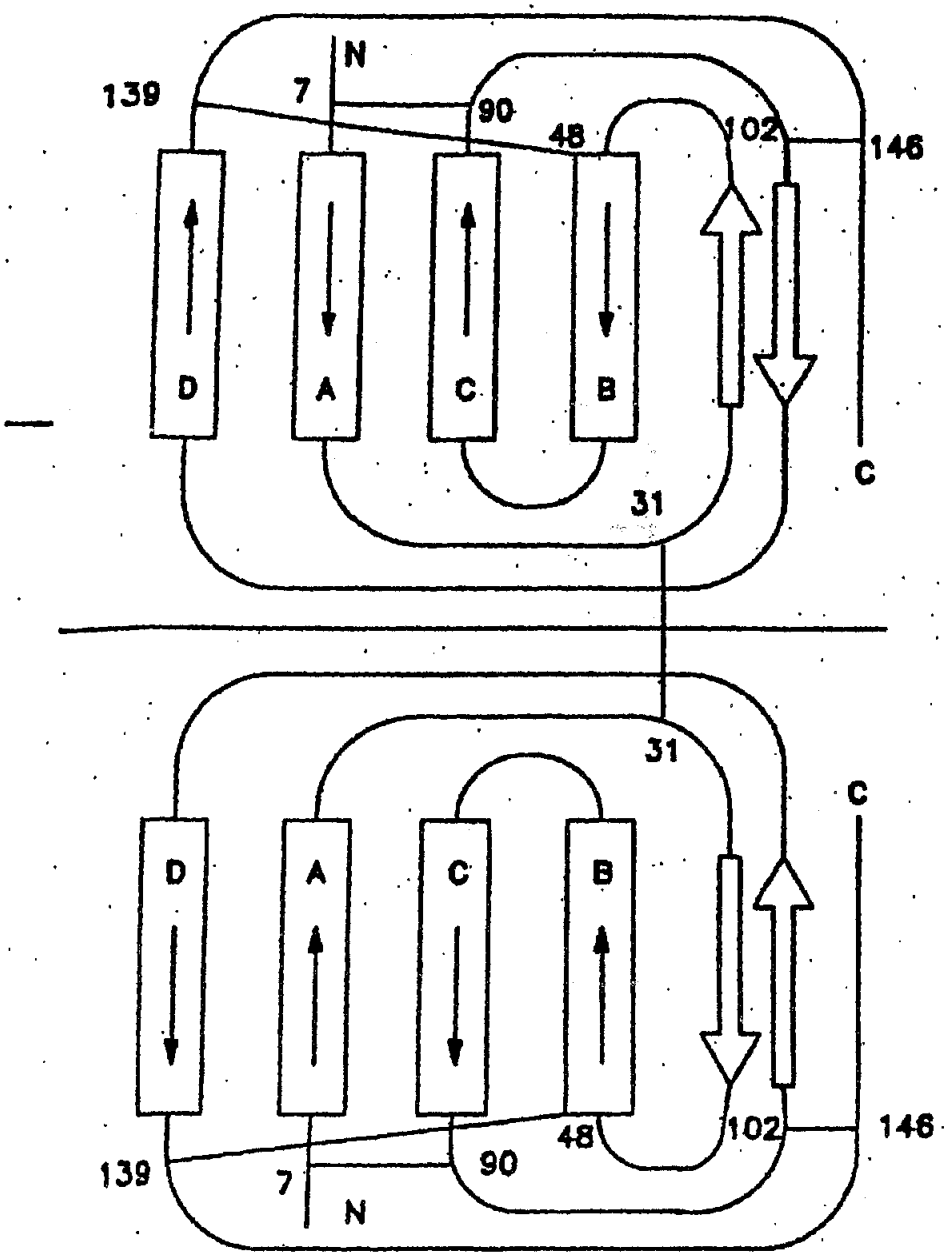
FIG. 1



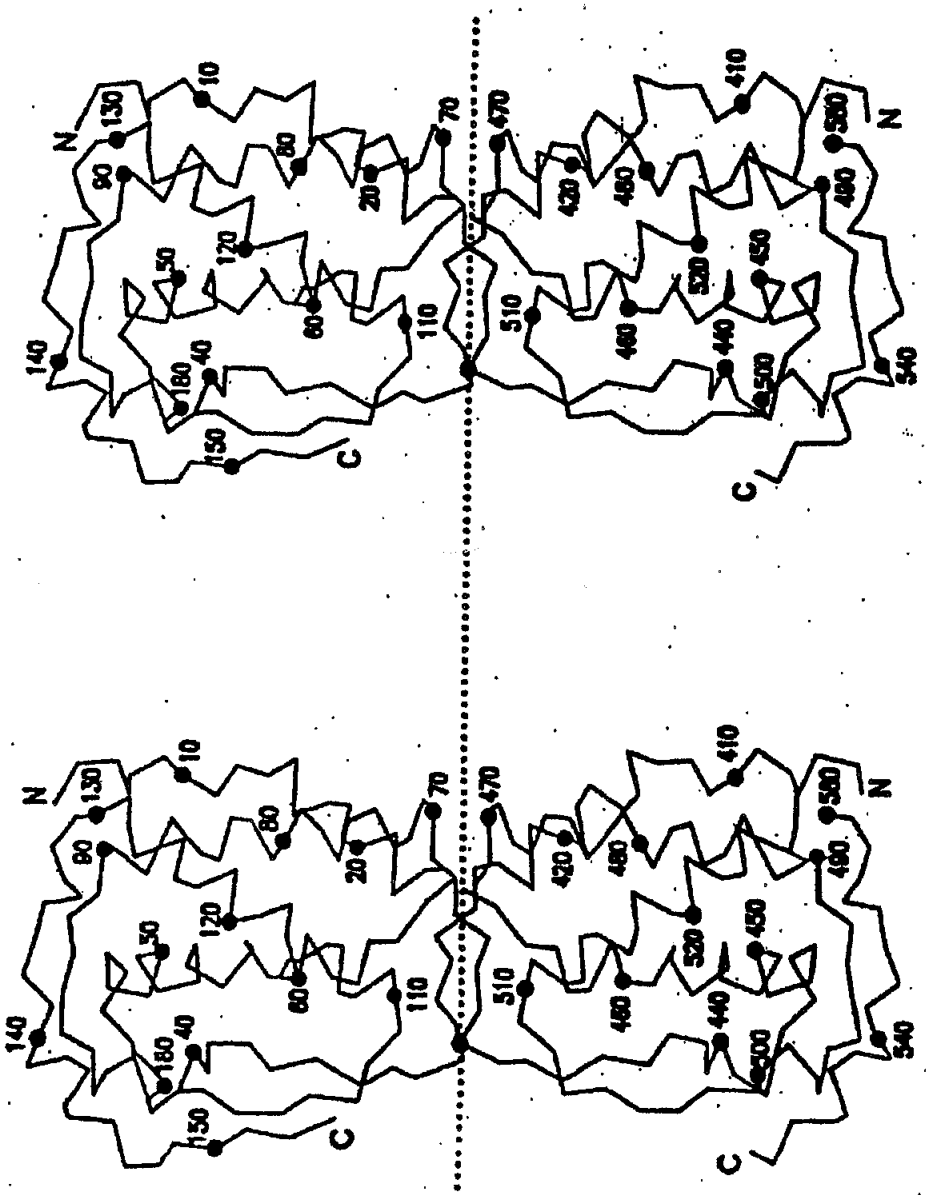

N
C
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
410
420
430
440
450
460
470
480
490
500
510
520
530
540
550

FIG. 2

FIG. 3

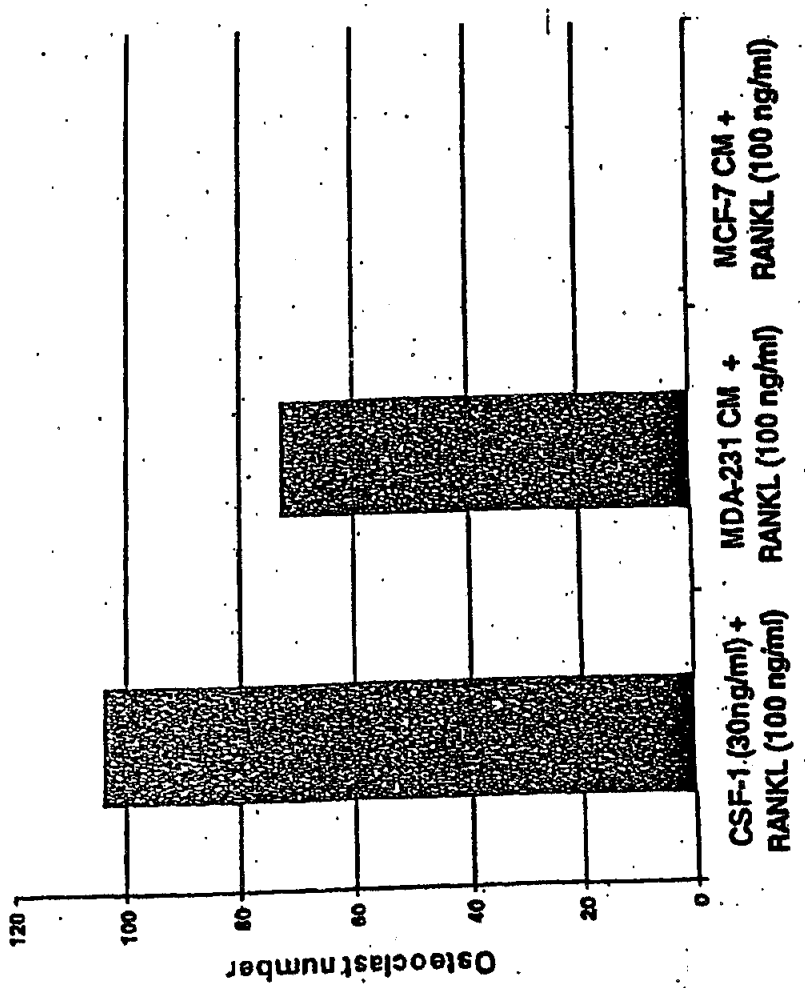

Osteoclast number
120
100
80
60
40
20
0
CSF-1 (30ng/ml) + RANKL (100 ng/ml)
MDA-231 CM + RANKL (100 ng/ml)
MCF-7 CM + RANKL (100 ng/ml)

Fig. 4A

RX1 Light chain amino acid sequence:

1 2 3

DILLTQSPAILSVSPGERVSFSC**RASQSIGTSIH**WYQQRTNGSPRLLIK**YASESIS**GIPSRFSGSGSGTDFTLSINSVESEDIADYYC**QQINSWPTT**FGGGTKLEIKRADAAPTVSIFPPSSE
QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

RX1 Heavy Chain amino acid sequence:

