

FIG. 1A

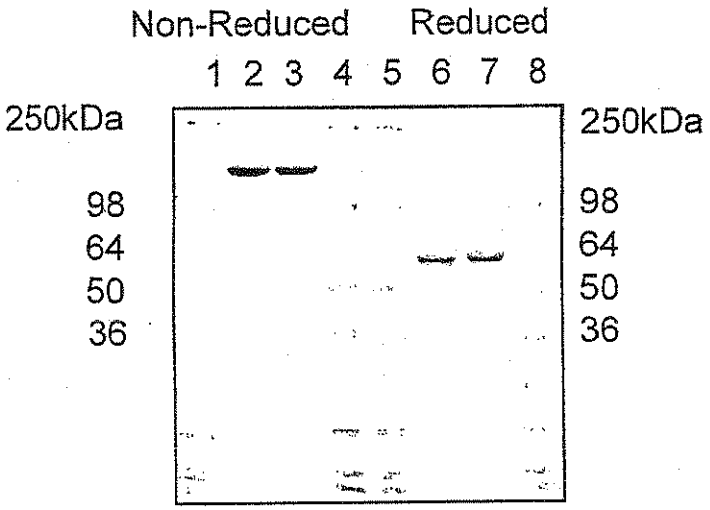


FIG. 1B

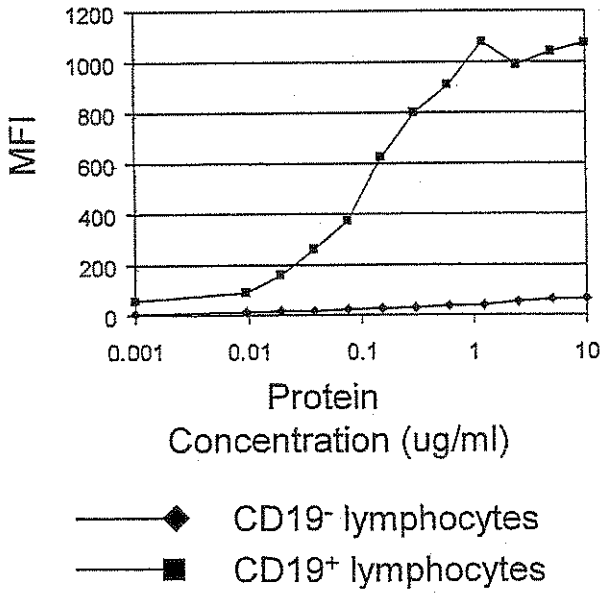


FIG. 1C

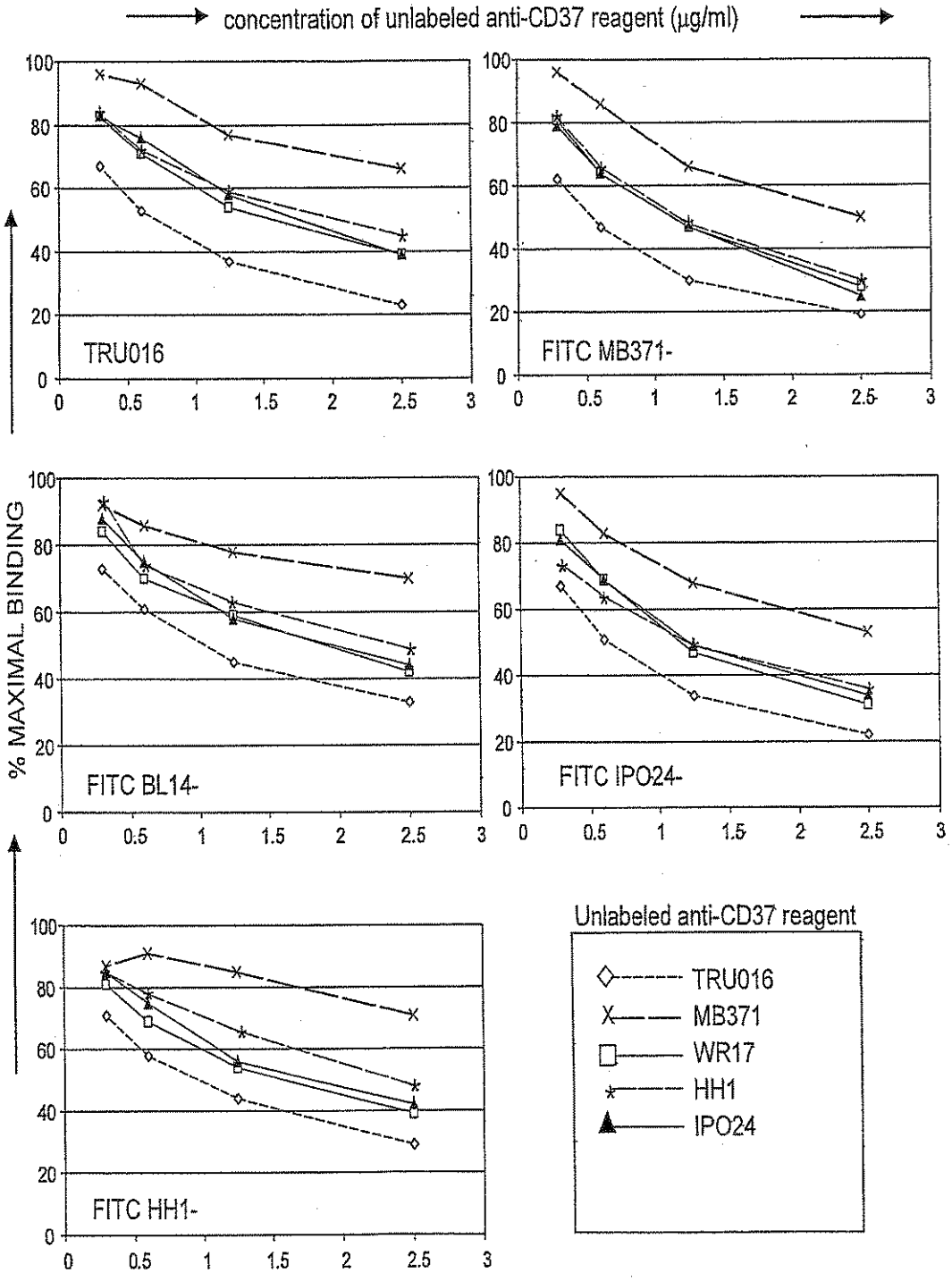

concentration of unlabeled anti-CD37 reagent (µg/ml)
% MAXIMAL BINDING
TRU016
FITC MB371-
FITC BL14-
FITC IPO24-
FITC HH1-
Unlabeled anti-CD37 reagent
TRU016
MB371
WR17
HH1
IPO24

FIG. 2

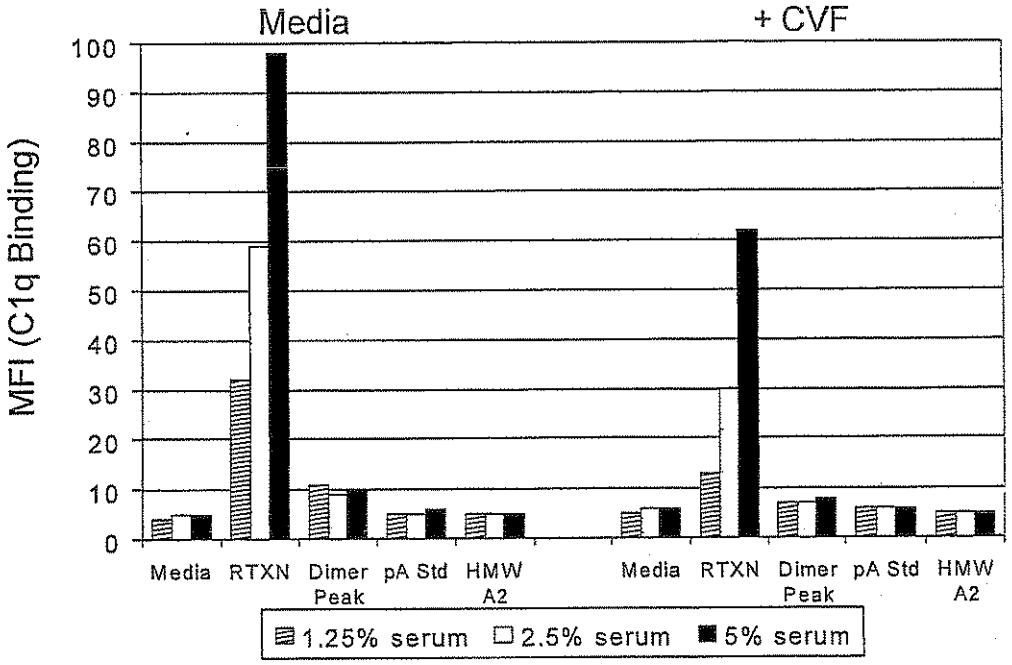

Media
+ CVF
MFI (C1q Binding)
100
90
80
70
60
50
40
30
20
10
0
Media
RTXN
Dimer Peak
pA Std
HMW A2
Media
RTXN
Dimer Peak
pA Std
HMW A2
1.25% serum
2.5% serum
5% serum

FIG. 3A

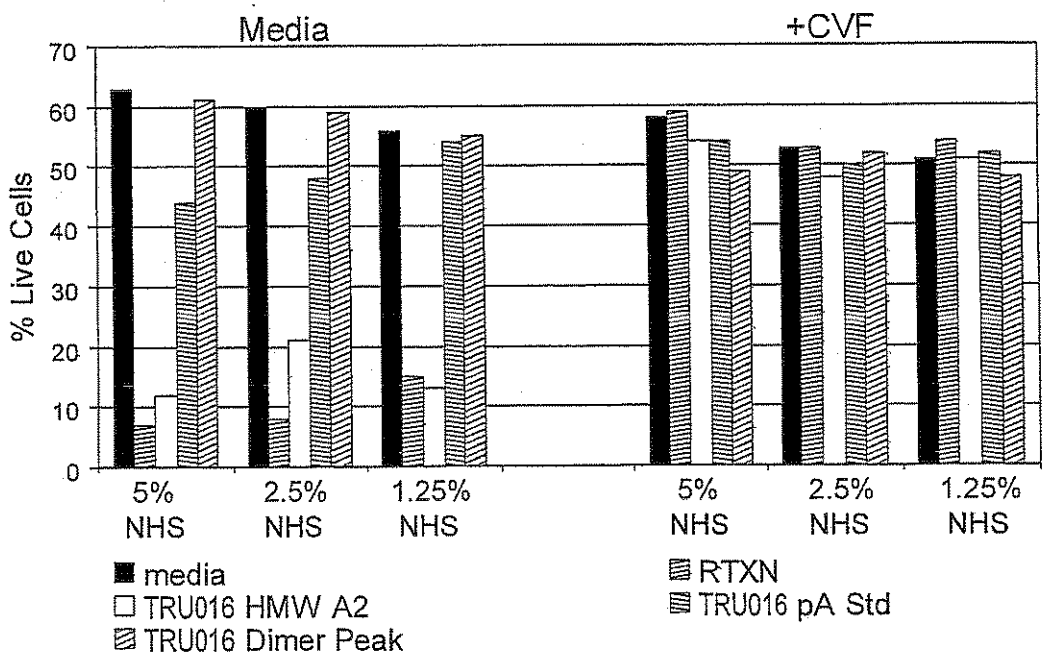

Media
+CVF
% Live Cells
70
60
50
40
30
20
10
0
5% NHS
2.5% NHS
1.25% NHS
5% NHS
2.5% NHS
1.25% NHS
media
TRU016 HMW A2
TRU016 Dimer Peak
RTXN
TRU016 pA Std

FIG. 3B

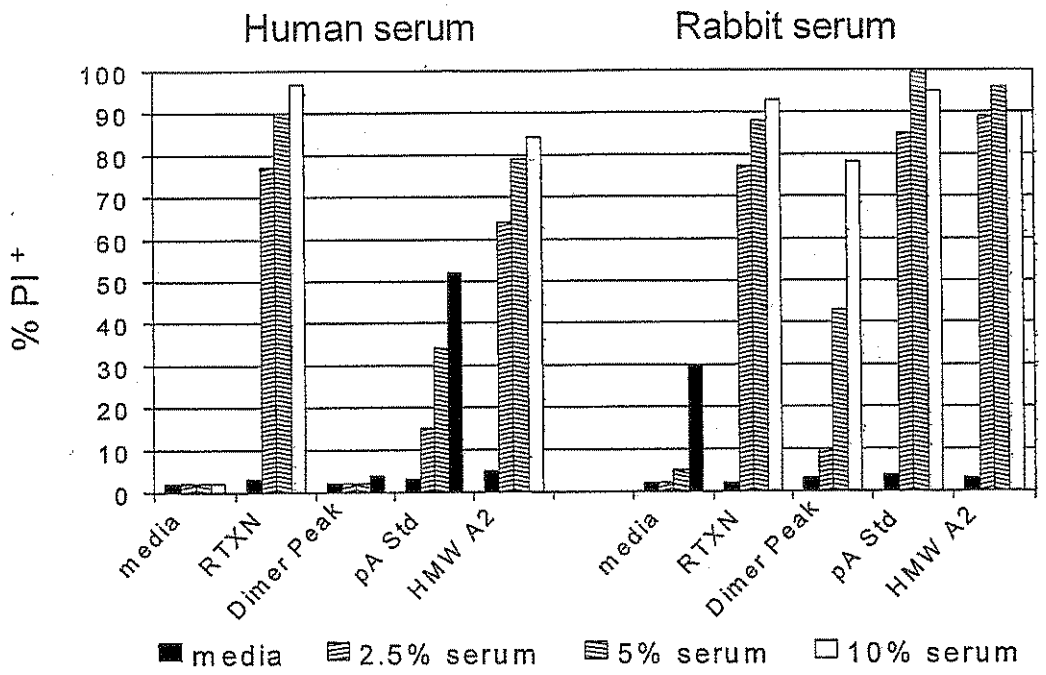

Human serum
Rabbit serum
% PI +
100
90
80
70
60
50
40
30
20
10
0
media
RTXN
Dimer Peak
pA Std
HMW A2
media
RTXN
Dimer Peak
pA Std
HMW A2
media
2.5% serum
5% serum
10% serum

