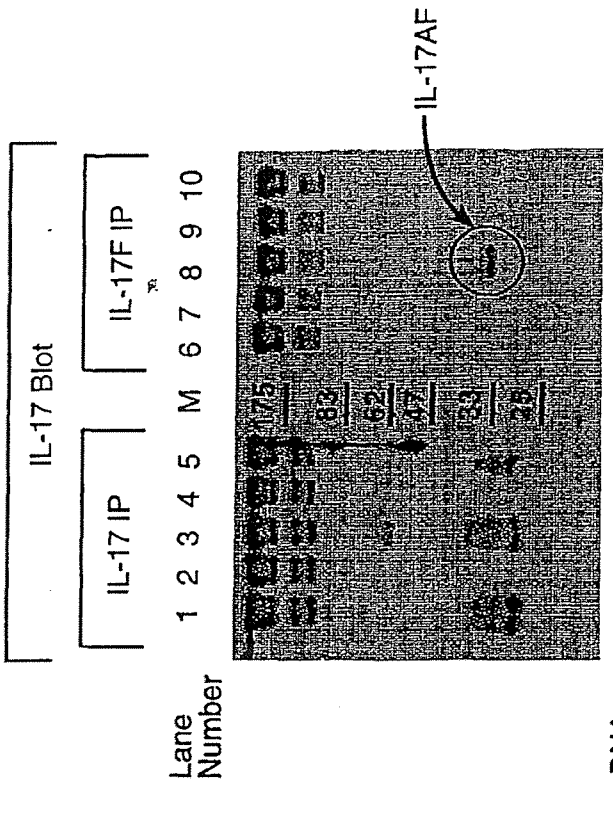

IL-17 Blot
IL-17 IP
IL-17F IP
Lane Number
1 2 3 4 5 M 6 7 8 9 10
175
83
62
47
33
25
IL-17AF
cDNA
IL-17 + - + - + + - + - +
IL-17F + + + +
IL-17C + + + +

FIG. 1A

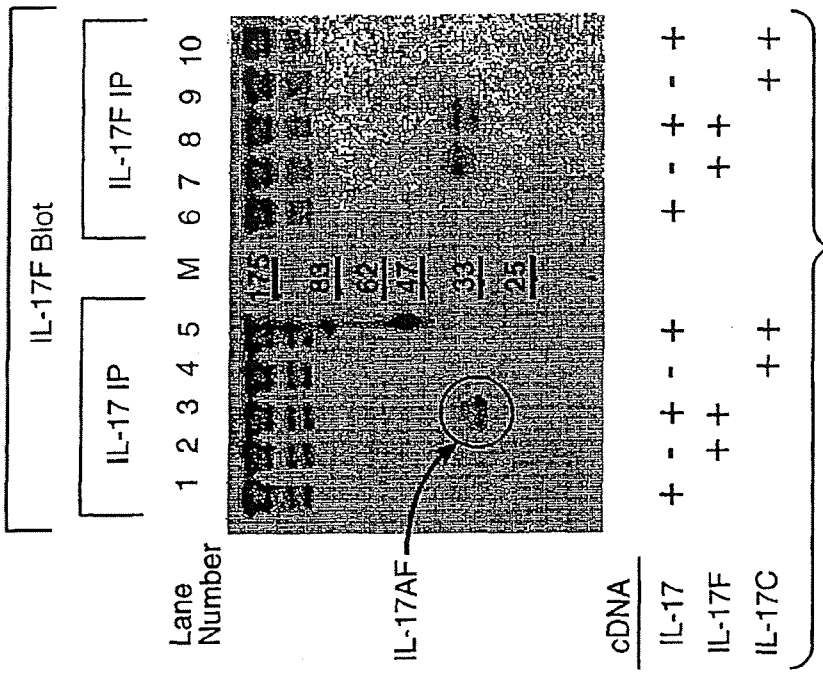

IL-17F Blot
IL-17 IP
IL-17F IP
Lane Number
1 2 3 4 5 M 6 7 8 9 10
125
83
62
47
33
25
IL-17AF
cDNA
IL-17 + - + - + + - + - +
IL-17F + + + +
IL-17C + + + +

FIG. 1B

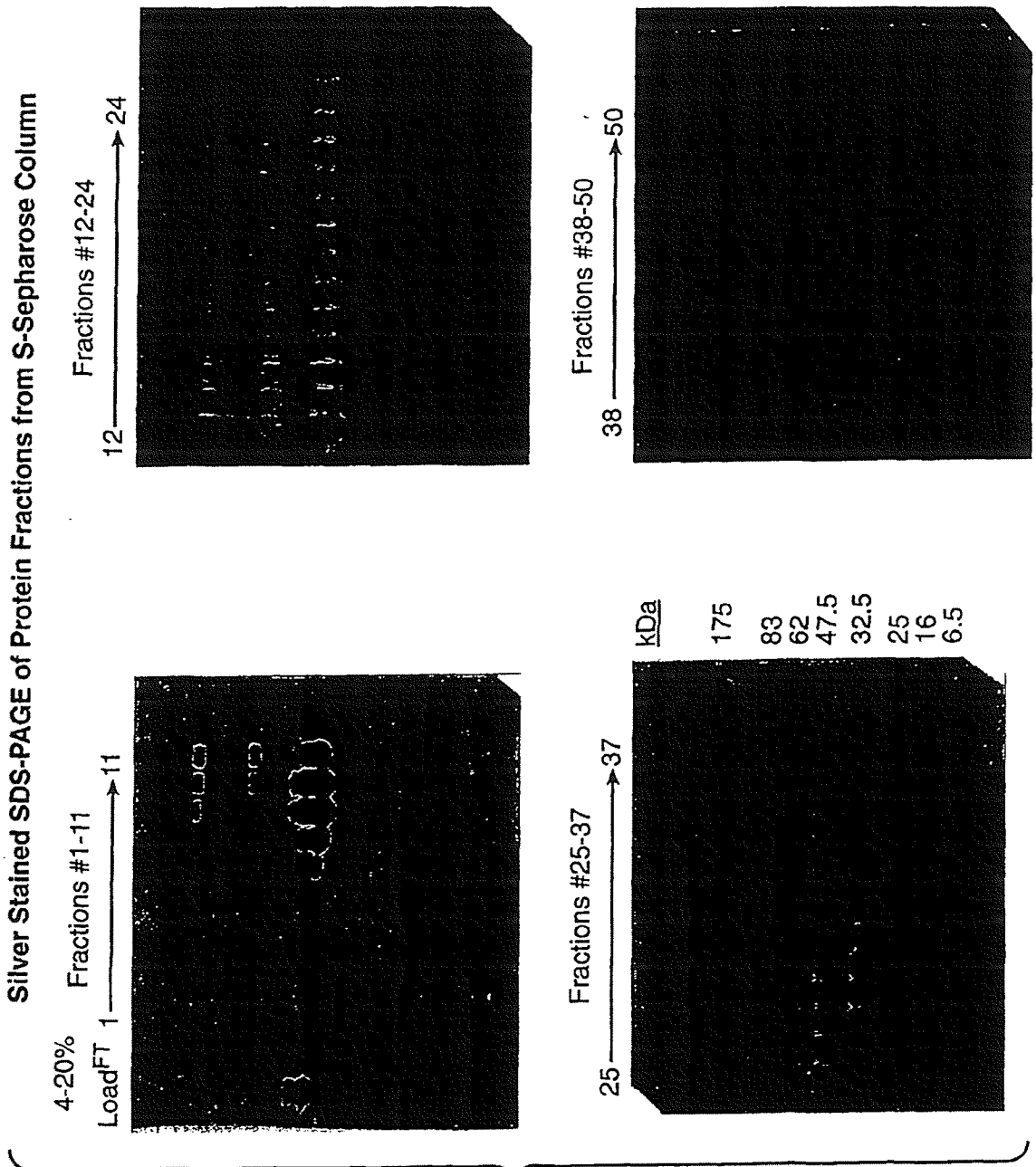

Silver Stained SDS-PAGE of Protein Fractions from S-Sepharose Column
4-20%
Load FT
Fractions #1-11
1
11
Fractions #12-24
12
24
Fractions #25-37
25
37
Fractions #38-50
38
50
kDa
175
83
62
47.5
32.5
25
16
6.5