4 5 6

DVQLQESGPGLVKPSQSLSLTCTVTDYSIT**SDYAWN**WIRQFPGNKLEWMG**YISYSGSTSYNPSLKS**RISITRDTSKNQFFLQLNSVTTEDTATYYCAS**FDYAHAMDY**WGQGTSVTVSSAKTTA
PSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP
KIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPpEEEMTKKQVTLTCM
VTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHhttKSFSRTPG

RX1 heavy chain nucleotide sequence:

atgggttggtcctgtatcatcctattcctggtggccactgccacaggtgtgcactccgacgtgcagcttcaggagtcaggacctggcctcgtgaaaccttctcagagtctgtccctcacctgt
actgtcactgactactccatcaccagtgattacgcctggaactggatacggcaattcccagggaataaacttgagtggatggggtacataagctacagtggtagcacttcctacaatccatct
ctcaaaagtcggatctccatcactcgagacacatccaagaaccagttcttcctgcagctgaactctgtgactactgaggacacagccacatattactgtgcatccttcgactatgcccacgcc
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actgtaacctcgagcacctggcccagccagtccatcacctgcaatgtggcccacccggcaagcagcaccaaggtggacaagaaaattgagcccagagggcccacaatcaagccctgtcctcca
tgcaaatgcccagcacctaacctcttgggtggaccatccgtcttcatcttccctccaaagatcaaggatgtactcatgatctccctgagccccatagtcacatgtgtggtggtggatgtgagc
gaggatgacccagatgtccagatcagctggtttgtgaacaacgtggaagtacacacagctcagacacaaacccatagagaggattacaacagtactctccgggtggtcagtgccctccccatc
cagcaccaggactggatgagtggcaaggagttcaaatgcaaggtcaacaacaaagacctcccagcgcccatcgagagaaccatctcaaaacccaaagggtcagtaagagctccacaggtatat
gtcttgcctccaccagaagaagagatgactaagaaacaggtcactctgacctgcatggtcacagacttcatgcctgaagacatttacgtggagtggaccaacaacgggaaaacagagctaaac
tacaagaacactgaaccagtcctggactctgatggttcttacttcatgtacagcaagctgagagtggaaaagaagaactgggtggaaagaaatagctactcctgttcagtggtccacgagggt
ctgcacaatcaccacacgactaagagcttctcccggactccgggtaaa

RX1 light chain nucleotide sequence:

atggtatccacacctcagttccttgtatttttgcttttctggattccagcctccagaggtgacatcttgctgactcagtctccagccatcctgtctgtgagtccaggagaaagagtcagtttc
tcctgcagggccagtcagagcattggcacaagcatacactggtatcagcaaagaacaaatggttctccaaggcttctcataaagtatgcttctgagtctatctctgggatcccttccaggttt
agtggcagtggatcagggacagattttactcttagcatcaacagtgtggagtctgaagatattgcagattattactgtcaacaaattaatagctggccaaccacgttcggcgggggacaaag
ttggaaataaaacgggctgatgctgcaccaactgtatccatcttcccaccatccagtgagcagttaacatctggaggtgcctcagtcgtgtgcttcttgaacaacttctaccccaaagacatc
aatgtcaagtggaagattgatggcagtgaacgacaaaatggcgtcctgaacagttggactgatcaggacagcaaagacagcacctacagcatgagcagcaccctcacgttgaccaaggacgag
tatgaacgacataacagctatacctgtgaggccactcacaagacatcaacttcacccattgtcaagagcttcaacaggaatgagtgt

FIG. 4B

CHIR-R1X Light Chain Risk Assignments

V-Region	Amino Acids 1-52
Risk	LHLHLHLMLLMLHLMLLLHLHLHLHMHHHHHHHHHHHHHHHHMHLMLLMHMHHHHHHH
Mouse	DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH----WYQQRTNGSPRLLIKYAS

V-Region	Amino Acids 53-109
Risk	HLMMLHMLMHLHLHLHLLLHLHLHLLHLLLHLHHHHHHHHHHHHHHHHHHHHHHLHHLHLLLLLL
Mouse	ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA

FIG. 4C

CHIR-RX1Heavy Chain Risk Assignments

V-Region	Amino Acids 1-57
Risk	MHLHLHLHMLLMLMLLLHLHLHLHMHHHHHHHHHHHHHHHHMHLMLLMHMHHHHHHHHHHHHHH
Mouse	DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWN-WIRQFPGNKLEWMGYIS---YSGST

V-Region	Amino Acids 58-113
Risk	HMHMMHMLMHLHLHLMLLMLHLHLHLLHLLLHLHMHHHHHHHHHHHHHHHHHHHHHHHHHHHHLHHLHLHLL
Mouse	SYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDYAHAM----------DYWGQGTSVTVSS

FIG. 5A

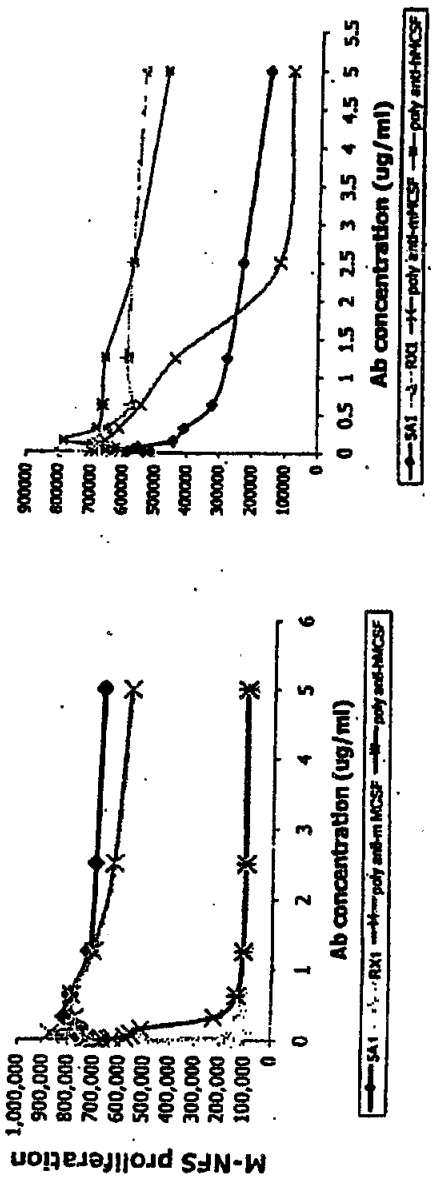
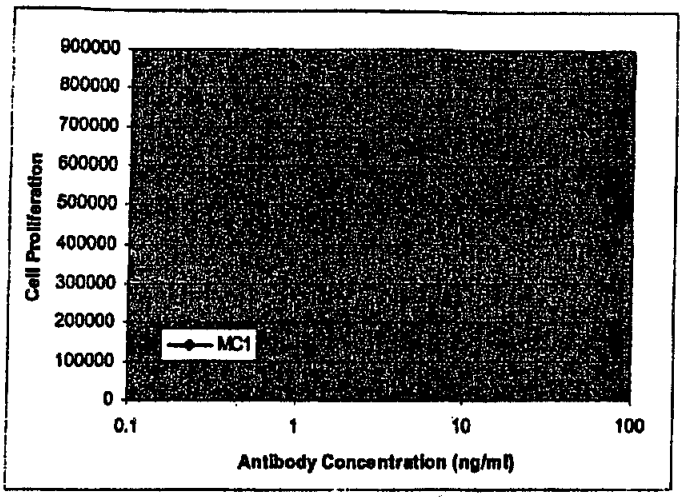

M-NFS proliferation
1,000,000
900,000
800,000
700,000
600,000
500,000
400,000
300,000
200,000
100,000
0
0 1 2 3 4 5 6
Ab concentration (ug/ml)
SA1
RX1
poly anti-mMCSF
poly anti-hMCSF
900000
800000
700000
600000
500000
400000
300000
200000
100000
0
0 0.5 1 1.5 2 2.5 3 3.5 4 4.5 5 5.5
Ab concentration (ug/ml)
SA1
RX1
poly anti-mMCSF
poly anti-hMCSF