FIG. 3C

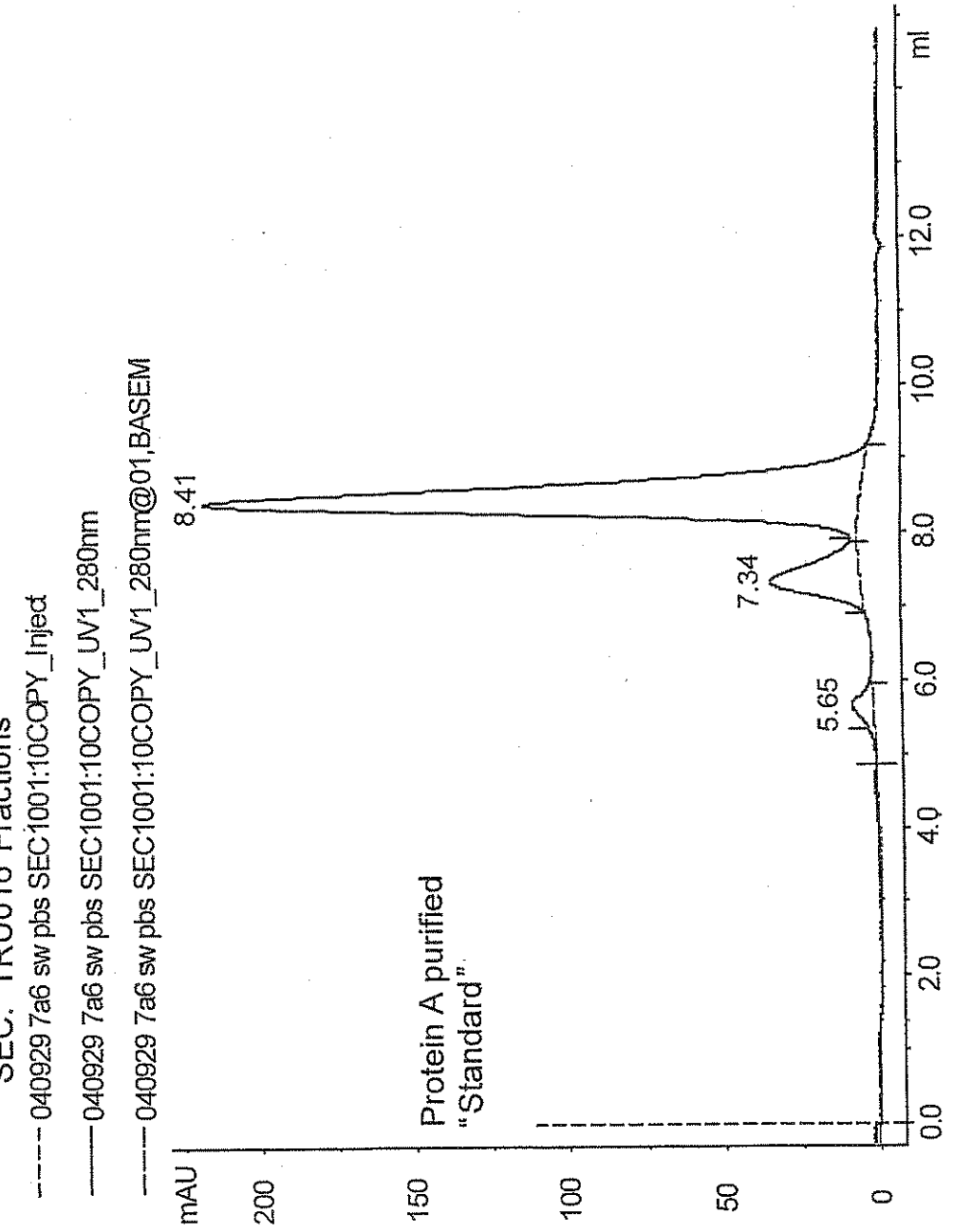

SEC: TRU016 Fractions
040929 7a6 sw pbs SEC1001:10COPY_Inject
040929 7a6 sw pbs SEC1001:10COPY_UV1_280nm
040929 7a6 sw pbs SEC1001:10COPY_UV1_280nm@01,BASEM
mAU
200
150
100
50
0
Protein A purified
"Standard"
8.41
7.34
5.65
0.0
2.0
4.0
6.0
8.0
10.0
12.0
ml

FIG. 4A

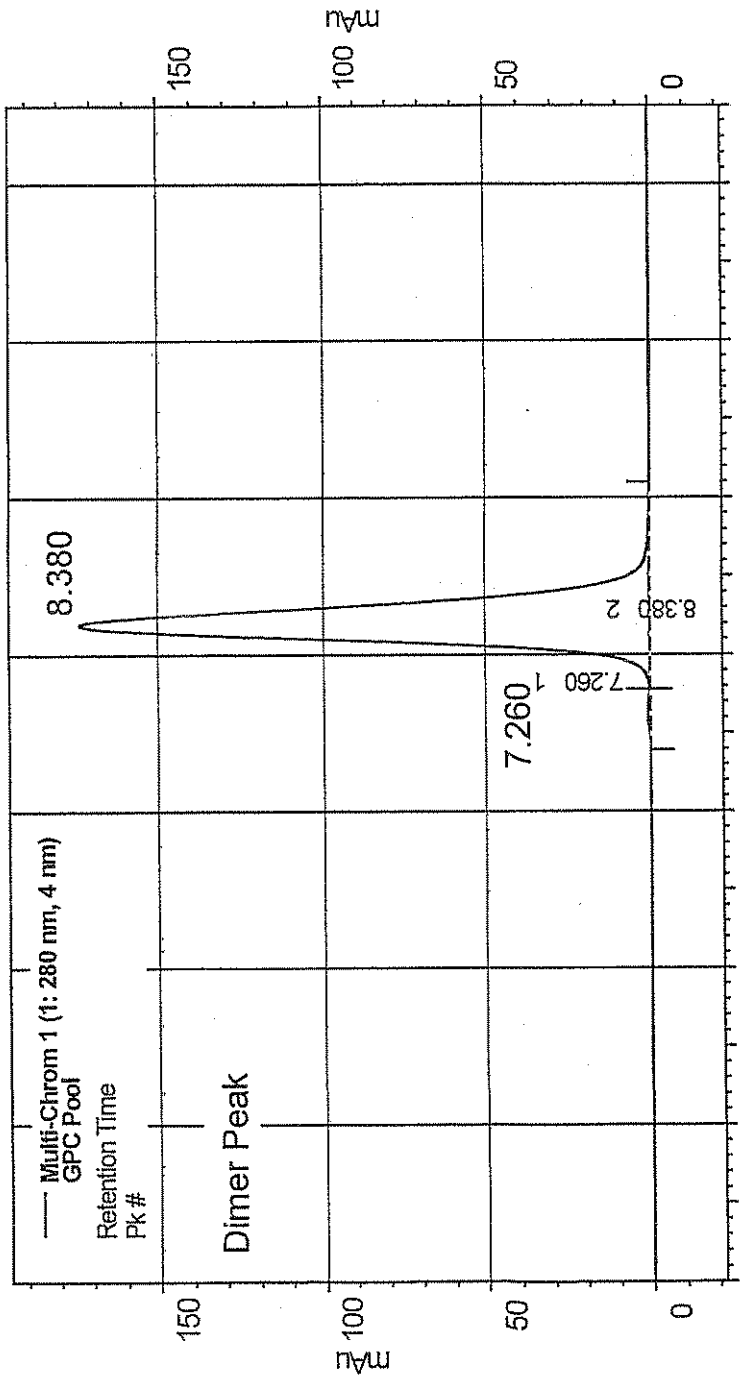

mAu
150
100
50
0
Multi-Chrom 1 (1: 280 nm, 4 nm)
GPC Pool
Retention Time
Pk #
Dimer Peak
8.380
7.260
8.380 2
7.260 1

FIG. 4B

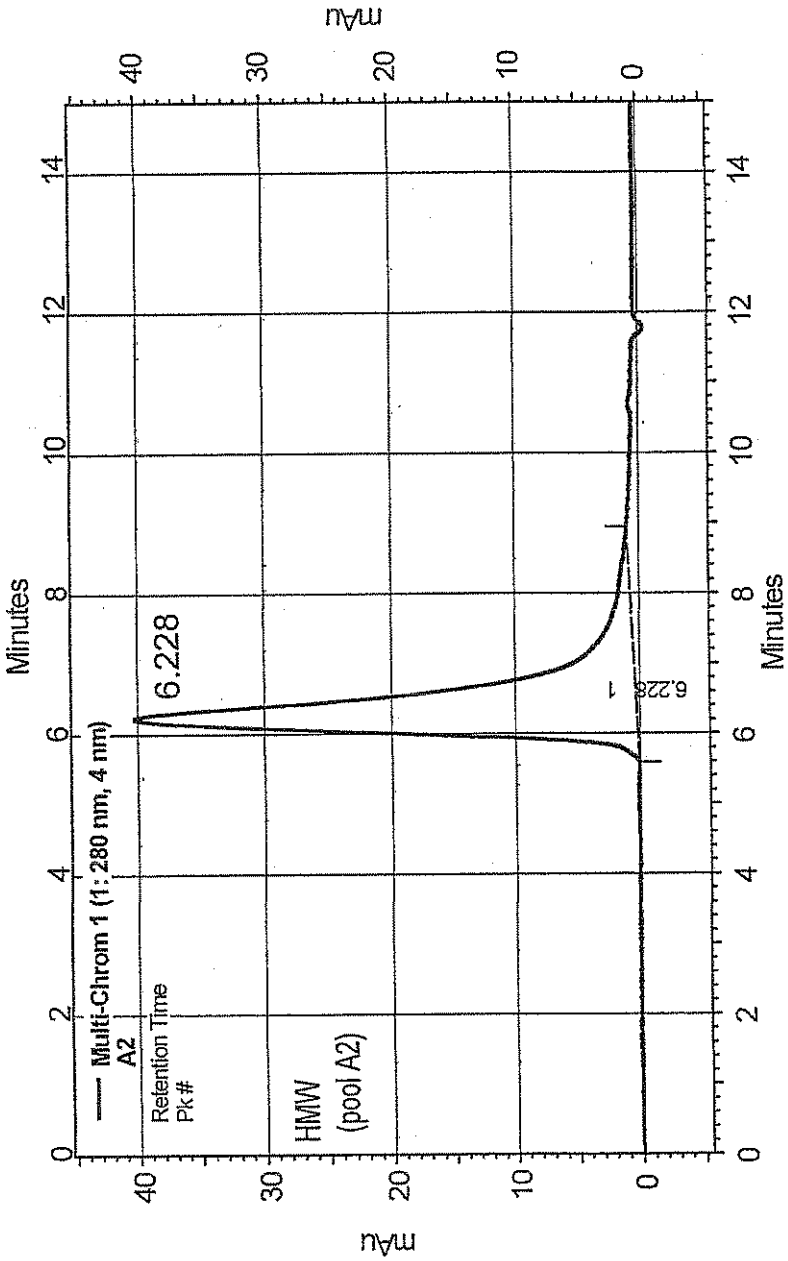
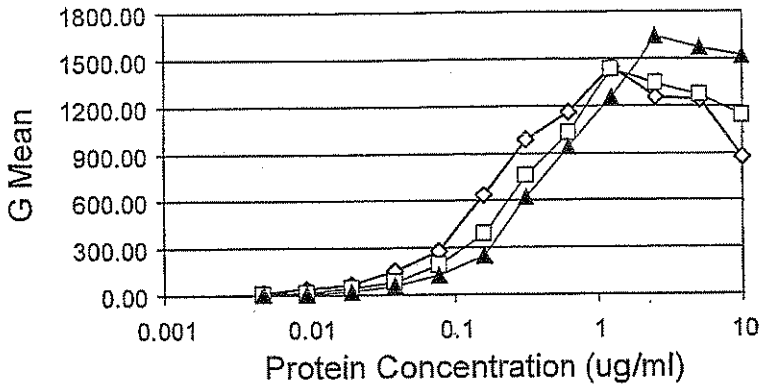
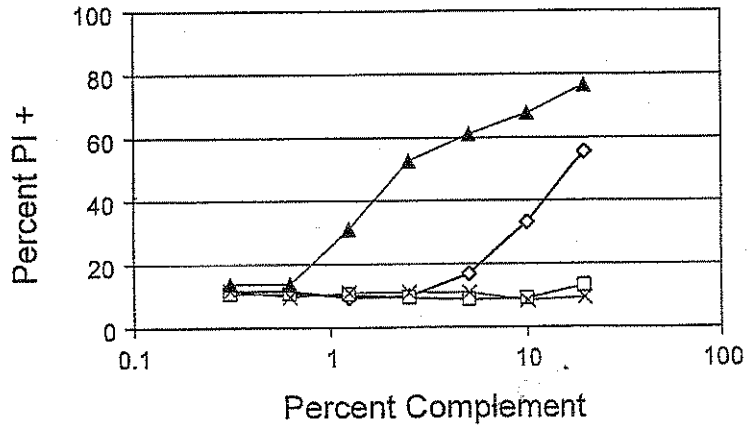

mAu
40
30
20
10
0
Minutes
0
2
4
6
8
10
12
14
Multi-Chrom 1 (1: 280 nm, 4 nm)
A2
Retention Time
Pk #
6.228
HMW
(pool A2)
6.228
1

FIG. 4C


1800.00
1500.00
1200.00
900.00
600.00
300.00
0.00
G Mean
0.001
0.01
0.1
1
10
Protein Concentration (ug/ml)


100
80
60
40
20
0
Percent PI +
0.1
1
10
100
Percent Complement

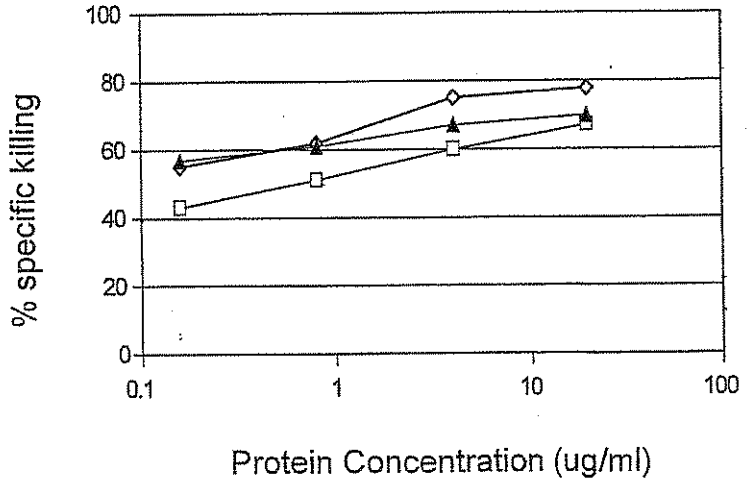

100
80
60
40
20
0
% specific killing
0.1
1
10
100
Protein Concentration (ug/ml)
TRU016 protein A standard (pA std)
TRU016 Dimer Peak
TRU016 HMW A2 (agg)
Media

FIG. 5

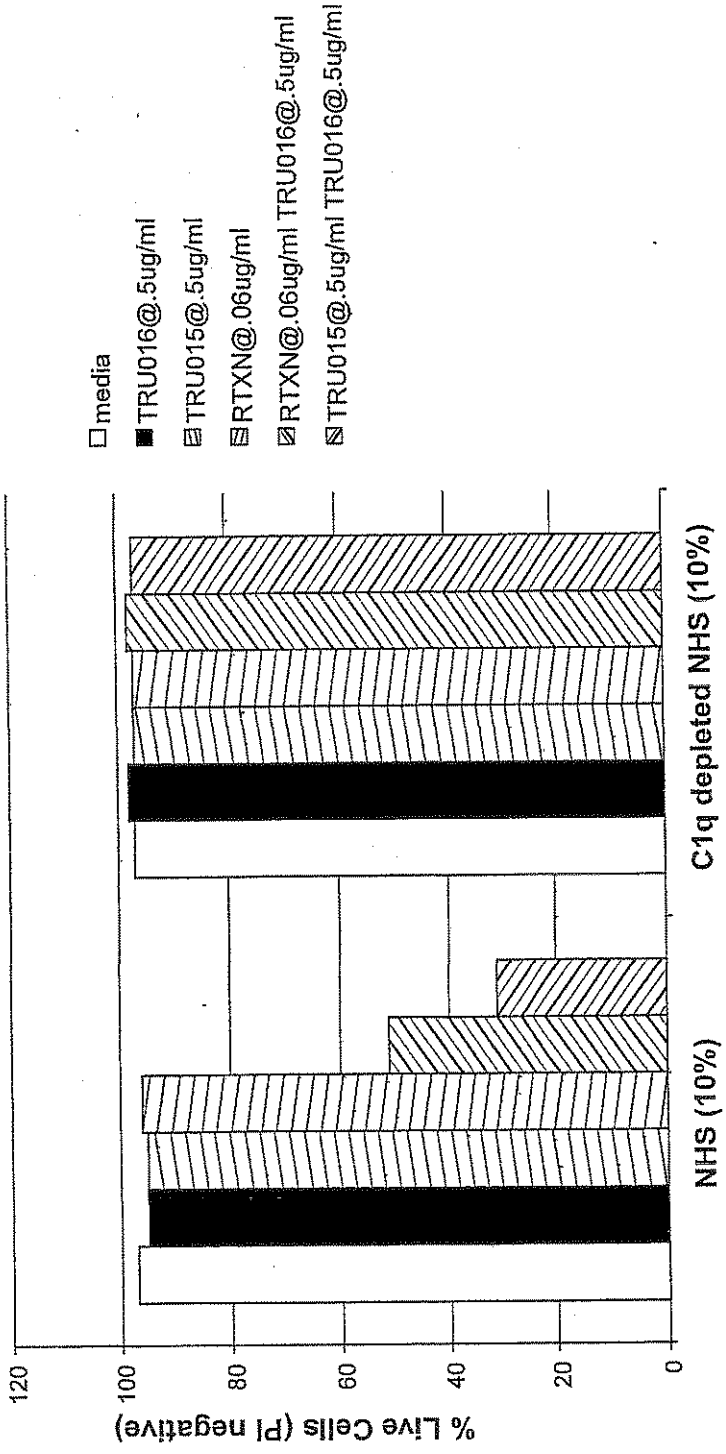

media
TRU016@.5ug/ml
TRU015@.5ug/ml
RTXN@.06ug/ml
RTXN@.06ug/ml TRU016@.5ug/ml
TRU015@.5ug/ml TRU016@.5ug/ml
% Live Cells (PI negative)
120
100
80
60
40
20
0
NHS (10%)
C1q depleted NHS (10%)

