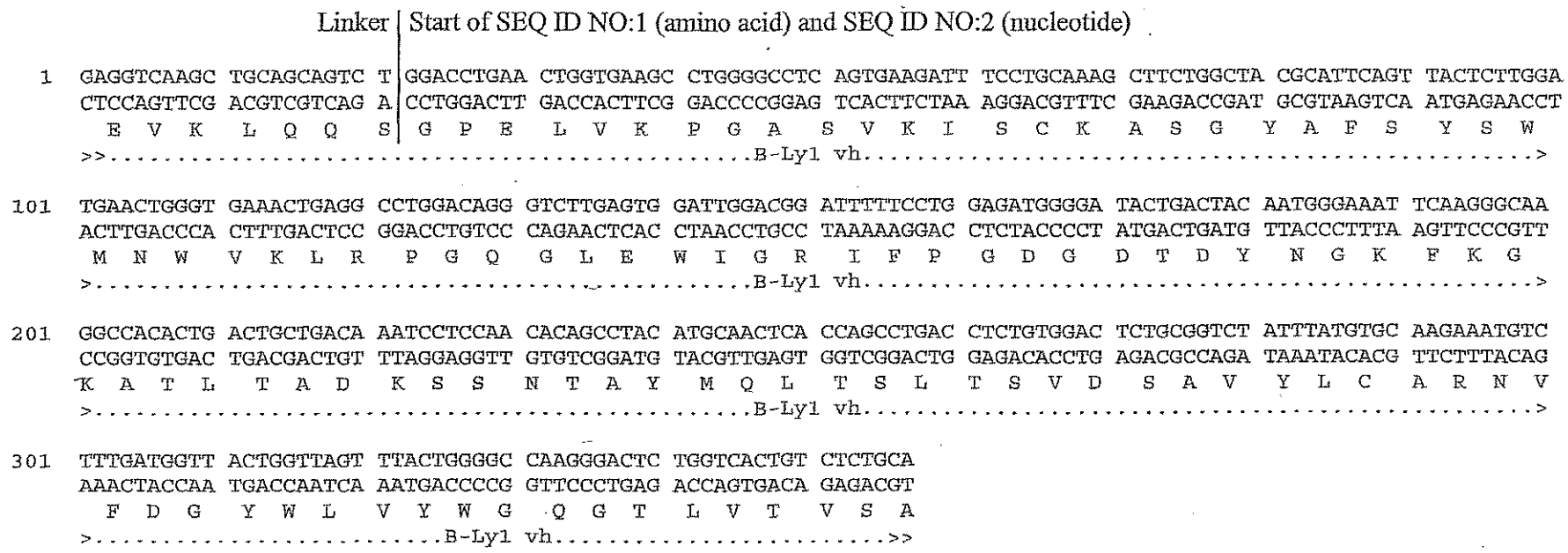

Linker | Start of SEQ ID NO:1 (amino acid) and SEQ ID NO:2 (nucleotide)
1 GAGGTCAAGC TGCAGCAGTC T|GGACCTGAA CTGGTGAAGC CTGGGGCCTC AGTGAAGATT TCCTGCAAAG CTTCTGGCTA CGCATTCAGT TACTCTTGGA
CTCCAGTTCG ACGTCGTCAG A|CCTGGACTT GACCACTTCG GACCCCGGAG TCACTTCTAA AGGACGTTTC GAAGACCGAT GCGTAAGTCA ATGAGAACCT
E V K L Q Q S| G P E L V K P G A S V K I S C K A S G Y A F S Y S W
>>.....B-Ly1 vh.....>
101 TGAACTGGGT GAAACTGAGG CCTGGACAGG GTCTTGAGTG GATTGGACGG ATTTTTCCTG GAGATGGGGA TACTGACTAC AATGGGAAAT TCAAGGGCAA
ACTTGACCCA CTTTGACTCC GGACCTGTCC CAGAACTCAC CTAACCTGCC TAAAAAGGAC CTCTACCCCT ATGACTGATG TTACCCTTTA AGTTCCCGTT
M N W V K L R P G Q G L E W I G R I F P G D G D T D Y N G K F K G
>.....B-Ly1 vh.....>
201 GGCCACACTG ACTGCTGACA AATCCTCCAA CACAGCCTAC ATGCAACTCA CCAGCCTGAC CTCTGTGGAC TCTGCGGTCT ATTTATGTGC AAGAAATGTC
CCGGTGTGAC TGACGACTGT TTAGGAGGTT GTGTCGGATG TACGTTGAGT GGTCGGACTG GAGACACCTG AGACGCCAGA TAAATACACG TTCTTTACAG
K A T L T A D K S S N T A Y M Q L T S L T S V D S A V Y L C A R N V
>.....B-Ly1 vh.....>
301 TTTGATGGTT ACTGGTTAGT TTACTGGGGC CAAGGGACTC TGGTCACTGT CTCTGCA
AAACTACCAA TGACCAATCA AATGACCCCG GTTCCCTGAG ACCAGTGACA GAGACGT
F D G Y W L V Y W G Q G T L V T V S A
>.....B-Ly1 vh.....>>