FIG. 5B

MC1 Neutralizes human MCSF activity



MC3 Neutralizes human MCSF activity

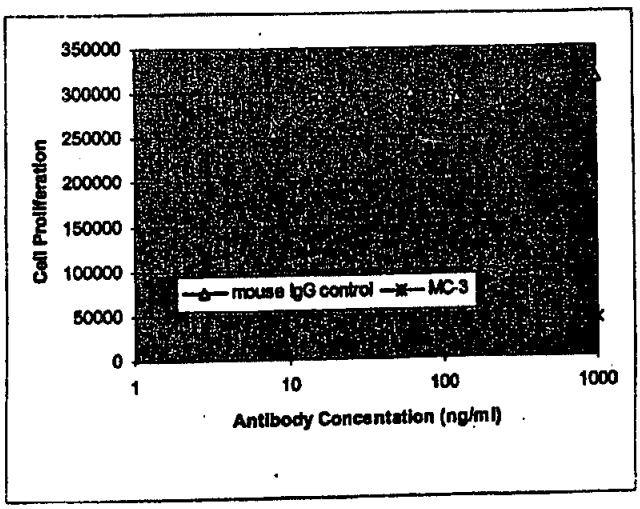


Fig. 6

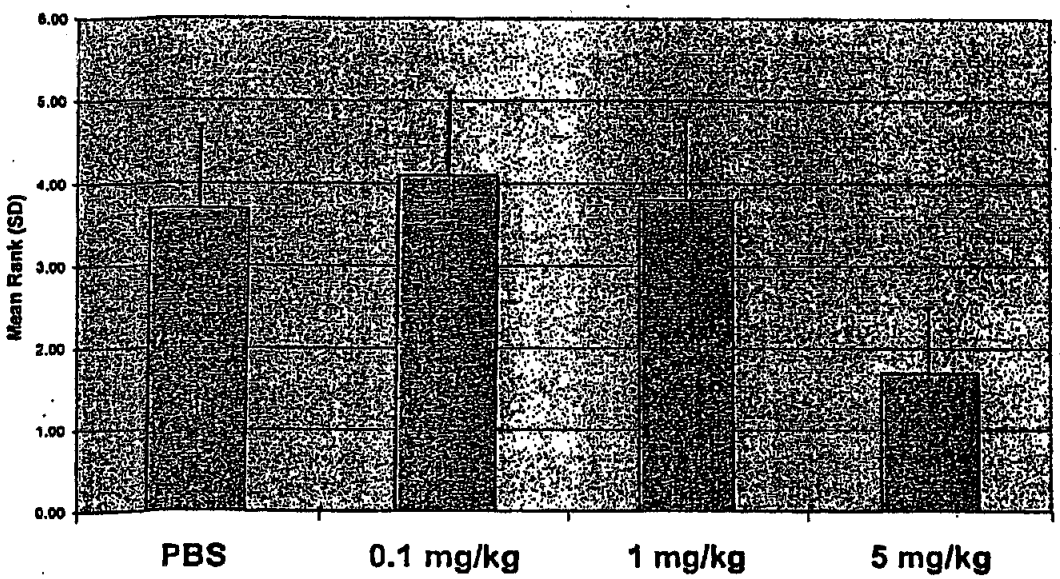

6.00
5.00
4.00
3.00
2.00
1.00
0.00
Mean Rank (SD)
PBS
0.1 mg/kg
1 mg/kg
5 mg/kg

Fig. 7

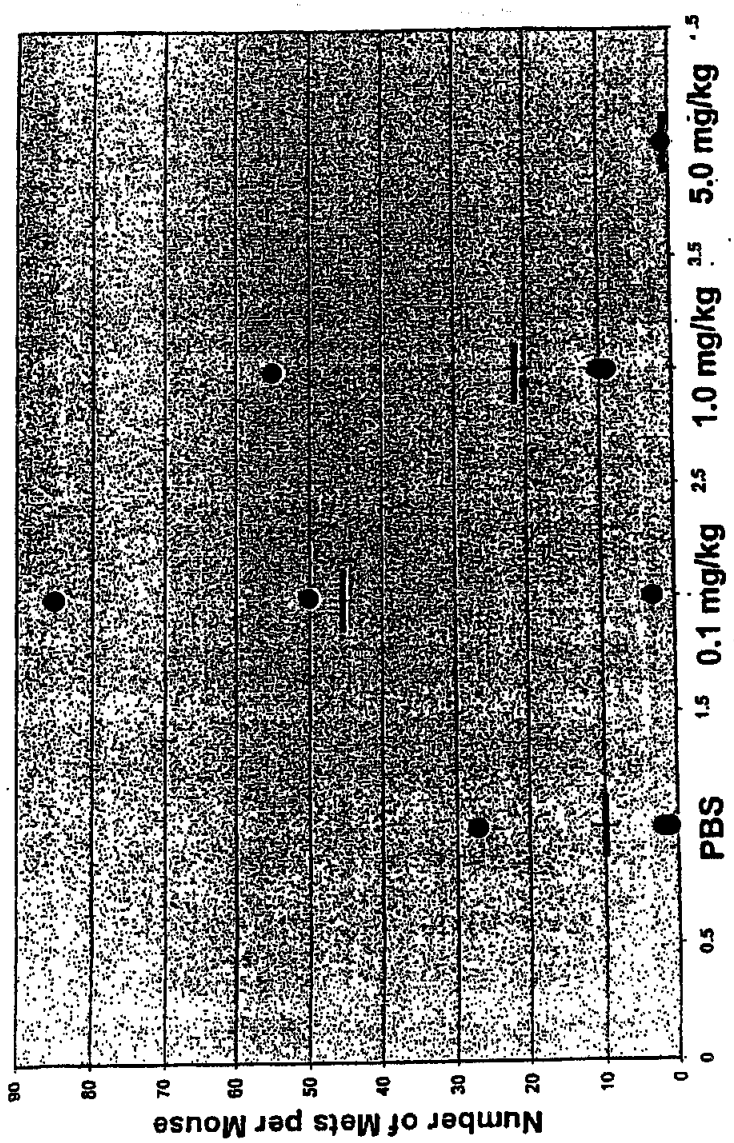

Number of Mets per Mouse
90
80
70
60
50
40
30
20
10
0
0
0.5
PBS
1.5
0.1 mg/kg
2.5
1.0 mg/kg
3.5
5.0 mg/kg
4.5

FIG. 8A

Binding of MCSF-specific antibody to breast cancer cell line MDA231

Red: no antibody control
Black: M-CSF antibody 1 ug/ml
Green: M-CSF antibody 10 ug/ml
Blue: M-CSF antibody 50 ug/ml

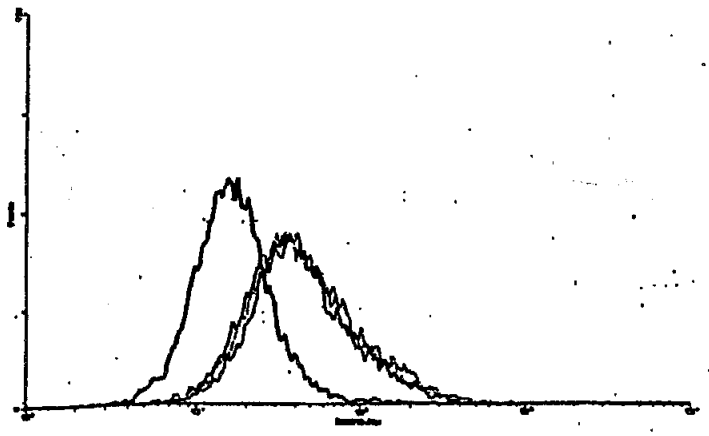


FIG. 8B

Binding of MCSF-specific antibody to multiple myeloma cancer cell line ARH77

Red: no antibody control
Green: M-CSF antibody 5 ug/ml
Blue: control IgG2a 5 ug/ml

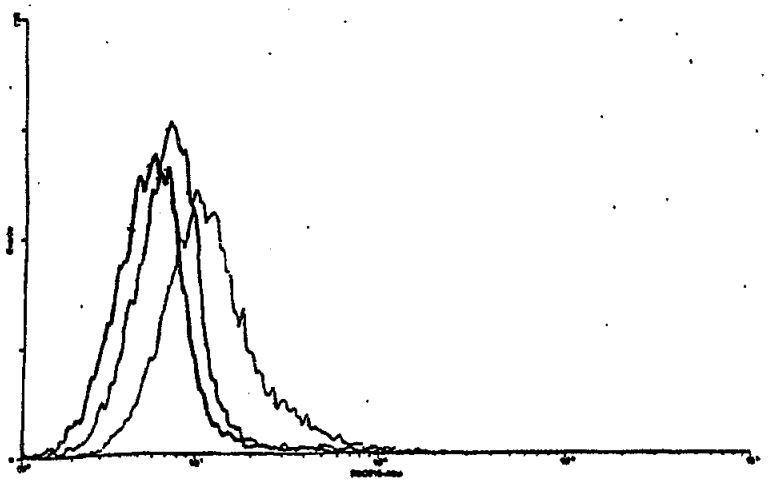


FIG. 9

Cancer Type	Cancer Status	Score 0	Score 1	Score 2	Score 3	Score 4	% with scores 3 or higher
adrenal	normal	10	5	5	0	0	0
basal cell	cancer	5	0	0	0	0	0
bladder	normal	6	1	2	1	0	10
brain	normal	17	1	2	0	0	0
breast	cancer	6	5	13	62	0	72
breast	normal	7	5	7	6	0	24
carcinoids	cancer	9	2	2	0	0	0
carcinoids (muscle)	cancer	1	0	1	0	0	0
choriocarcinoma	cancer	1	0	0	0	0	0
colon	normal	4	0	2	0	0	0
colon	cancer	9	0	1	4	0	27
fibrosarcoma	cancer	3	1	0	0	0	0
gallbladder	normal	2	1	0	1	0	25
germ cell	cancer	1	0	0	0	0	0
heart	normal	7	3	2	4	0	25
kidney	normal	5	10	1	4	0	20
kidney	cancer	6	1	0	3	0	25
leiomyosarcoma	cancer	5	0	0	0	0	0
liver	normal	11	3	4	1	0	5
liver	cancer	5	3	0	3	0	27
lung	normal	19	0	1	0	0	0
lung	cancer	3	1	0	3	0	43
lymphoma	cancer	13	0	3	2	0	12
melanoma	cancer	7	0	2	5	0	36
melanoma(inflammation)	cancer	0	0	0	1	0	100
mesothelioma	cancer	6	0	0	0	0	0
neuroblastoma	cancer	1	0	0	0	0	0
ovary	normal	6	0	2	0	0	0
ovary	cancer	8	2	0	4	0	29
pancreas	normal	9	2	5	4	0	20
pancreas	cancer	6	1	0	3	0	25
prostate	normal	0	3	8	3	0	21
prostate	cancer	9	1	1	4	0	27
sarcoma all	cancer	6	0	2	2	0	20
sarcoma	cancer	3	0	2	1	0	17
sarcoma (kidney)	cancer	3	0	2	1	0	17
sarcoma mfh	cancer	2	0	0	0	0	0
seminoma	cancer	3	0	0	0	0	0
small intestine	normal	2	1	0	1	0	25
spleen	normal	14	2	3	0	0	0
squamous cell	cancer	3	0	0	0	0	0
stomach	normal	3	2	2	1	0	13
stomach	cancer	7	1	1	1	0	10
teratoma	cancer	1	0	0	0	0	0
testis	normal	5	1	3	3	0	25
thyroid	normal	15	0	0	0	0	0
thyroid	cancer	6	2	1	2	0	18
undiff all	cancer	6	0	2	1	0	11
undif	cancer	5	0	2	0	0	0

Fig. 10

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                  10                  15

Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
            20                  25                  30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35                  40                  45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50                  55                  60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65                  70                  75                  80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
                85                  90                  95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100                 105                 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115                 120                 125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130                 135                 140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145                 150                 155                 160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
                165                 170                 175

Glu Cys Ser Ser Gln Gly His Glu Arg Gln Ser Glu Gly Ser Ser Ser
            180                 185                 190

Pro Gln Leu Gln Glu Ser Val Phe His Leu Leu Val Pro Ser Val Ile
        195                 200                 205

Leu Val Leu Leu Ala Val Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg
    210                 215                 220

Arg Ser His Gln Glu Pro Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro
225                 230                 235                 240

Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg Gln Val Glu Leu Pro Val
                245                 250                 255
```

Fig. 11

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                  10                  15
Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
            20                  25                  30
Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35                  40                  45
Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50                  55                  60
Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65                  70                  75                  80
Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
                85                  90                  95
Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100                 105                 110
Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115                 120                 125
Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130                 135                 140
Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145                 150                 155                 160
Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
                165                 170                 175
Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
            180                 185                 190
Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
        195                 200                 205
Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
    210                 215                 220
Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225                 230                 235                 240
Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
                245                 250                 255
Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
            260                 265                 270
Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
        275                 280                 285
Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
    290                 295                 300
Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305                 310                 315                 320
Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Ser Met Gln Thr Glu
                325                 330                 335
Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
            340                 345                 350
Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala Leu Pro
        355                 360                 365
Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His Thr Pro
    370                 375                 380
Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
385                 390                 395                 400
Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Gly Leu Ser Asn Pro
                405                 410                 415
Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
            420                 425                 430
Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
        435                 440                 445
Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala
    450                 455                 460
Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
465                 470                 475                 480
His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
                485                 490                 495
Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
            500                 505                 510
Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
        515                 520                 525
Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
    530                 535                 540
Gln Asp Asp Arg Gln Val Glu Leu Pro Val
```