FIG. 6

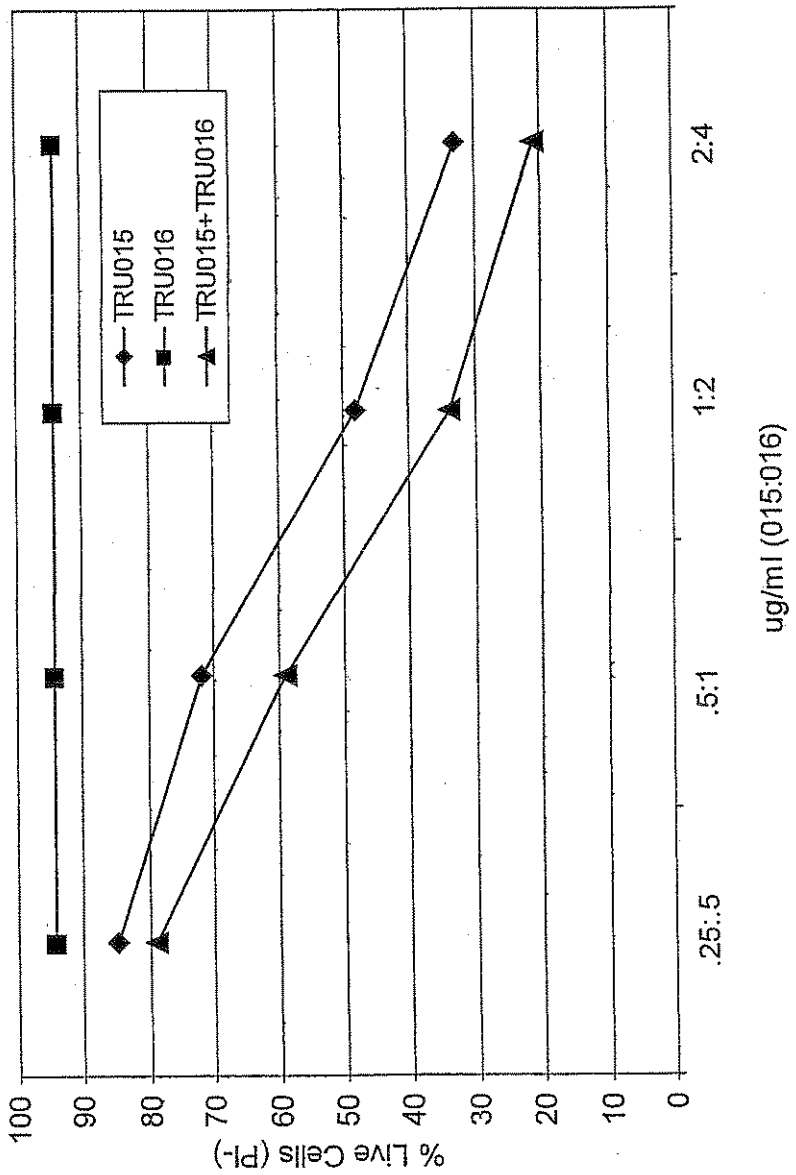

% Live Cells (PI-)
100
90
80
70
60
50
40
30
20
10
0
TRU015
TRU016
TRU015+TRU016
.25:.5
.5:1
1:2
2:4
ug/ml (015:016)

FIG. 7

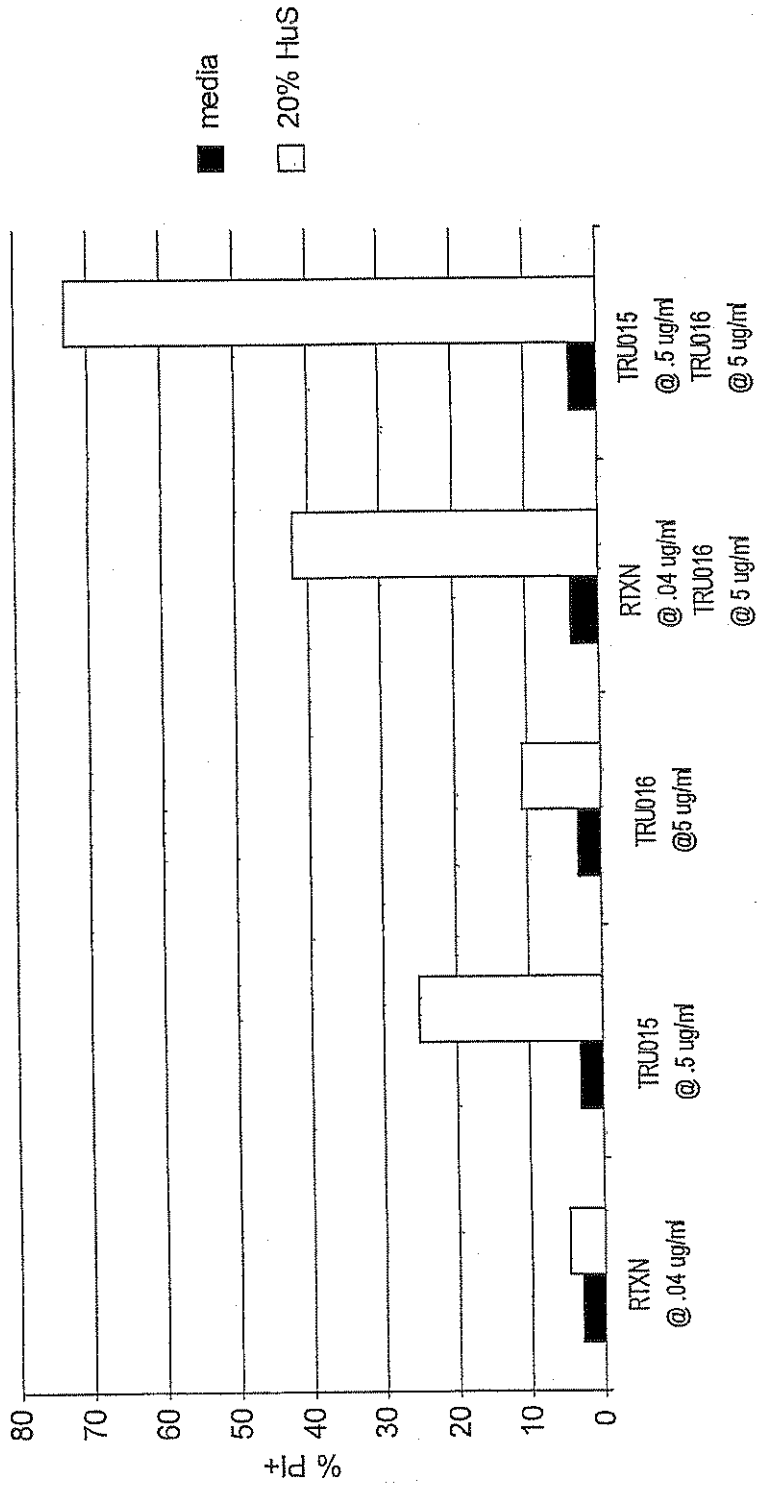

media
20% HuS
% PI+
80
70
60
50
40
30
20
10
0
RTXN @ .04 ug/ml
TRU015 @ .5 ug/ml
TRU016 @5 ug/ml
RTXN @ .04 ug/ml TRU016 @ 5 ug/ml
TRU015 @ .5 ug/ml TRU016 @ 5 ug/ml

FIG. 8

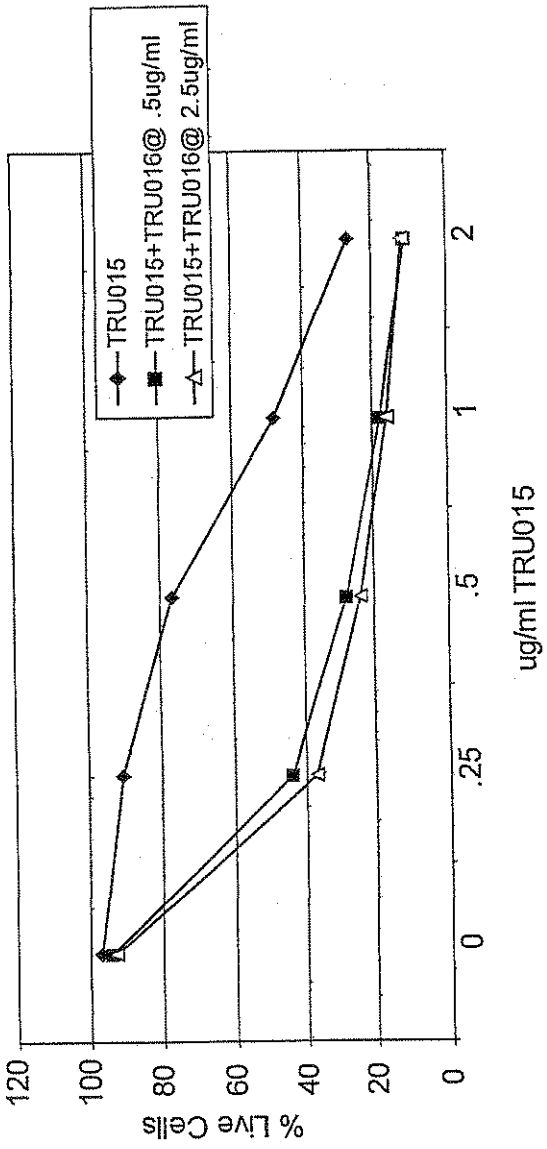

TRU015
TRU015+TRU016@ .5ug/ml
TRU015+TRU016@ 2.5ug/ml
% Live Cells
120
100
80
60
40
20
0
0
.25
.5
1
2
ug/ml TRU015

FIG. 9

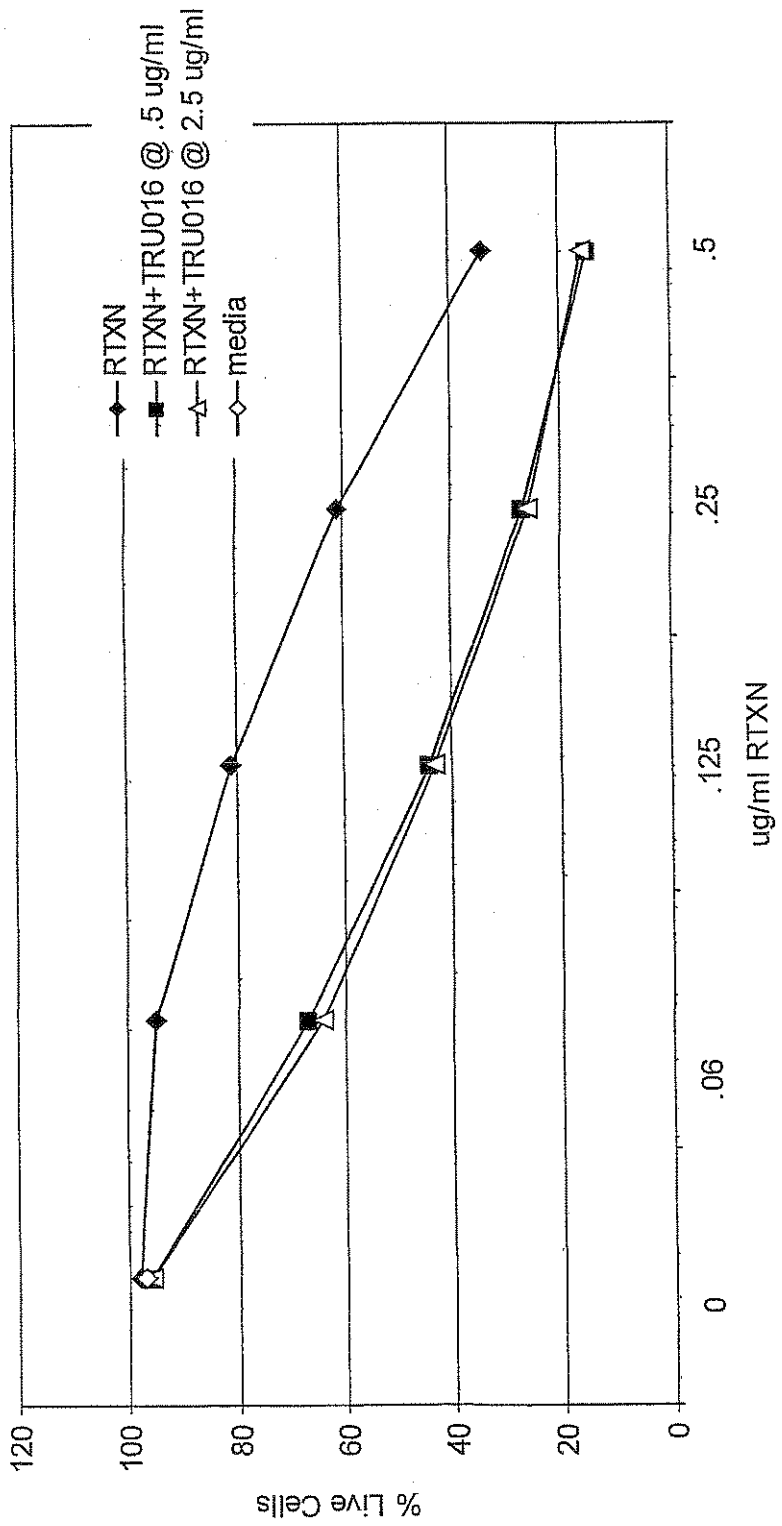

RTXN
RTXN+TRU016 @ .5 ug/ml
RTXN+TRU016 @ 2.5 ug/ml
media
% Live Cells
120
100
80
60
40
20
0
0
.06
.125
.25
.5
ug/ml RTXN

FIG. 10

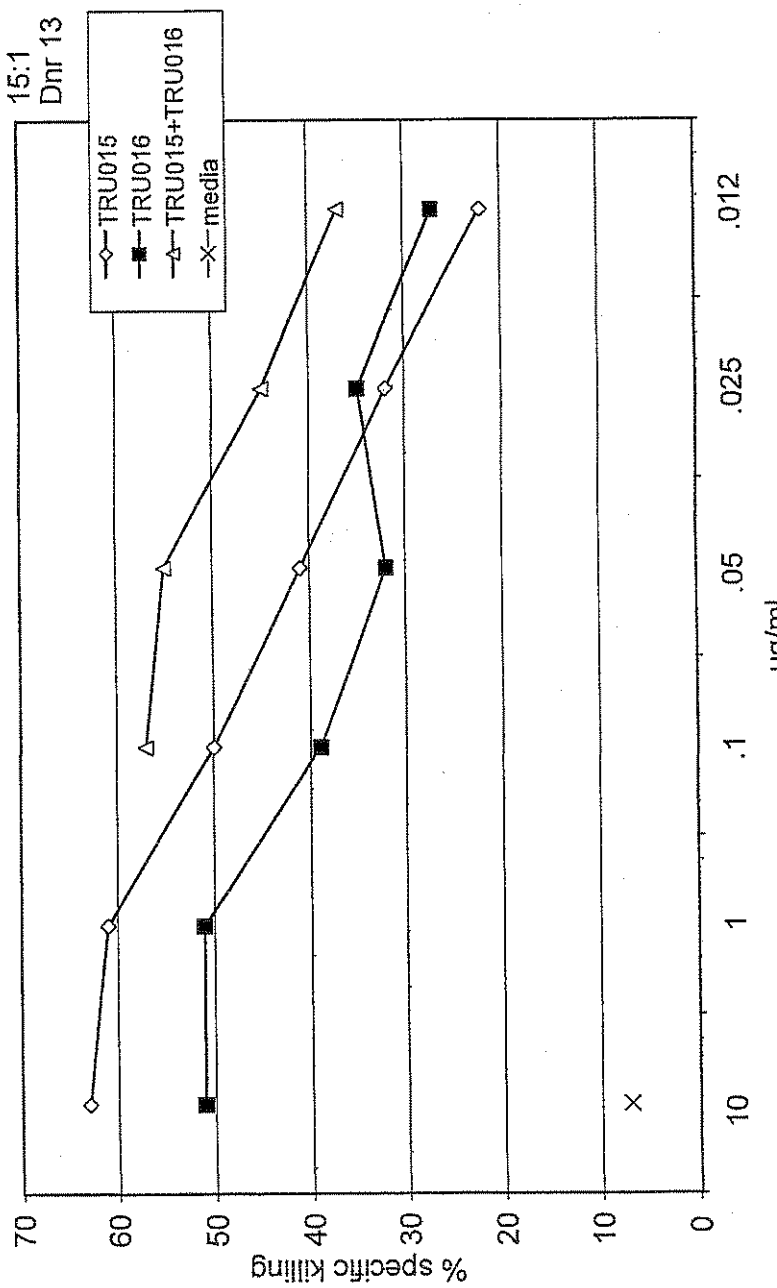

15:1
Dnr 13
TRU015
TRU016
TRU015+TRU016
media
% specific killing
70
60
50
40
30
20
10
0
10
1
.1
.05
.025
.012
ug/ml