FIG. 1

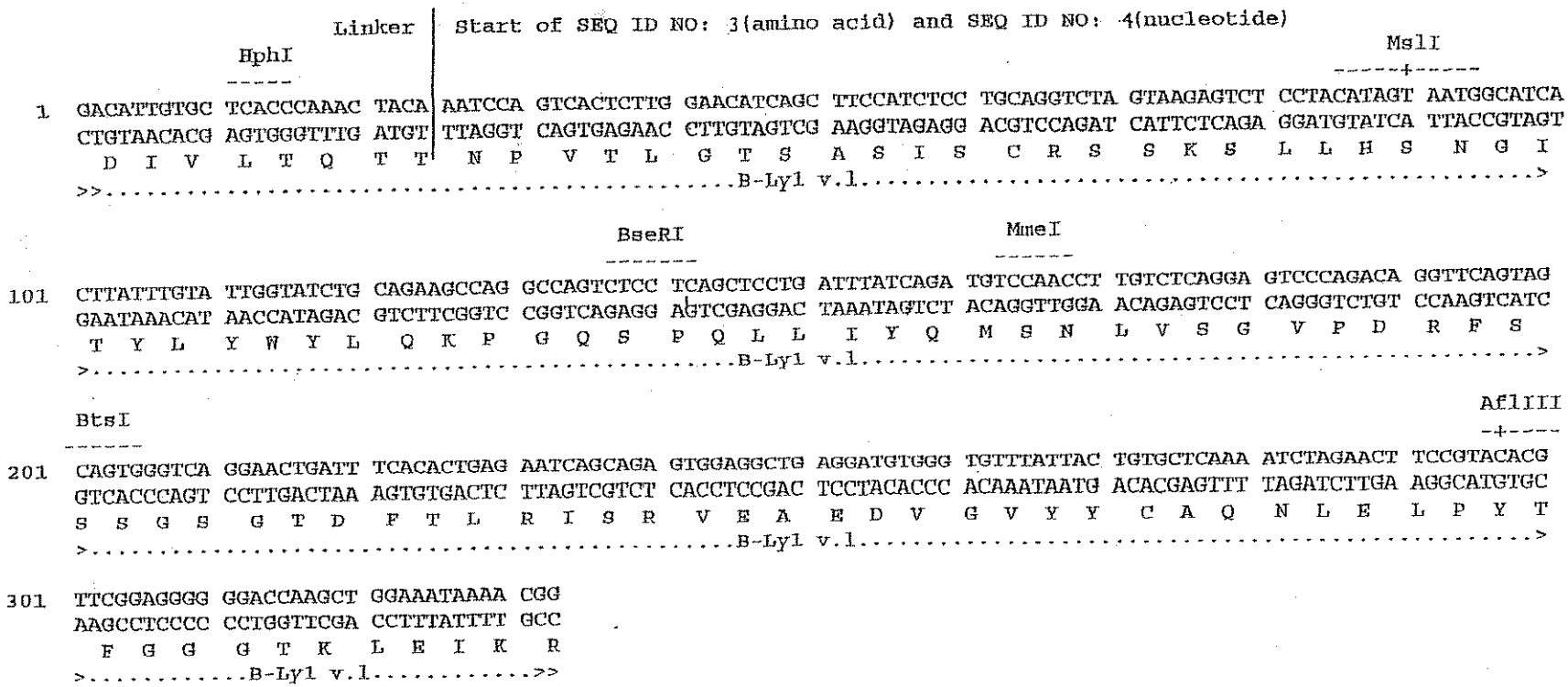

Linker
Start of SEQ ID NO: 3(amino acid) and SEQ ID NO: 4(nucleotide)
HphI
MslI
1 GACATTGTGC TCACCCAAAC TACA AATCCA GTCACTCTTG GAACATCAGC TTCCATCTCC TGCAGGTCTA GTAAGAGTCT CCTACATAGT AATGGCATCA
CTGTAACACG AGTGGGTTTG ATGT TTAGGT CAGTGAGAAC CTTGTAGTCG AAGGTAGAGG ACGTCCAGAT CATTCTCAGA GGATGTATCA TTACCGTAGT
D I V L T Q T T N P V T L G T S A S I S C R S S K S L L H S N G I
>>.....B-Ly1 v.1.....>
BseRI
MmeI
101 CTTATTTGTA TTGGTATCTG CAGAAGCCAG GCCAGTCTCC TCAGCTCCTG ATTTATCAGA TGTCCAACCT TGTCTCAGGA GTCCCAGACA GGTTCAGTAG
GAATAAACAT AACCATAGAC GTCTTCGGTC CGGTCAGAGG AGTCGAGGAC TAAATAGTCT ACAGGTTGGA ACAGAGTCCT CAGGGTCTGT CCAAGTCATC
T Y L Y W Y L Q K P G Q S P Q L L I Y Q M S N L V S G V P D R F S
>.....B-Ly1 v.1.....>
BtsI
AflIII
201 CAGTGGGTCA GGAACTGATT TCACACTGAG AATCAGCAGA GTGGAGGCTG AGGATGTGGG TGTTTATTAC TGTGCTCAAA ATCTAGAACT TCCGTACACG
GTCACCCAGT CCTTGACTAA AGTGTGACTC TTAGTCGTCT CACCTCCGAC TCCTACACCC ACAAATAATG ACACGAGTTT TAGATCTTGA AGGCATGTGC
S S G S G T D F T L R I S R V E A E D V G V Y Y C A Q N L E L P Y T
>.....B-Ly1 v.1.....>
301 TTCGGAGGGG GGACCAAGCT GGAAATAAAA CGG
AAGCCTCCCC CCTGGTTCGA CCTTTATTTT GCC
F G G G T K L E I K R
>.....B-Ly1 v.1.....>>

FIG. 2

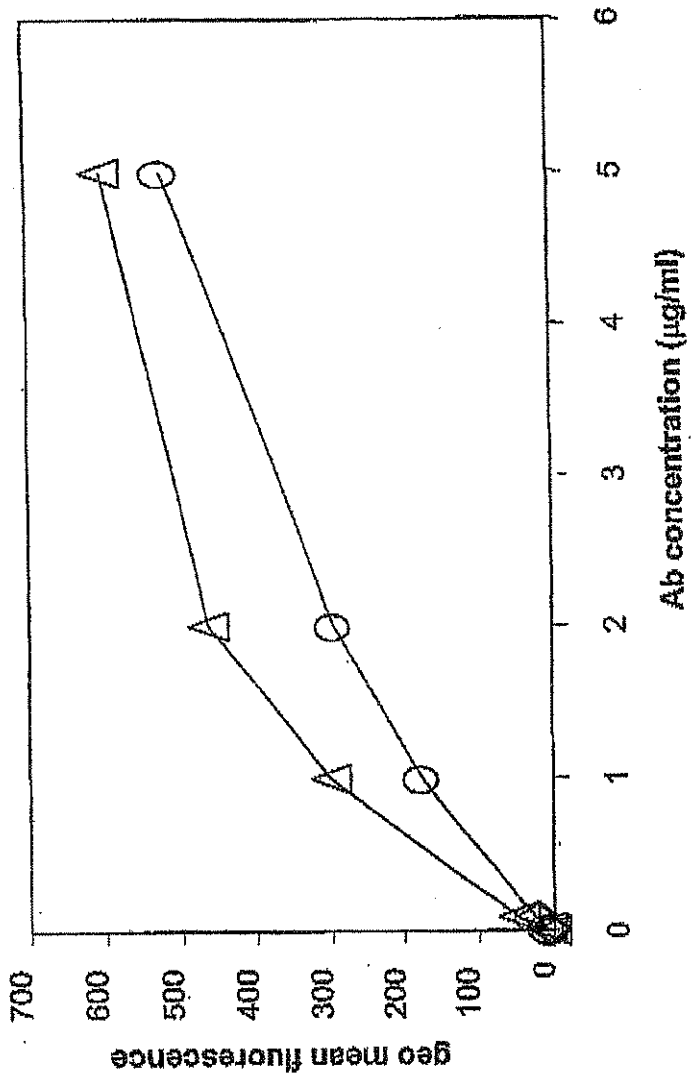

geo mean fluorescence
700
600
500
400
300
200
100
0
0
1
2
3
4
5
6
Ab concentration (µg/ml)

FIG. 3

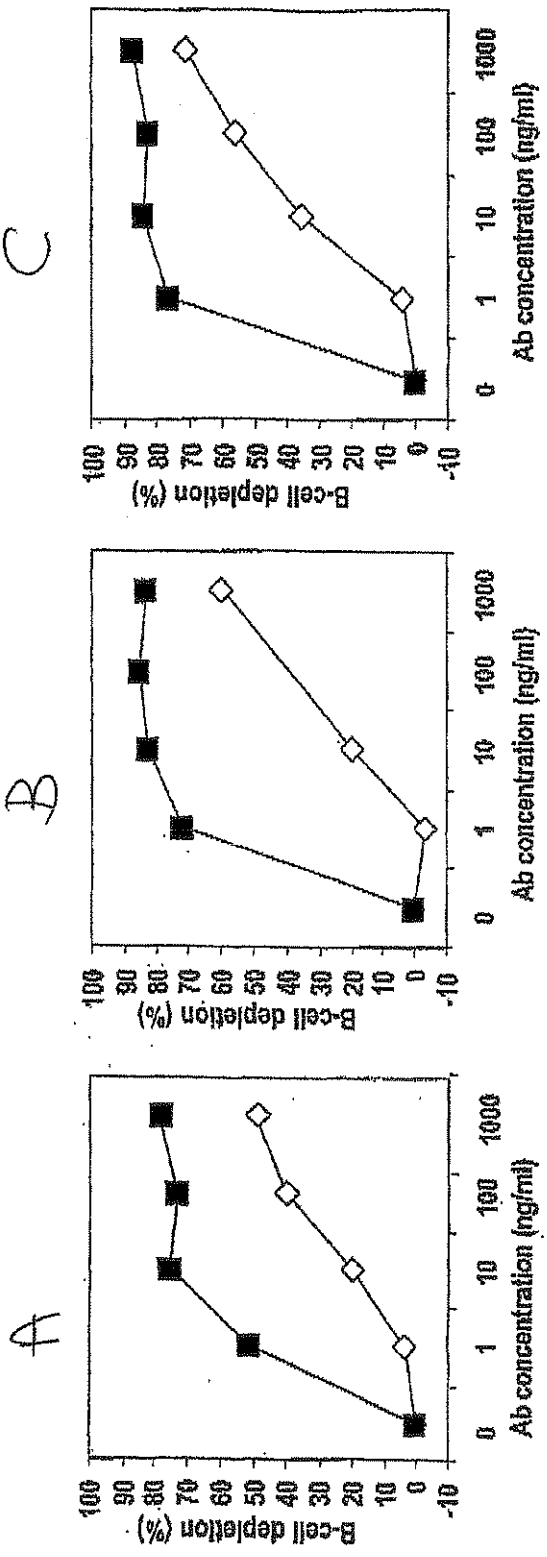
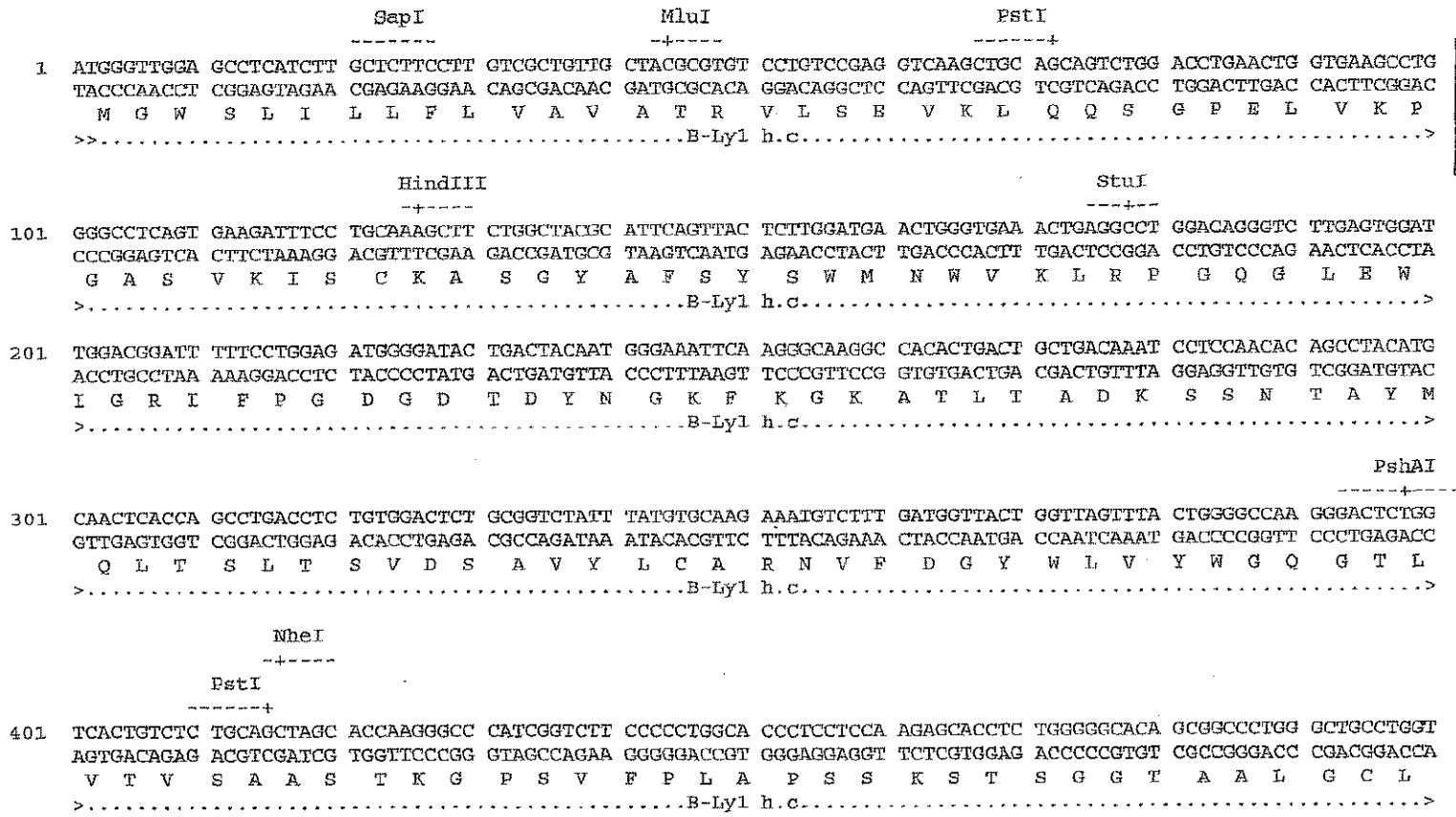