FIG. 2A

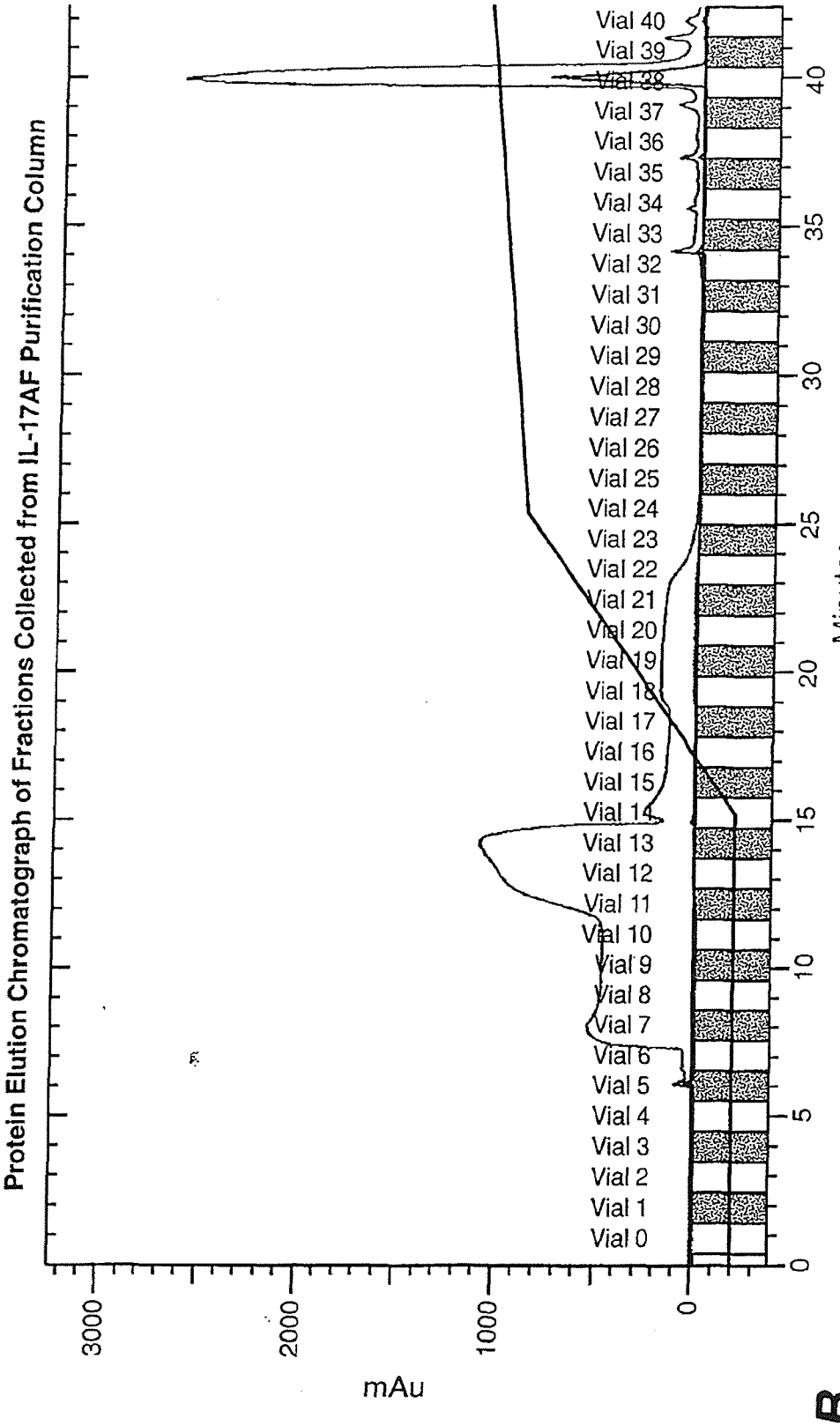


FIG. 2B-1

FIG. 2B

FIG. 2B-1 FIG. 2B-2

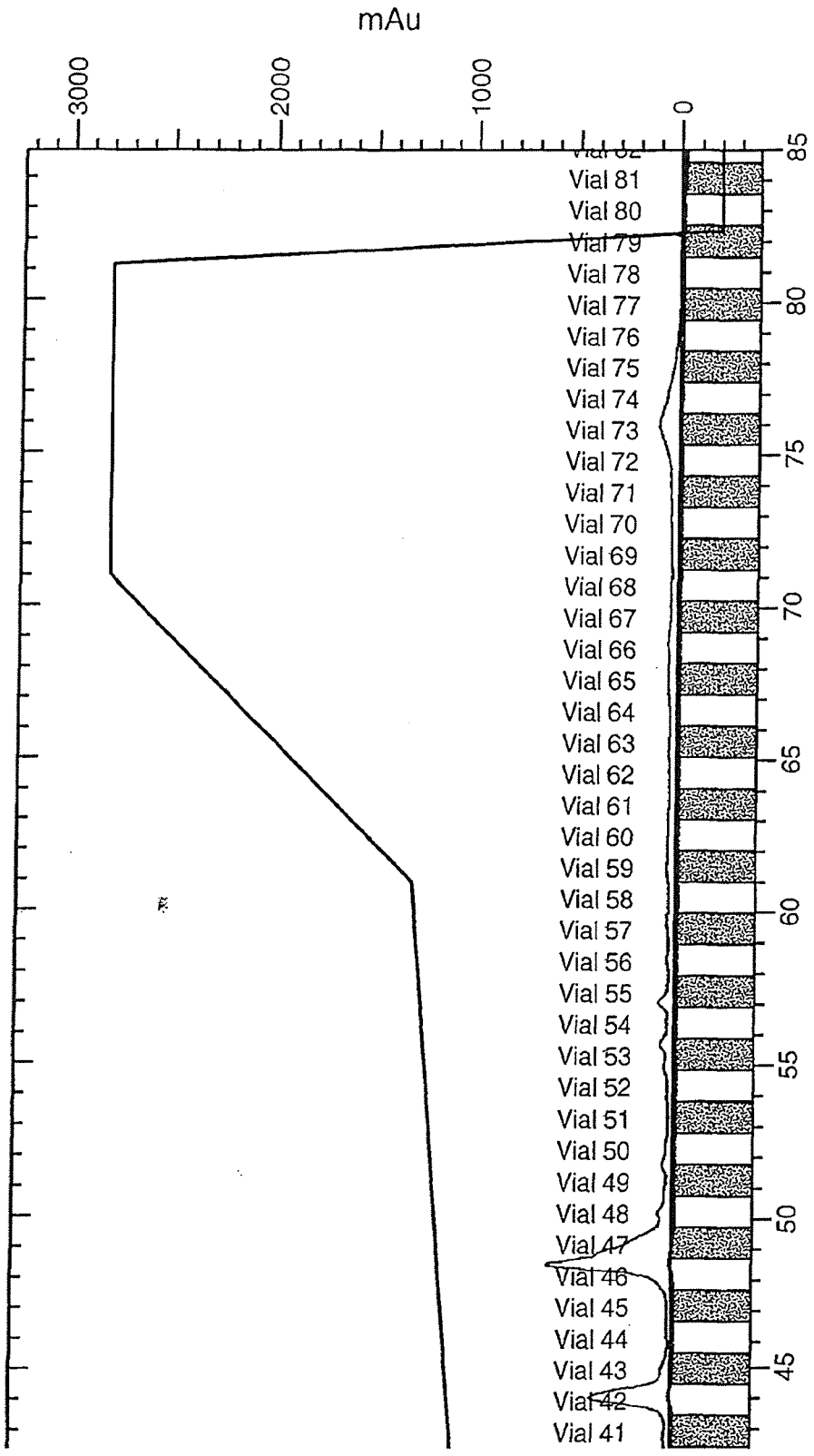

mAu
3000
2000
1000
0
Vial 81
Vial 80
Vial 79
Vial 78
Vial 77
Vial 76
Vial 75
Vial 74
Vial 73
Vial 72
Vial 71
Vial 70
Vial 69
Vial 68
Vial 67
Vial 66
Vial 65
Vial 64
Vial 63
Vial 62
Vial 61
Vial 60
Vial 59
Vial 58
Vial 57
Vial 56
Vial 55
Vial 54
Vial 53
Vial 52
Vial 51
Vial 50
Vial 49
Vial 48
Vial 47
Vial 46
Vial 45
Vial 44
Vial 43
Vial 42
Vial 41
85
80
75
70
65
60
55
50
45
Minutes

FIG. 2B-2

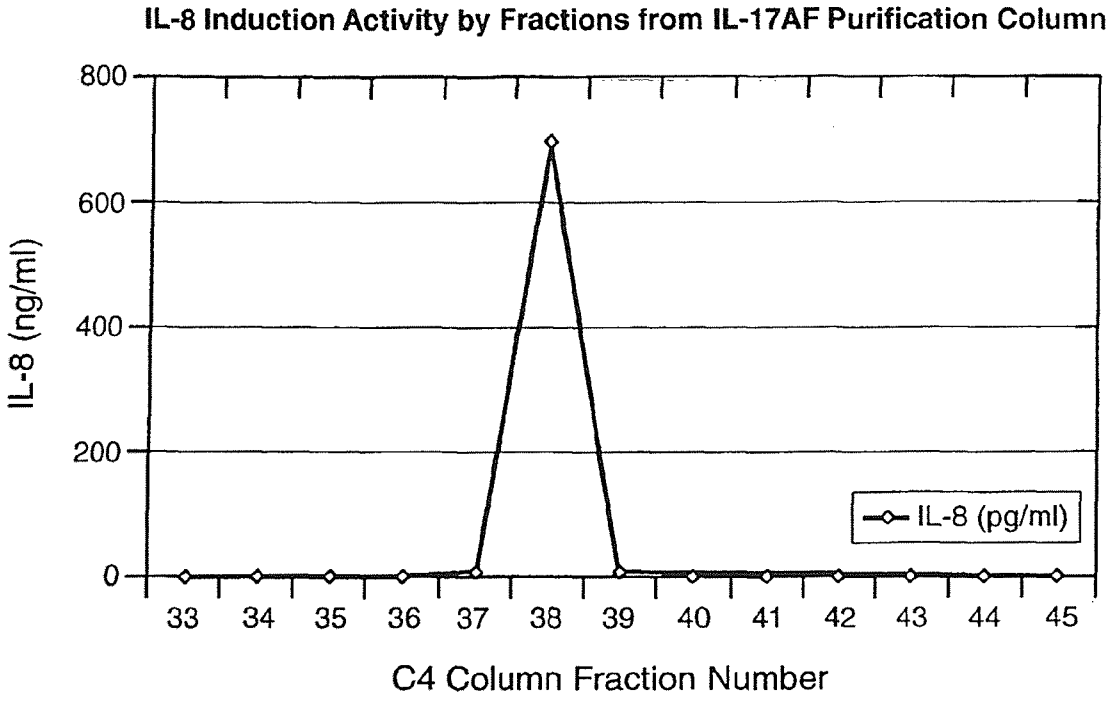

IL-8 Induction Activity by Fractions from IL-17AF Purification Column
800
600
400
200
0
IL-8 (ng/ml)
IL-8 (pg/ml)
33
34
35
36
37
38
39
40
41
42
43
44
45
C4 Column Fraction Number

FIG. 2C

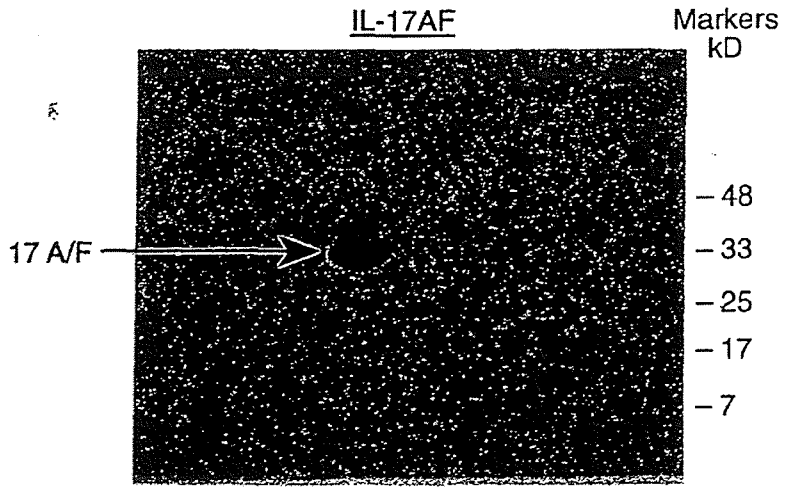

IL-17AF
Markers
kD
17 A/F
48
33
25
17
7

FIG. 3A

SEQ ID NO:	Sequence Data Results												
	Cycle / Run	1 / 3	2 / 4	3 / 5	4 / 6	5 / 7	6 / 8	7 / 9	8 / 10	9 / 11	10 / 12	11 / 13	12 / 14
SEQ ID NO:1	Sequence 1	G 11.353	I 16.037	T 6.719	I 16.620	P 10.757	R 3.563	N 4.106	P 8.529	G 4.488	C 0.076	P 7.599	N 3.502
SEQ ID NO:2	Sequence 2	R 16.186	K 3.857	I 25.186	P 6.655	K 2.679	V 7.060	G 2.385	H 3.082	T 2.395	F 3.263	(F) 7.163	Q 4.522

