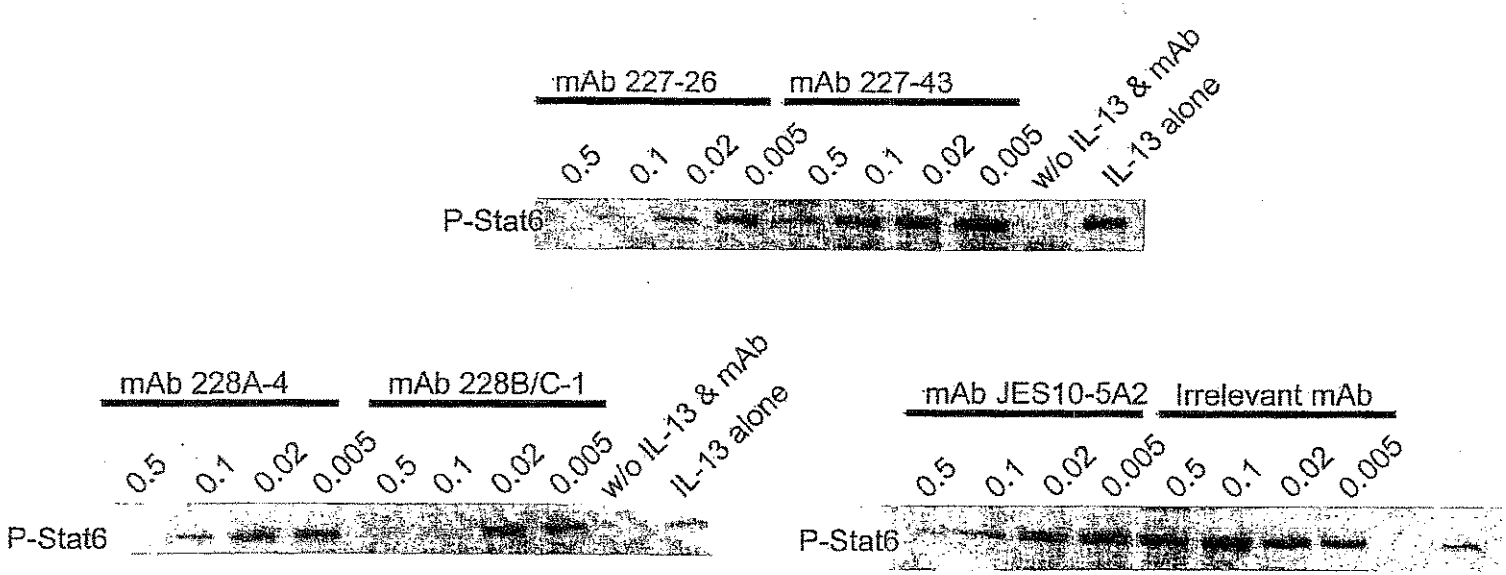


FIGURE 8

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 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

	SEQ ID NO	FM1 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	CDR1	FR2 35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	CDR2	SEQ ID NO
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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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FIGURE 11 C

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HT2-dp27 #279	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 #298	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	A	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
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	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	29
HT2-dp27 #7	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
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 #58	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	
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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	
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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 #199	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #203	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 #198	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 #1656	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 #276	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #278	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #279	W	Y	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	
HT2-dp27 #298	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	
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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