A
B
C
B-cell depletion (%)
100
90
80
70
60
50
40
30
20
10
0
-10
0
1
10
100
1000
Ab concentration (ng/ml)

FIG. 4



SEQ ID NO: 11 (nucleic acid) and SEQ ID NO: 13 (amino acid)

FIG. 5A



SEQ ID NO: 11 (nucleic acid) and SEQ ID NO: 13 (amino acid)

FIG. 5B

```
                                SmaI
                                ---+--
1101  ACAGGTGTAC ACCCTGCCCC CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG
      TGTCCACATG TGGGACGGGG GTAGGGCCCT ACTCGACTGG TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCCGAAGA TAGGGTCGCT GTAGCGGCAC
      P  Q  V  Y   T  L  P   P  S  R   D  E  L  T   K  N  Q   V  S  L   T  C  L  V   K  G  F   Y  P  S   D  I  A  V
      >.....................................................B-Ly1 h.c.....................................................>

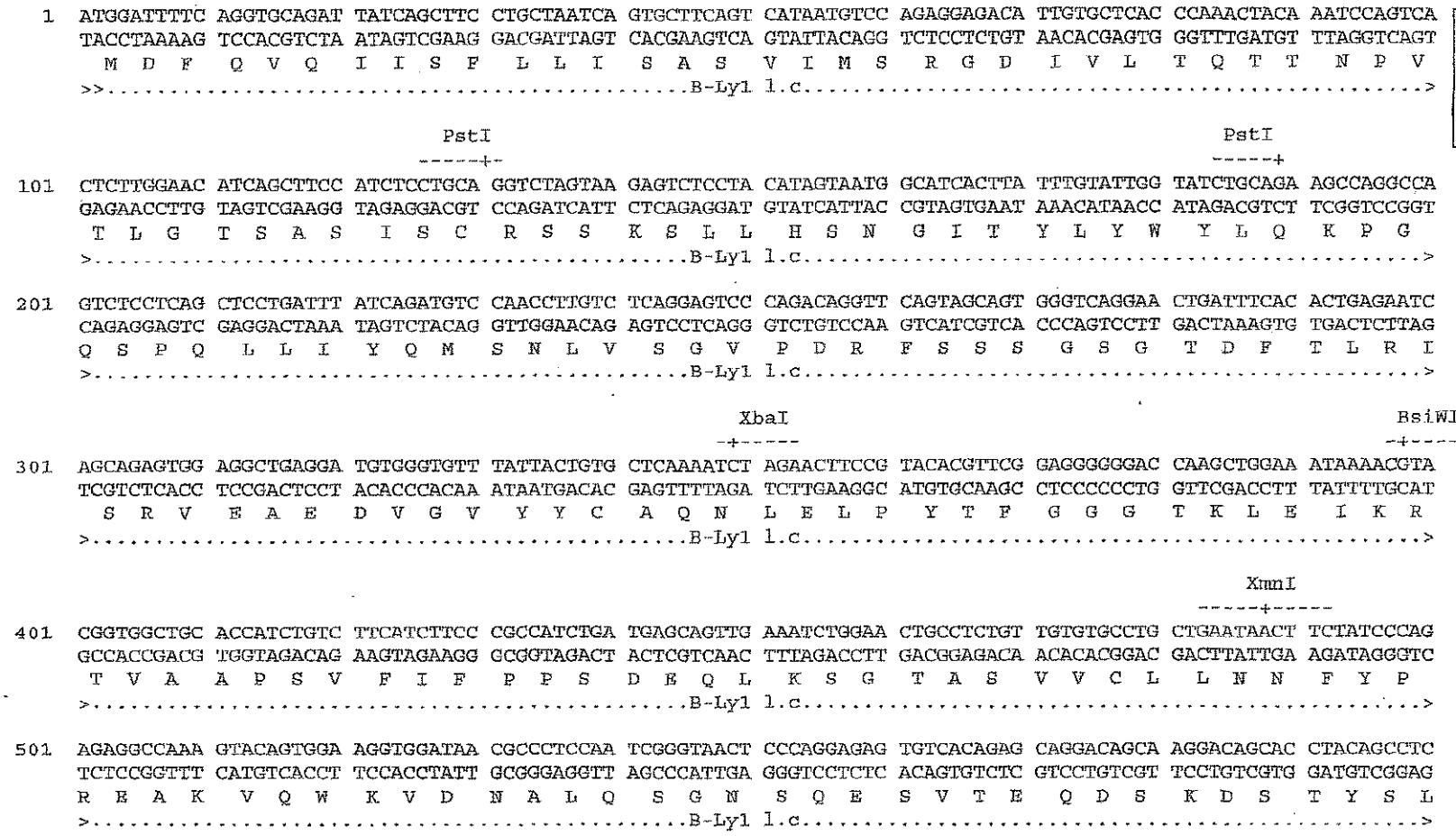
1201  GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG
      CTCACCCTCT CGTTACCCGT CGGCCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTC GAGTGGCACC
        E  W  E   S  N  G   Q  P  E  N   N  Y  K   T  T  P   P  V  L  D   S  D  G   S  F  F   L  Y  S  K   L  T  V
      >.....................................................B-Ly1 h.c.....................................................>

                                                                                    SapI
                                                                                    --------
1301  ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG
      TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTTGGTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCCC
       D  K  S   R  W  Q  Q   G  N  V   F  S  C   S  V  M  H   E  A  L   H  N  H   Y  T  Q  K   S  L  S   L  S  P
      >.....................................................B-Ly1 h.c.....................................................>

1401  TAAATGA
      ATTTACT
      G  K  -
      >....>> B-Ly1 h.c.
```