FIG. 3B

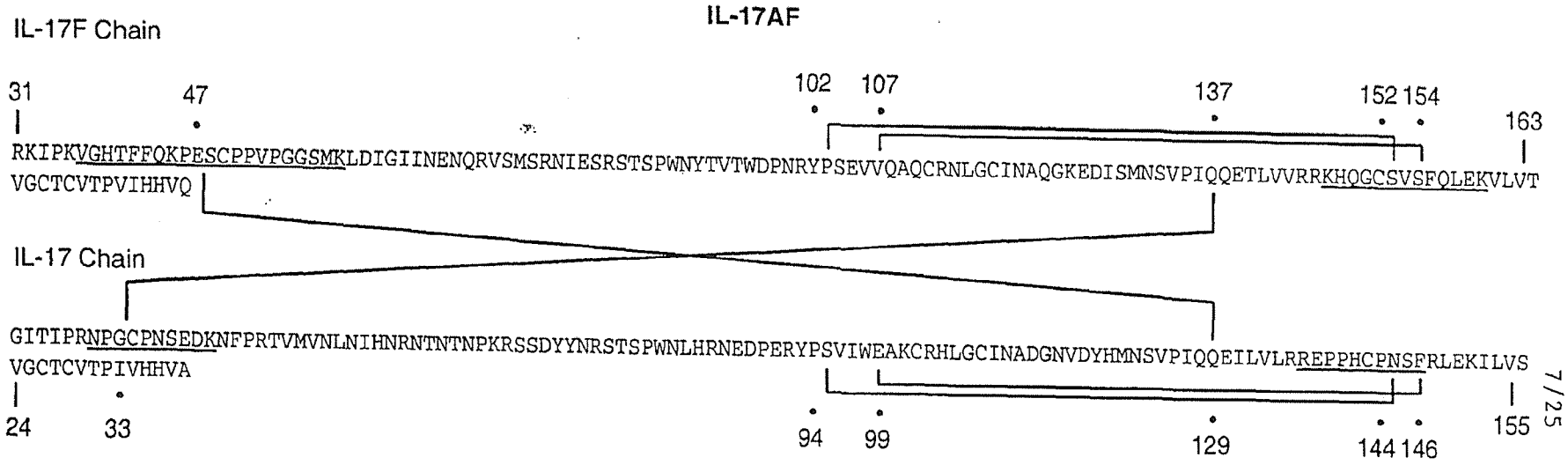
IL-17

MTPGKTSLVSLLLLLSLEAIVKA**GITIPRNPGCPN**SEDKNFPRTVMVNLNIHNRNTNTN
PKRSSDYYNRSTSPWNLHRNEDPERYPSVIWEAKCRHLGCINADGNVDYHMNSVPIQQEI
LVLRREPPHCPNSFRLEKILVSVGCTCVTPIVHHVA (SEQ ID NO:3)

IL-17F

MTVKTLHGPAMVKYLLLSILGLAFLSEAAA**RKIPKVGHTFFQ**KPESCPPVPGGSMKL
DIGIINENQRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISM
NSVPIQQETLVVRRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ (SEQ ID NO:4)

FIG. 3C



IL-17AF contains two interchain disulfide linkages:

IL-17F chain cysteine residue 47 and IL-17 chain cysteine residue 129

IL-17F chain cysteine residue 137 and IL-17 chain cysteine residue 33

FIG. 4A

IL-17AF Disulfide Bond Fragment #1

VGHTFFQKPESCPPVPGGSMK (IL-17F chain trypsin digest peptide amino acids 36-56)
|
EPPHCPNSFR (IL-17F chain trypsin digest peptide amino acids 125-134)

monoisotopic $[M+H]^+$ = 3410.58 Da

IL-17AF Disulfide Bond Fragment #2

HQGCSVSFQLEK (IL-17F chain trypsin digest peptide amino acids 134-145)
|
NPGCPNSEDK (IL-17 chain trypsin digest peptide amino acids 30-39)

monoisotopic $[M+H]^+$ = 2420.05 Da

FIG. 4B

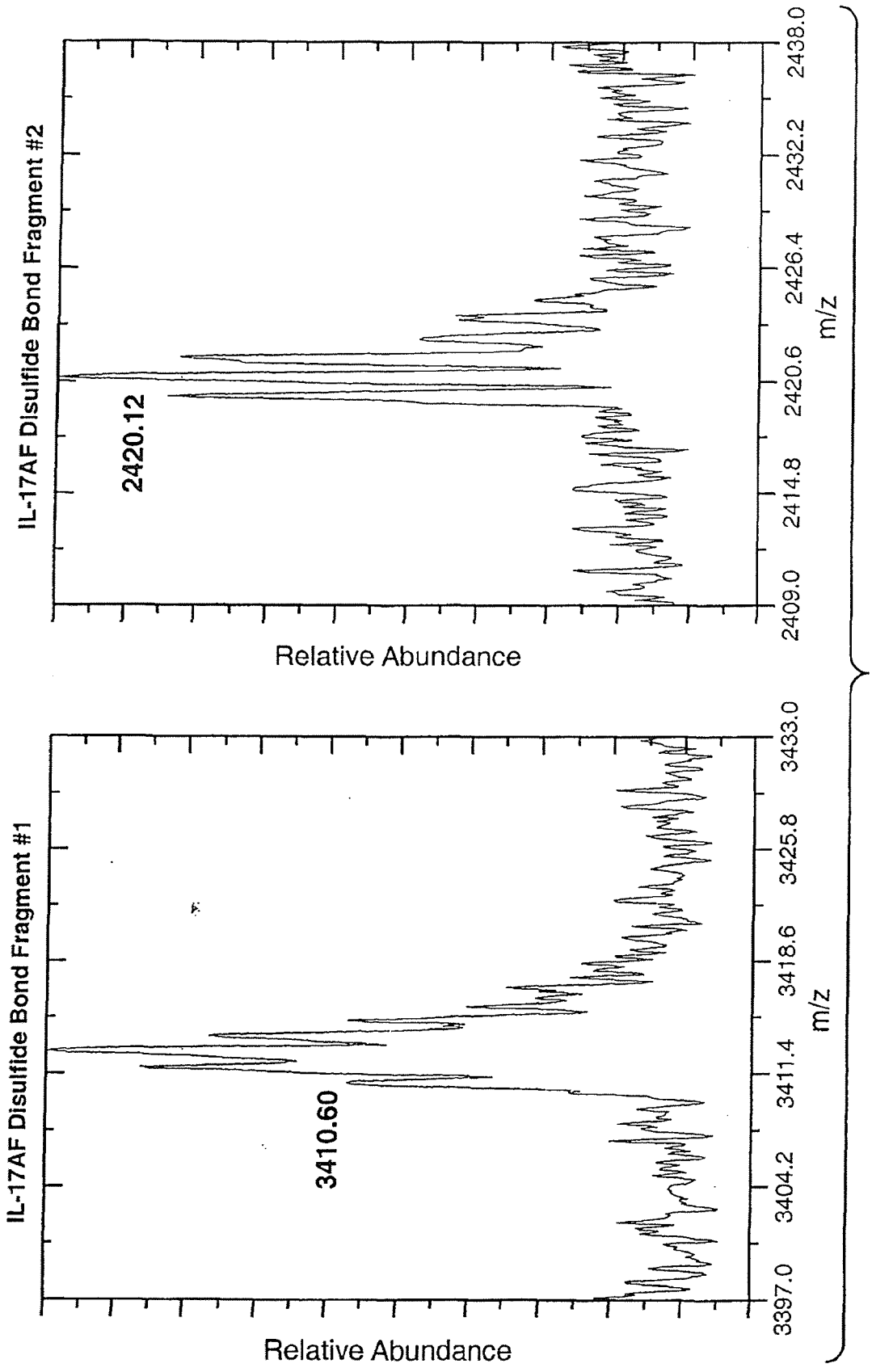

IL-17AF Disulfide Bond Fragment #2
2420.12
Relative Abundance
2409.0
2414.8
2420.6
2426.4
2432.2
2438.0
m/z
IL-17AF Disulfide Bond Fragment #1
3410.60
Relative Abundance
3397.0
3404.2
3411.4
3418.6
3425.8
3433.0
m/z

FIG. 4C

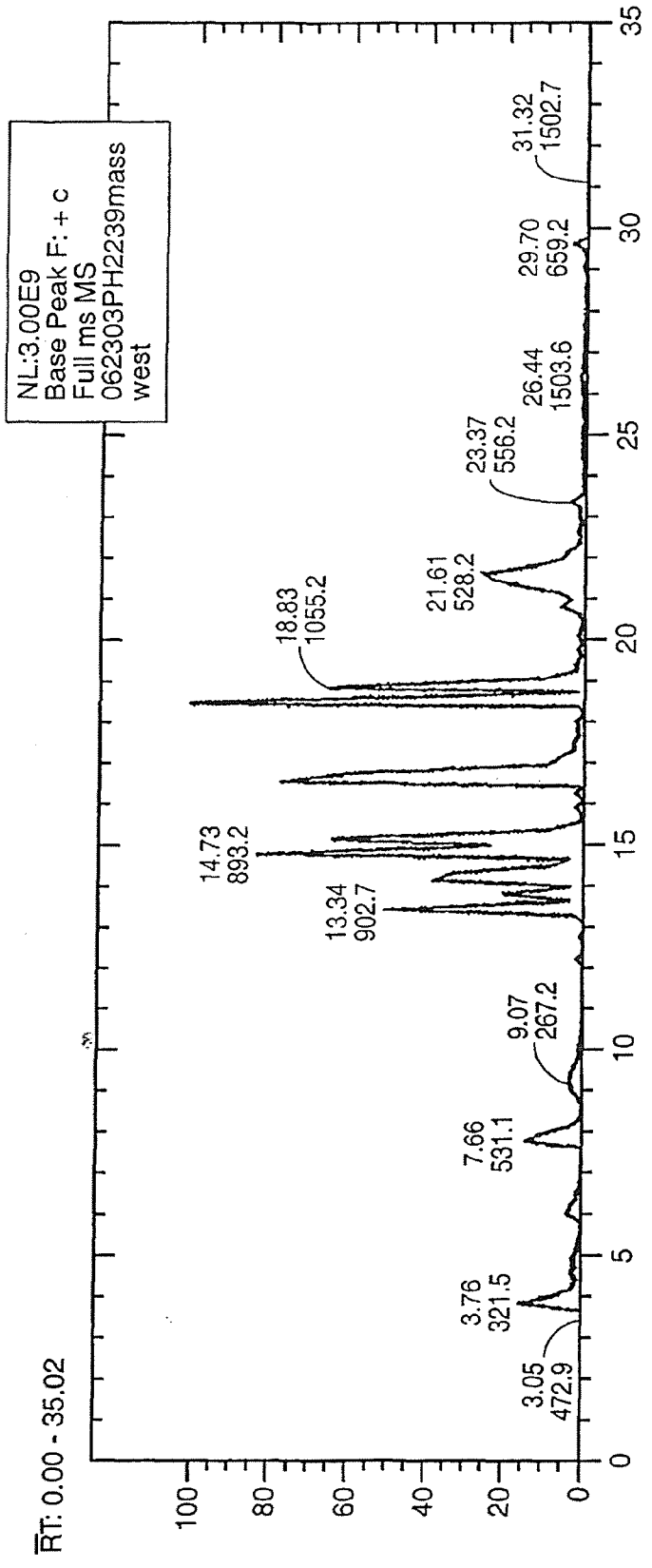

NL:3.00E9
Base Peak F: + c
Full ms MS
062303PH2239mass
west
RT: 0.00 - 35.02
Time (Min)
3.05
472.9
3.76
321.5
7.66
531.1
9.07
267.2
13.34
902.7
14.73
893.2
18.83
1055.2
21.61
528.2
23.37
556.2
26.44
1503.6
29.70
659.2
31.32
1502.7