Fig. 12

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                  10                  15
Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
            20                  25                  30
Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35                  40                  45
Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50                  55                  60
Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65                  70                  75                  80
Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
                85                  90                  95
Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100                 105                 110
Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115                 120                 125
Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130                 135                 140
Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145                 150                 155                 160
Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
                165                 170                 175
Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
            180                 185                 190
Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
        195                 200                 205
Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
    210                 215                 220
Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225                 230                 235                 240
Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
                245                 250                 255
Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
            260                 265                 270
Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
        275                 280                 285
Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
    290                 295                 300
Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305                 310                 315                 320
Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
                325                 330                 335
Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
            340                 345                 350
Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly His Glu Arg Gln
        355                 360                 365
Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu
    370                 375                 380
Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu
385                 390                 395                 400
Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp
                405                 410                 415
Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg
            420                 425                 430
Gln Val Glu Leu Pro Val
```

FIG. 13

5H4 heavy chain protein sequence:

```
  1   EIQLQQSGPE LVKTGTSVKI SCKASGYSFT GYFMHWVKQS HGKSLEWIGY
 51   ISCYNGDTNY NQNFKGKATF TVDTSSSTAY MQFNSLTSED SAVYYCAREG
101   GNYPAYWGQG TLVTVSAAKT TPPSVYPLAP GSAAQTNSMV TLGCLVKGYF
151   PEPVTVTWNS GSLSSGVHTF PAVLQSDLYT LSSSVTVPSS TWPSETVTCN
201   VAHPASSTKV DKKIVPRDCG CKPCICTVPE VSSVFIFPPK PKDVLTITLT
251   PKVTCVVVDI SKDDPEVQFS WFVDDVEVHT AQTQPREEQF NSTFRSVSEL
301   PIMHQDWLNG KEFKCRVNSA AFPAPIEKTI SKTKGRPKAP QVYTIPPPKE
351   QMAKDKVSLT CMITDFFPED ITVEWQWNGQ PAENYKNTQP IMDTDGSYFV
401   YSKLNVQKSN WEAGNTFTCS VLHEGLHNHH TEKSLSHSPG K
```

5H4 light chain protein sequence:

```
  1   DIVMTQSHKF MSTSVGDRVT ITCKASQNVG TAVTWYQQKP GQSPKLLIYW
 51   TSTRHAGVPD RFTGSGSGTD FTLTISDVQS EDLADYFCQQ YSSYPLTFGA
101   GTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
151   DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201   STSPIVKSFN RNEC
```

FIG. 14

MC-1 heavy chain protein sequence:

```
  1   EVKLVESGGG LVQPGGSLKL SCATSGFTFS DYYMYWVRQT PEKRLEWVAY
 51   ISNGGGSTYY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARQG
101   SYGYPFAYWG QGTLVTVSAA KTTAPSVYPL APVCGDTTGS SVTLGCLVKG
151   YFPEPVTLTW NSGSLSSGVH TFPAVLQSDL YTLSSSVTVT SSTWPSQSIT
201   CNVAHPASST KVDKKIEPRG PTIKPCPPCK CPAPNLLGGP SVFIFPPKIK
251   DVLMISLSPI VTCVVVDVSE DDPDVQISWF VNNVEVHTAQ TQTHREDYNS
301   TLRVVSALPI QHQDWMSGKE FKCKVNNKDL PAPIERTISK PKGSVRAPQV
351   YVLPPPEEEM TKKQVTLTCM VTDFMPEDIY VEWTNNGKTE LNYKNTEPVL
401   DSDGSYFMYS KLRVEKKNWV ERNSYSCSVV HEGLHNHHTT KSFSRTPGK
```

MC-1 light chain protein sequence:

```
  1   AIQMTQTTSS LSASLGDRVT ISCSASQGIS NYLNWYQQKP DGTVKLLIYY
 51   TSSLHSGVPS RFSGSGSGTD YSLTISNLEP EDIATYYCQQ YSKLPWTFGG
101   GTKLEIKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
151   DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201   STSPIVKSFN RNEC
```

FIG. 15

MC-3 heavy chain protein sequence:

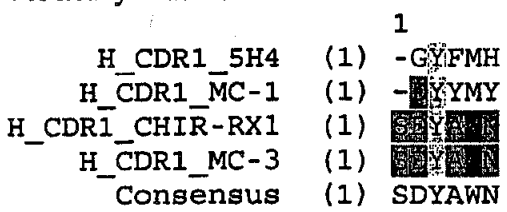
```
  1   DVQLQESGPG LVKPSQSLSL TCTVTGYSIT SDYAWNWIRQ FPGNKLEWMG
 51   YISYSGSTSY NPSLKSRISI TRDTSKNQFF LQLNSVTTED TATYYCARLE
101   TWLFDYWGQG TTLTVSSAKT TPPSVYPLAP GCGDTTGSSV TLGCLVKGYF
151   PESVTVTWNS GSLSSSVHTF PALLQSGLYT MSSSVTVPSS TWPSQTVTCS
201   VAHPASSTTV DKKLEPSGPI STINPCPPCK ECHKCPAPNL EGGPSVFIFP
251   PNIKDVLMIS LTPKVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQTQTHRE
301   DYNSTIRVVS TLPIQHQDWM SGKEFKCKVN NKDLPSPIER TISKIKGLVR
351   APQVYILPPP AEQLSRKDVS LTCLVVGFNP GDISVEWTSN GHTEENYKDT
401   APVLDSDGSY FIYSKLNMKT SKWEKTDSFS CNVRHEGLKN YYLKKTISRS
451   PGLDLDDICA EAKDGELDGL WTTITIFISL FLLSVCYSAS VTLFKVKWIF
501   SSVVELKQKI SPDYRNMIGQ GA
```

MC-3 light chain protein sequence:

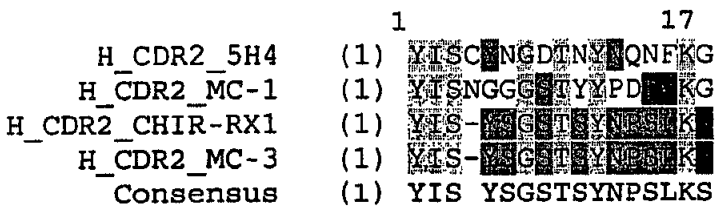
```
  1   DILLTQSPAI LSVSPGERVS FSCRASQSIG TSIHWYQQRT NGSPRLLIKY
 51   ASESISGIPS RFSGSGSGTD FTLSINSVES EDIADYYCQQ SNSWPTTFGG
101   GTKLEIKWAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
151   DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201   STSPIVKSFN RNEC
```

FIG. 16A

For heavy chain CDR1:



For heavy chain CDR2:



For heavy chain CDR3:

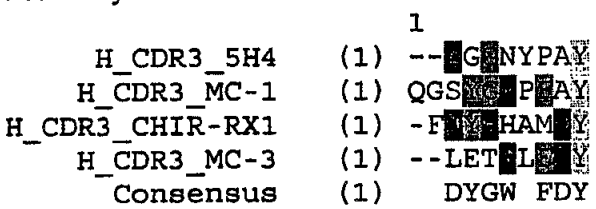
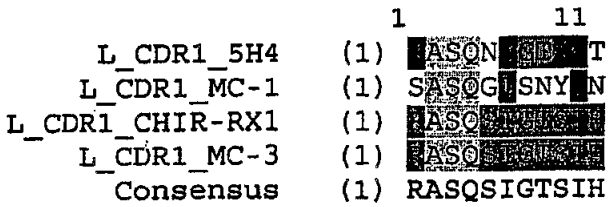
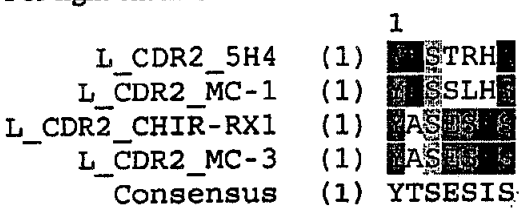


FIG. 16B

For light chain CDR1:



For light chain CDR2:



For light chain CDR3:

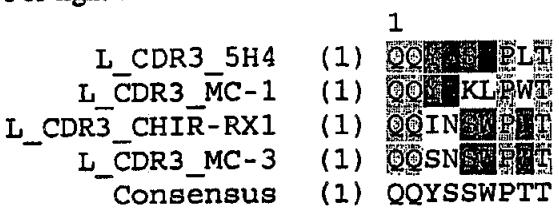


FIG. 17

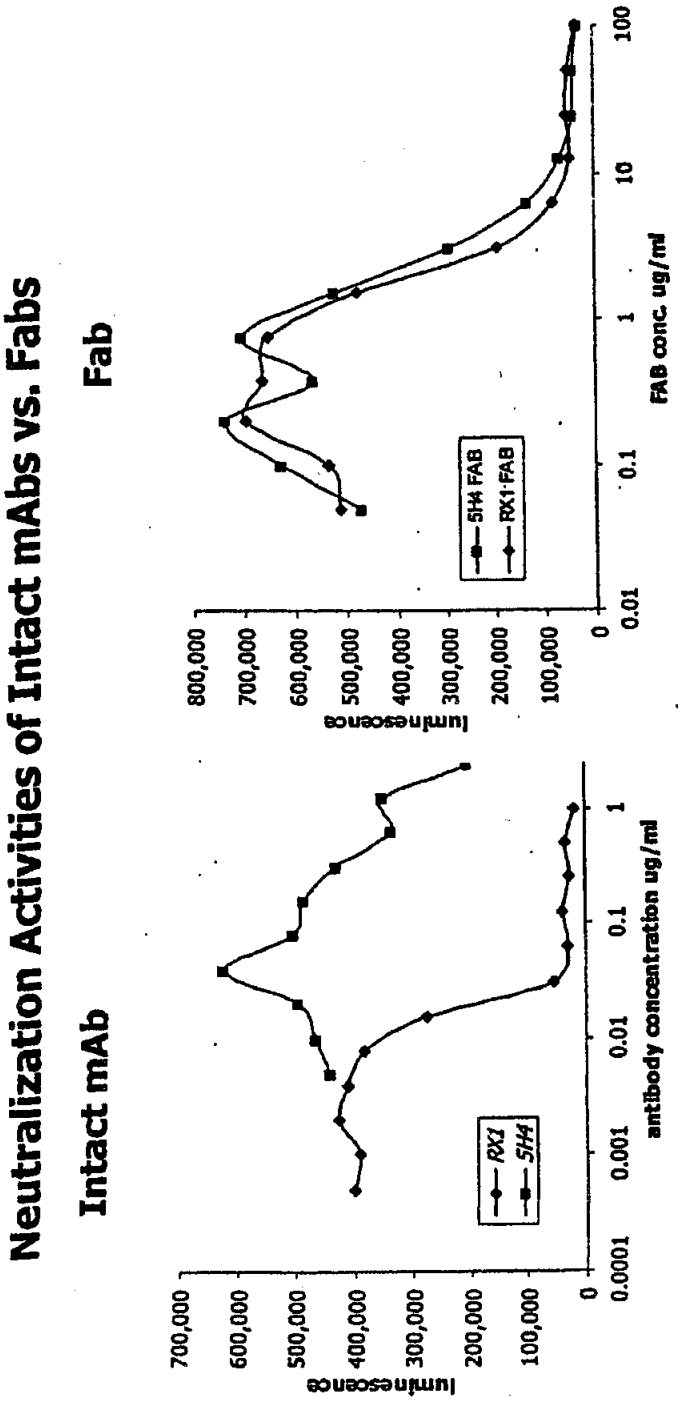

Neutralization Activities of Intact mAbs vs. Fabs
Intact mAb
Fab
luminescence
antibody concentration ug/ml
FAB conc. ug/ml
RX1
5H4
5H4 FAB
RX1 FAB

FIG. 18

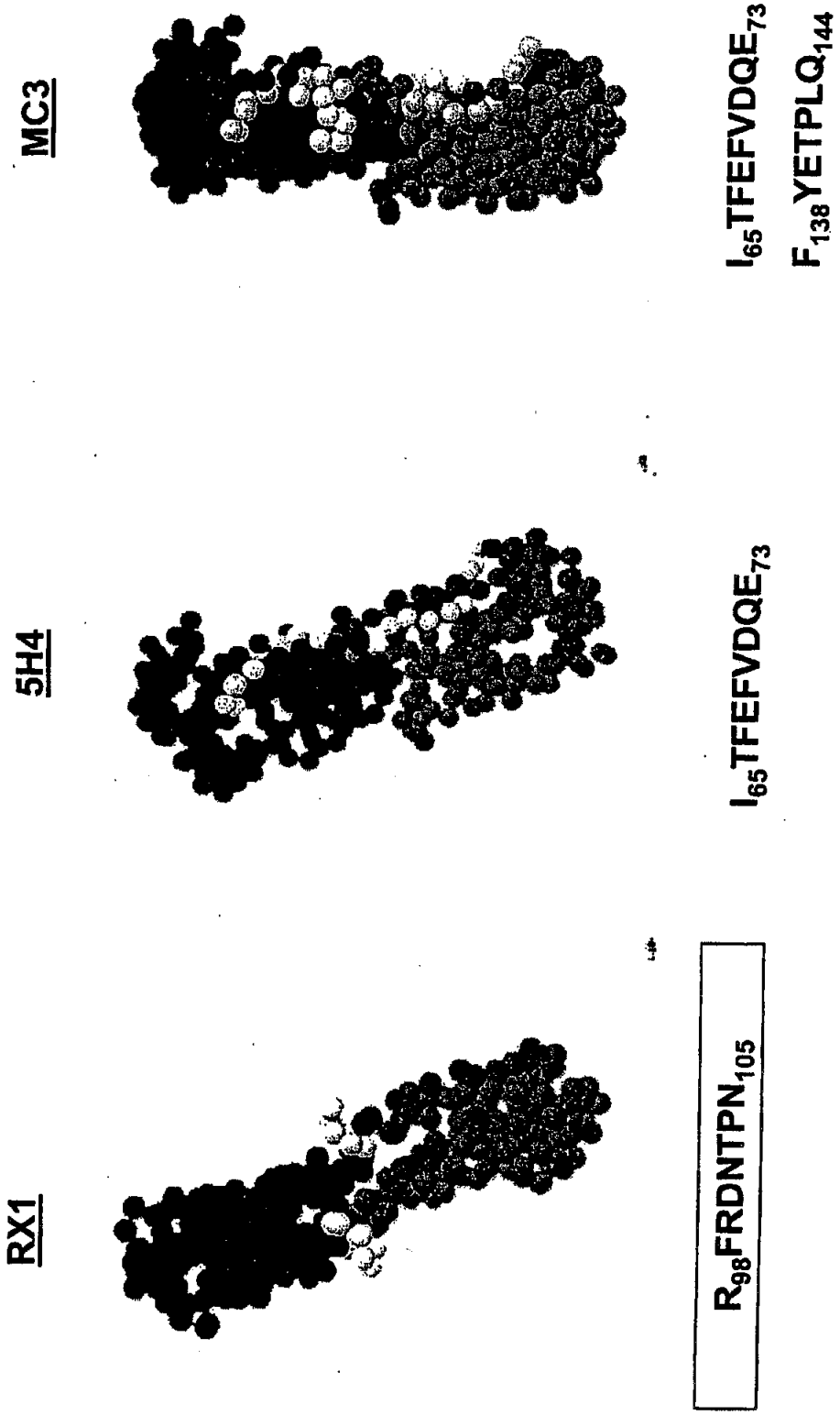

MCSF Structure with RX1 Epitopes Highlighted
RX1
5H4
MC3
R_{98}FRDNTPN$_{105}$
I_{65}TFEFVDQE$_{73}$
I_{65}TFEFVDQE$_{73}$
F_{138}YETPLQ$_{144}$

FIG. 19A

Heavy Chain

V-Region	No.of Changes	Amino Acids 1-57
Risk		MHLHLHLHMLLMLMLLLHLHLHLHMHHHHHHHHHHHHHHHHMHLMLLMHMHHHHHHHHHHHHHH
Mouse		DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWN-WIRQFPGNKLEWMGYIS---YSGST
Human		qvqLqesGpgLVkPsqTLsLTCxvsGxsxSsxxxxxxWiRQpPgkgLEWigxiyyraxxgxt
Low Risk	2	DVQLQESGPGLVKPSQ**T**LSLTCTVTDYSITSDYAWN-WIRQFPG**K**KLEWMGYIS---YSGST
Low+Mod	5	QVQLQESGPGLVKPSQ**T**LSLTCTV**S**DYSITSDYAWN-WIRQFPG**K**GLEWMGYIS---YSGST

V-Region	No.of Changes	Amino Acids 58-113
Risk		HMHMMHMLMHLHLHLMLLMLHLHLHLLHLLLHLHMHHHHHHHHHHHHHHHHHHHHHHHHHHLHHLHLHLL
Mouse		SYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDYAHAM----------DYWGQGTSVTVSS
Human		xynpSlksRvTisvDTSKNQfsLxlxsvtaaDTAvYyCArxxxxxxxxxxxxxxxxxfdxWGqGtxVTVSS
Low Risk	6	SYNPSLKSRI**T**I**S**RDTSKNQF**S**LQLNSVT**AA**DTATYYCASFDYAHAM----------DYWGQGT**T**VTVSS
Low+Mod	7	SYNPSLKSRI**T**I**S**RDTSKNQF**S**LQLNSVT**AA**DTAVYYCASFDYAHAM----------DYWGQGT**T**VTVSS

FIG. 19B

Low Risk Heavy Chain Vs. Kabat Vh2 Consensus:

Protein Seq:

DVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWNWIRQFPGKKLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSLQLNSVTAADTATYYCASFDYAHAMD
YWGQGTTVTVSS

DNA Seq:

GACGTACAACTTCAAGAATCTGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTACGCTT
GGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCTCCTACAATCCTTCTCTGAAATCACGCATCAC
AATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATTCTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACG
CCATGGATTATTGGGGACAGGGTACTACCGTTACCGTAAGCTCA

Low Risk + Moderate Risk Heavy Chain Vs. Kabat Vh2 Consensus:

Protein Seq:

QVQLQESGPGLVKPSQTLSLTCTVSDYSITSDYAWNWIRQFPGKGLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSLQLNSVTAADTAVYYCASFDYAHAMD
YWGQGTTVTVSS

DNA Seq:

CAAGTTCAACTTCAAGAATCAGGCCCCGGACTCGTTAAACCCTCTCAAACTCTCTCTCTTACTTGCACTGTATCCGATTACTCTATTACTTCAGACTACGCTTG
GAACTGGATCAGACAATTTCCCGGAAAAGGACTCGAATGGATGGGATATATCTCTTACTCTGGCTCAACCTCTTACAACCCCTCTCTCAAATCTCGAATAAC
AATCTCACGCGATACTTCTAAAAATCAATTCTCACTTCAACTTAACTCCGTTACTGCCGCCGACACTGCCGTTTACTACTGTGCTTCCTTCGATTACGCCCACG
CTATGGATTATTGGGGACAAGGAACTACCGTCACTGTCAGCTCA

FIG. 20A

Light Chain

V-Region	No.of Changes	Amino Acids 1-52
Risk		LHLHLHLMLLMLHLMLLLHLHLHLHMHHHHHHHHHHHHHHHMHLMLLMHMHHHHHHH
Mouse		DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH----WYQQRTNGSPRLLIKYAS
Human		EIVlTQSPgTLSlSPGERaTLSCRASQSvsssyL---AWYQQkPGQAPRLLIYgAS
Low Risk	8	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH----WYQQKTGQSPRLLIKYAS
Low+Mod	9	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH----WYQQKTGQAPRLLIKYAS

V-Region	No.of Changes	Amino Acids 53-109
Risk		HLMMLHMLMHLHLHLHLLLHLHLHLLHLLLLHLHHHHHHHHHHHHHHHHHHHHHHLHHLHLLLLLL
Mouse		ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA
Human		sRATGIPdRFSGSGSGTDFTLTISrLepEDFAVYYCQQygsspp-----xTFGqGTKvEI-KRT
Low Risk	8	ERISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT
Low+Mod	10	ERATGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT

FIG. 20B

Low Risk Light Chain Vs. Kabat Vk3 Consensus:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQSPRLLIKYASERISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTCCTTACCCAATCTCCCGGAACCCTCTCAGTATCTCCCGGCGAACGAGTAACCTTTTCATGTAGAGCATCCCAATCCATCGGCACTTCAATTCACT
GGTATCAGCAGAAAACAGGTCAATCCCCACGGCTTCTTATAAAATATGCATCAGAAAGAATATCAGGCATTCCAGACAGATTCTCAGGTTCAGGTTCAGGC
ACAGACTTCACACTTACAATTTCCCGCGTCGAATCCGAAGACTTCGCTGACTATTACTGCCAACAAATCAACTCATGGCCTACTACTTTCGGTCAAGGCACC
AAACTCGAAATTAAACGTACG

Low Risk + Moderate Risk Light Chain Vs. Kabat Vk3 Consensus:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQAPRLLIKYASERATGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTTCTTACTCAATCCCCCGGTACACTCTCAGTTTCCCCAGGCGAACGCGTCACTTTTTCTTGCAGAGCATCACAATCAATCGGCACTTCAATTCATT
GGTATCAACAAAAAACAGGACAGGCCCCACGACTTCTTATTAAATATGCATCAGAACGAGCCACAGGCATCCCAGACAGATTTTCAGGTTCAGGATCAGGC
ACCGATTTCACACTTACAATATCCAGAGTCGAATCAGAAGATTTTGCAGATTACTATTGTCAACAAATAAACAGCTGGCCCACTACATTCGGACAAGGCACA
AAACTCGAAATTAAACGTACG

FIG. 21A

Light Chain – Changes back to Murine

V-Region	No.of Changes	Amino Acids 1-52
Risk		LHLHLHLMLLMLHLMLLLHLHLHLHMHHHHHHHHHHHHHHHMHLMLLMHMHHHHHHH
Mouse		DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH----WYQQRTNGSPRLLIKYAS
Human		EIVlTQSPgTLSlSPGERaTLSCRASQSvsssyL---AWYQQkPGQAPRLLIYgAS
Low Risk	8	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH----WYQQKTGQSPRLLIKYAS
Low+Mod	9	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH----WYQQKTGQAPRLLIKYAS

V-Region	No.of Changes	Amino Acids 53-109
Risk		HLMMLHMLMHLHLHLHLLHLHLHLLHLLLHLHHHHHHHHHHHHHHHHHHHHHHHLHHLHLLLLLL
Mouse		ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA
Human		sRATGIPdRFSGSGSGTDFTLTISrLepEDFAVYYCQQygsspp-----xTFGqGTKvEI-KRT
Low Risk	8	ERISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT
Low+Mod	10	ERATGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT
Low+Mod Altnernate	7	ESISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT

FIG. 21B

Low Risk Light Chain Vs. Kabat Vk3 Consensus; AA54 changed back to murine:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQSPRLLIKYASESISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTCCTTACCCAATCTCCCGGAACCCTCTCAGTATCTCCCGGCGAACGAGTAACCTTTTCATGTAGAGCATCCCAATCCATCGGCACTTCAATTCACT
GGTATCAGCAGAAAACAGGTCAATCCCCACGGCTTCTTATAAAATATGCATCAGAATCAATTTCTGGCATCCCAGACAGATTTTCAGGTTCAGGATCAGGCA
CCGATTTCACACTTACAATATCCAGAGTCGAATCAGAAGATTTTGCAGATTACTATTGTCAACAAATAAACAGCTGGCCCACTACATTCGGACAAGGCACAA
AACTCGAAATTAAACGTACG

Low Risk + Moderate Risk Light Chain Vs. Kabat Vk3 Consensus; AA54, 55, 56 changed back to murine:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQAPRLLIKYASESISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTTCTTACTCAATCCCCCGGTACACTCTCAGTTTCCCCAGGCGAACGCGTCACTTTTTCTTGCAGAGCATCACAATCAATCGGCACTTCAATTCATT
GGTATCAACAAAAAACAGGACAGGCCCCACGACTTCTTATTAAATATGCATCAGAATCAATTTCTGGCATCCCAGACAGATTTTCAGGTTCAGGATCAGGCA
CCGATTTCACACTTACAATATCCAGAGTCGAATCAGAAGATTTTGCAGATTACTATTGTCAACAAATAAACAGCTGGCCCACTACATTCGGACAAGGCACAA
AACTCGAAATTAAACGTACG

FIG. 22A

Light Chain – Changes based on HK6 2-1-1(A14)

V-Region	No.of Changes	Amino Acids 1-52
Risk		LHLHLHLMLLMLHLMLLLHLHLHLHMHHHHHHHHHHHHHHHMHLMLLMHMHHHHHHH
Mouse		DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH----WYQQRTNGSPRLLIKYAS
Human		DVVMTQSPAFLSVTPGEKVTITCQASEGIGNYLY----WYQQKPDQAPKLLIKYAS
Low Risk	10	DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIH----WYQQKTDQSPRLLIKYAS
Low+Mod	12	DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIH----WYQQKTDQAPKLLIKYAS

V-Region	No.of Changes	Amino Acids 53-109
Risk		HLMMLHMLMHLHLHLHLLLHLHLHLLHLLLHLHHHHHHHHHHHHHHHHHHHHHHHLHHLHLLLLLL
Mouse		ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA
Human		QSISGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQGNKHP------LTFGGGTKVEI-KRT
Low Risk	5	ESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQINSWPT------TFGGGTKLEI-KRT
Low+Mod	5	ESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQINSWPT------TFGGGTKLEI-KRT

FIG. 22B

Low Risk Light Chain vs. VK6 Subgroup 2-1-(1) A14:

Protein Seq:

DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIHWYQQKTDQSPRLLIKYASESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQINSWPTTFGGGTKLEIKRT

Nucleotide Seq: Not synthesized

Low Risk + Moderate Risk Light Chain vs. VK6 Subgroup 2-1-(1) A14:

DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIHWYQQKTDQAPKLLIKYASESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQI
NSWPTTFGGGTKLEIKRT

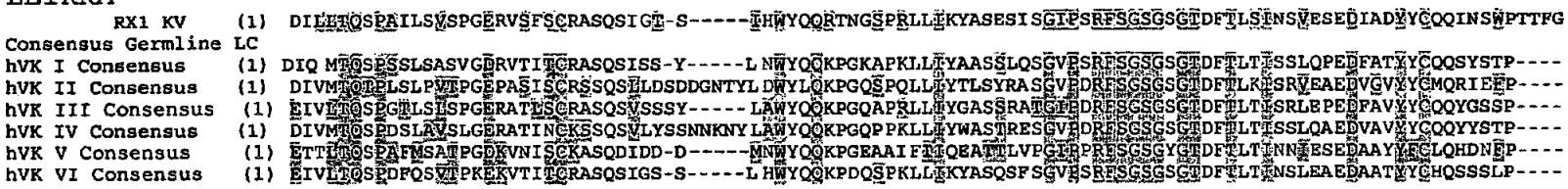
Nucleotide Seq:

GACATAGTTCTCACACAATCACCAGCATTCCTCTCAGTTACACCCGGCGAAAAAGTAACCTTTACCTGTCAGGCTTCTCAATCTATCGGCACTTCTATTCACT
GGTATCAACAAAAAACCGATCAAGCTCCTAAACTCCTCATAAAATACGCATCCGAATCCATCTCCGGTATCCCCTCCAGATTTTCAGGCTCCGGCTCCGGCA
CAGATTTCACCCTTACCATTAGCTCAGTTGAAGCCGAAGACGCAGCTGATTACTACTGTCAACAAATAAACTCATGGCCCACTACTTTCGGCGGCGGCACTA
AACTCGAAATAAAACGTACG

FIG. 23A

Murine RX-1 Light Chain:

DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPTTFGGGTK
LEIKRA



LIGHT CHAIN amino half

RX-1 DILLTQSPAILSVSPGERVSFSCRASQSI--GTSIH----WYQQRTNGSPRLLIKYAS

pos... 10 20 abcdef 30 40 50

Kabat:

HK1...DIQMTQSPSSLSASVGDRVTITCRASQSLVXX-XISXXLXWYQQKPGKAPKLLIYXAS
HK2...DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSXDGXXYLNWYLQKPGQSPQLLIYXXS
HK3...EIVLTQSPGTLSLSPGERATLSCRASQS-----VSSSYLAWYQQKPGQAPRLLIYGAS
HK4...DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWAS

Germline Consensus (with JK4):

hVK1 DIQMTQSPSSLSASVGDRVTITCRASQS------ISSYLNWYQQKPGKAPKLLIYAAS
hVK2 DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLLIYTLS
hVK3 EIVLTQSPGTLSLSPGERATLSCRASQS-----VSSSYLAWYQQKPGQAPRLLIYGAS
hVK4 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWAS
hVK5 ETTLTQSPAFMSATPGDKVNISCKASQDIDD------DMNWYQQKPGEAAIFIIQEAT
hVK6 EIVLTQSPDFQSVTPKEKVTITCRASQSIG------SSLHWYQQKPDQSPKLLIKYAS

FIG. 23B

LIGHT CHAIN carboxy half