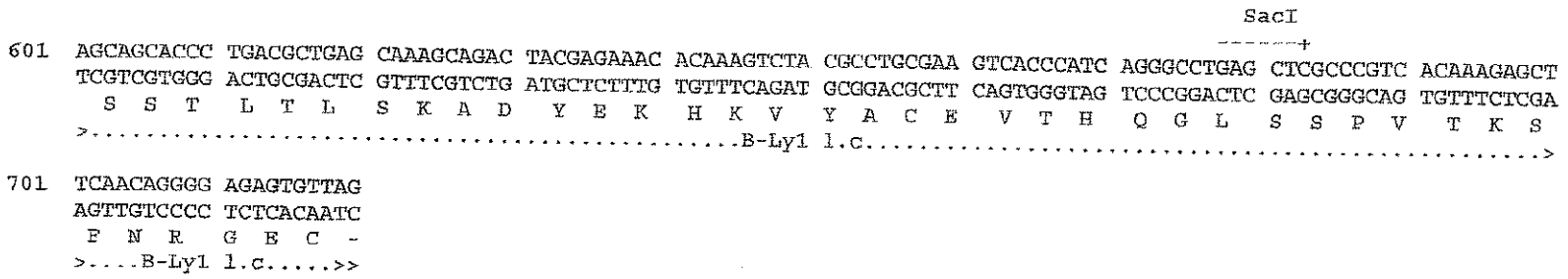
SEQ ID NO: 11 (nucleic acid) and SEQ ID NO: 13 (amino acid)

FIG. 5C



SEQ ID NO 12 (nucleic acid) and SEQ ID NO. 14 (amino acid)

FIG. 6A



SEQ ID NO: 12 (nucleic acid) and SEQ ID NO. 14 (amino acid)

FIG 6B

A

CDR1(Kabat):	
TACTCTTGGATGAAC	SEQ ID NO: 5
TyrSerTrpMetAsn	SEQ ID NO: 15
CDR1(Chothia):	
GGCTACGCATTCAGTTAC	SEQ ID NO: 6
GlyTyrAlaPheSerTyr	SEQ ID NO: 16
CDR1(AbM):	
GGCTACGCATTCAGTTACTCTTGGATGAAC	SEQ ID NO: 7
GlyTyrAlaPheSerTyrSerTrpMetAsn	SEQ ID NO: 17
CDR2(Kabat):	
CGGATTTTTCCTGGAGATGGGGATACTGACTACAATGGGAAATTCAAGGGC	SEQ ID NO: 21
ArgIlePheProGlyAspGlyAspThrAspTyrAsnGlyLysPheLysGly	SEQ ID NO: 25
CDR2(Chothia):	
TTTCCTGGAGATGGGGATACTGAC	SEQ ID NO: 22
PheProGlyAspGlyAspThrAsp	SEQ ID NO: 26
CDR2(AbM):	
CGGATTTTTCCTGGAGATGGGGATACTGAC	SEQ ID NO: 23
ArgIlePheProGlyAspGlyAspThrAsp	SEQ ID NO: 27
CDR3(Kabat, Chothia, AbM):	
AATGTCTTTGATGGTTACTGGTTAGTTTAC	SEQ ID NO: 24
AsnValPheAspGlyTyrTrpLeuValTyr	SEQ ID NO: 28

B

CDR1(Kabat):	
AGGTCTAGTAAGAGTCTCCTACATAGTAATGGCATCACTTATTTGTAT	SEQ ID NO: 8
ArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyrLeuTyr	SEQ ID NO: 18
CDR2(Kabat):	
CAGATGTCCAACCTTGTCTCA	SEQ ID NO: 9
GlnMetSerAsnLeuValSer	SEQ ID NO: 19
CDR3(Kabat):	
GCTCAAAATCTAGAACTTCCGTACACG	SEQ ID NO: 10
AlaGlnAsnLeuGluLeuProTyrThr	SEQ ID NO: 20

FIG. 7

1.relative percentages

	Bly-1 m1 031024 016	+ EndoH Bly-1 m1 031024 017
1053		
1256		
1282		
1298		3.70%
1339	18.60%	17.90%
1460		4.30%
1486	5.90%	5.50%
1502	5.10%	3.70%
1543	35.00%	39.20%
1622		
1647	4.60%	3.00%
1664	7%	
1680		
1688	11.00%	10.30%
1705	7.20%	7.30%
1810		
1826		
1850	5.90%	5.20%
1972		
2012		
	100%	100%

FIG. 8A

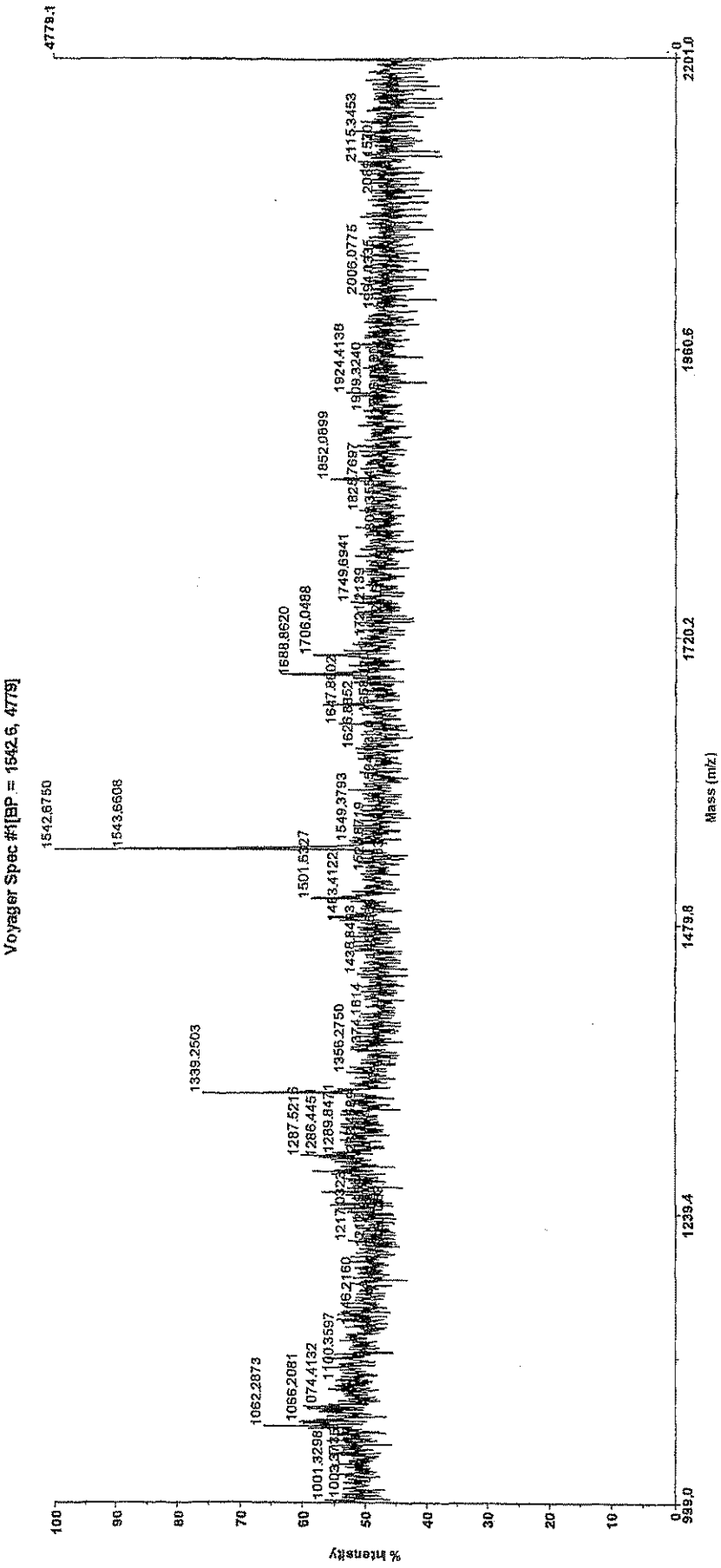

Voyager Spec #1[BP = 1542.6, 4779]
1542.6750
1543.6608
1339.2503
1062.2873
1056.2081
1074.4132
1100.3587
1001.3296
1003.3113
1287.5215
1286.445
1289.8471
1356.2750
1501.5327
1549.3793
1688.8620
1706.0488
1749.6941
1852.0699
1924.4138
2006.0775
2115.3453
4778.1
0
2201.0
1960.6
1720.2
1479.8
1239.4
999.0
Mass (m/z)
% Intensity
100
90
80
70
60
50
40
30
20
10
0