FIG. 4D-1

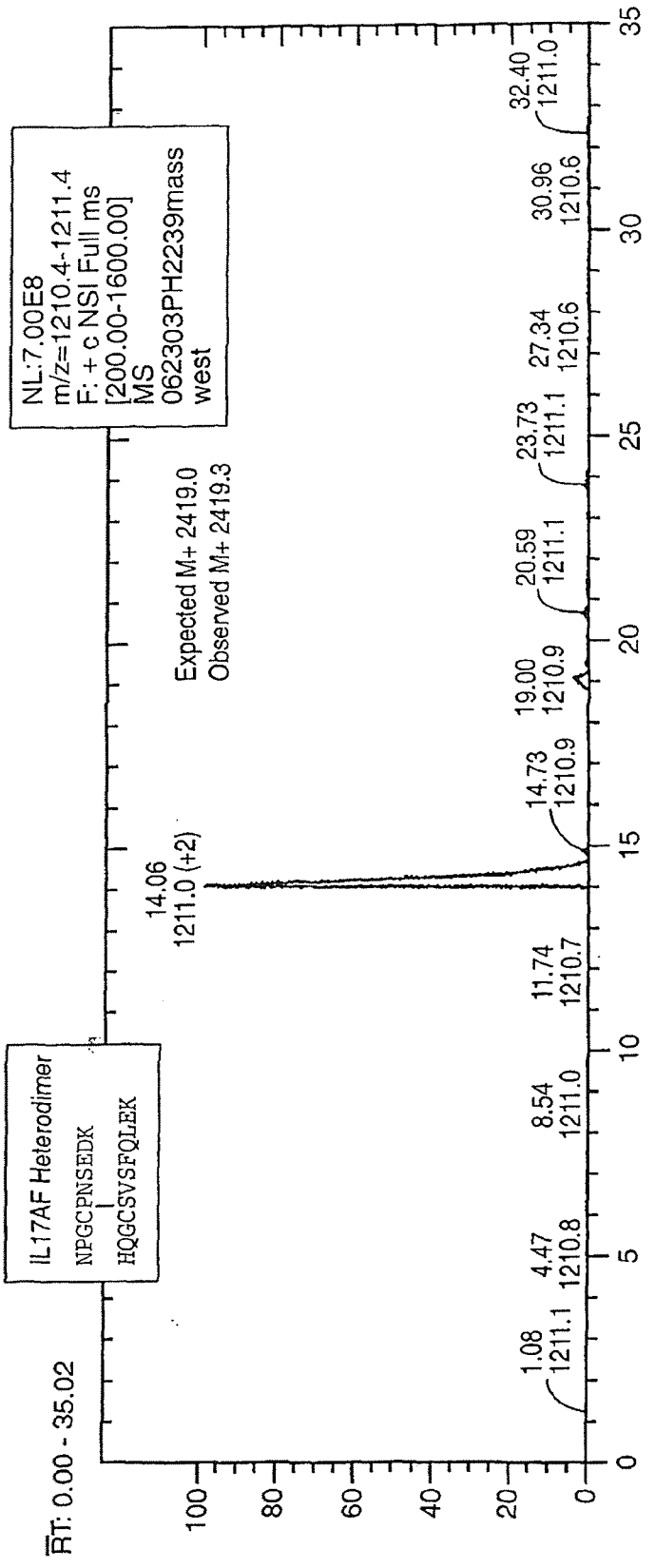

RT: 0.00 - 35.02
IL17AF Heterodimer
NPGCPNSEDK
HQGCSVSFQLEK
NL:7.00E8
m/z=1210.4-1211.4
F: + c NSI Full ms
[200.00-1600.00]
MS
062303PH2239mass
west
Expected M+ 2419.0
Observed M+ 2419.3
14.06
1211.0 (+2)
1.08
1211.1
4.47
1210.8
8.54
1211.0
11.74
1210.7
14.73
1210.9
19.00
1210.9
20.59
1211.1
23.73
1211.1
27.34
1210.6
30.96
1210.6
32.40
1211.0
Time (Min)

FIG. 4D-2

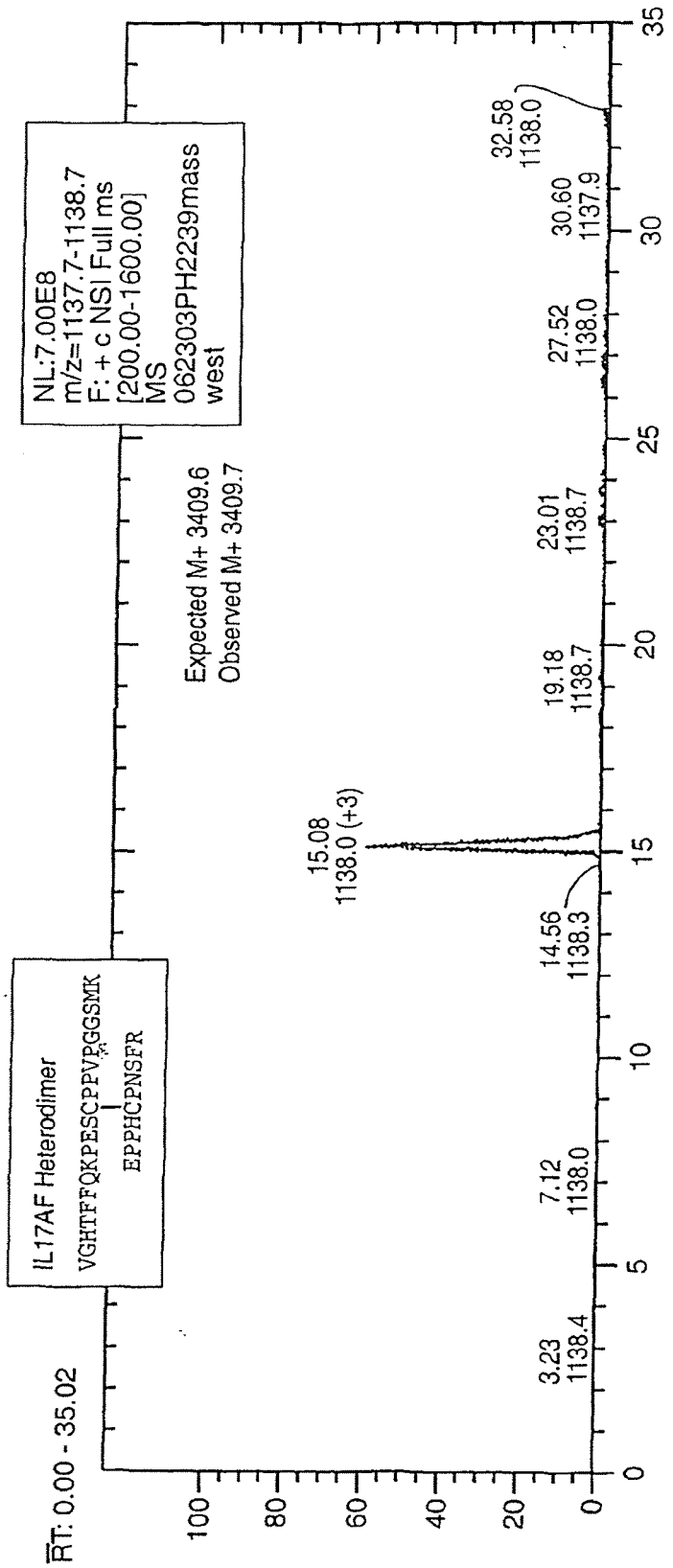

RT: 0.00 - 35.02
IL17AF Heterodimer
VGHTFFQKPESCPPVPGGSMK
EPPHCPNSFR
NL:7.00E8
m/z=1137.7-1138.7
F: + c NSI Full ms
[200.00-1600.00]
MS
062303PH2239mass
west
Expected M+ 3409.6
Observed M+ 3409.7
3.23
1138.4
7.12
1138.0
14.56
1138.3
15.08
1138.0 (+3)
19.18
1138.7
23.01
1138.7
27.52
1138.0
30.60
1137.9
32.58
1138.0
Time (Min)

FIG. 4D-3

Dose Response of IL-17AF Activity in the Induction of IL-8:
Distinct Potency Compared to IL-17 and IL-17F