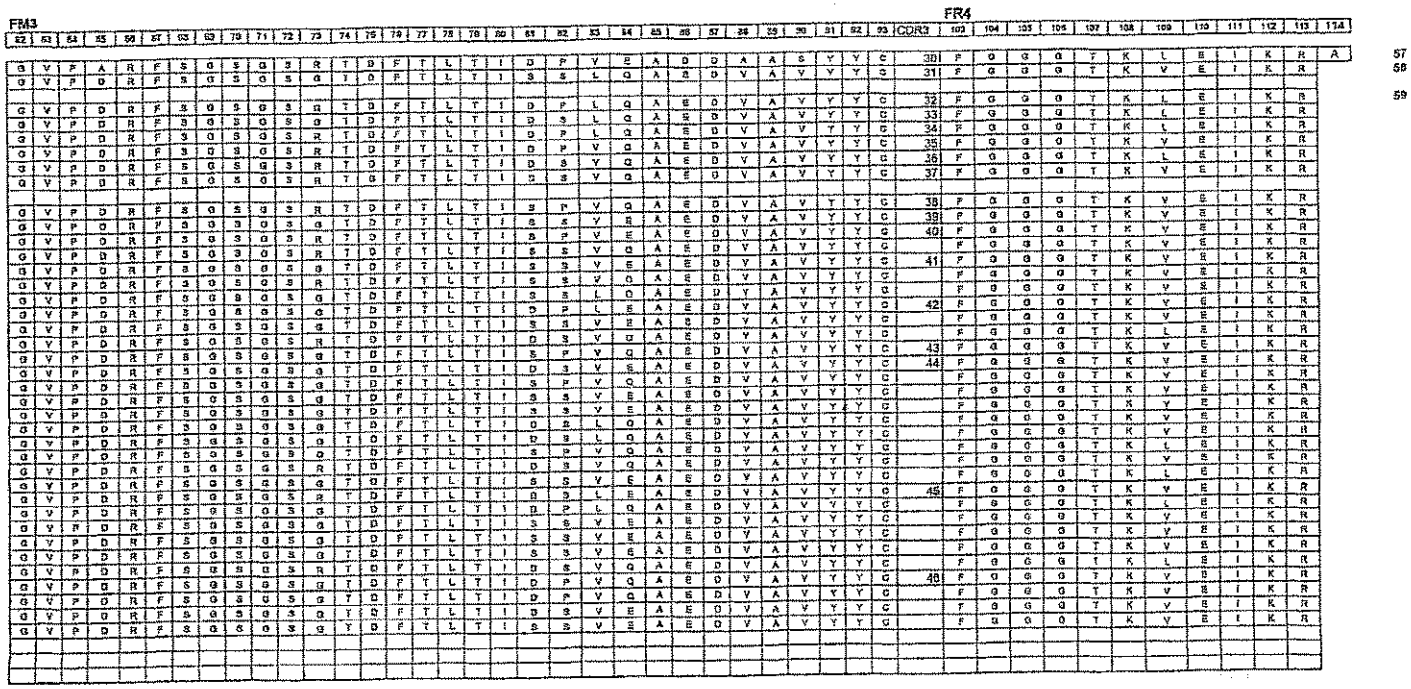


FIGURE 11 D

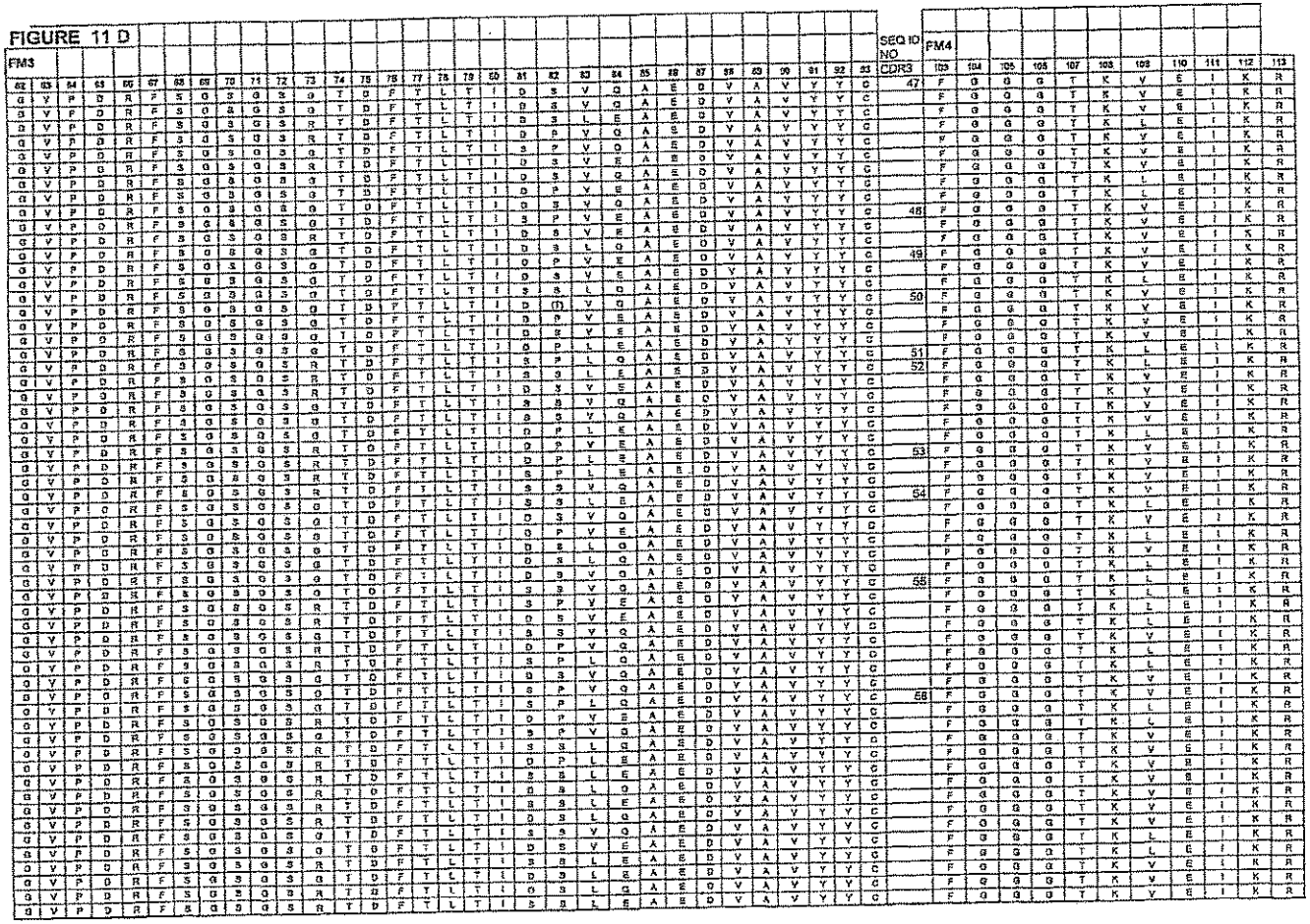


FIGURE 12A

VH CHAIN

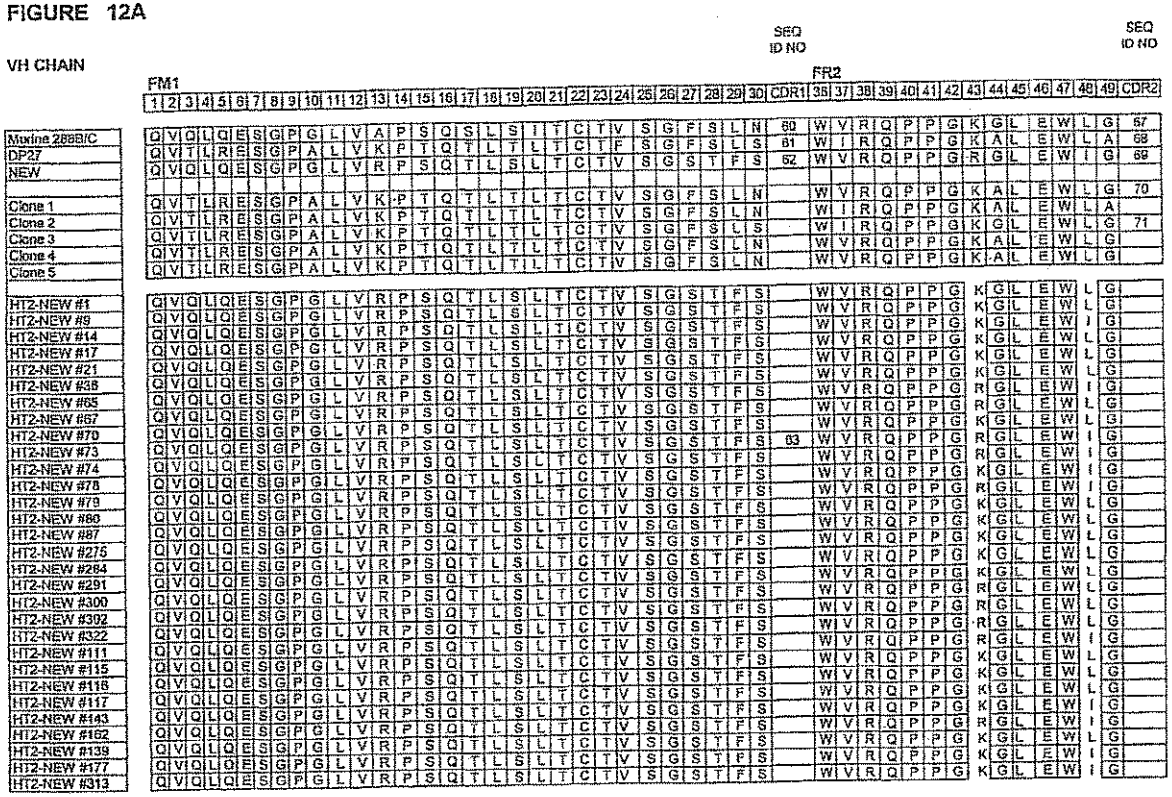


FIGURE 12C

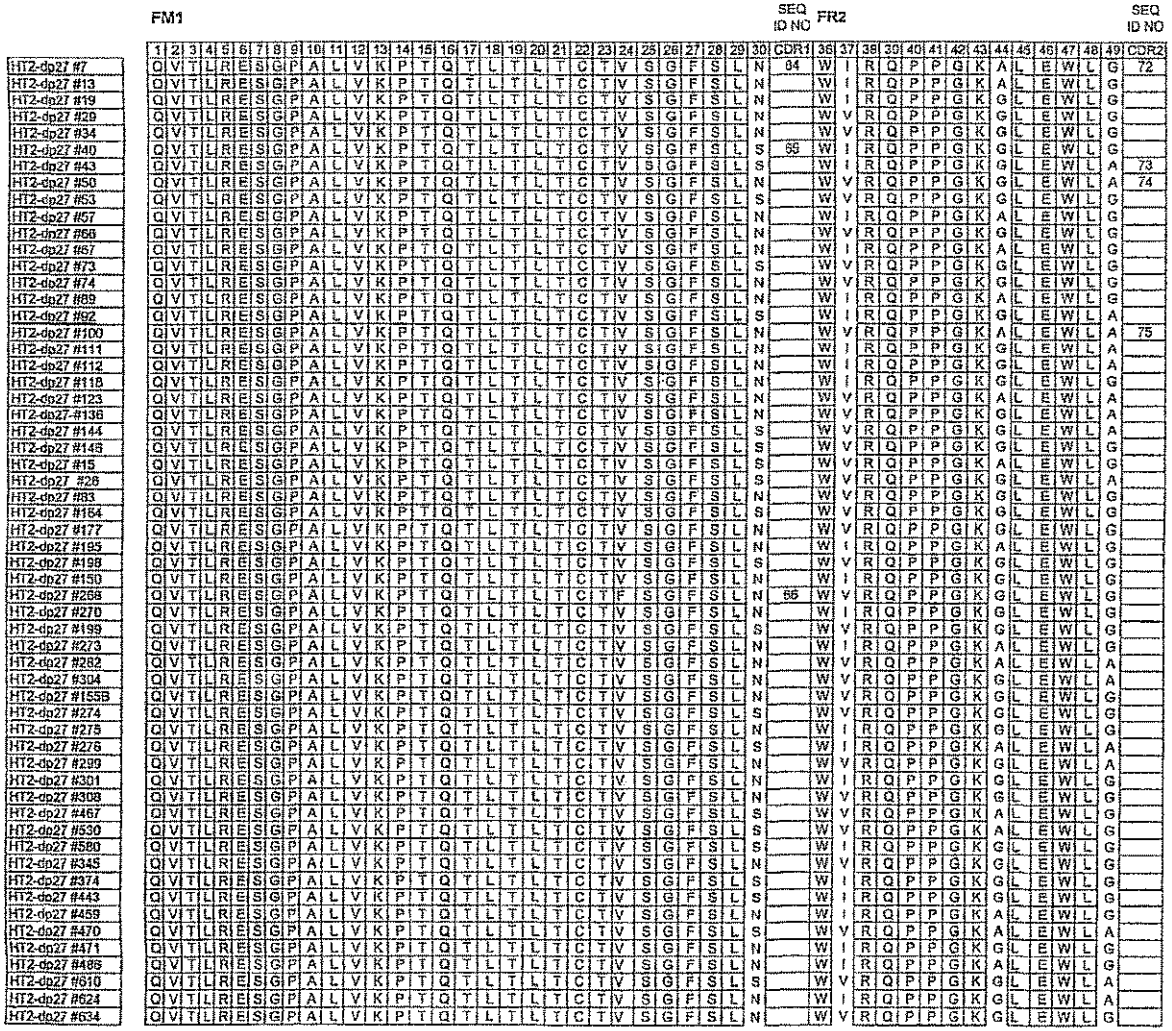

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FR2
SEQ ID NO
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CDR2
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HT2-dp27 #19
HT2-dp27 #29
HT2-dp27 #34
HT2-dp27 #40
HT2-dp27 #43
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HT2-dp27 #67
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HT2-dp27-#136
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HT2-dp27 #146
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HT2-dp27 #195
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HT2-dp27 #443
HT2-dp27 #459
HT2-dp27 #470
HT2-dp27 #471
HT2-dp27 #486
HT2-dp27 #610
HT2-dp27 #624
HT2-dp27 #634