FIG. 8B

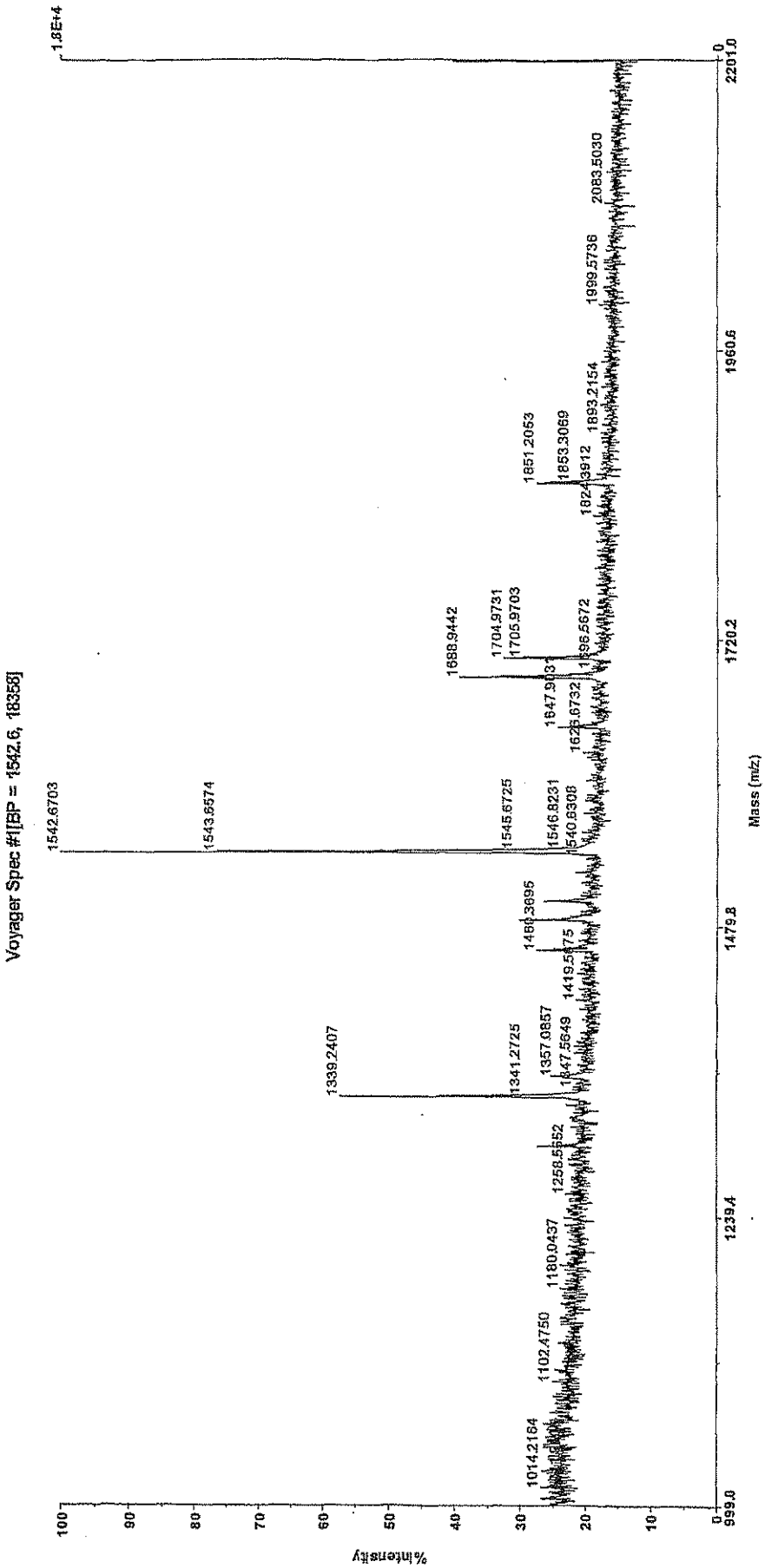

Voyager Spec #1[BP = 1542.6, 18358]
1.8E+4
0
100
90
80
70
60
50
40
30
20
10
0
%Intensity
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
Mass (m/z)
1542.6703
1543.6574
1545.6725
1546.8231
1540.6308
1626.6732
1647.9083
1688.9442
1704.9731
1705.9703
1696.5672
1824.3912
1851.2053
1853.3069
1893.2154
1999.5736
2083.5030
1480.3695
1419.5875
1341.2725
1339.2407
1357.0857
1647.5649
1258.5552
1180.0437
1102.4750
1014.2164

FIG. 8C

Figure 9

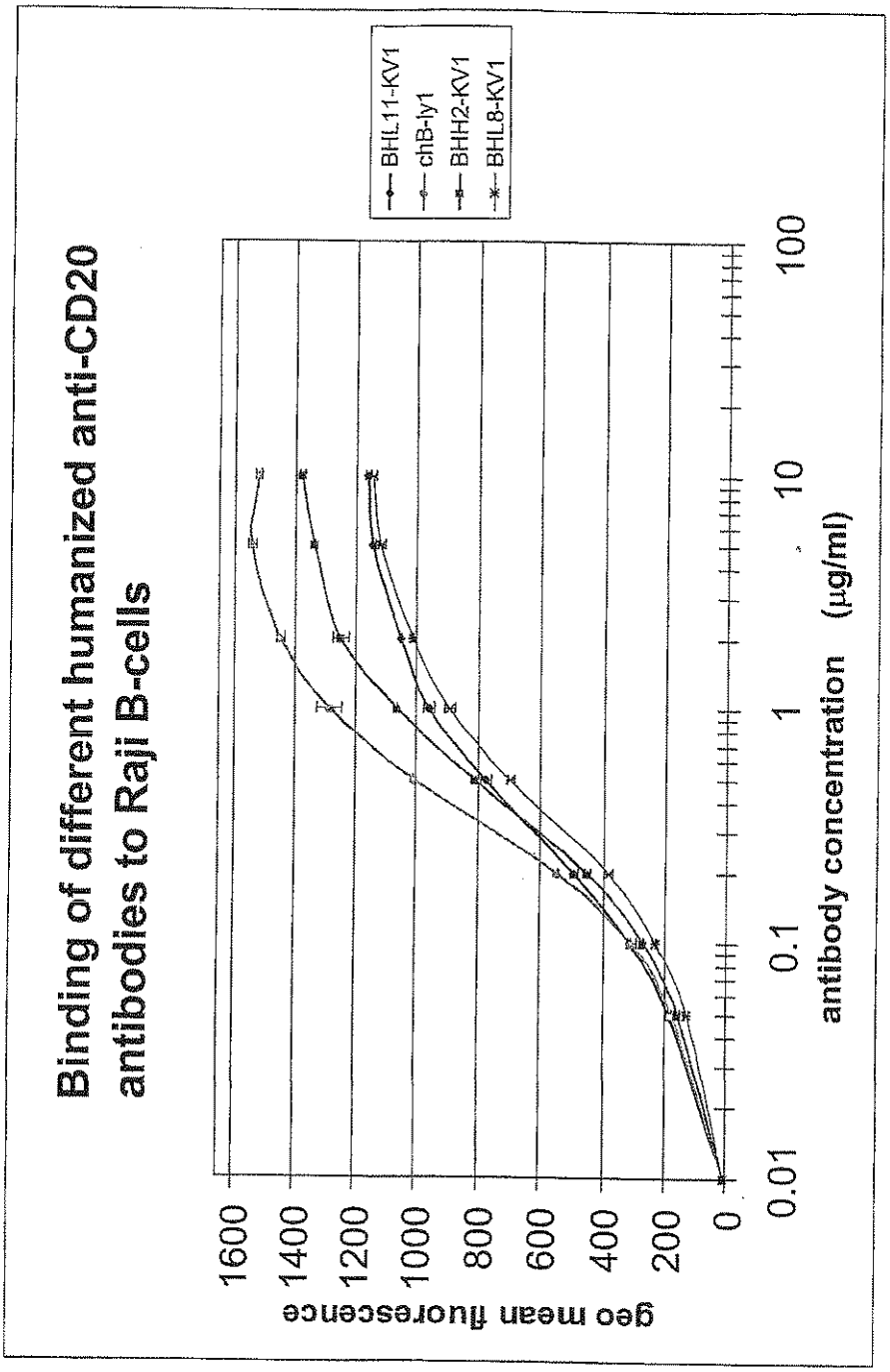

Binding of different humanized anti-CD20 antibodies to Raji B-cells
BHL11-KV1
chB-ly1
BHH2-KV1
BHL8-KV1
geo mean fluorescence
1600
1400
1200
1000
800
600
400
200
0
0.01
0.1
1
10
100
antibody concentration (µg/ml)