FIG. 11

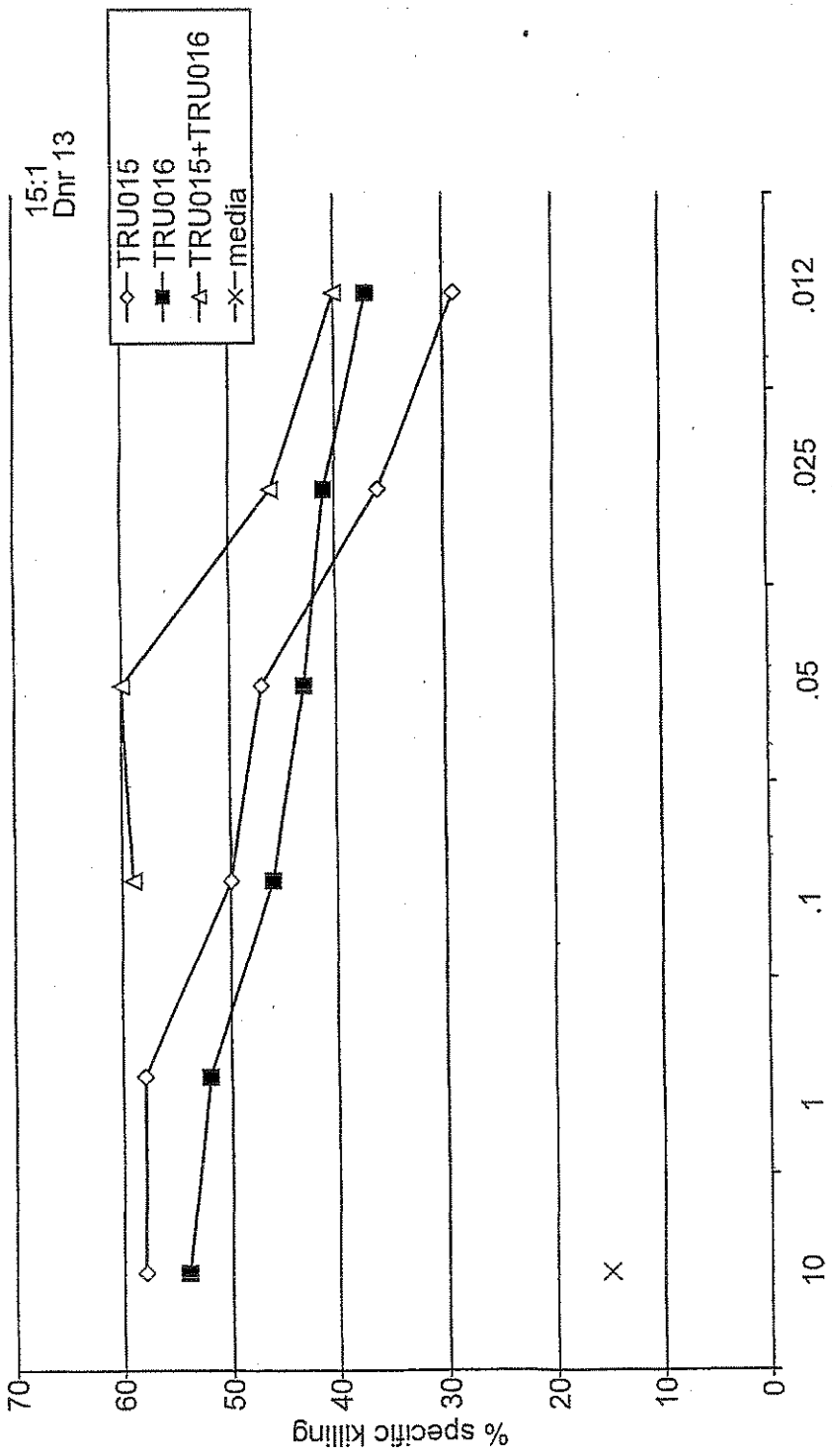

15:1
Dnr 13
TRU015
TRU016
TRU015+TRU016
media
% specific killing
70
60
50
40
30
20
10
0
10
1
.1
.05
.025
.012
ug/ml

FIG. 12

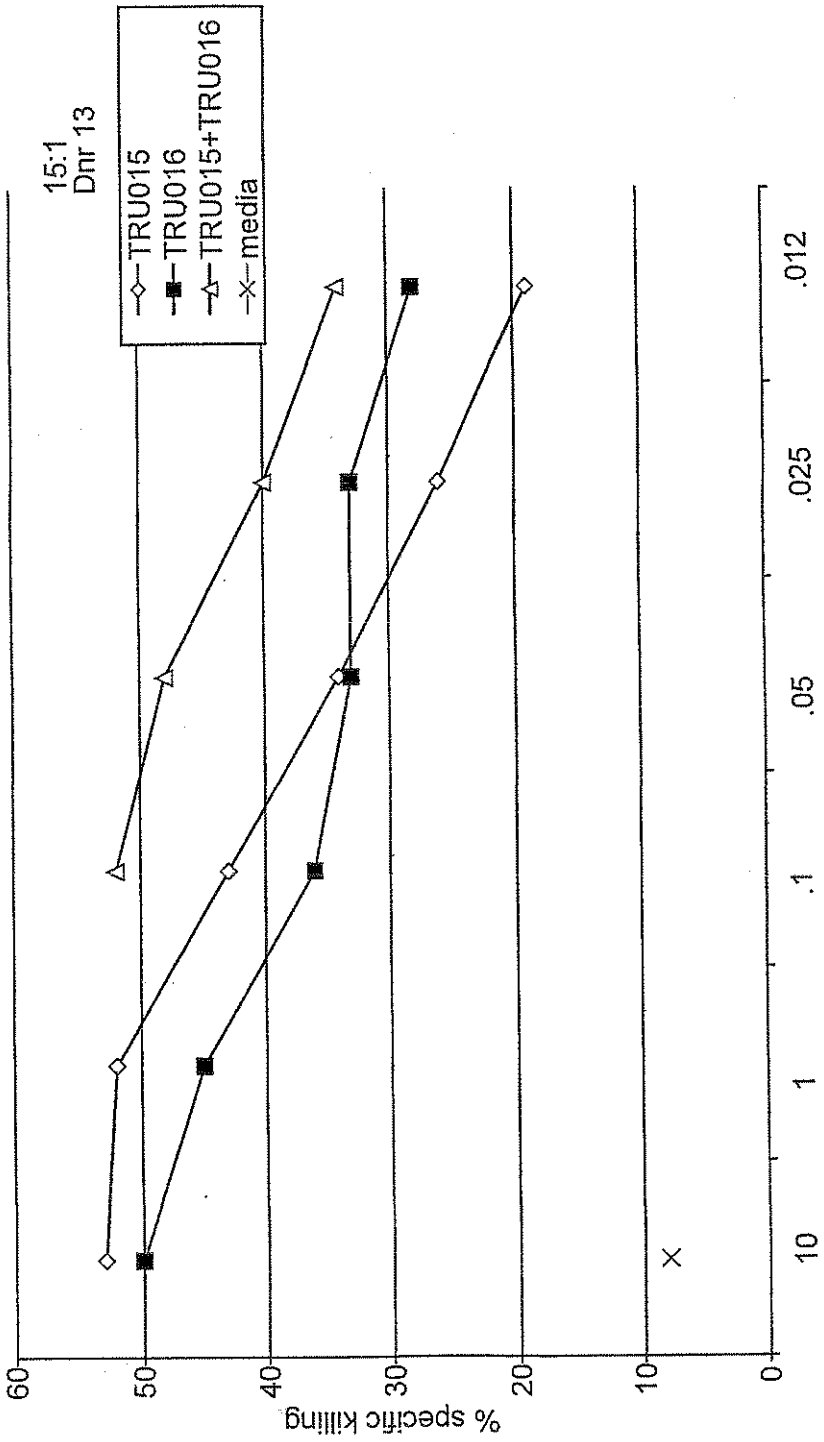

15:1
Dnr 13
TRU015
TRU016
TRU015+TRU016
media
% specific killing
60
50
40
30
20
10
0
10
1
.1
.05
.025
.012
ug/ml

FIG. 13

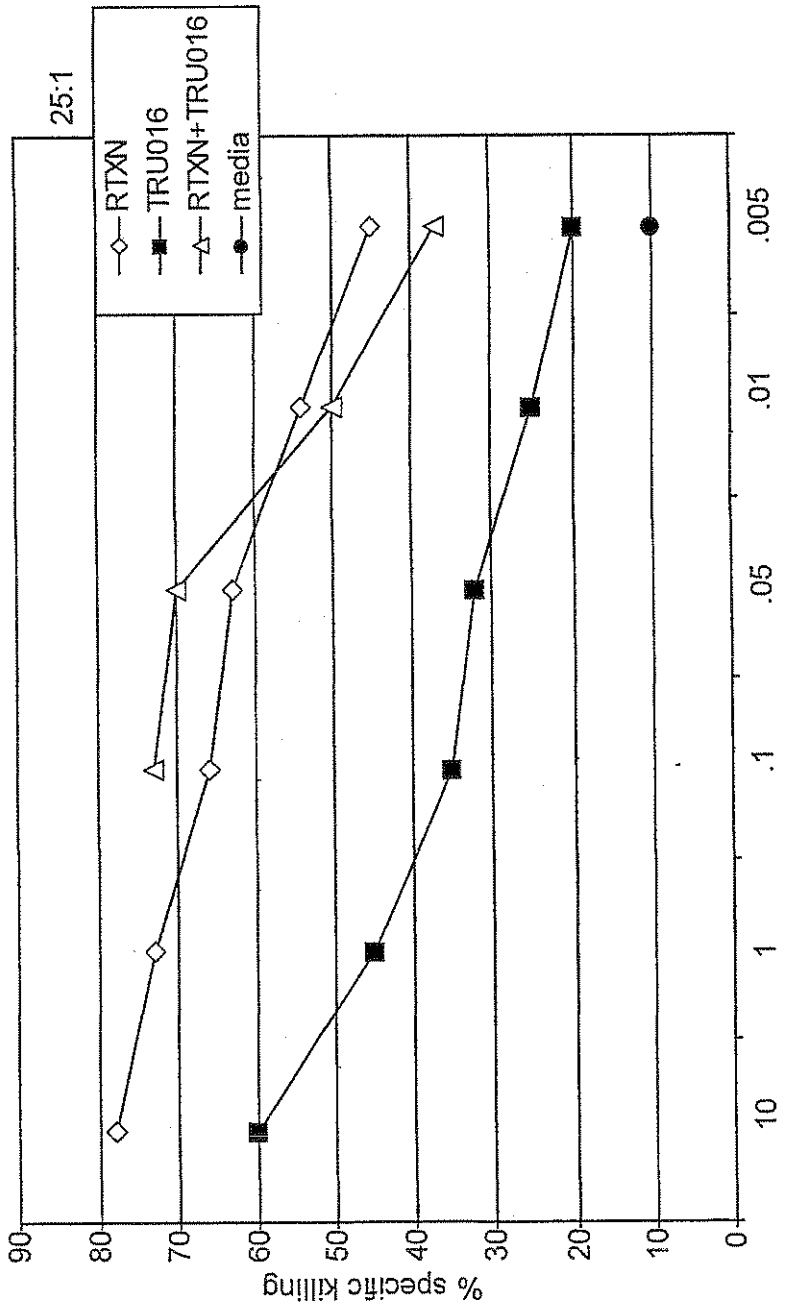

25:1
RTXN
TRU016
RTXN+TRU016
media
% specific killing
90
80
70
60
50
40
30
20
10
0
10
1
.1
.05
.01
.005
ug/ml

FIG. 14

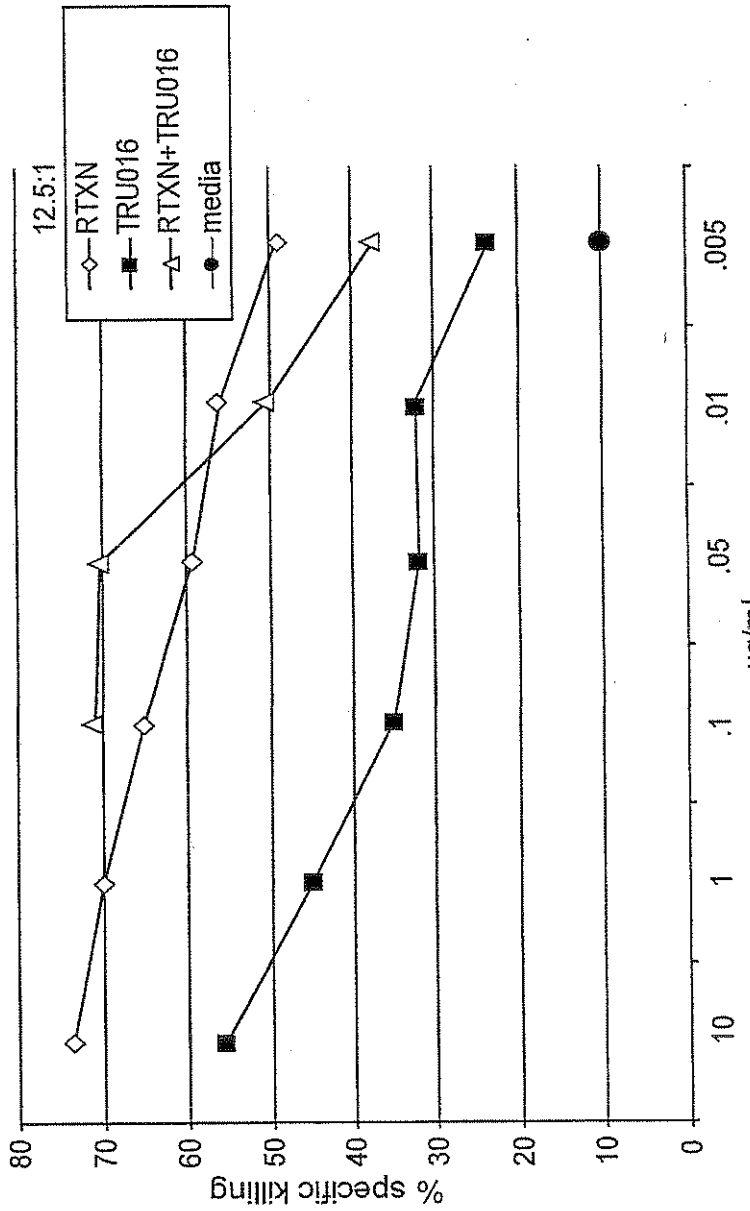

12.5:1
RTXN
TRU016
RTXN+TRU016
media
% specific killing
0
10
20
30
40
50
60
70
80
10
1
.1
.05
.01
.005
ug/ml