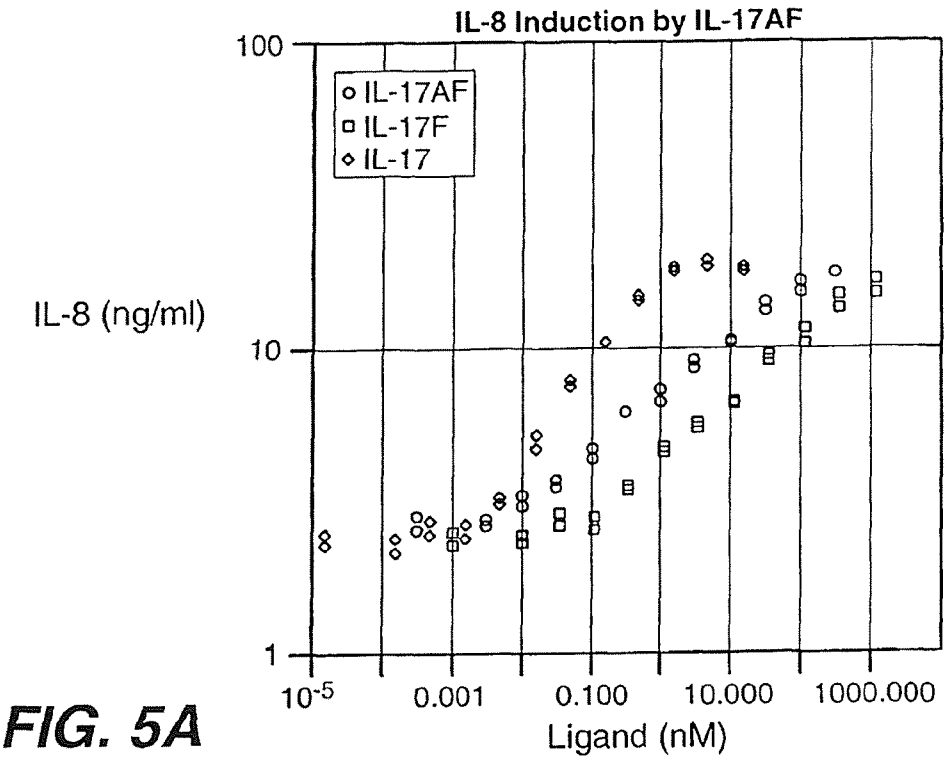


FIG. 5A

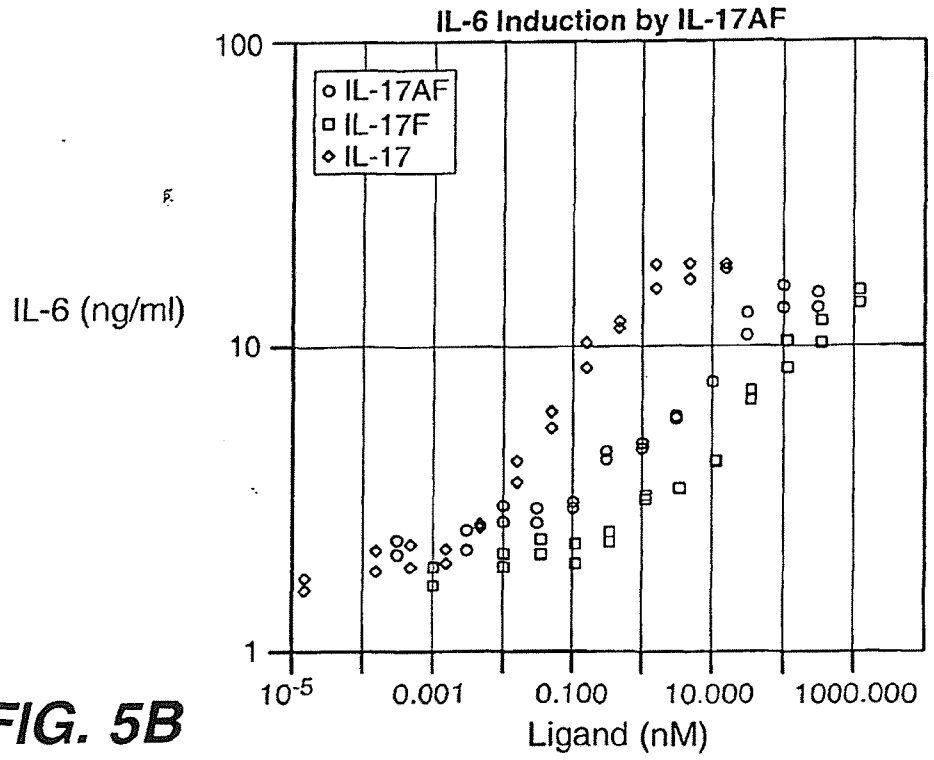


FIG. 5B

Amino Acid Sequence of Region of Heavy Chain Variable Region Containing CDR H1-H3 from Fab that Bind IL-17AF

Clone #	CDR-H1	CDR-H2	CDR-H3
1	LSCAAS**GFTISDSAIH**WVRQAPGKGLEWV**AGITPYSGYTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AKEAREGYDVGYA**MDYWGQ		
2	LSCAAS**GFTISDSYIH**WVRQAPGKGLEWV**AEISPPGGDTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARLLWWWDGA**MDYWGQ		
3	LSCAAS**GFTITNTWIH**WVRQAPGKGLEWV**AVITPYGGATYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARESMWSKF**DYWGQ		
4	LSCAAS**GFTINSSAIH**WVRQAPGKGLEWV**GYITPDNGDTNYADSVK**GRFTISADTSKNTAYLQMNSLIAEDTAVYYC**ARGHGNFYGTWAA**MDYWGQ		
5	LSCAAS**GFTISGSDIH**WVRQAPGKGLEWV**AYINPYGGSTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARAYEMWYV**MDYWGQ		
6	LSCAAS**GFTITNSWIH**WVRQAPGKGLEWV**GVITPSSGSTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREVFPDIGDCSNAYCYA**MDYWGQ		
7	LSCAAS**GFTITSTYIH**WVRQAPGKGLEWV**AWISPYSGYTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREVGWGDSYA**MDYWGQ		
8	LSCAAS**GFTISGSWIH**WVRQAPGKGLEWV**AGIYPYDGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREAEGLYQSGIYDAGM**DYWGQ		
9	LSCAAS**GFTITSYYIH**WVRQAPGKGLEWV**AWIYPADGATYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARGSYFGGYD**MDYWGQ		
10	LSCAAS**GFTINDSDIH**WVRQAPGKGLEWV**GIIYPYDGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARSNLDNNLF**DYWGQ		
11	LSCAAS**GFTINGYWIH**WVRQAPGKGLEWV**ADINPNGGSTNYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARAYRCGGLADWAGA**MDYWGQ		
12	LSCAAS**GFTISGSWIH**WVRQAPGKGLEWV**AIITPSGGNTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREVFAVSTAGYPWV**MDYWGQ		
13	LSCAAS**GFTITDSWIH**WVRQAPGKGLEWV**GSITPYNGNTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARRGESDEAYAAV**MDYWGQ		
14	LSCAAS**GFTISSSDIH**WVRQAPGKGLEWV**GTINPASGSTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARGANSSFYALQYV**MDYWGQ		
15	LSCAAS**GFTITDNYIH**WVRQAPGKGLEWV**GWISPYSGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARETLFYDKDQYSYV**MDYWGQ		
16	LSCAAS**GFTISSSYIH**WVRQAPGKGLEWV**AWISPYSGYTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREGLLRWGYA**MDYWGQ		
17	LSCAAS**GFTITDNGIH**WVRQAPGKGLEWV**GWITPTSGYTNYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARDGDTWKWDAPYV**MDYWGQ		
18	LSCAAS**GFTITNTYIH**WVRQAPGKGLEWV**AWISPYSGYTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREILLDYGSAGYA**MDYWGQ		
19	LSCAAS**GFTITSTWIH**WVRQAPGKGLEWV**GVITPTNGSTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREVWWWGDGHGYV**MDYWGQ		
20	LSCAAS**GFTISSSAIH**WVRQAPGKGLEWV**GGITPASGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARSPGGVFVDGGV**MDYWGQ		
21	LSCAAS**GFTINSTDIH**WVRQAPGKGLEWV**GRINPSGGSTNYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARTSAYTTWAVDWFIGYV**MDYWGQ		
22	LSCAAS**GFTITGYGIH**WVRQAPGKGLEWV**AWISPSNGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARRVSYYVYRHDWVRGYV**MDYWGQ		
23	LSCAAS**GFTITDTWIH**WVRQAPGKGLEWV**GVITPYGGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARDGGFF**DYWGQ		
24	LSCAAS**GFTISDSSIH**WVRQAPGKGLEWV**AFIYPTSGSTYYANSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARASYGVSKWTF**DYWGQ		
25	LSCAAS**GFTITGYGIH**WVRQAPGKGLEWV**AWISPSNGYTYYADSVK**GRFTISAYTSKNTAYLQMNSLRAEDTAVYYC**ARRVSYYVYRHDWVRGYV**MDYQGQ		
26	LSCAAS**GFTITGTYIH**WVRQAPGKGLEWV**AWISPYSGYTNYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**AREARSSLSADYA**MDYWGQ		
27	LSCAAS**GFTITDNYIH**WVRQAPGKGLEWV**AWISPYSGYTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARESGFSACNTRAYA**MDYWGQ		
28	LSCAAS**GFTITDSWIH**WVRQAPGKGLEWV**GSITPYNGNTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARRGESDEAYPAV**MDYWGQ		
29	LSCAAS**GFTITSTAIH**WVRQAPGKGLEWV**AWITPYDGYTDYADSVK**GRFTISADTSKNTAYLLMNSLRAEDTAVYYC**ARTWFTLASAMELLGSA**		
30	LSCAAS**GFTITGNGIH**WVRQAPGKGLEWV**AWISPTNGSTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARRVDYQVYHDRFEEGYA**MDYWGQ		
31	LSCAAS**GFTINSYWIH**WVRQAPGKGLEWV**GWISPDNGATNYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARKFWGWDWGG**MDYWGQ		
32	LSCAAS**GFTISDSYIH**WVRQAPGKGLEWV**GDITPTDGYTDYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARNLMWWDSSA**MDYWGQ		
33	LSCAAS**GFTISDSGIH**WVRQAPGKGLEWV**GFIYPNGGSTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARMSLIGFSYA**MDYWGQ		
34	LSCAAS**GFTINSTWIH**WVRQAPGKGLEWV**AWINPYNGSTYYADSVK**GRFTISADTSKNTAYLQMNSLRAEDTAVYYC**ARDLYDYDIGF**DYWGQ		