```
RX-1  ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA

pos...      60        70        80        90     abcdef  100       a
```

Kabat:

```
HK1...XLXSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQXXXXPE-----XTFGQGTKVEI-KRT
HK2...NRXSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAXQXPR-----XTFGQGTKVEI-KRT
HK3...SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPP-----XTFGQGTKVEI-KRT
HK4...TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP------XTFGQGTKVEI-KRT
```

Germline Consensus (with JK4):

```
hVK1  SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP------LTFGGGTKVEI-KRT
hVK2  YRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP------LTFGGGTKVEI-KRT
hVK3  SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP------LTFGGGTKVEI-KRT
hVK4  TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP------LTFGGGTKVEI-KRT
hVK5  TLVPGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP------LTFGGGTKVEI-KRT
hVK6  QSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP------LTFGGGTKVEI-KRT
```

FIG. 24A

Murine RX-1 Heavy Chain:

DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYC
ASFDYAHAMDYWGQGTSVTVSS

```
RX1 VH                (1) D VQLQESGPGLVKPSQSLS LTCTVTDYSITS-DYAWNWIRQFPGNKLEWMGYISYSGSTS---YNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDY
Consensus Germline
hVH I Consensus       (1)  QVQLVQSGAEVKKPGASVKVSCKASGYTFTG--YYMHWVRQAPGQGLEWMGWINP--NSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR---
hVH II Consensus      (1)  QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKR---YSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHR--
hVH III Consensus     (1) E VQLVESGGGLVQPGGSLRLSCAASGFTFSS--YWMSWVRQAPGKGLEWVANIKQ--DGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR---
hVH IV Consensus      (1)  QVQLQESGPGLVKPSGTLSLTCAVSGGSISSS-NWWSWVRQPPGKGLEWIGEIYHSGSTN---YNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCAR---
hVH V Consensus       (1) E VQLVQSGAEVKKPGESLKISCKGSGYSFTS--YWIGWVRQMPGKGLEWMGIIYP--GDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---
hVH VI Consensus      (1)  QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWYN-DYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAR---
hVH VII Consensus     (1)  QVQLVQSGSELKKPGASVKVSCKASGYTFTS--YAMNWVRQAPGQGLEWMGWINT--NTGNPTYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCAR---
```

HEAVY CHAIN amino half

```
      DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWN-WIRQFPGNKLEWMGYIS---YSGST

pos ...        10        20        30     ab   40        50  abc
```

Kabat:

```
HH1 ...XVQLVQSGAEVKKPGXSVKVSCKASGYTFXSYXIX--WVRQAPGQGLEWMGXIXPY-XXGXT
HH2 ...QVQLQESGPGLVKPSQTLSLTCXVSGXSXSSXXXXXXWIRQPPGKGLEWIGXIYYRAXXGXT
HH3 ...EVQLVESGGGLVQPGGSLRLSCAASGFTFSXYXMX--WVRQAPGKGLEWVXXIXXKXXGXXT
```

Germline Consensus (with JH4):

```
hVHI   QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMH--WVRQAPGQGLEWMGWINP--NSGGT
hVHII  QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIY---WNDDK
hVHIII EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMS--WVRQAPGKGLEWVANIK--QDGSEK
hVHIV  QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWW-SWVRQPPGKGLEWIGEIY---HSGST
hVHV   EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIG--WVRQMPGKGLEWMGIIYP--GDSDT
hVHVI  QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYY-RSKWYN
hVHVII QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMN--WVRQAPGQGLEWMGWINT--NTGNP
```

FIG. 24B

HEAVY CHAIN carboxy half