Figure 10

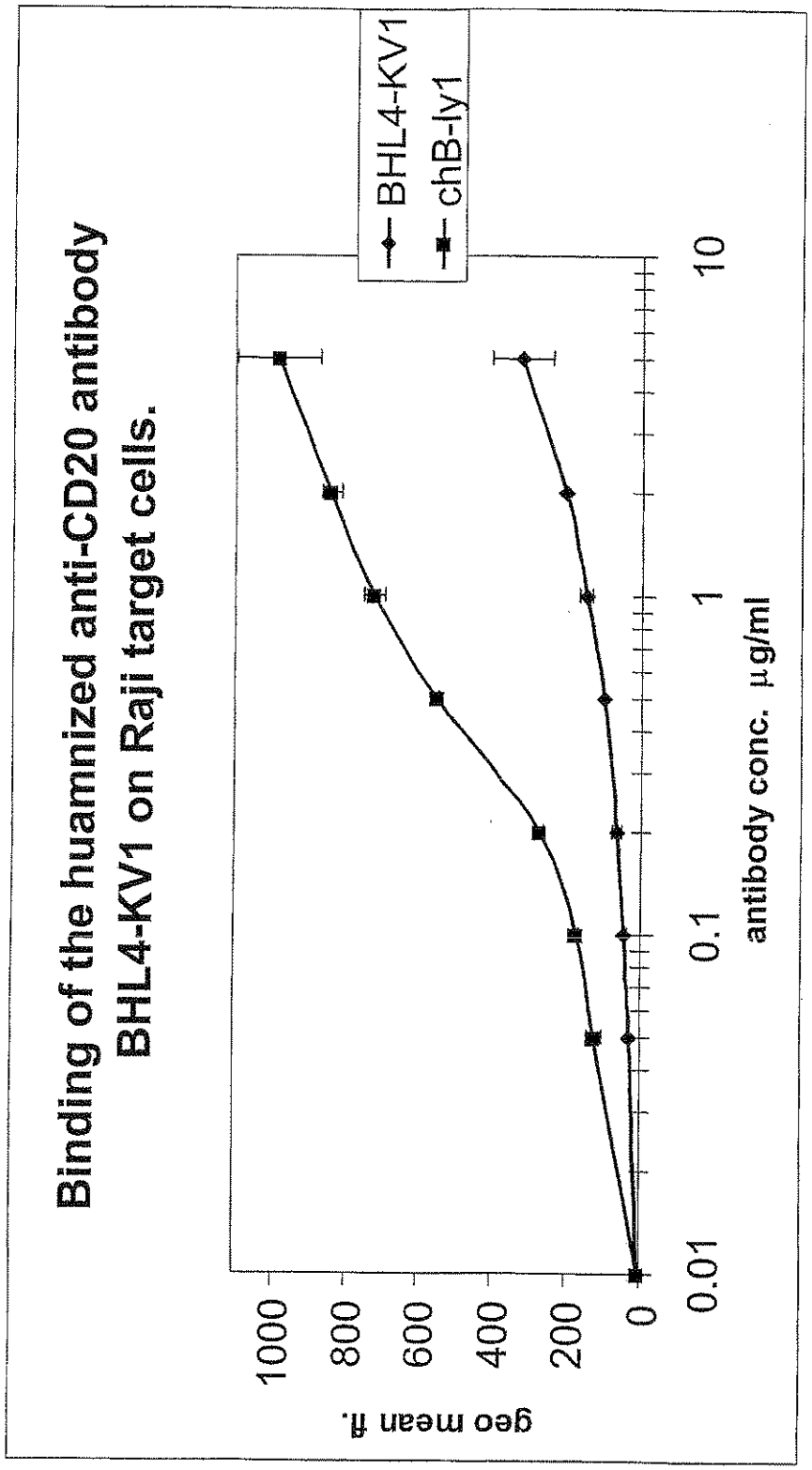

Binding of the huamnized anti-CD20 antibody
BHL4-KV1 on Raji target cells.
BHL4-KV1
chB-Iy1
geo mean fl.
1000
800
600
400
200
0
0.01
0.1
1
10
antibody conc. µg/ml

Figure 11

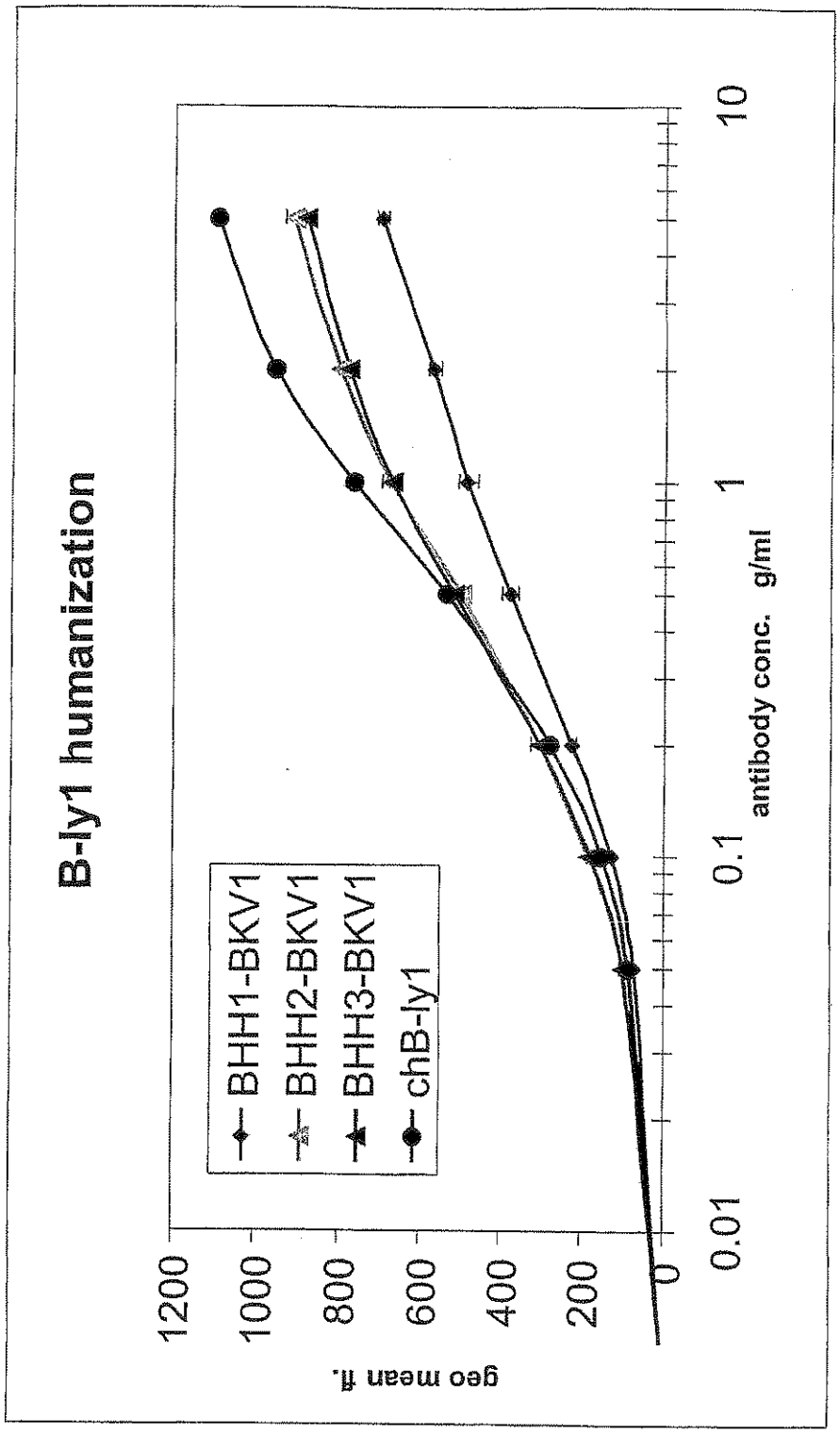

B-ly1 humanization
BHH1-BKV1
BHH2-BKV1
BHH3-BKV1
chB-ly1
geo mean fl.
1200
1000
800
600
400
200
0
0.01
0.1
1
10
antibody conc. g/ml