FIG. 15

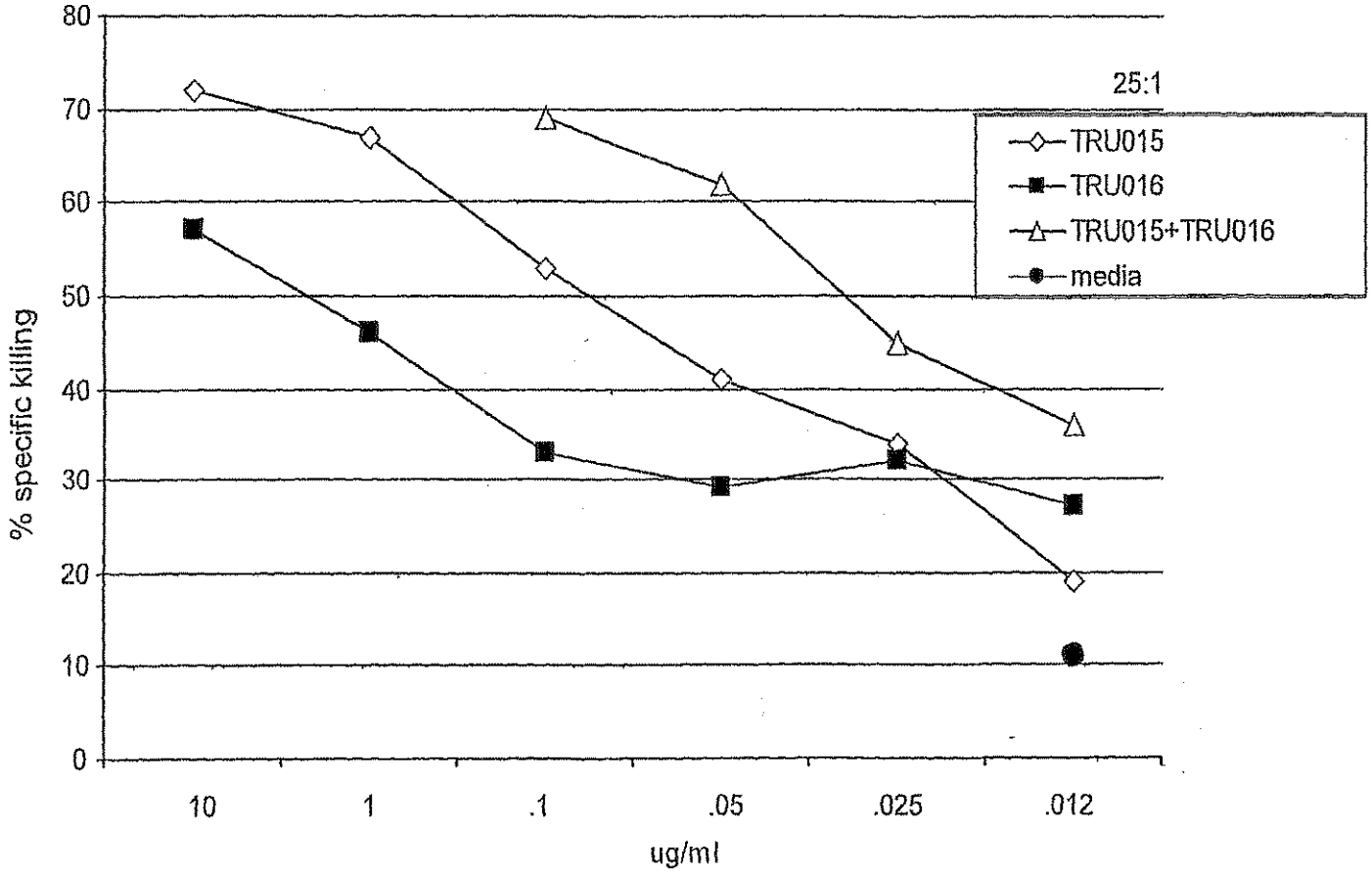

80
70
60
50
40
30
20
10
0
% specific killing
25:1
TRU015
TRU016
TRU015+TRU016
media
10
1
.1
.05
.025
.012
ug/ml

FIG. 16

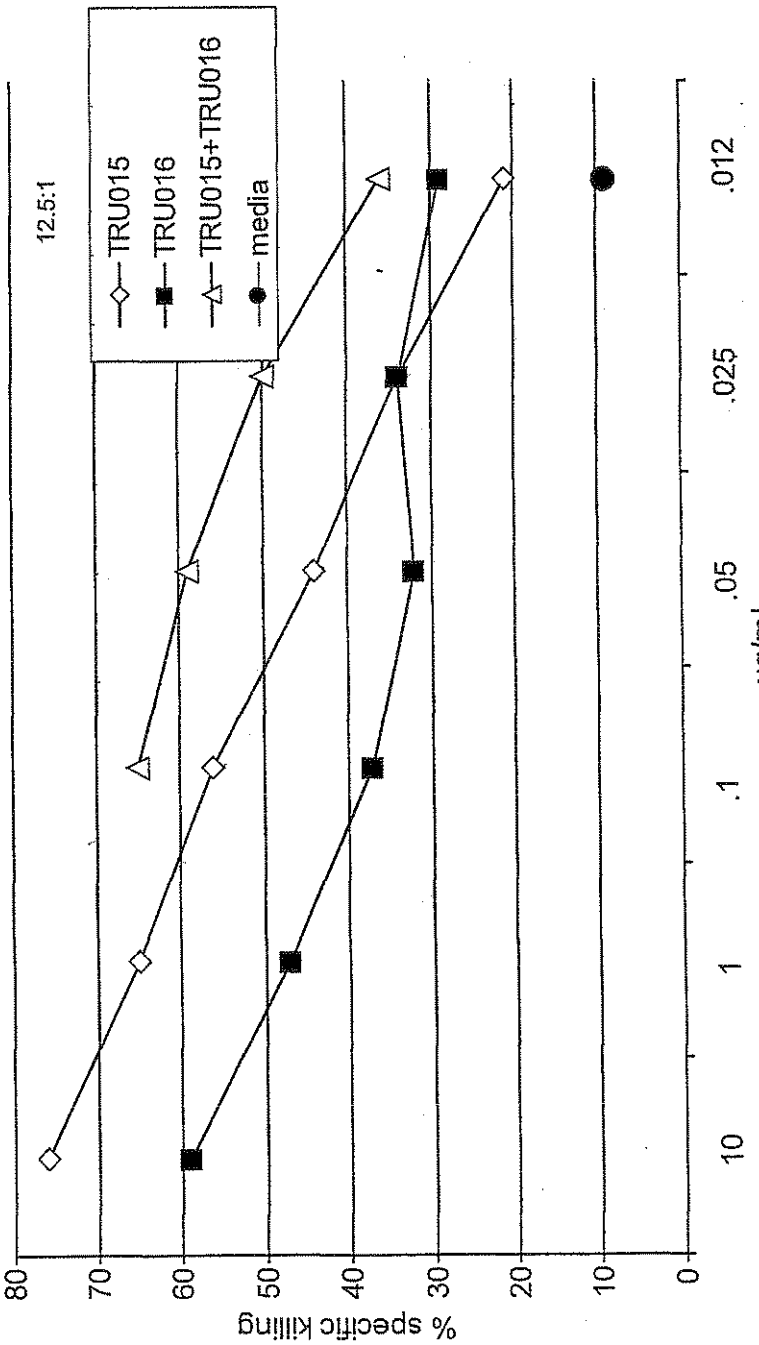

12.5:1
TRU015
TRU016
TRU015+TRU016
media
% specific killing
0
10
20
30
40
50
60
70
80
10
1
.1
.05
.025
.012
ug/ml