```
       SYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDYAHAM----------DYWGQGTSVTVSS

pos ... 60        70        80  abc     90        100abcdefghijk       110
```

Kabat:

```
HH1 ...NYAQKFQGRVTITXDXSTSTAYMELSSLRSXDTAVYYCARXXXXXXXXXXXXXDXXFDXWGQGTLVTVSS
HH2 ...XYNPSLKSRVTISVDTSKNQFSLXLXSVTAADTAVYYCARXXXXXXXXXXXXXXXXXFDXWGQGTXVTVSS
HH3 ...YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAXXXXXXXXXXXXXXYYXXFDXWGQGTLVTVSS
```

Germline Consensus (with JH4):

```
hVHI   NYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHII  RYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHIII YYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHIV  NYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHV   RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHVI  DYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHVII TYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
```

Figure 24C:

Kabat numbering of 5H4:

5H4 heavy chain protein sequence:

1-30: EIQLQQSGPE LVKTGTSVKI SCKASGYSFT
31-35: GYFMH
36-49: WVKQSHGKSLEWIG
50-65: YIS C (52A) YNGDTNY NQNFKG
66-94: KATF TVDTSSSTAY MQF N (82A) S(82B) L(82C) TSED SAVYYCAR
95-102: EGGNYPAY
103-437: WGQG TLVTVSAAKT TPPSVYPLAP GSAAQTNSMV
TLGCLVKGYFPEPVTVTWNS GSLSSGVHTF PAVLQSDLYT LSSSVTVPSS TWPSETVTCN
VAHPASSTKV DKKIVPRDCG CKPCICTVPE VSSVFIFPPK PKDVLTITLT PKVTCVVVDI
SKDDPEVQFS WFVDDVEVHT AQTQPREEQF NSTFRSVSEL PIMHQDWLNG KEFKCRVNSA
AFPAPIEKTI SKTKGRPKAP QVYTIPPPKE QMAKDKVSLT CMITDFFPED ITVEWQWNGQ
PAENYKNTQP IMDTDGSYFV YSKLNVQKSN WEAGNTFTCS VLHEGLHNHH TEKSLSHSPG K

5H4 light chain protein sequence:

1-23: DIVMTQSHKF MSTSVGDRVT ITC
24-34: KASQNVG TAVT
35-49: WYQQKPGQSPKLLIY
50-56: WTSTRHA
57-88: GVPD RFTGSGSGTD FTLTISDVQS EDLADYFC
89-97: QQYSSYPLT
98-214: FGAGTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
STSPIVKSFN RNEC

Figure 24D:

Kabat numbering of MC1

MC-1 heavy chain protein sequence:

```
1-30:       EVKLVESGGG LVQPGGSLKL SCATSGFTFS
31-35:      DYYMY
36-49:      WVRQTPEKRLEWVA
50-65:      YIS N (52A) GGGSTYY PDTVKG
66-94:      RFTI SRDNAKNTLY LQM S (82A) R (82B) L (82C) KSED TAMYYCAR
95-102:     QGSYGYPFAY
103-449:    WG QGTLVTVSAA KTTAPSVYPL APVCGDTTGS SVTLGCLVKG YFPEPVTLTW
NSGSLSSGVH TFPAVLQSDL YTLSSSVTVT SSTWPSQSIT CNVAHPASST KVDKKIEPRG
PTIKPCPPCK CPAPNLLGGP SVFIFPPKIK DVLMISLSPI VTCVVVDVSE DDPDVQISWF
VNNVEVHTAQ TQTHREDYNS TLRVVSALPI QHQDWMSGKE FKCKVNNKDL PAPIERTISK
PKGSVRAPQV YVLPPPEEEM TKKQVTLTCM VTDFMPEDIY VEWTNNGKTE LNYKNTEPVL
DSDGSYFMYS KLRVEKKNWV ERNSYSCSVV HEGLHNHHTT KSFSRTPGK
```

MC-1 light chain protein sequence:

```
1-23:       AIQMTQTTSS LSASLGDRVT ISC
24-34:      SASQGIS NYLN
35-49:      WYQQKP DGTVKLLIY
50-56:      YTSSLHS
57-88:      GVPS RFSGSGSGTD YSLTISNLEP EDIATYYC
89-97:      QQ YSKLPWT
98-214:     FGGGTKLEIKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT STSPIVKSFN
RNEC
```

Figure 24E

Kabat numbering of MC3

MC-3 heavy chain protein sequence:

1-30: DVQLQESGPG LVKPSQSLSL TCTVTGYSIT
31-35: SDYAW N (35A)
36-49: WIRQ FPGNKLEWMG
50-65: YISYSGSTSY NPSLKS
66-94: RISIT RDTSKNQFFL QL **N (82A) S (82B) V (82C)** TTEDT ATYYCAR
95-102: LETWLFDY

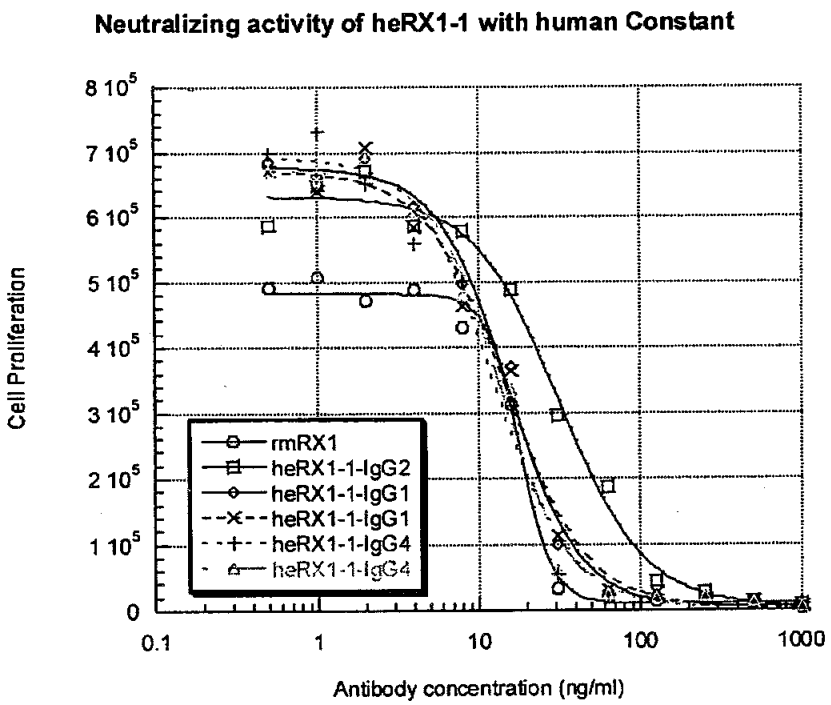
103-522: WGQG TTLTVSSAKT TPPSVYPLAP GCGDTTGSSV TLGCLVKGYF PESVTVTWNS
GSLSSSVHTF PALLQSGLYT MSSSVTVPSS TWPSQTVTCS VAHPASSTTV
DKKLEPSGPI STINPCPPCK ECHKCPAPNL EGGPSVFIFP PNIKDVLMIS
LTPKVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQTQTHRE DYNSTIRVVS
TLPIQHQDWM SGKEFKCKVN NKDLPSPIER TISKIKGLVR APQVYILPPP
AEQLSRKDVS LTCLVVGFNP GDISVEWTSN GHTEENYKDT APVLDSDGSY
FIYSKLNMKT SKWEKTDSFS CNVRHEGLKN YYLKKTISRS PGLDLDDICA
EAKDGELDGL WTTITIFISL FLLSVCYSAS VTLFKVKWIF SSVVELKQKI
SPDYRNMIGQ GA

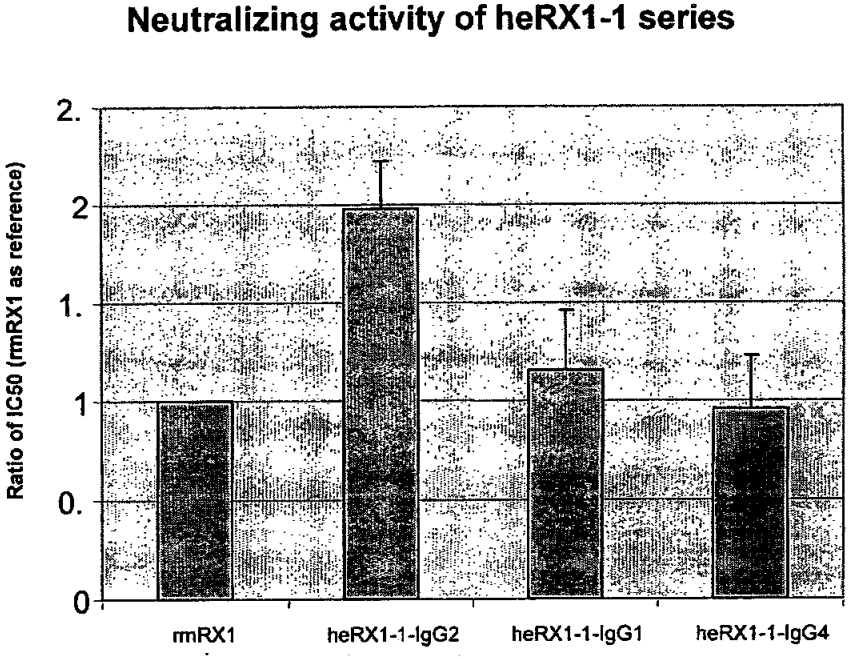
MC-3 light chain protein sequence:

1-23: DILLTQSPAI LSVSPGERVS FSC
24-34: RASQSIG TSIH
35-49: WYQQRT NGSPRLLIK
50-56: YASESIS
57-88: GIPS RFSGSGSGTD FTLSINSVES EDIADYYC
89-97: QQ SNSWPTT
98-214: FGG GTKLEIKWAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
STSPIVKSFN RNEC

Fig. 25

Measurement of Neutralizing Activity of heRX1 With Different IgG Subclass Constant Regions

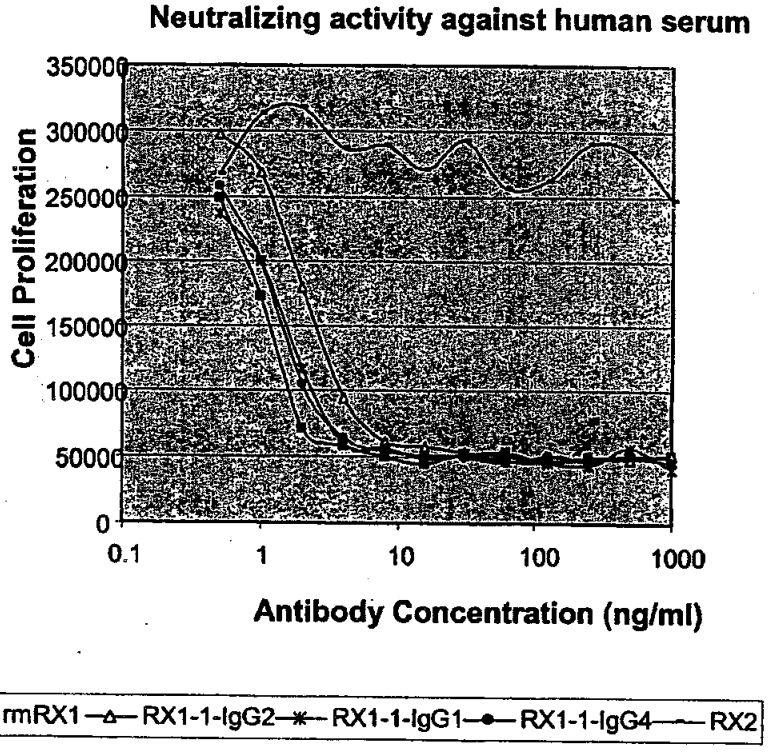




Against recombinant human MCSF

Fig. 26

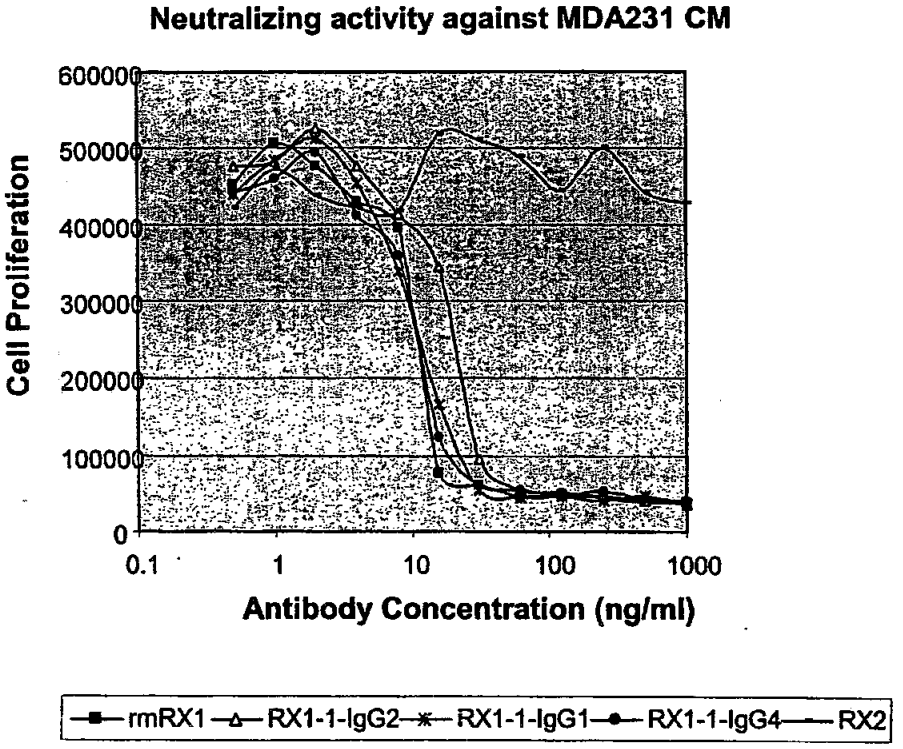
Activity of heRX1-1 With Different IgG Subclasses Against Other Forms of MCSF



Similar results observed against Cyno MCSF in serum and recombinant Cyno MCSF

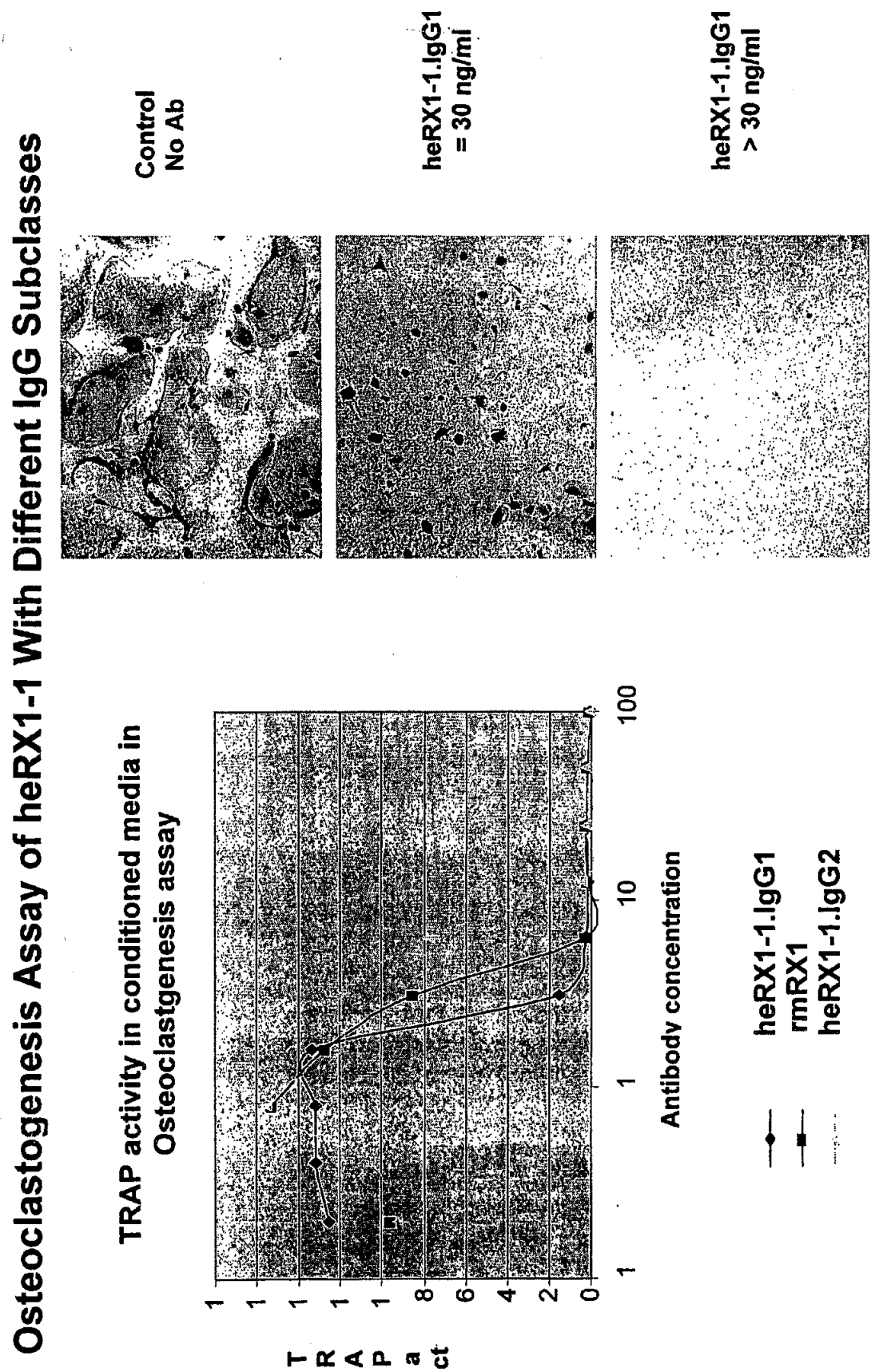
Fig. 27

Activity of heRX1-1 With Different IgG Subclasses Against Other Forms of MCSF



Similar results observed against Cyno MCSF in serum and recombinant Cyno MCSF

Fig. 28


Osteoclastogenesis Assay of heRX1-1 With Different IgG Subclasses
TRAP activity in conditioned media in Osteoclastgenesis assay
TRAP act
1
1
1
1
1
8
6
4
2
0
1
1
10
100
Antibody concentration
heRX1-1.IgG1
rmRX1
heRX1-1.IgG2
Control No Ab
heRX1-1.IgG1 = 30 ng/ml
heRX1-1.IgG1 > 30 ng/ml

Amino Acids

MGWSCIILFLVATATGVHS

DVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWNWIRQFPGKKLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSL
QLNSVTAADTATYYCASFDYAHAMDYWGQGTTVTVSS

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPGK•

Nucleotides

ATGGGATGGAGTTGCATTATACTTTTCCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACTTCAAGAATC
TGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCT
CCTACAATCCTTCTCTGAAATCACGCATCACAATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA
CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGT
GGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGG
GGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
AGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
AGAGCCTCTCCCTGTCCCCGGGTAAATGA

Amino Acids

MGWSCIILFLVATATGVHS

QVQLQESGPGLVKPSQTLSLTCTVSDYSITSDYAWNWIRQFPGKGLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSL
QLNSVTAADTAVYYCASFDYAHAMDYWGQGTTVTVSS

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPGK•

Nucleotides

ATGGGTTGGTCTTGCATCATTCTCTTTCTCGTCGCTACCGCAACTGGTGTACACTCCCAAGTTCAACTTCAAGAATCA
GGCCCCGGACTCGTTAAACCCTCTCAAACTCTCTCTCTTACTTGCACTGTATCCGATTACTCTATTACTTCAGACTAC
GCTTGGAACTGGATCAGACAATTTCCCGGAAAAGGACTCGAATGGATGGGATATATCTCTTACTCTGGCTCAACCT
CTTACAACCCCTCTCTCAAATCTCGAATAACAATCTCACGCGATACTTCTAAAAATCAATTCTCACTTCAACTTAAC
TCCGTTACTGCCGCCGACACTGCCGTTTACTACTGTGCTTCCTTCGATTACGCCCACGCTATGGATTATTGGGGACA
AGGAACTACCGTCACTGTCAGCTCAGCCAGCACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGC
ACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT
CAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGG
TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGG
GGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG
GAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGG
ACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA
GAAGAGCCTCTCCCTGTCCCCGGGTAAATGA

Fig. 30

HeRX-1 Low Risk Heavy Chain Gamma-4

Amino Acids

MGWSCIILFLVATATGVHSDVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWNWIRQFPGKKLEWMGYISYSGSTSYN
PSLKSRITISRDTSKNQFSLQLNSVTAADTATYYCASFDYAHAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKY
GPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Nucleotides

cDNA

ATGGGATGGAGTTGCATTATACTTTTCCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACTTCAAGAATC
TGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCT
CCTACAATCCTTCTCTGAAATCACGCATCACAATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA
CCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGT
GGACAAGAGAGTTGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCA
GTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGA
CGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAC
GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTG
ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC
TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCA
GGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCTGGGTAAATGA

Genomic

ATGGGATGGAGTTGCATTATACTTTTCCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACTTCAAGAATC
TGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCT
CCTACAATCCTTCTCTGAAATCACGCATCACAATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA
CCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGT
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GACCACCCCACTCATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCGGGCAGCCACAGGCTGGATGC
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GCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTG
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CCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTG
ACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCC
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GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGT
CTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGG
GCCACATGGACAGAGGTCAGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGG
GCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC
CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA
CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGG
TGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCT
CCCTGTCTCTGGGTAAATGA