FIGURE 12 B

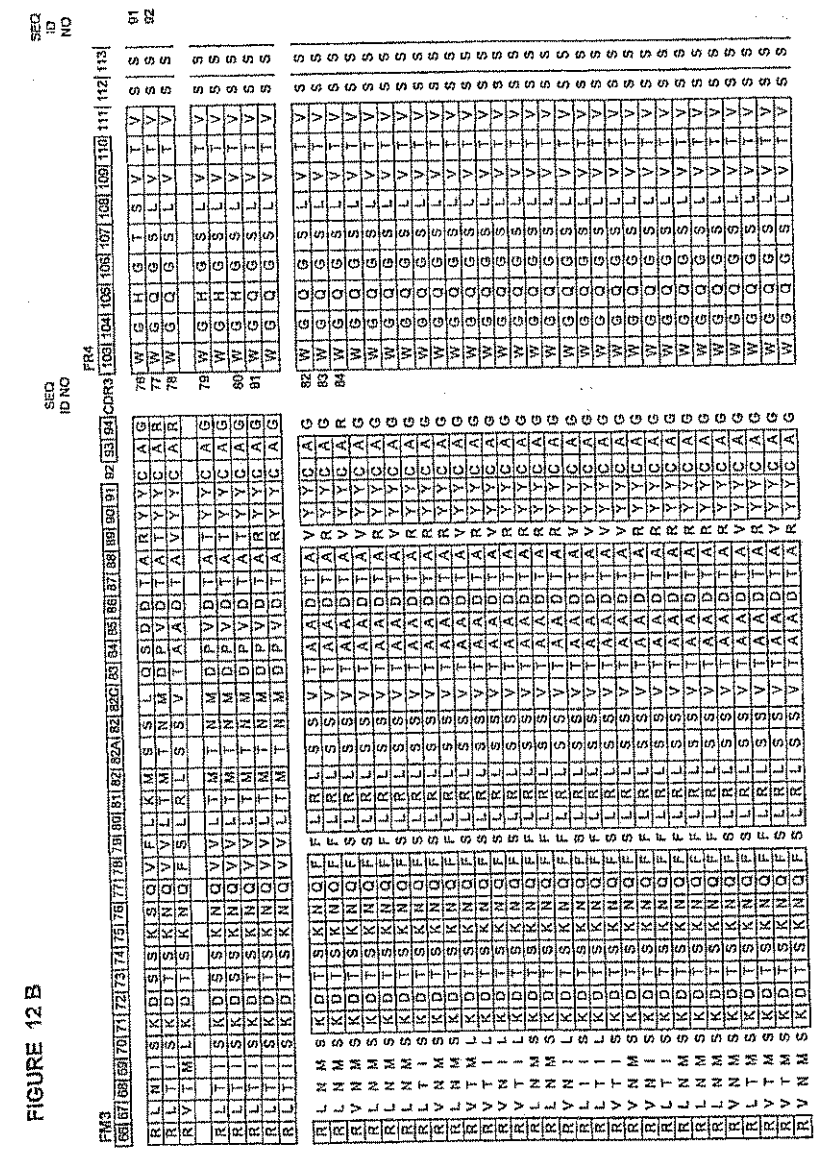


FIGURE 12D

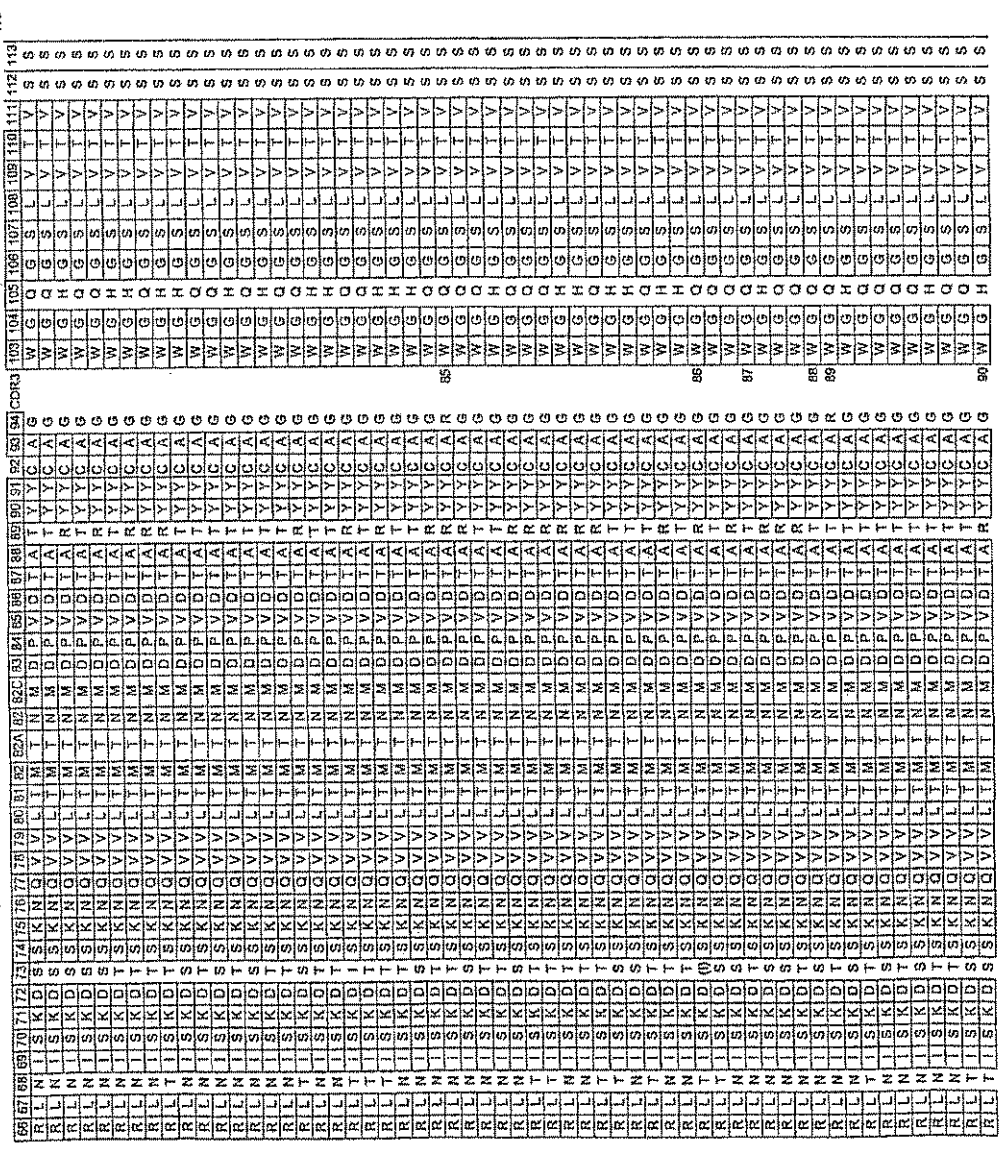


FIGURE 13 A

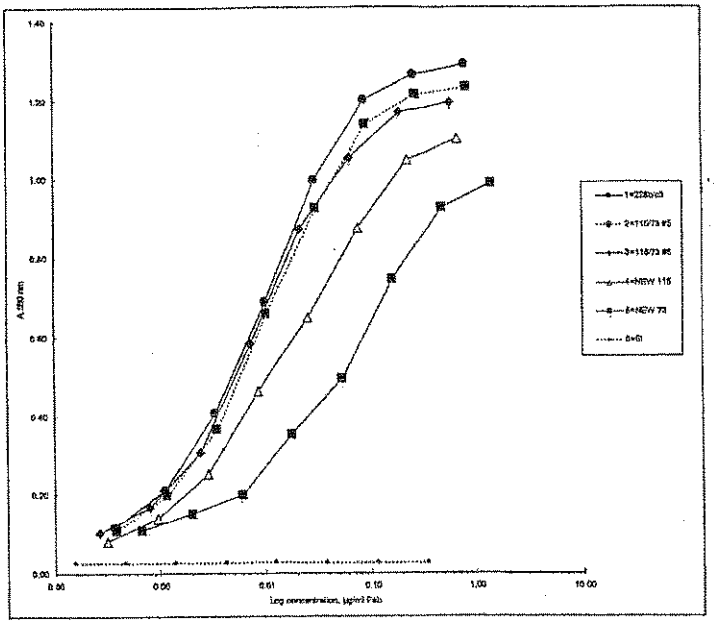


FIGURE 13 B

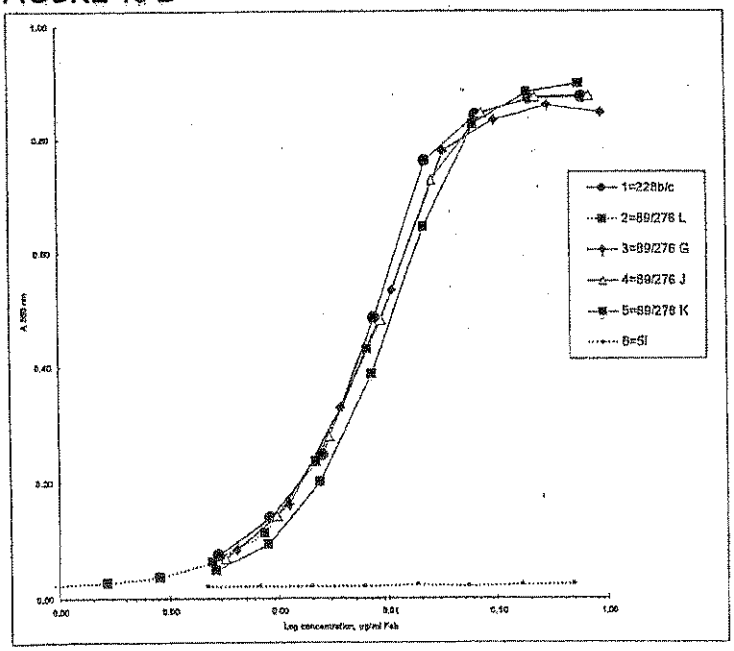


FIGURE 13 C

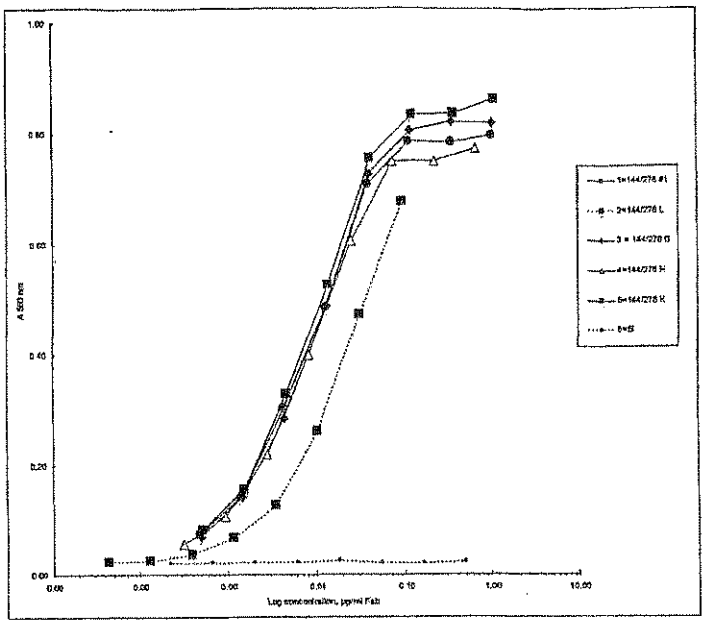


FIGURE 13 D