FIG. 6

GCAGGCACAAACTCATCCATCCCCAGTTGATTGGAAGAAACAACGATGACTCCTGGGAAG
ACCTCATTGGTGTCACTGCTACTGCTGCTGAGCCTGGAGGCCATAGTGAAGGCAGGAATC
ACAATCCCACGAAATCCAGGATGCCCAAATTCTGAGGACAAGAACTTCCCCCGGACTGTG
ATGGTCAACCTGAACATCCATAACCGGAATACCAATACCAATCCCAAAAGGTCCTCAGAT
TACTACAACCGATCCACCTCACCTTGGAATCTCCACCGCAATGAGGACCCTGAGAGATAT
CCCTCTGTGATCTGGGAGGCAAAGTGCCGCCACTTGGGCTGCATCAACGCTGATGGGAAC
GTGGACTACCACATGAACTCTGTCCCCATCCAGCAAGAGATCCTGGTCCTGCGCAGGGAG
CCTCCACACTGCCCCAACTCCTTCCGGCTGGAGAAGATACTGGTGTCCGTGGGCTGCACC
TGTGTCACCCCGATTGTCCACCATGTGGCCTAAGAGCTCTGGGGAGCCCACACTCCCCAA
AGCAGTTAGACTATGGAGAGCCGACCCAGCCCCTCAGGAACCCTCATCCTTCAAAGACAG
CCTCATTTCGGACTAAACTCATTAGAGTTCTTAAGGCAGTTTGTCCAATTAAAGCTTCAG
AGGTAACACTTGGCCAAGATATGAGATCTGAATTACCTTTCCCTCTTTCCAAGAAGGAAG
GTTTGACTGAGTACCAATTTGCTTCTTGTTTACTTTTTTAAGGGCTTTAAGTTATTTATG
TATTTAATATGCCCTGAGATAACTTTGGGGTATAAGATTCCATTTTAATGAATTACCTAC
TTTATTTTGTTTGTCTTTTTAAAGAAGATAAGATTCTGGGCTTGGGAATTTTATTATTTA
AAAGGTAAAACCTGTATTTATTTGAGCTATTTAAGGATCTATTTATGTTTAAGTATTTAG
AAAAAGGTGAAAAAGCACTATTATCAGTTCTGCCTAGGTAAATGTAAGATAGAATTAAAT
GGCAGTGCAAAATTTCTGAGTCTTTACAACATACGGATATAGTATTTCCTCCTCTTTGTT
TTTAAAAGTTATAACATGGCTGAAAAGAAAGATTAAACCTACTTTCATATGTATTAATTT
AAATTTTGCAATTTGTTGAGGTTTTACAAGAGATACAGCAAGTCTAACTCTCTGTTCCAT
TAAACCCTTATAATAAAATCCTTCTGTAATAATAAAGTTTCAAAAGAAAATGTTTATTTG
TTCTCATTAAATGTATTTTAGCAAACTCAGCTCTTCCCTATTGGGAAGAGTTATGCAAAT
TCTCCTATAAGCAAAACAAAGCATGTCTTTGAGTAACAATGACCTGGAAATACCCAAAAT
TCCAAGTTCTCGATTTCACATGCCTTCAAGACTGAACACCGACTAAGGTTTTCATACTAT
TAGCCAATGCTGTAGACAGAAGCATTTTGATAGGAATAGAGCAAATAAGATAATGGCCCT
GAGGAATGGCATGTCATTATTAAAGATCATATGGGGAAAATGAAACCCTCCCCAAAATAC
AAGAAGTTCTGGGAGGAGACATTGTCTTCAGACTACAATGTCCAGTTTCTCCCCTAGACT
CAGGCTTCCTTTGGAGATTAAGGCCCCTCAGAGATCAACAGACCAACATTTTTCTCTTCC
TCAAGCAACACTCCTAGGGCCTGGCTTCTGTCTGATCAAGGCACCACACAACCCAGAAAG
GAGCTGATGGGGCAGAACGAACTTTAAGTATGAGAAAAGTTCAGCCCAAGTAAAATAAAA
ACTCAATCACATTCAATTCCAGAGTAGTTTCAAGTTTCACATCGTAACCATTTTCGCCC

FIG. 7

MTPGKTSLVSLLLLLSLEAIVKAGITIPRNPGCPNSEDKNFPRTVMVNLNIHNRNTNTNP
KRSSDYYNRSTSPWNLHRNEDPERYPSVIWEAKCRHLGCINADGNVDYHMNSVPIQQEIL
VLRREPPHCPNSFRLEKILVSVGCTCVTPIVHHVA

FIG. 8

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCTGCAT
GGCCCAGCCATGGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCTTTCTGAGTGAG
GCGGCAGCTCGGAAAATCCCCAAAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGC
CCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGCATCATCAATGAAAACCAGCGC
GTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTGGAATTACACTGTCACT
TGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGAACTTGGGCTGC
ATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACC
CTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCTG
GTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCAT
ATCCACTCAGCTGAAGAAG

FIG. 9

MTVKTLHGPAMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIG
IINENQRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNS
VPIQQETLVVRRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:	Amino acids 1-30
N-glycosylation site:	Amino acids 83-86
N-myristoylation sites:	Amino acids 106-111;136-141

FIG. 10

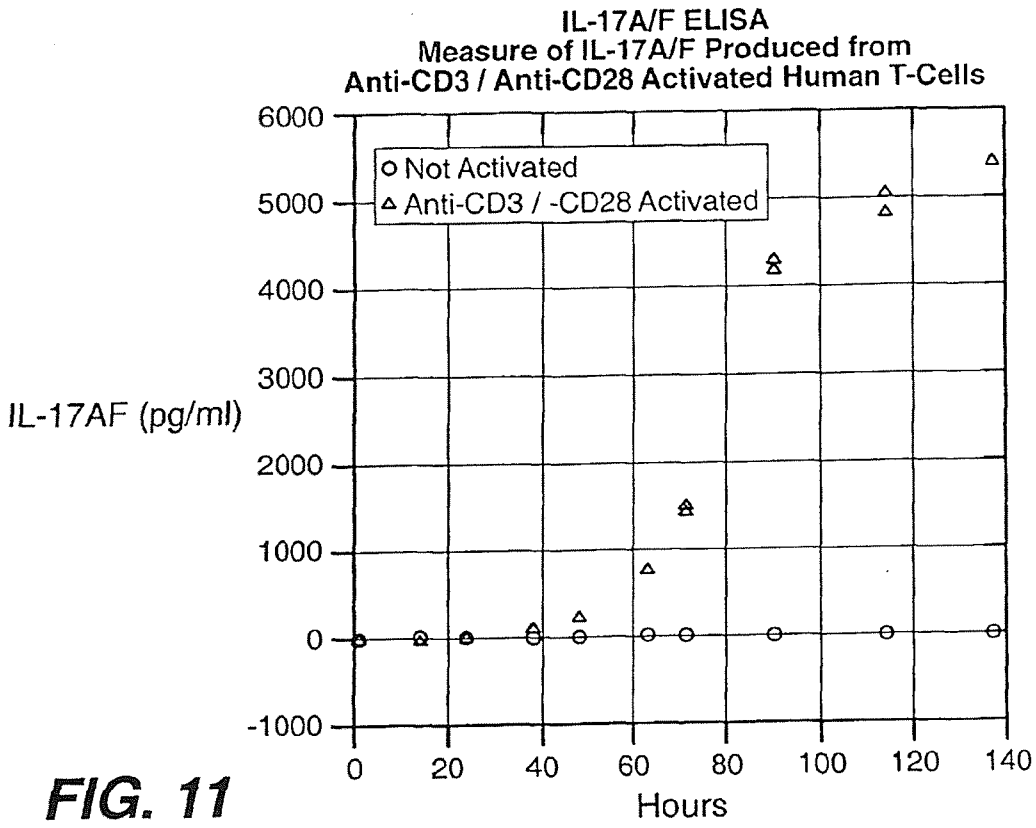

IL-17A/F ELISA
Measure of IL-17A/F Produced from
Anti-CD3 / Anti-CD28 Activated Human T-Cells
Not Activated
Anti-CD3 / -CD28 Activated
IL-17AF (pg/ml)
6000
5000
4000
3000
2000
1000
0
-1000
0
20
40
60
80
100
120
140
Hours

FIG. 11

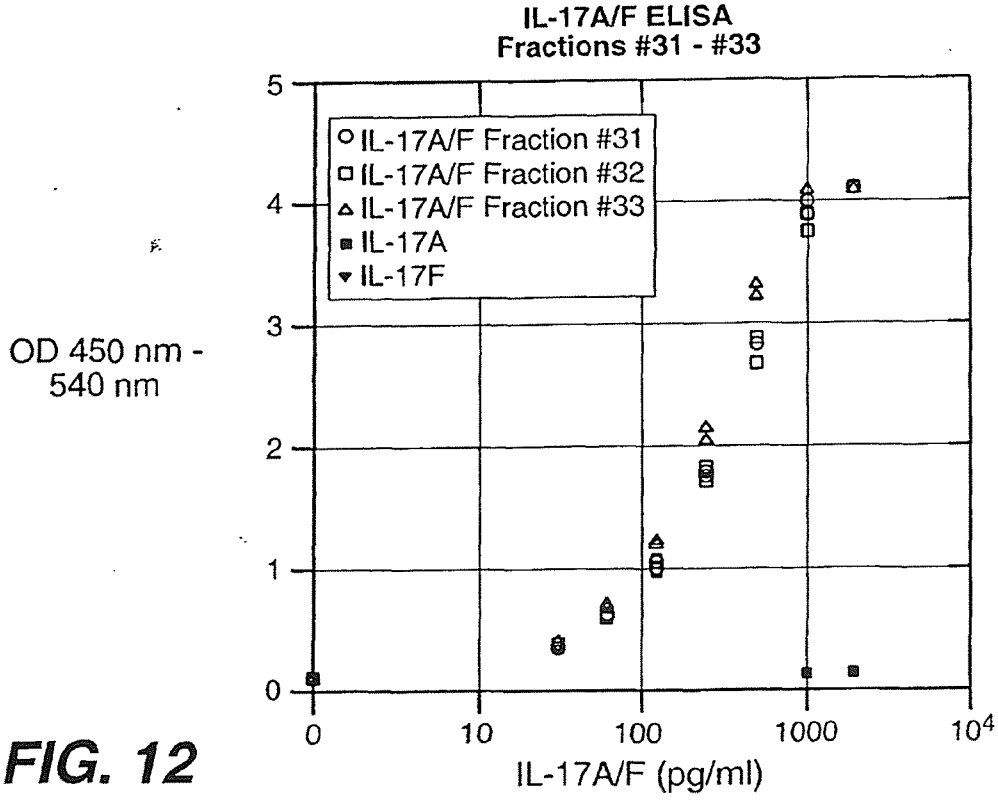
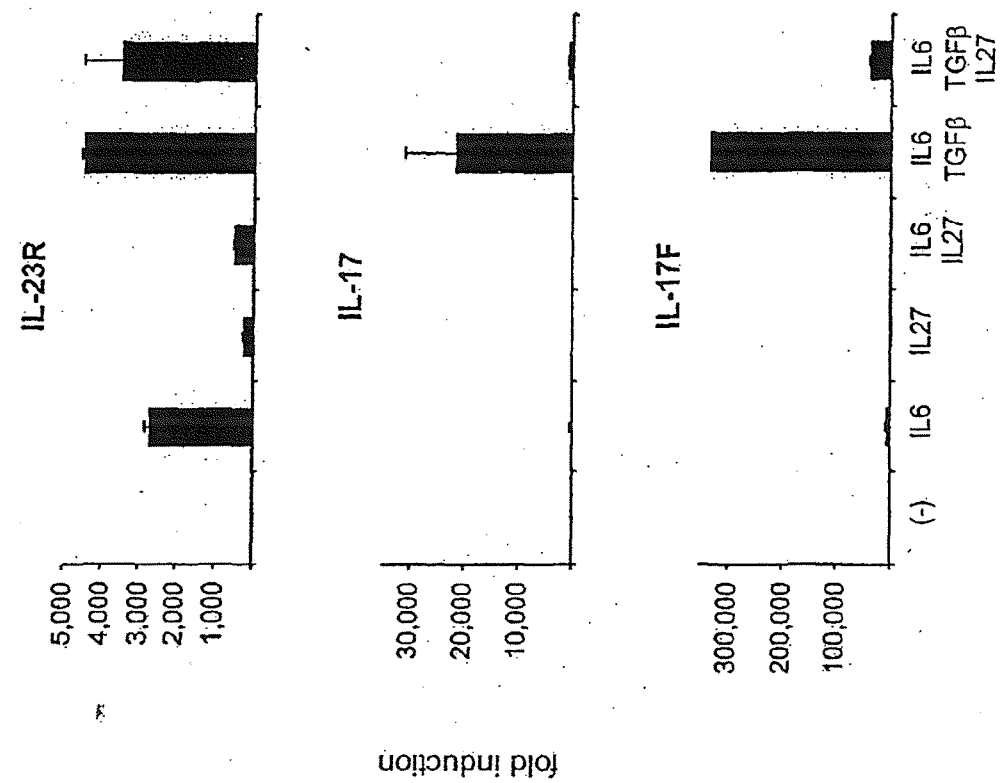