FIG. 17

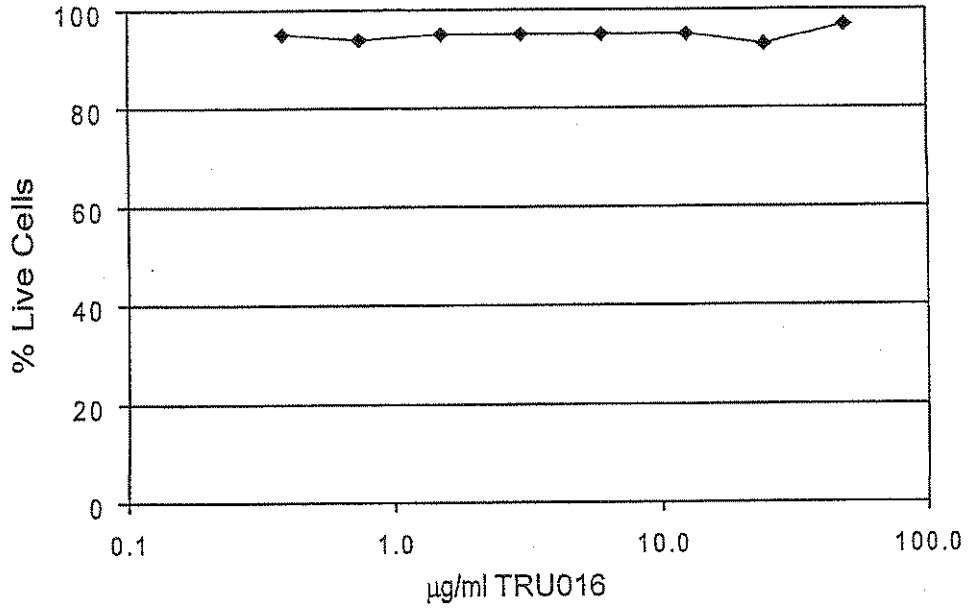


FIG. 18A

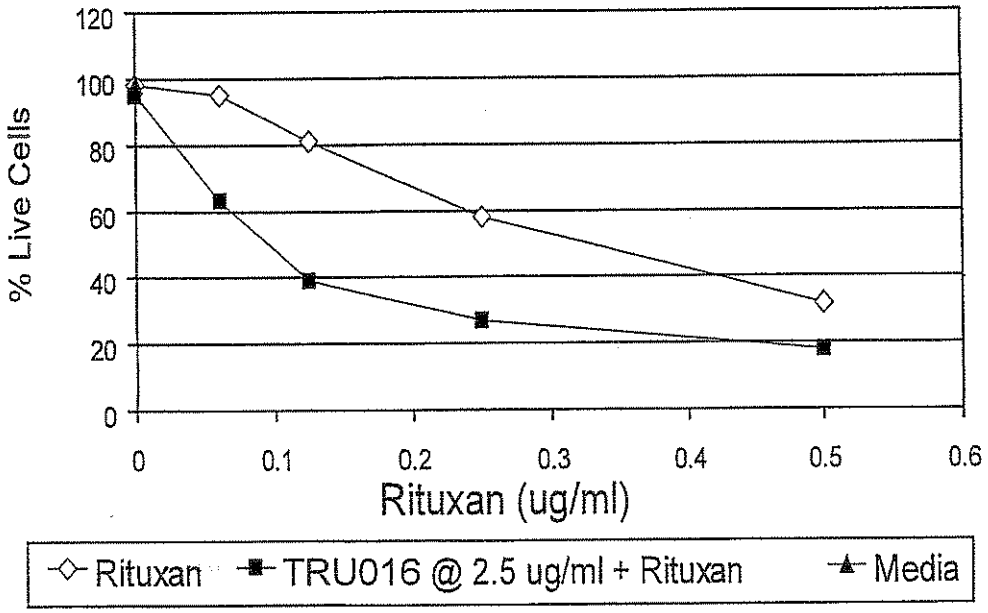


FIG. 18B

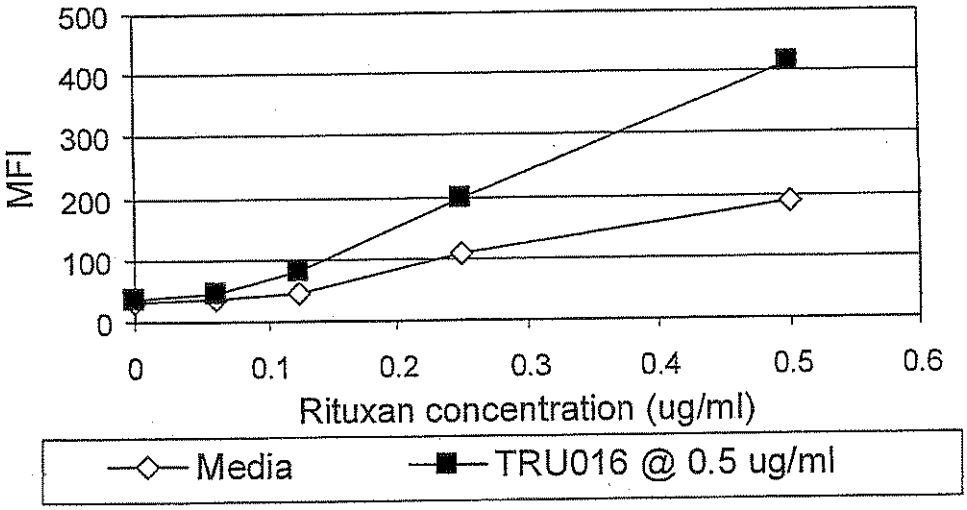


FIG. 18C

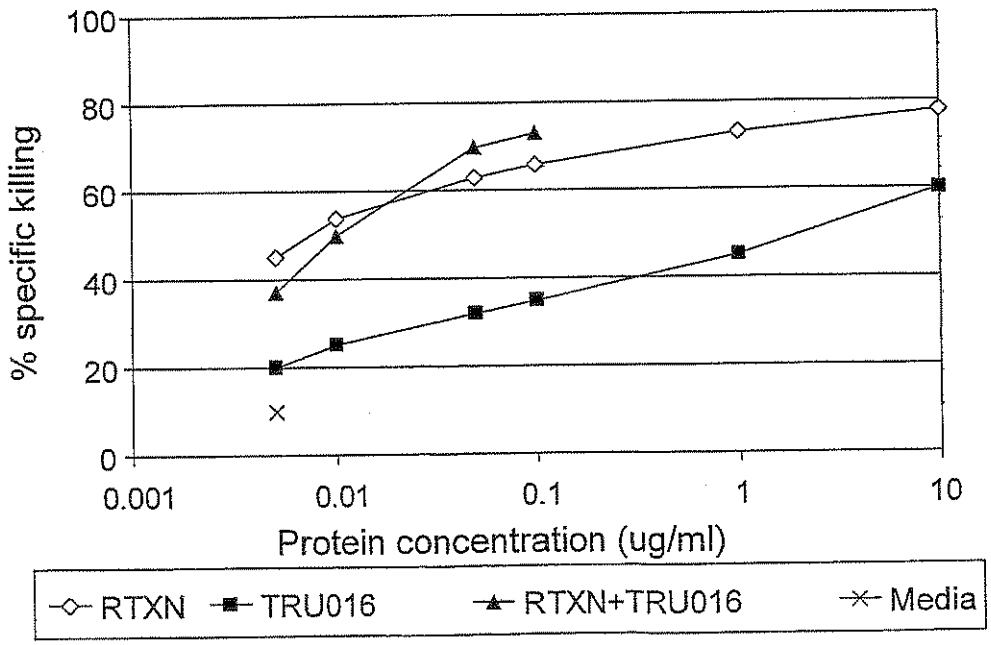


FIG. 18D

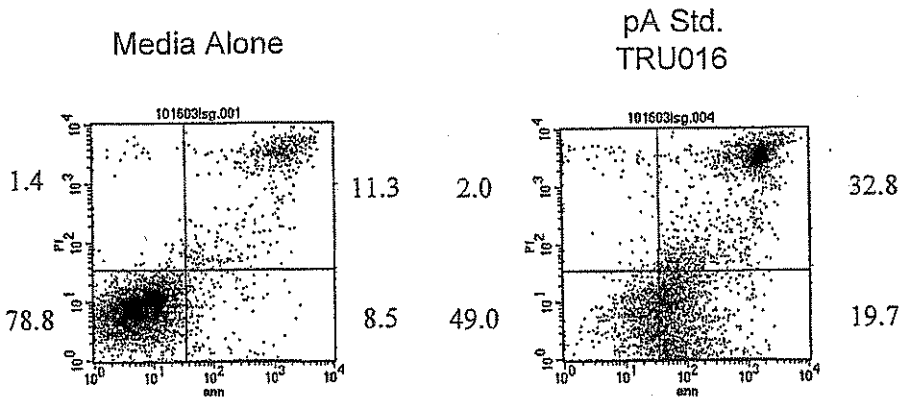


FIG. 19A

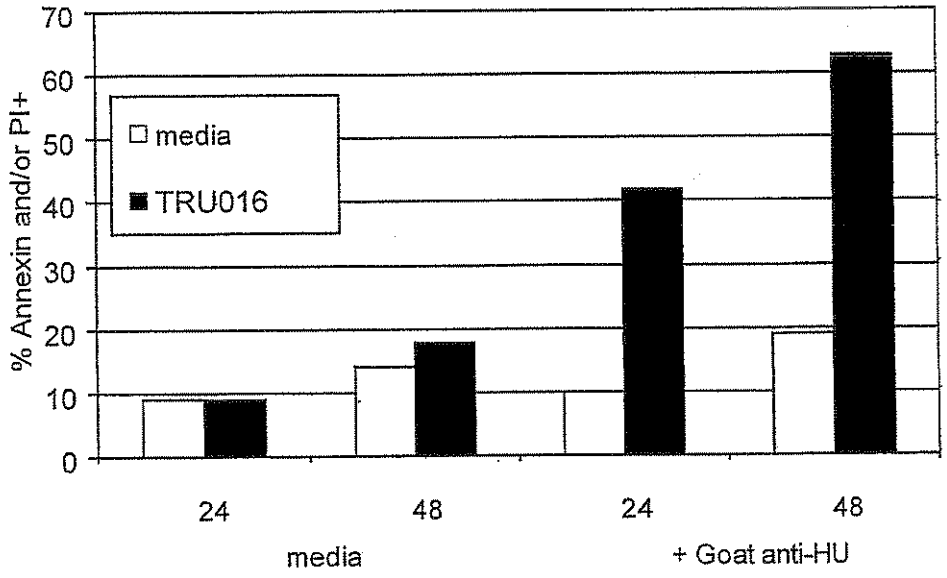


FIG. 19B

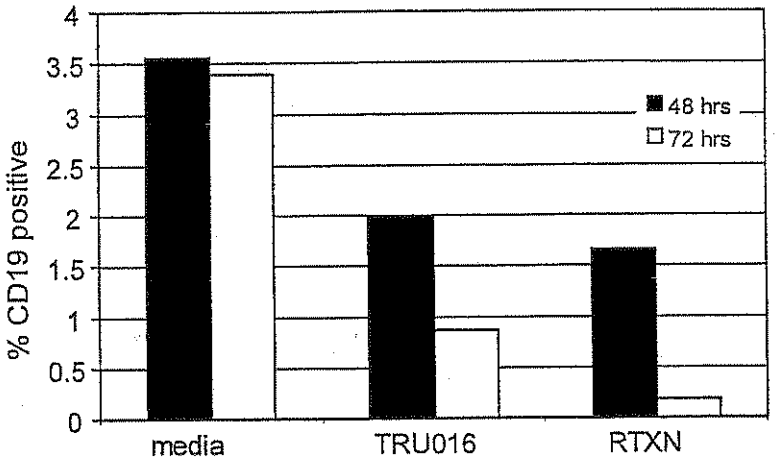


FIG. 20A

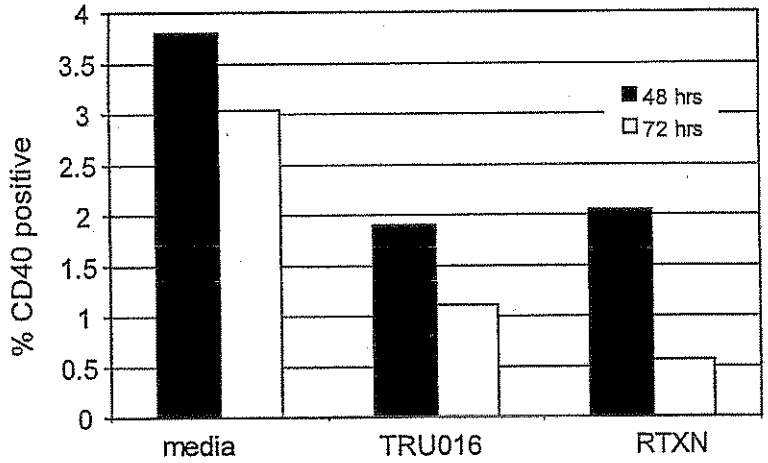


FIG. 20B

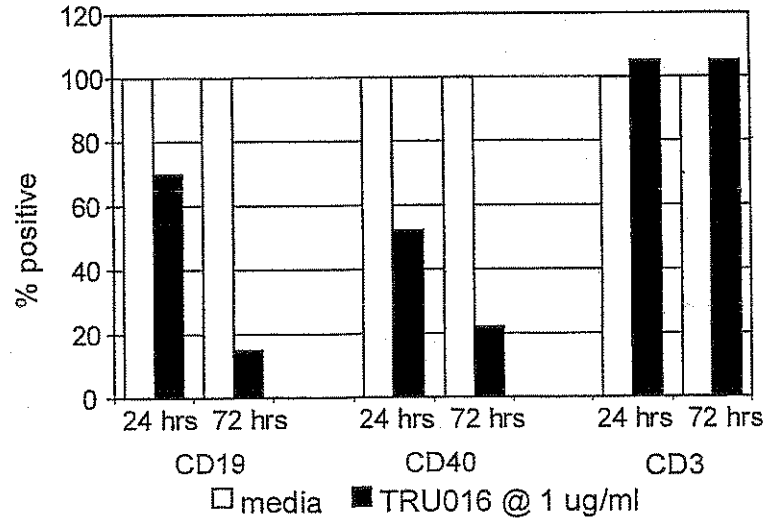


FIG. 20C

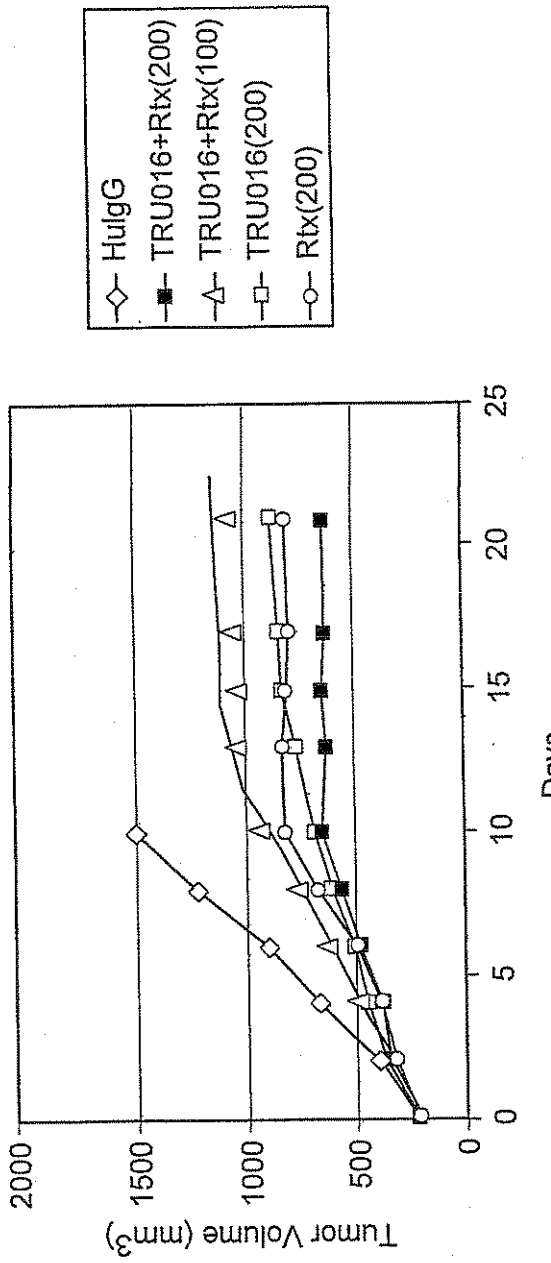

HulgG
TRU016+Rtx(200)
TRU016+Rtx(100)
TRU016(200)
Rtx(200)
Tumor Volume (mm3)
2000
1500
1000
500
0
0
5
10
15
20
25
Days

FIG. 21

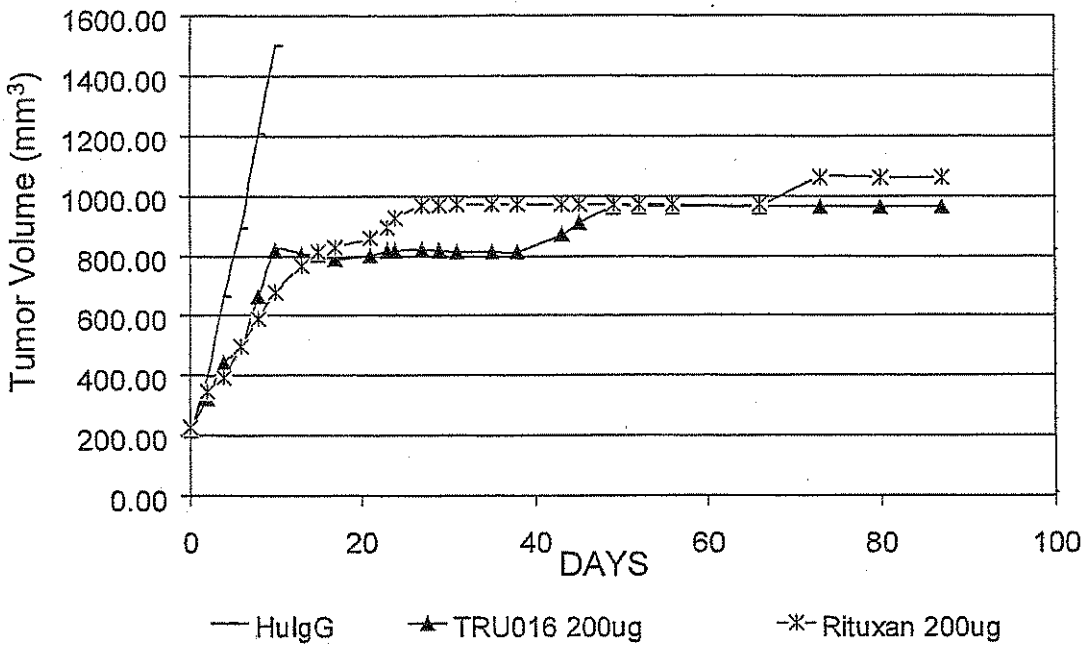


FIG. 22A

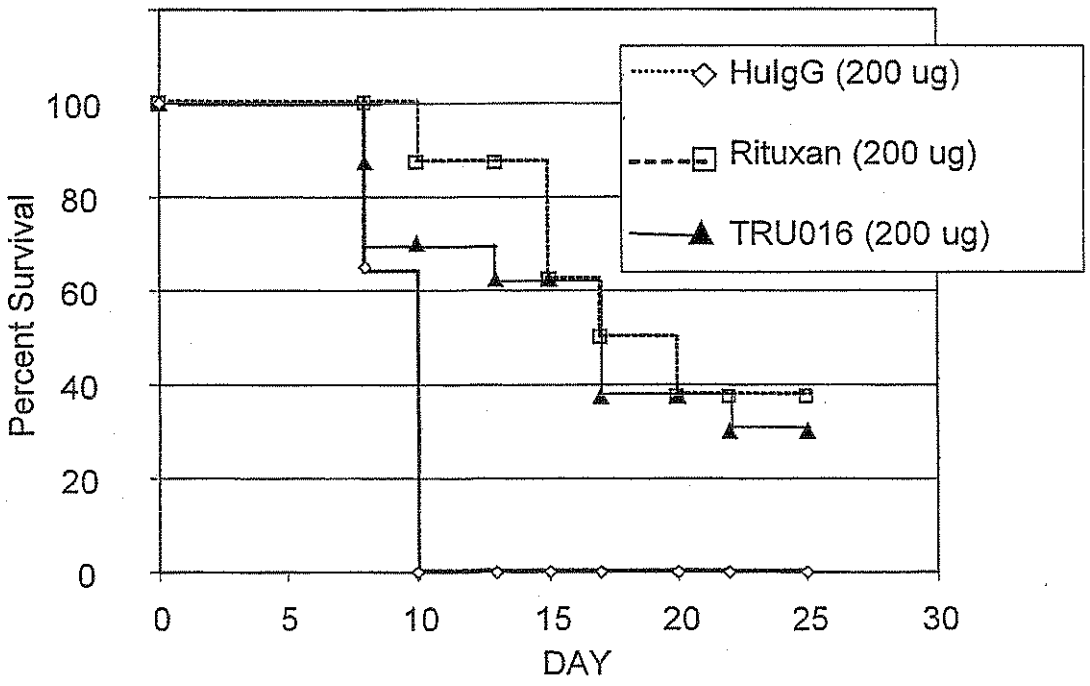


FIG. 22B

FIG. 23A

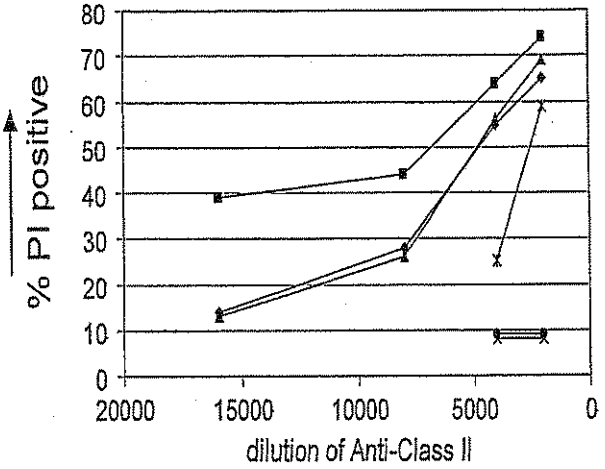
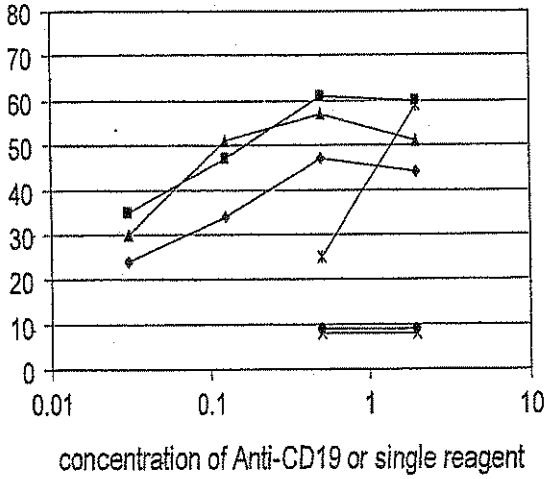
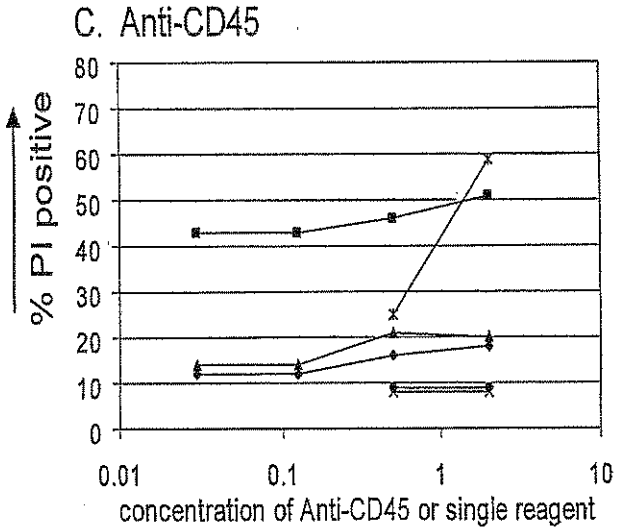