Figure 12

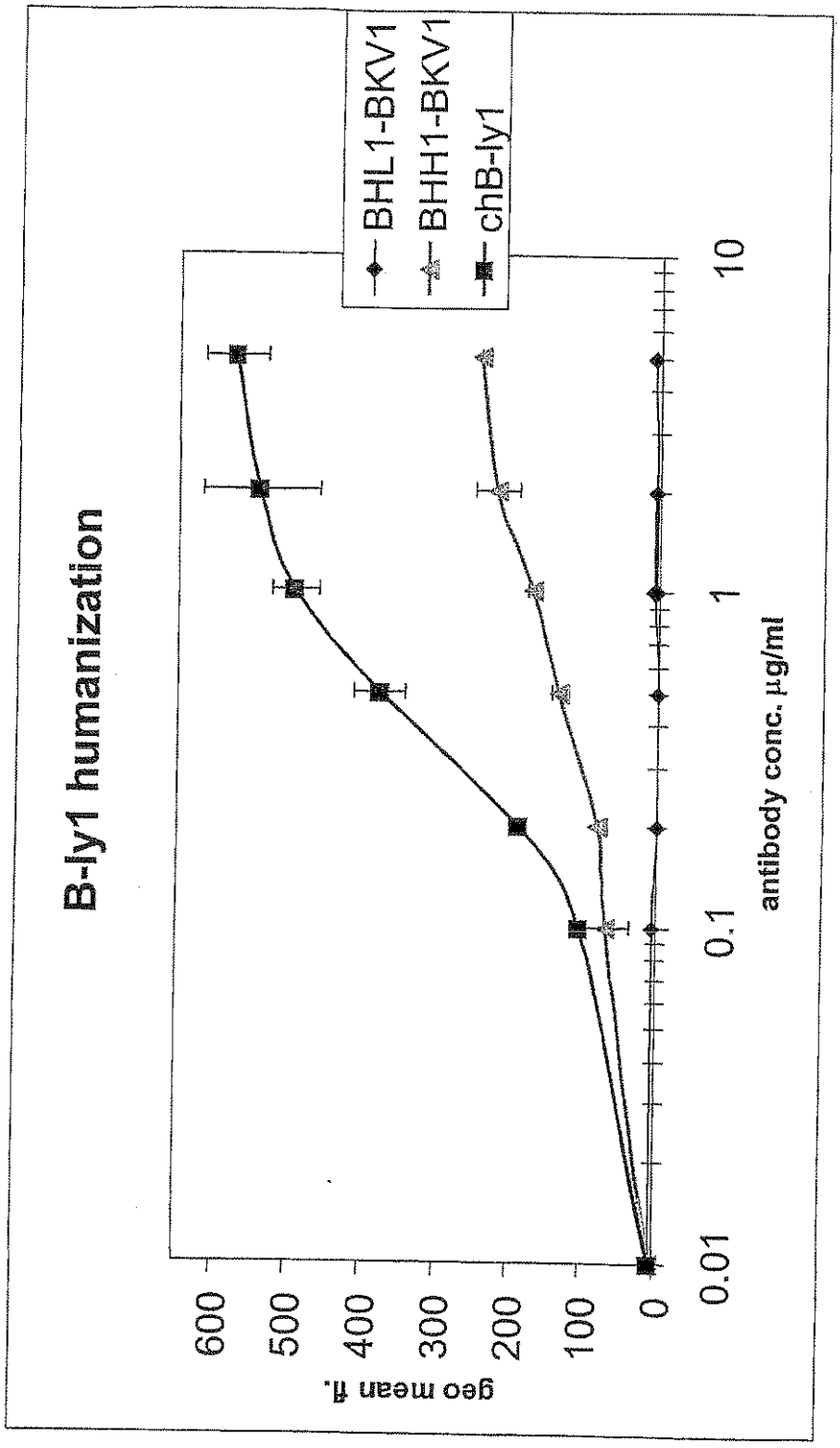

B-ly1 humanization
BHL1-BKV1
BHH1-BKV1
chB-ly1
geo mean fl.
600
500
400
300
200
100
0
0.01
0.1
1
10
antibody conc. µg/ml

Figure 13

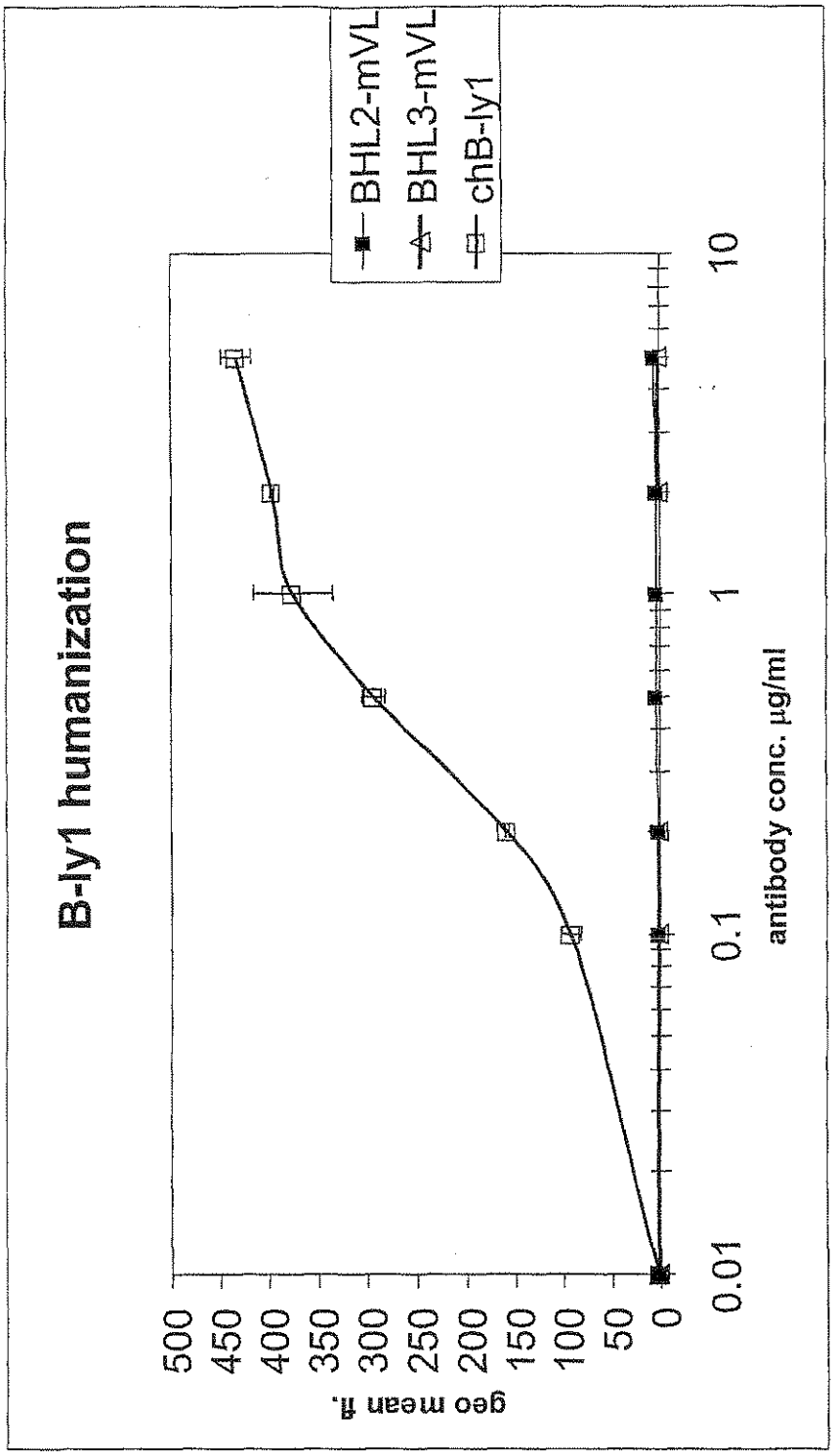

B-ly1 humanization
BHL2-mVL
BHL3-mVL
chB-ly1
geo mean fl.
500
450
400
350
300
250
200
150
100
50
0
0.01
0.1
1
10
antibody conc. µg/ml