IL-17A/F ELISA
Fractions #31 - #33
IL-17A/F Fraction #31
IL-17A/F Fraction #32
IL-17A/F Fraction #33
IL-17A
IL-17F
OD 450 nm -
540 nm
5
4
3
2
1
0
0
10
100
1000
10^4
IL-17A/F (pg/ml)

FIG. 12

FIGURE 13


IL-23R
IL-17
IL-17F
fold induction
5,000
4,000
3,000
2,000
1,000
30,000
20,000
10,000
300,000
200,000
100,000
(-)
IL6
IL27
IL6 IL27
IL6 TGFβ
IL6 TGFβ IL27

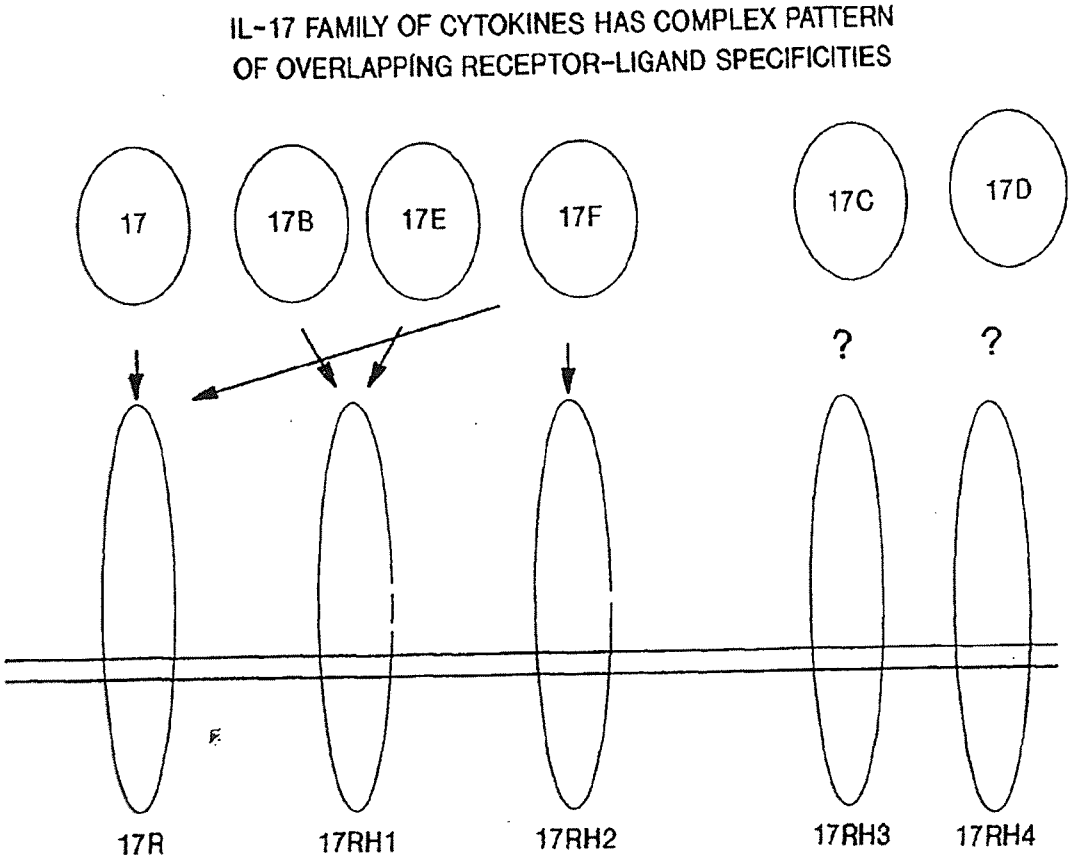
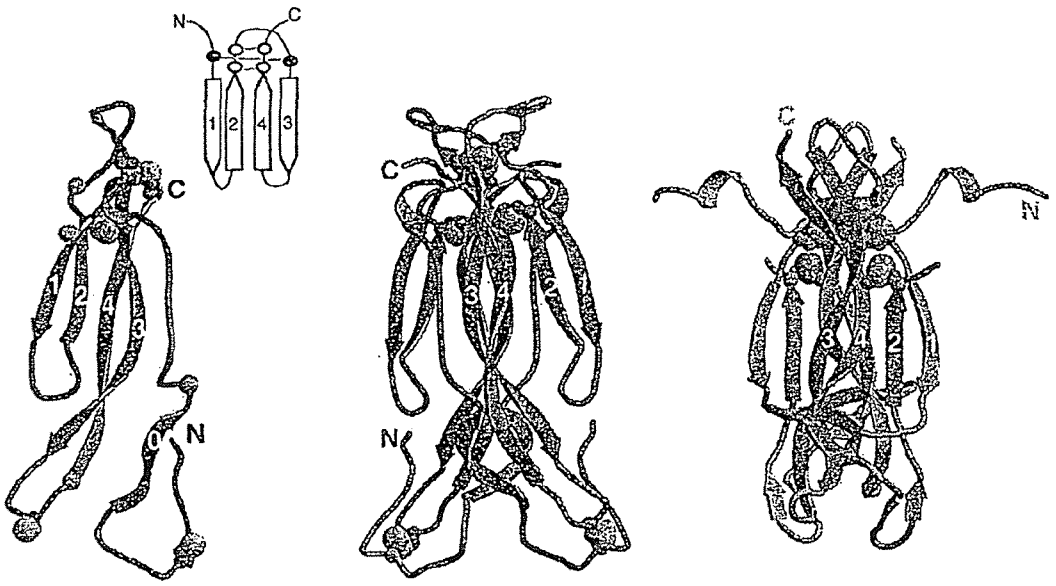

IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN
OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES
17
17B
17E
17F
17C
17D
?
?
17R
17RH1
17RH2
17RH3
17RH4

FIGURE 14



A B C

FIGURE 15

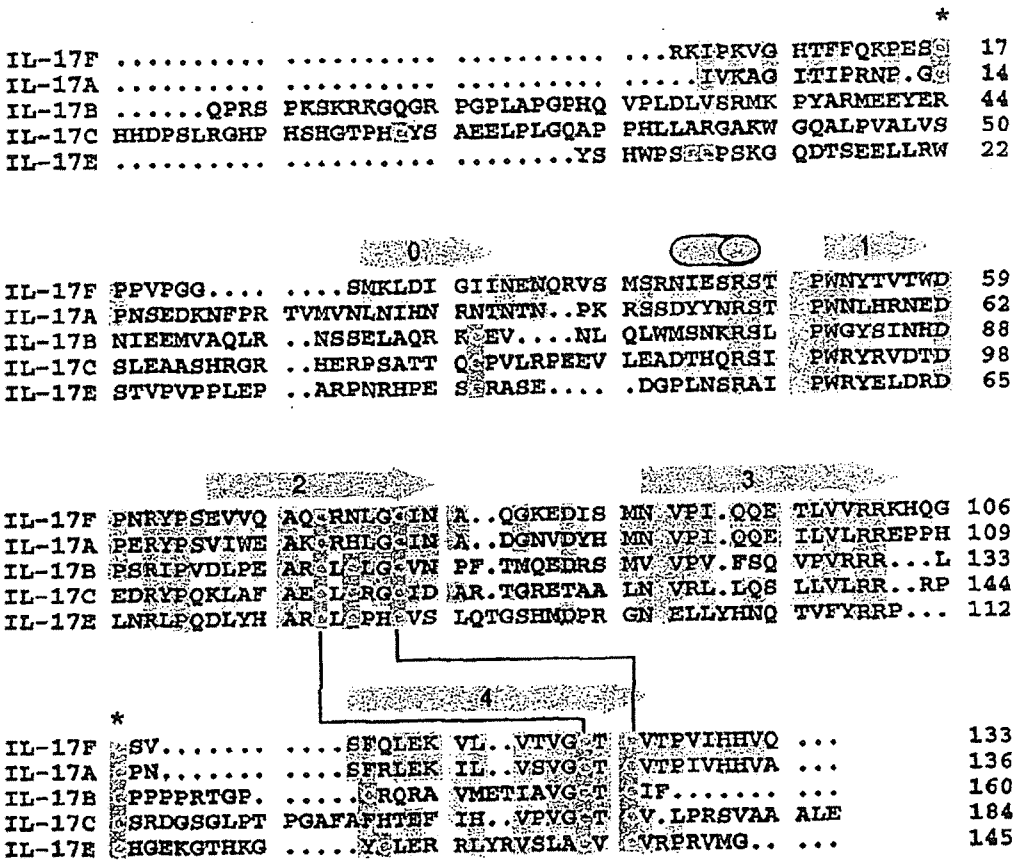

IL-17F ....RKIPKVG HTFFQKPESS 17
IL-17A ....IVKAG ITIPRNP.GS 14
IL-17B .....QPRS PKSKRKGQGR PGPLAPGPHQ VPLDLVSRMK PYARMEEYER 44
IL-17C HHDPSLRGHP HSHGTPHSYS AEELPLGQAP PHLLARGAKW GQALPVALVS 50
IL-17E ....YS HWPSFAPSKG QDTSEELLRW 22
0
1
IL-17F PPVPGG.... ....SMKLDI GIINENQRVS MSRNIESRST PWNYTVTWD 59
IL-17A PNSEDKNFPR TVMVNLNIHN RNTNTN..PK RSSDYYNRST PWNLHRNED 62
IL-17B NIEEMVAQLR ..NSSELAQR KSEV....NL QLWMSNKRSL PWGYSINHD 88
IL-17C SLEAASHRGR ..HERPSATT QSPVLRPEEV LEADTHQRSI PWRYRVDTD 98
IL-17E STVPVPPLEP ..ARPNRHPE SSRASE.... .DGPLNSRAI PWRYELDRD 65
2
3
IL-17F PNRYPSEVVQ AQSRNLGSIN A..QGKEDIS MNSVPI.QQE TLVVRRKHQG 106
IL-17A PERYPSVIWE AKSRHLGSIN A..DGNVDYH MNSVPI.QQE ILVLRREPPH 109
IL-17B PSRIPVDLPE ARSILSLGSVN PF.TMQEDRS MVSVPV.FSQ VPVRRR...L 133
IL-17C EDRYPQKLAF AESLSRGSID AR.TGRETAA LNSVRL.LQS LLVLRR..RP 144
IL-17E LNRLPQDLYH ARSLSPHSVS LQTGSHMDPR GNSELLYHNQ TVFYRRP... 112
4
IL-17F SV..... ....SFQLEK VL..VTVGST VTPVIHHVQ ... 133
IL-17A PN..... ....SFRLEK IL..VSVGST VTPIVHHVA ... 136
IL-17B PPPPRTGP. .....SRQRA VMETIAVGST IF..... ... 160
IL-17C SRDGSGLPT PGAFAFHTEF IH..VPVGST V.LPRSVAA ALE 184
IL-17E HGEKGTHKG .....YSLER RLYRVSLASV VRPRVMG.. ... 145