FIG. 23B





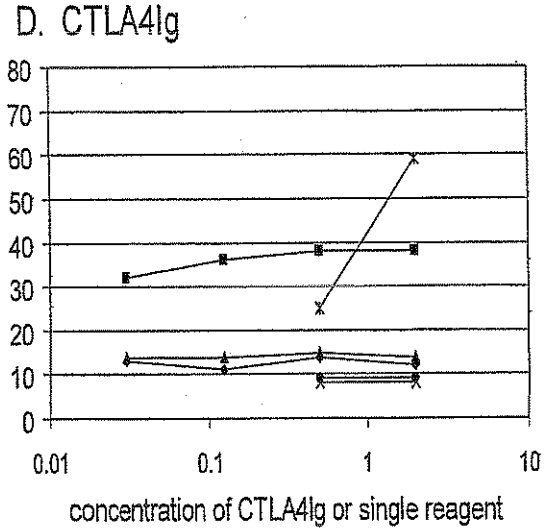


FIG. 23C

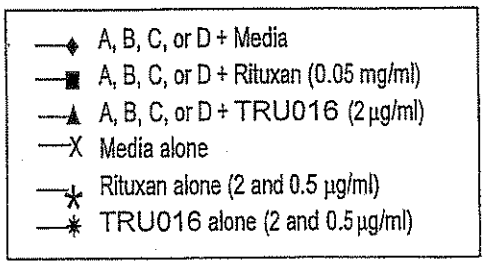


FIG. 23D

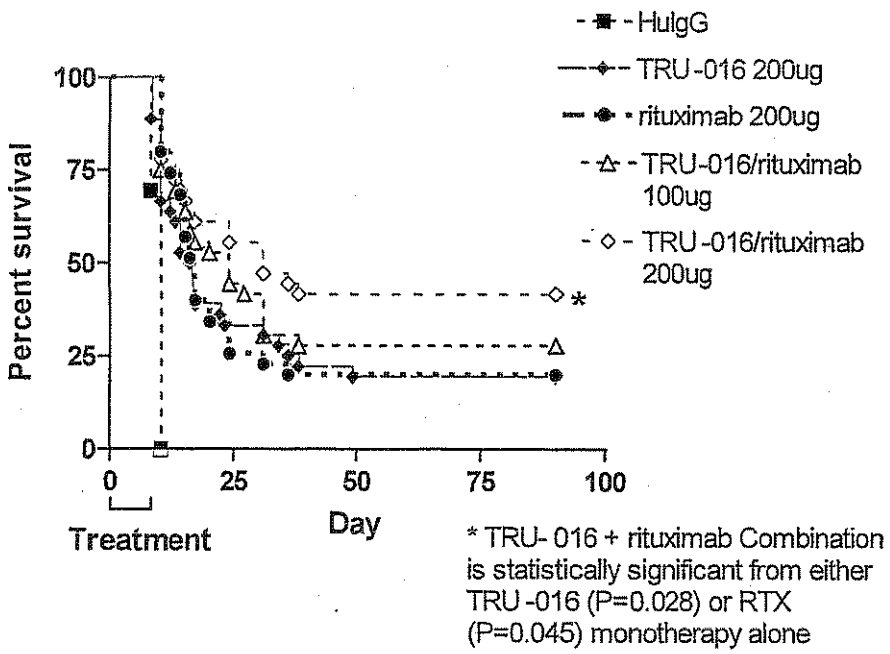

HuIgG
TRU-016 200ug
rituximab 200ug
TRU-016/rituximab 100ug
TRU-016/rituximab 200ug
Percent survival
100
75
50
25
0
0
25
50
75
100
Day
Treatment
*
* TRU- 016 + rituximab Combination is statistically significant from either TRU-016 (P=0.028) or RTX (P=0.045) monotherapy alone

FIG. 24

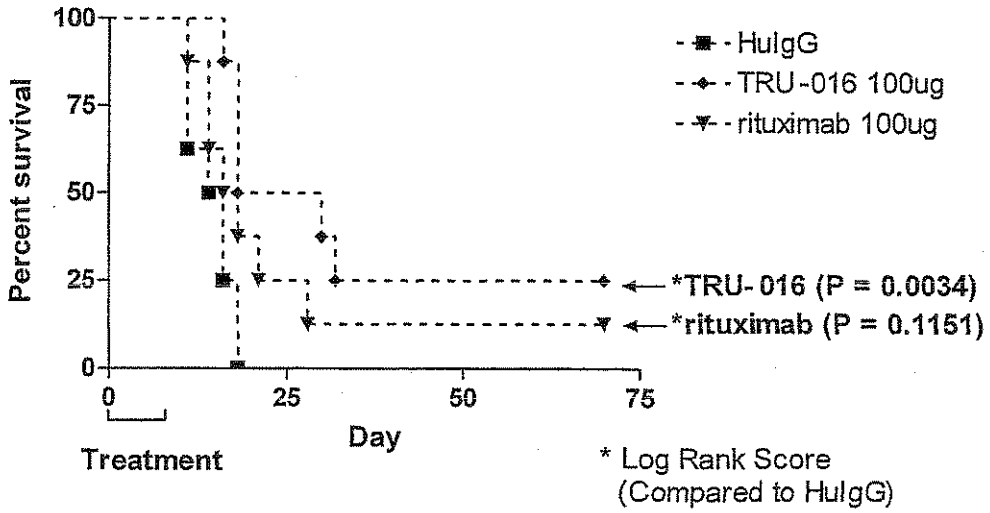
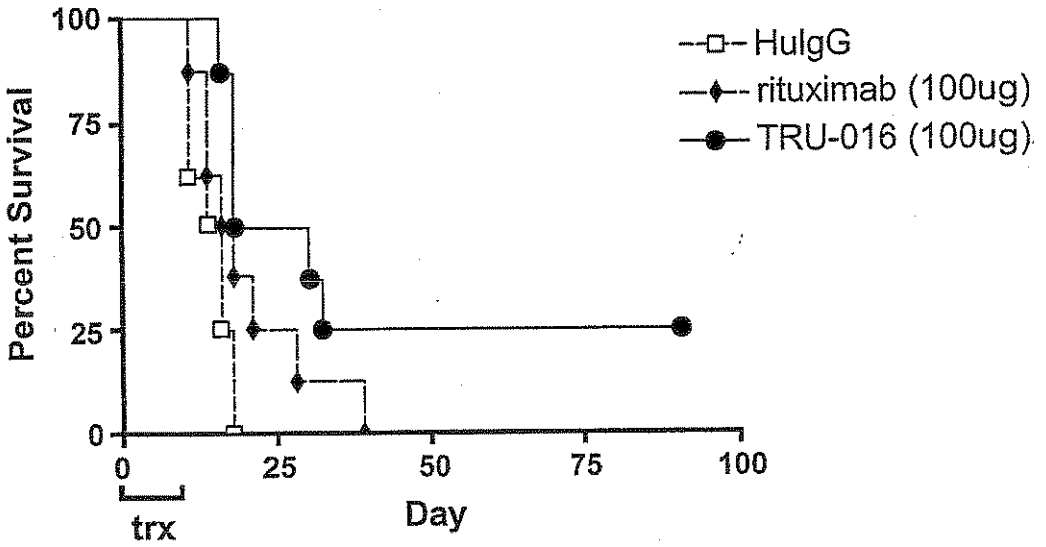

HuIgG
TRU-016 100ug
rituximab 100ug
Percent survival
100
75
50
25
0
0
25
50
75
Day
Treatment
*TRU- 016 (P = 0.0034)
*rituximab (P = 0.1151)
* Log Rank Score (Compared to HuIgG)

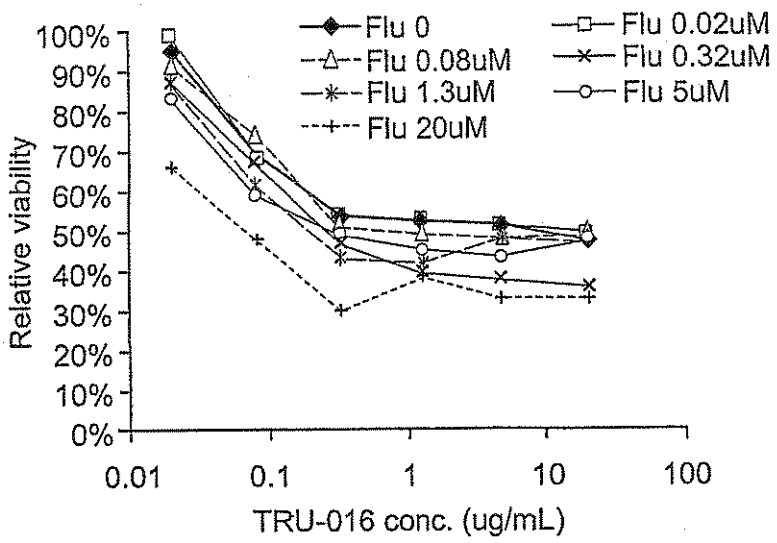
FIG. 25



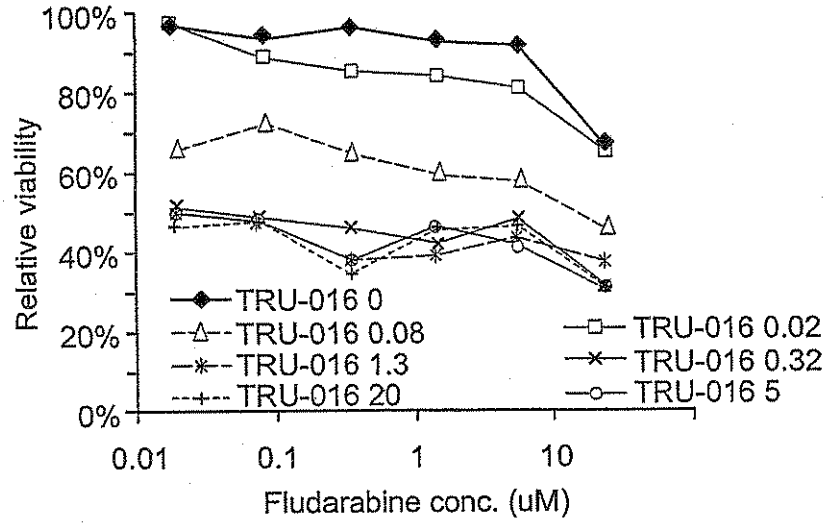
Log Rank Scores
TRU-016 vs. HulgG control P+0.003
rituximab vs. HulgG control P=0.115

FIG. 26

a


Flu 0
Flu 0.02uM
Flu 0.08uM
Flu 0.32uM
Flu 1.3uM
Flu 5uM
Flu 20uM
Relative viability
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
0.01
0.1
1
10
100
TRU-016 conc. (ug/mL)

b


Relative viability
100%
80%
60%
40%
20%
0%
TRU-016 0
TRU-016 0.08
TRU-016 1.3
TRU-016 20
TRU-016 0.02
TRU-016 0.32
TRU-016 5
0.01
0.1
1
10
Fludarabine conc. (uM)

c

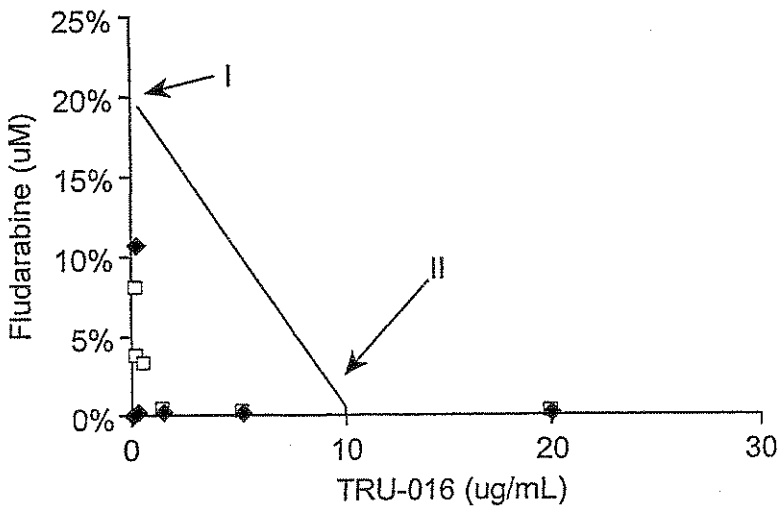

Fludarabine (uM)
25%
20%
15%
10%
5%
0%
I
II
0
10
20
30
TRU-016 (ug/mL)

FIG. 27

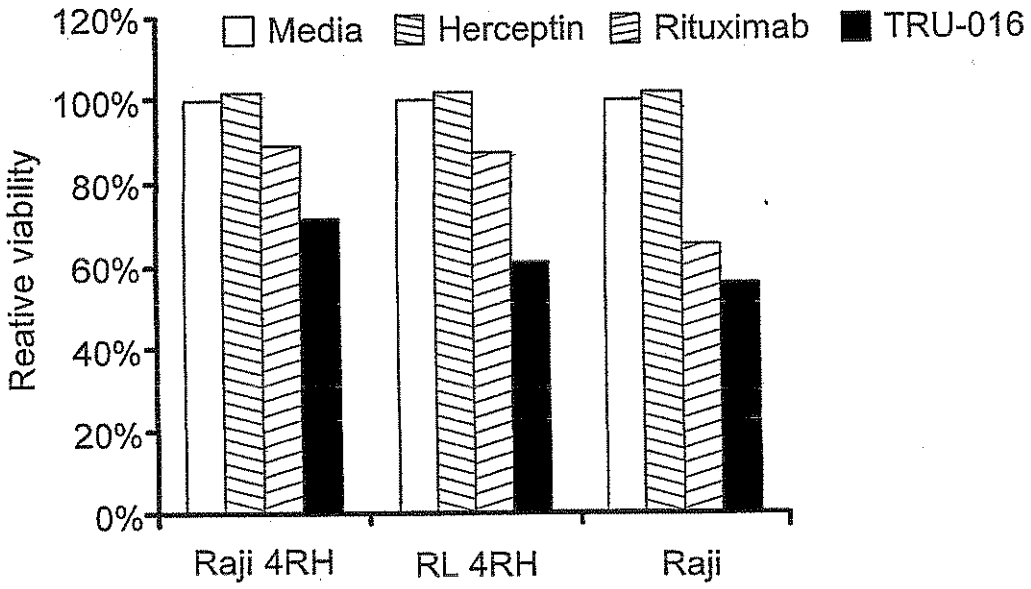

120%
100%
80%
60%
40%
20%
0%
Reative viability
Media
Herceptin
Rituximab
TRU-016
Raji 4RH
RL 4RH
Raji

FIG. 28

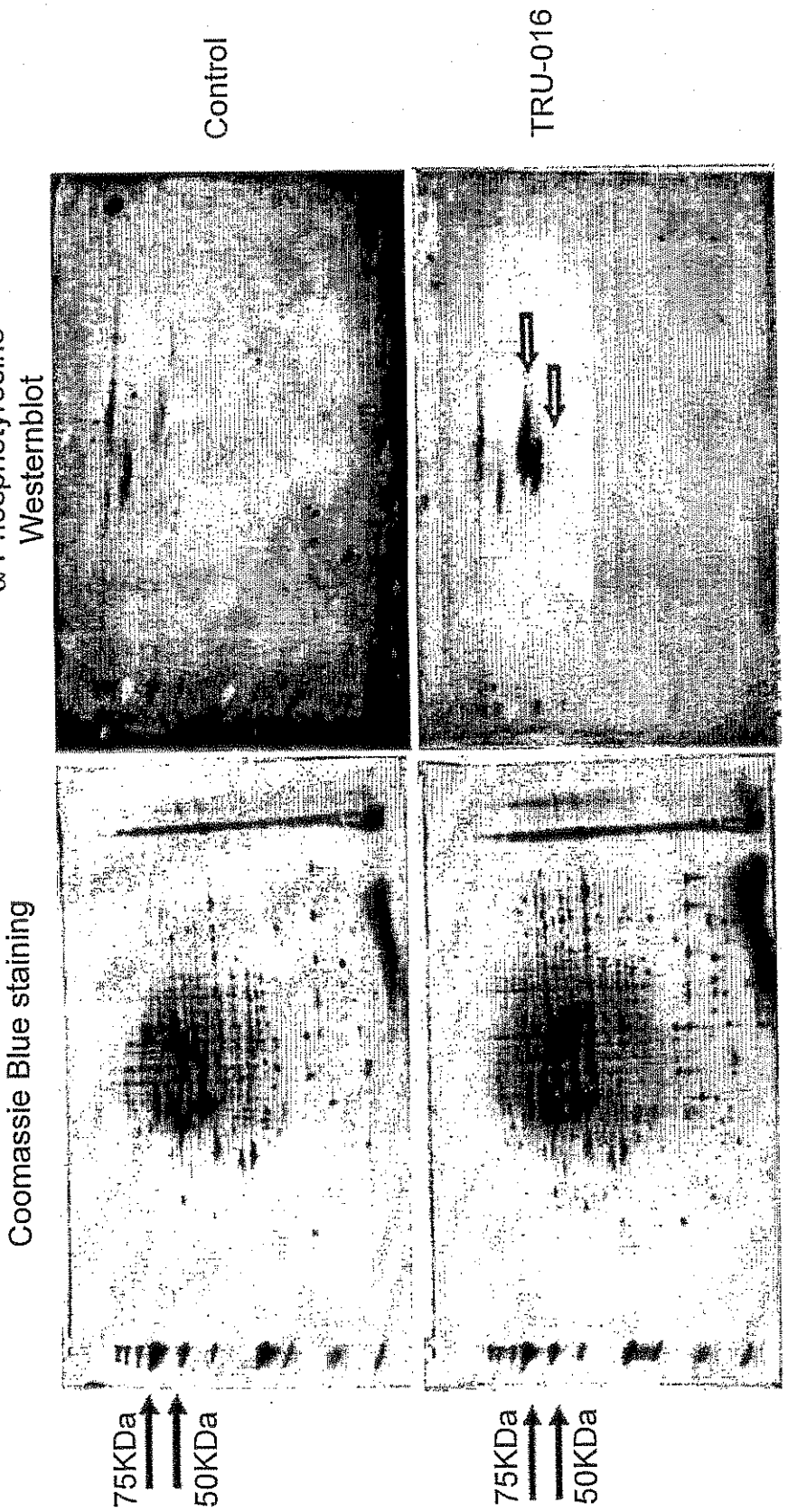

α-Phosphotyrosine Westernblot
Coomassie Blue staining
Control
TRU-016
75KDa
50KDa
75KDa
50KDa