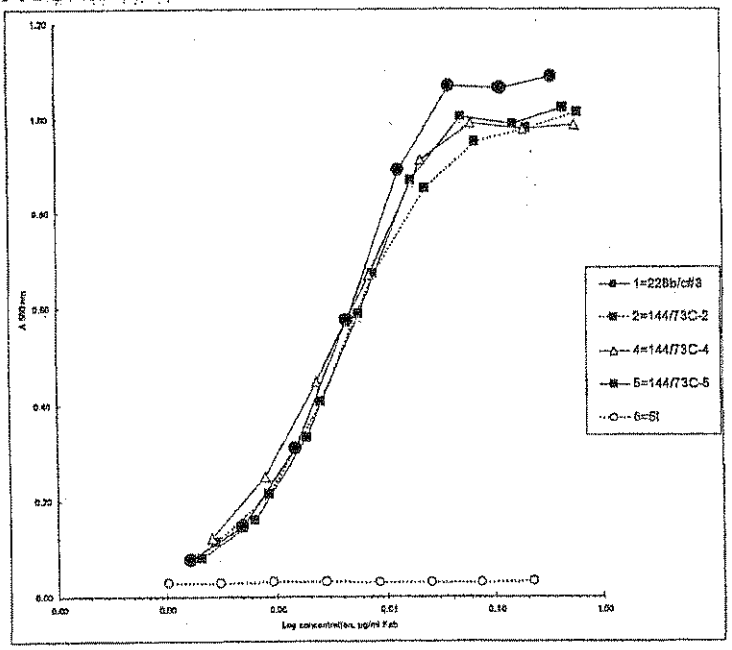


FIGURE 14 A

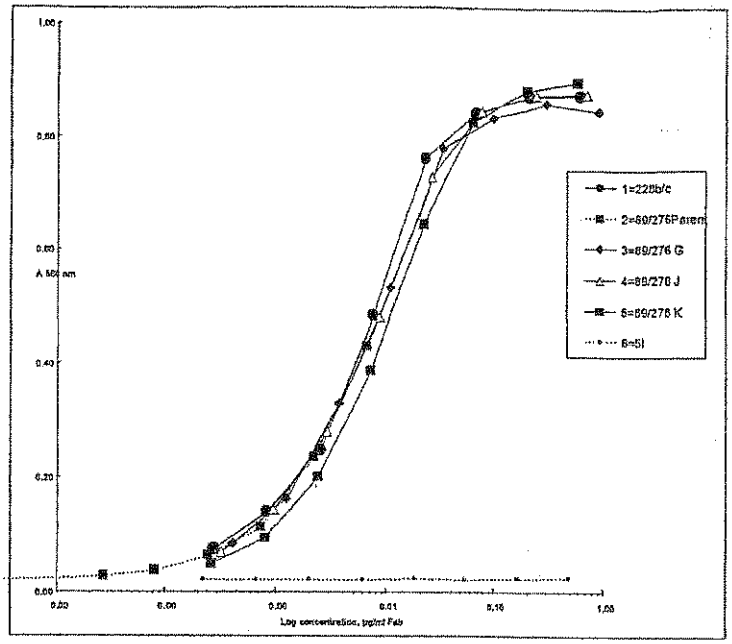


FIGURE 14B

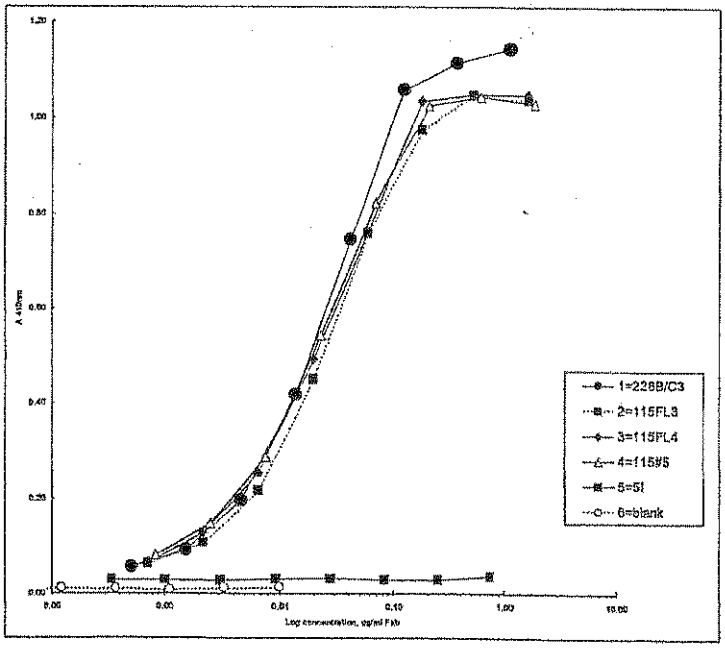


FIGURE 15

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

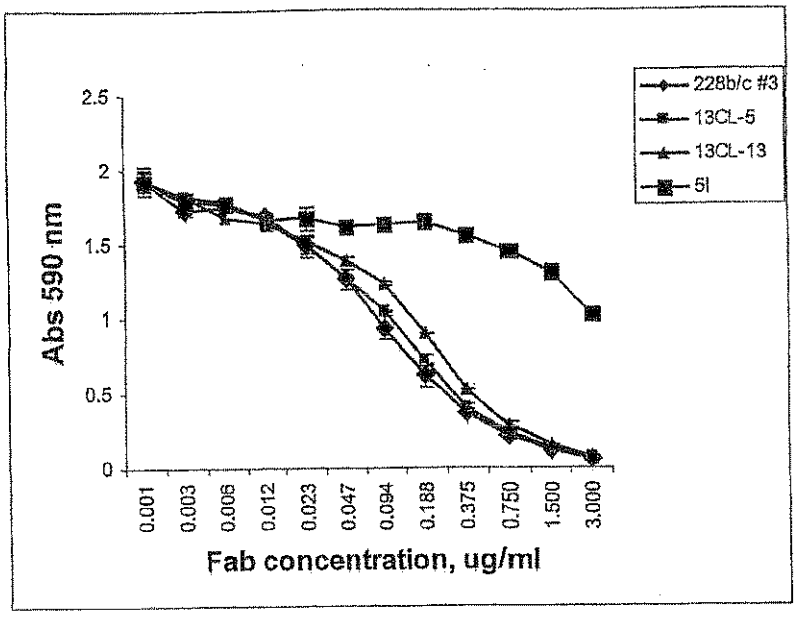

228b/c #3
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13CL-13
5I
Abs 590 nm
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2
1.5
1
0.5
0
0.001
0.003
0.006
0.012
0.023
0.047
0.094
0.188
0.375
0.750
1.500
3.000
Fab concentration, ug/ml

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
Majority
Human.pro
Monkey-cyn
Bovine.pro
Dog.pro
Rat.pro
Mouse.pro
Gerbil.pro