FIGURE 16

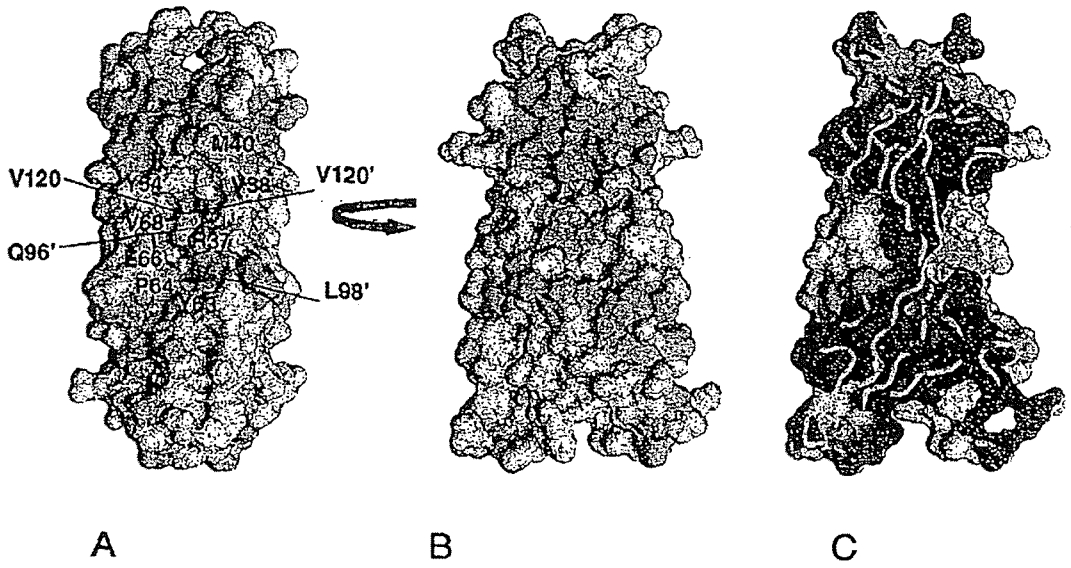


FIGURE 17

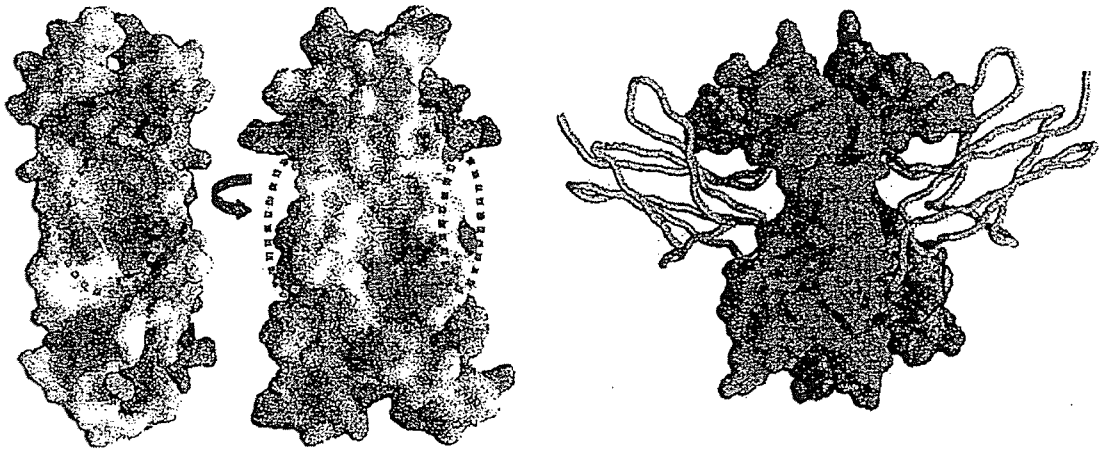


FIGURE 18

IL-17A/F antibodies in CIA model

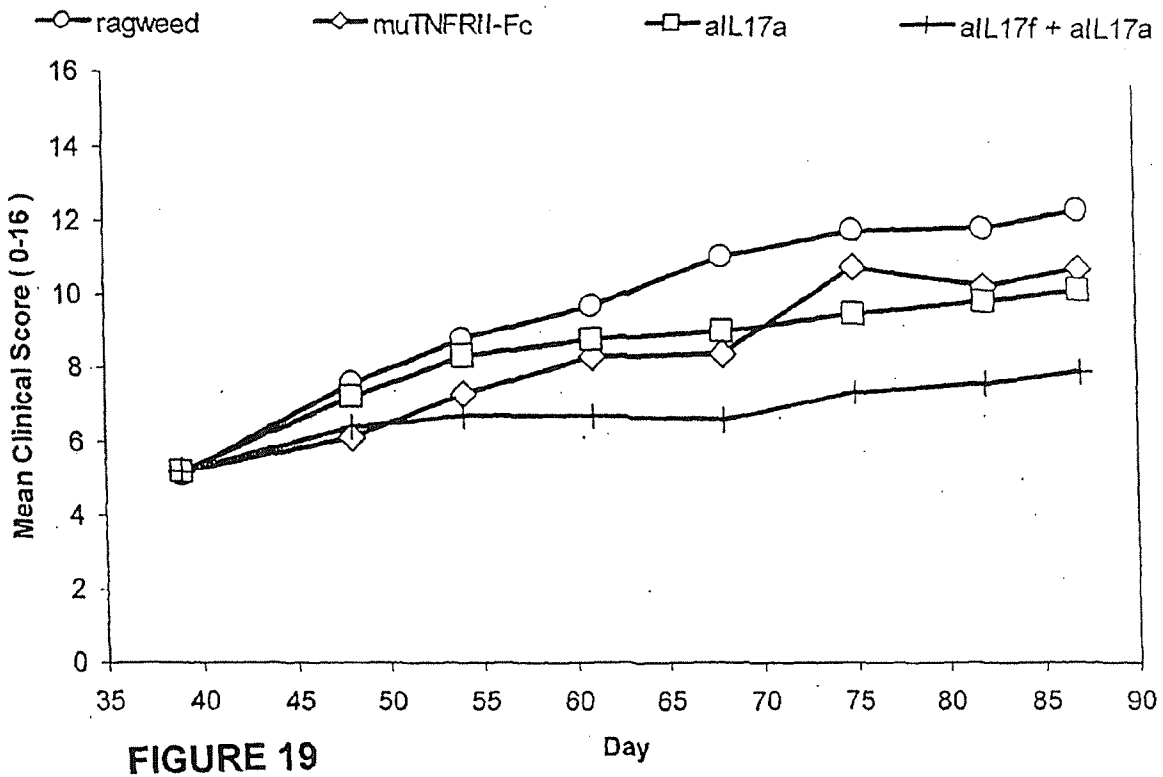
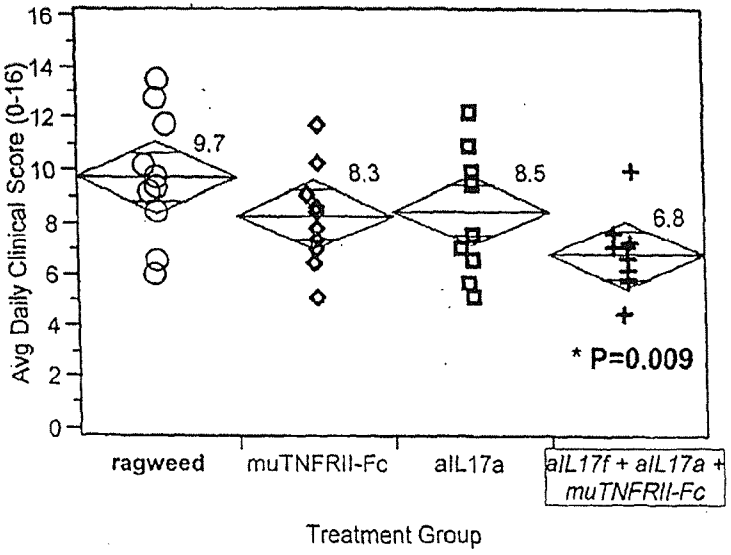


FIGURE 19

IL-17A/F antibodies in CIA model



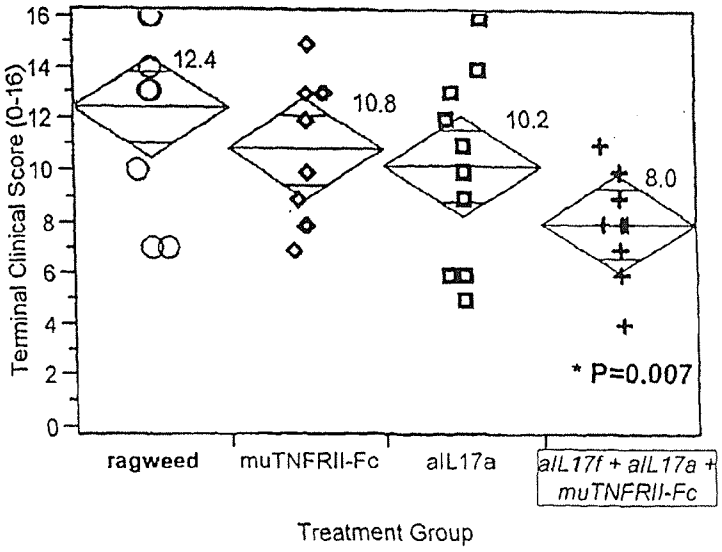


FIGURE 20