FIG. 29

```
                    L-FR1           L-CDR1        L-FR2
                    1                                                49
  O16_-_G28-1       DIQMTQSPASLSASVGETVTITC RTSENVYSYLA WYQQKQGKSPQLLVS
 HO16_-_O19001      EIVLTQSPATLSLSPGERATLSC RTSENVYSYLA WYQQKPGQAPRLLIY

    Consensus        I  TQSPA LS S GE  T  C RTSENVYSYLA WYQQK G  P LL

                     L-CDR2          L-FR3                      L-CDR3
                     50                                              97
  O16_-_G28-1       FAKTLAE GVPSRFSGSGSGTQFSLKISSLQPEDSGSYFC QHHSDNPWT
 HO16_-_O19001      FAKTLAE GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QHHSDNPWT

    Consensus       FAKTLAE G P RFSGSGSGT F L ISSL PED   Y C QHHSDNPWT

                     L-FR4     (G4S)3 linker             H-FR1
                     98                          1                    30
  O16_-_G28-1       FGGGTELEIK GGGGSGGGGSGGGGSS AVQLQQSGPESEKPGASVKISCKASGYSFT
 HO16_-_O19001      FGQGTKVEIK GGGGSGGGGSGGGGTG EVQLVQSGAEVKKPGESLKISCKGSGYSFT

    Consensus       FG GT  EIK GGGGSGGGGSGGGG    VQL QSG E  KPG S KISCK SGYSFT

                   H-CDR1    H-FR2          H-CDR2
                   31                                             76
  O16_-_G28-1      GYNMN WVKQNNGKSLEWIG NIDPYYGGTTYNRKFKG KATLTVDKSSS
 HO16_-_O19001     GYNMN WVRQMPGKGLEWMG NIDPYYGGTTYNRKFKG QVTISADKSIS

    Consensus      GYNMN WV Q  GK LEW G NIDPYYGGTTYNRKFKG   T   DKS S

                     H-FR3               H-CDR3    H-FR4
                     77                              113
  O16_-_G28-1       TAYMQLKSLTSEDSAVYYCAR SVGPMDY WGQGTSVTVSS
 HO16_-_O19001      TAYLQWSSLKASDTAMYYCAR SVGPMDY WGRGTLVTVSS

    Consensus       TAY Q  SL   D A YYCAR SVGPMDY WG GT VTVSS
```

FIG. 30A

```
                1                                                  50
H016_-_019001   EIVLTQSPATLSLSPGERATLSCRTSENVYSYLAWYQQKPGQAPRLLIYF
H016_-_019008   EIVLTQSPATLSLSPGERATLSCRTSENVYSYLAWYQQKPGQAPRLLIYF
H016_-_019009   EIVLTQSPATLSLSPGERATLSCRTSENVYSYLAWYQQKPGQAPRLLIYF

                51                                                 100
H016_-_019001   AKTLAEGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHSDNPWTFGQ
H016_-_019008   AKTLAEGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHSDNPWTFGQ
H016_-_019009   AKTLAEGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHHSDNPWTFGQ

                101                                                150
H016_-_019001   GTKVEIKGGGGSGGGGSGGGGTGEVQLVQSGAEVKKPGESLKISCKGSGY
H016_-_019008   GTKVEIKGGGGSGGGGSGGGGASEVQLVQSGAESKKPGESLKISCKGSGY
H016_-_019009   GTKVEIKGGGGSGGGGSGGGGASEVQLVQSGAESKKPGESLRISCKGSGY
                                  **                 *

                151                                                200
H016_-_019001   SFTGYNMNWVRQMPGKGLEWMGNIDPYYGGTTYNRKFKGQVTISADKSIS
H016_-_019008   SFTGYNMNWVRQMPGKGLEWMGNIDPYYGGTTYNRKFKGQVTISADKSIS
H016_-_019009   SFTGYNMNWVRQMPGKGLEWMGNIDPYYGGTTYNRKFKGHVTISADKSIS
                                                    *

                201                                239
H016_-_019001   TAYLQWSSLKASDTAMYYCARSVGPMDYWGRGTLVTVSS
H016_-_019008   TAYLQWSSLKASDTAMYYCARSVGPMDYWGRGTLVTVSS
H016_-_019009   TAYLQWSSLKASDTAMYYCARSVGPMDYWGRGTLVTVSS
```

FIG. 30B

Construct ID	Description	Hinge	DNA Sequence
019001	Vk3:VH5-51	SSC-P	atggaagccccagctcagcttctcttcctcctgctactctggctcccag
019041	Vk3:VH5-51	SSC-P	aagcttgccgccatggaagccccagcgcagcttctcttcctcctgcta
019044	Vk3:VH5-51	SSC-P	aagcttgccgccatggaagccccagcgcagcttctcttcctcctgcta

Amino Acid Sequence

meapaqllflllwlpdttgeivltqspatlslspgeratlscrtsenvysylawyqqkpgqaprlliyfaktlaegiparfsgsgsgtdftltisslepedfavyycqhhsdnpwtfgqgtkveikggggsggggsggggtgev
meapaqllflllwlpdttgeivltqspatlslspgeratlscrasenvysylawyqqkpgqaprlliyfaktlaegiparfsgsgsgtdftltisslepedfavyycqhhsdnpwtfgqgtkveikggggsggggsggggtge
meapaqllflllwlpdttgeivltqspatlslspgeratlscrasenvysylawyqqkpgqaprlliyfaktlaegiparfsgsgsgtdftltisslepedfavyycqhhsdnpwtfgqgtkveikggggsggggsggggtge

/qlvqsgaevkkpgeslkisckgsgysftgynmnwvrqmpgkglewmgnidpyyggttynrkfkgqvtisadksistaylqwsslkasdtamyycarsvgpmdywgrgtlvtvssdqepkssdkthtsppcpap
vqlvqsgaevkkpgeslkisckgsgysftgynmnwvrqmpgkglewmgnidpyyggttynrkfkgqvtisadksistaylqwsslkasdtamyycarsvgpfdywgqgtlvtvssdqepkssdkthtsppcpap
vqlvqsgaevkkpgeslkisckgsgysftgynmnwvrqmpgkglewmgnidpyyggttynrkfkgqvtisadksistaylqwsslkasdtamyycarsvgpfdswgqgtlvtvssdqepkssdkthtsppcpap

ellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlppsrdeltknqvsltclvkgfy
ellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlppsrdeltknqvsltclvkgfy
ellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlppsrdeltknqvsltclvkgfy

/psdiavewesngqpennykttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk
/psdiavewesngqpennykttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk*
/psdiavewesngqpennykttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk*

FIG. 31

FIG. 32A

```
LIGHT CHAIN  ........FR1.............  ___CDR1_____  ......FR2......
019041       EIVLTQSPATLSLSPGERATLSC RASENVYSYLA  WYQQKPGQAPRLLIY
019044       EIVLTQSPATLSLSPGERATLSC RASENVYSYLA  WYQQKPGQAPRLLIY
019001       EIVLTQSPATLSLSPGERATLSC RTSENVYSYLA  WYQQKPGQAPRLLIY

             _CDR2__  ..............FR3.............. __CDR3____  ....FR4...
019041       FAKTLAE  GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QHHSDNPWT  FGQGTKVEIK
019044       FAKTLAE  GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QHHSDNPWT  FGQGTKVEIK
019001       FAKTLAE  GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QHHSDNPWT  FGQGTKVEIK

HEAVY CHAIN  ..............FR1.............. CDR1  .....FR2......
019041       EVQLVQSGAEVKKPGESLKISCKGSGYSFT GYNMN WVRQMPGKGLEWMG
019044       EVQLVQSGAEVKKPGESLKISCKGSGYSFT GYNMN WVRQMPGKGLEWMG
019001       EVQLVQSGAEVKKPGESLKISCKGSGYSFT GYNMN WVRQMPGKGLEWMG

             ________CDR2_______ ..............FR3..............
019041       NIDPYYGGTTYNRKFKG QVTISADKSISTAYLQWSSLKASDTAMYYCAR
019044       NIDPYYGGTTYNRKFKG QVTISADKSISTAYLQWSSLKASDTAMYYCAR
019001       NIDPYYGGTTYNRKFKG QVTISADKSISTAYLQWSSLKASDTAMYYCAR

             __CDR3_ .....FR4...
019041       SVGPFDY WGQGTLVTVSS
019044       SVGPFDS WGQGTLVTVSS
019001       SVGPMDY WGRGTLVTVSS

CLUSTAL W (1.83) multiple sequence alignment

019041         ------------ATGGAAGCCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCA 48
019044         ------------ATGGAAGCCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCA 48
019001         AAGCTTGCCGCCATGGAAGCCCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCA 60
```

B

FIG. 32B




```
                    ********** ***********************************

019041      GATACCACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGC 108
019044      GATACCACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGC 108
019001      GATACCACCGGAGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGC 120
            ************************************************************

019041      GAAAGAGCCACCCTCTCCTGCCGAGCAAGTGAAAATGTTTACAGCTACTTAGCCTGGTAC 168
019044      GAAAGAGCCACCCTCTCCTGCCGAGCAAGTGAAAATGTTTACAGCTACTTAGCCTGGTAC 168
019001      GAAAGAGCCACCCTCTCCTGCCGAACAAGTGAAAATGTTTACAGCTACTTAGCCTGGTAC 180
            ************************ ***********************************

019041      CAACAGAAACCTGGCCAGGCTCCTAGGCTCCTCATCTATTTTGCAAAAACCTTAGCAGAA 228
019044      CAACAGAAACCTGGCCAGGCTCCTAGGCTCCTCATCTATTTTGCAAAAACCTTAGCAGAA 228
019001      CAACAGAAACCTGGCCAGGCTCCTAGGCTCCTCATCTATTTTGCAAAAACCTTAGCAGAA 240
            ************************************************************

019041      GGAATTCCAGCCAGGTTCAGTGGCAGTGGATCCGGGACAGACTTCACTCTCACCATCAGC 288
019044      GGAATTCCAGCCAGGTTCAGTGGCAGTGGATCCGGGACAGACTTCACTCTCACCATCAGC 288
019001      GGAATTCCAGCCAGGTTCAGTGGCAGTGGATCCGGGACAGACTTCACTCTCACCATCAGC 300
            ************************************************************

019041      AGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACATCATTCCGATAATCCGTGG 348
019044      AGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACATCATTCCGATAATCCGTGG 348
019001      AGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACATCATTCCGATAATCCGTGG 360
            ************************************************************

019041      ACATTCGGCCAAGGGACCAAGGTGGAAATCAAAGGTGGCGGCGGCTCGGGCGGTGGTGGA 408
019044      ACATTCGGCCAAGGGACCAAGGTGGAAATCAAAGGTGGCGGTGGCTCGGGCGGTGGTGGA 408
019001      ACATTCGGCCAAGGGACCAAGGTGGAAATCAAAGGTGGCGGTGGCTCGGGCGGTGGTGGA 420
            ************************************** ******************

019041      TCTGGAGGAGGTGGGACCGGTGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAG 468
019044      TCTGGAGGAGGTGGGACCGGTGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAG 468
019001      TCTGGAGGAGGTGGGACCGGTGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAG 480
            ************************************************************

019041      CCCGGAGAGTCTCTGAAGATTTCCTGTAAGGGATCCGGTTACTCATTCACTGGCTACAAT 528
019044      CCCGGAGAGTCTCTGAAGATTTCCTGTAAGGGATCCGGTTACTCATTCACTGGCTACAAT 528
019001      CCCGGAGAGTCTCTGAAGATTTCCTGTAAGGGATCCGGTTACTCATTCACTGGCTACAAT 540
            ************************************************************

019041      ATGAACTGGGTGCGCCAGATGCCCGGGAAAGGCCTCGAGTGGATGGGCAATATTGATCCT 588
019044      ATGAACTGGGTGCGCCAGATGCCCGGGAAAGGCCTCGAGTGGATGGGCAATATTGATCCT 588
019001      ATGAACTGGGTGCGCCAGATGCCCGGGAAAGGCCTCGAGTGGATGGGCAATATTGATCCT 600
            ************************************************************

019041      TATTATGGTGGTACTACCTACAACCGGAAGTTCAAGGGCCAGGTCACTATCTCCGCCGAC 648
```



FIG. 32C




```
019044          TATTATGGTGGTACTACCTACAACCGGAAGTTCAAGGGCCAGGTCACTATCTCCGCCGAC 648
019001          TATTATGGTGGTACTACCTACAACCGGAAGTTCAAGGGCCAGGTCACTATCTCCGCCGAC 660
                ************************************************************

019041          AAGTCCATCAGCACCGCCTACCTGCAATGGAGCAGCCTGAAGGCCTCGGACACCGCCATG 708
019044          AAGTCCATCAGCACCGCCTACCTGCAATGGAGCAGCCTGAAGGCCTCGGACACCGCCATG 708
019001          AAGTCCATCAGCACCGCCTACCTGCAATGGAGCAGCCTGAAGGCCTCGGACACCGCCATG 720
                ************************************************************

019041          TATTACTGTGCACGCTCAGTCGGCCCTTTCGACTACTGGGGCCAGGGCACCCTGGTCACT 768
019044          TATTACTGTGCACGCTCAGTCGGCCCTTTCGACTCCTGGGGCCAGGGCACCCTGGTCACT 768
019001          TATTACTGTGCACGCTCAGTCGGCCCTATGGACTACTGGGGCCGCGGCACCCTGGTCACT 780
                ***************************** * **** ********  ***************

019041          GTCTCCTCTGATCAGGAGCCCAAATCTTCTGACAAAACTCACACATCTCCACCGTGCCCA 828
019044          GTCTCCTCTGATCAGGAGCCCAAATCTTCTGACAAAACTCACACATCTCCACCGTGCCCA 828
019001          GTCTCCTCTGATCAGGAGCCCAAATCTTCTGACAAAACTCACACATCTCCACCGTGCCCA 840
                ************************************************************

019041          GCACCTGAACTCCTGGGTGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 888
019044          GCACCTGAACTCCTGGGTGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 888
019001          GCACCTGAACTCCTGGGTGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 900
                ************************************************************

019041          CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 948
019044          CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 948
019001          CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 960
                ************************************************************

019041          CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 1008
019044          CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 1008
019001          CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 1020
                ************************************************************

019041          CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1068
019044          CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1068
019001          CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1080
                ************************************************************

019041          CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1128
019044          CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1128
019001          CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1140
                ************************************************************

019041          CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1188
019044          CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1188
019001          CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1200
                ************************************************************
```






```
019041          CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1248
019044          CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1248
019001          CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1260
                ************************************************************

019041          GGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1308
019044          GGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1308
019001          GGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1320
                ************************************************************

019041          TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1368
019044          TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1368
019001          TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1380
                ************************************************************

019041          ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1428
019044          ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1428
019001          ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1440
                ************************************************************

019041          GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA------ 1482
019044          GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA------ 1482
019001          GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGATCTAGA 1500
                ************************************************
```

FIG. 32D