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

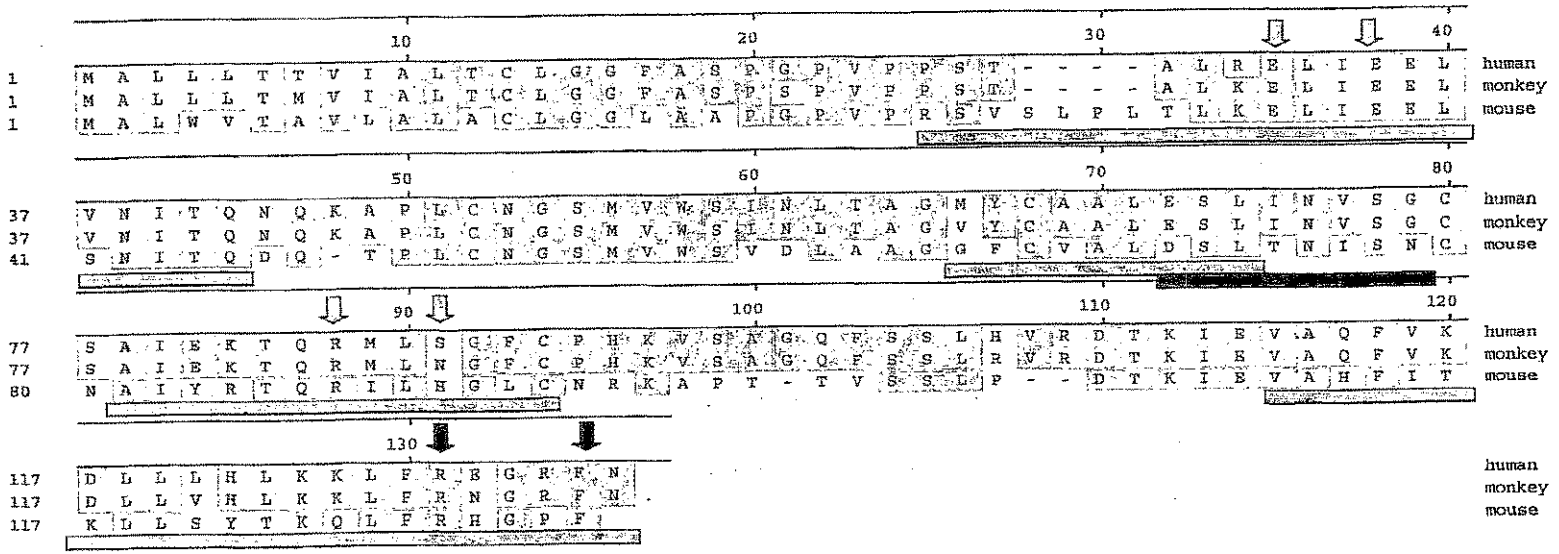


FIGURE 20

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P	RASKSVDSYGNSFMH	SEQ ID NO 99
V1	RASKSVDSYGQSFMH	SEQ ID NO 100
V2	RASKSVDSYGQSFLH	SEQ ID NO 101
V3	RASKSVDSYGNSYMH	SEQ ID NO 102
V4	RASKSVDSYGNSFLH	SEQ ID NO 103
	CDR-L2	
P	LASNLES	SEQ ID NO 104
V1	LASNLNS	SEQ ID NO 105
V2	LASNLQS	SEQ ID NO 106
V3	LATNLES	SEQ ID NO 107
V4	LASNLKS	SEQ ID NO 108
V5	LASNLEK	SEQ ID NO 109
V6	LASRLES	SEQ ID NO 110
V7	LASNLHS	SEQ ID NO 111
V8	LASNLSS	SEQ ID NO 112
V9	LASFLES	SEQ ID NO 113
V10	LANNLES	SEQ ID NO 114
	CDR-L3	
P	QQNNEDPRT	SEQ ID NO 115
V1	QQNAEDPRT	SEQ ID NO 116

	CDR-H1	
P	AYSVN	SEQ ID NO 117
V1	AKSVN	SEQ ID NO 118
V2	ANSVN	SEQ ID NO 119
V3	GYSVN	SEQ ID NO 120
V4	AHSVN	SEQ ID NO 121
V5	ARSVN	SEQ ID NO 122
	CDR-H2	
P	MIWGDGKIVYNSALKS	SEQ ID NO 123
V1	MIWGDGKISYNSALKS	SEQ ID NO 124
V2	MIWGDGKIVYNSALES	SEQ ID NO 125
V3	MIWGDGKIVYNSALKS	SEQ ID NO 126
V4	MIWGDGKIVYNSDLKS	SEQ ID NO 127
V5	MIWGDGKVVYNSALKS	SEQ ID NO 128
V6	MIWGDGKIVYNSELKS	SEQ ID NO 129
V7	MIWGDGKIAYNSALKS	SEQ ID NO 130
V8	MIWGDGKIVYNSALKE	SEQ ID NO 131
V9	MVWGDGKIVYNSALKS	SEQ ID NO 132
V10	MIWGDGKIVYNSALAS	SEQ ID NO 133
V11	MIWGDGKKVYNSALKS	SEQ ID NO 134
	CDR-H3	
P	DGYYPYAMDN	SEQ ID NO 135
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