Figure 14

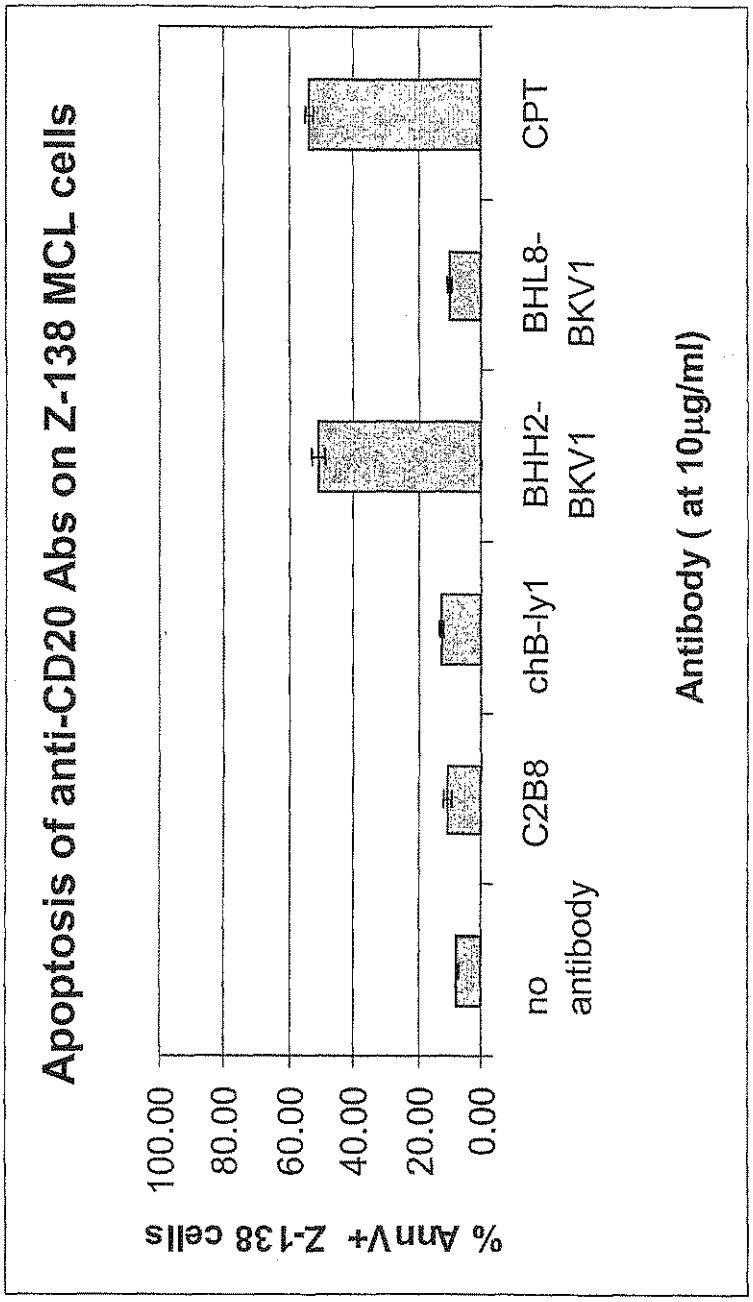

Apoptosis of anti-CD20 Abs on Z-138 MCL cells
% AnnV+ Z-138 cells
100.00
80.00
60.00
40.00
20.00
0.00
no antibody
C2B8
chB-ly1
BHH2-BKV1
BHL8-BKV1
CPT
Antibody (at 10µg/ml)

Figure15

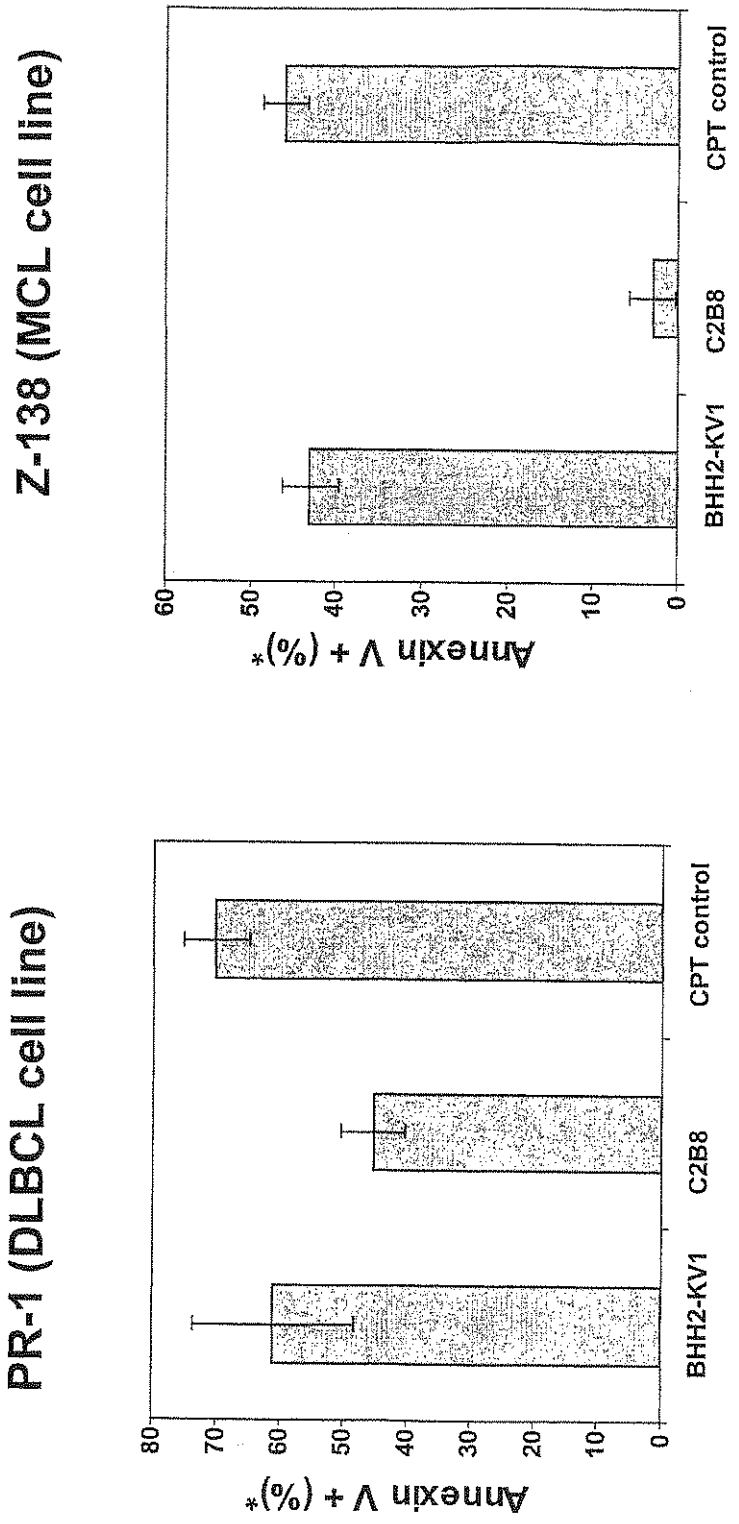

Z-138 (MCL cell line)
Annexin V + (%)*
0
10
20
30
40
50
60
BHH2-KV1
C2B8
CPT control
PR-1 (DLBCL cell line)
Annexin V + (%)*
0
10
20
30
40
50
60
70
80
BHH2-KV1
C2B8
CPT control

Figure 16

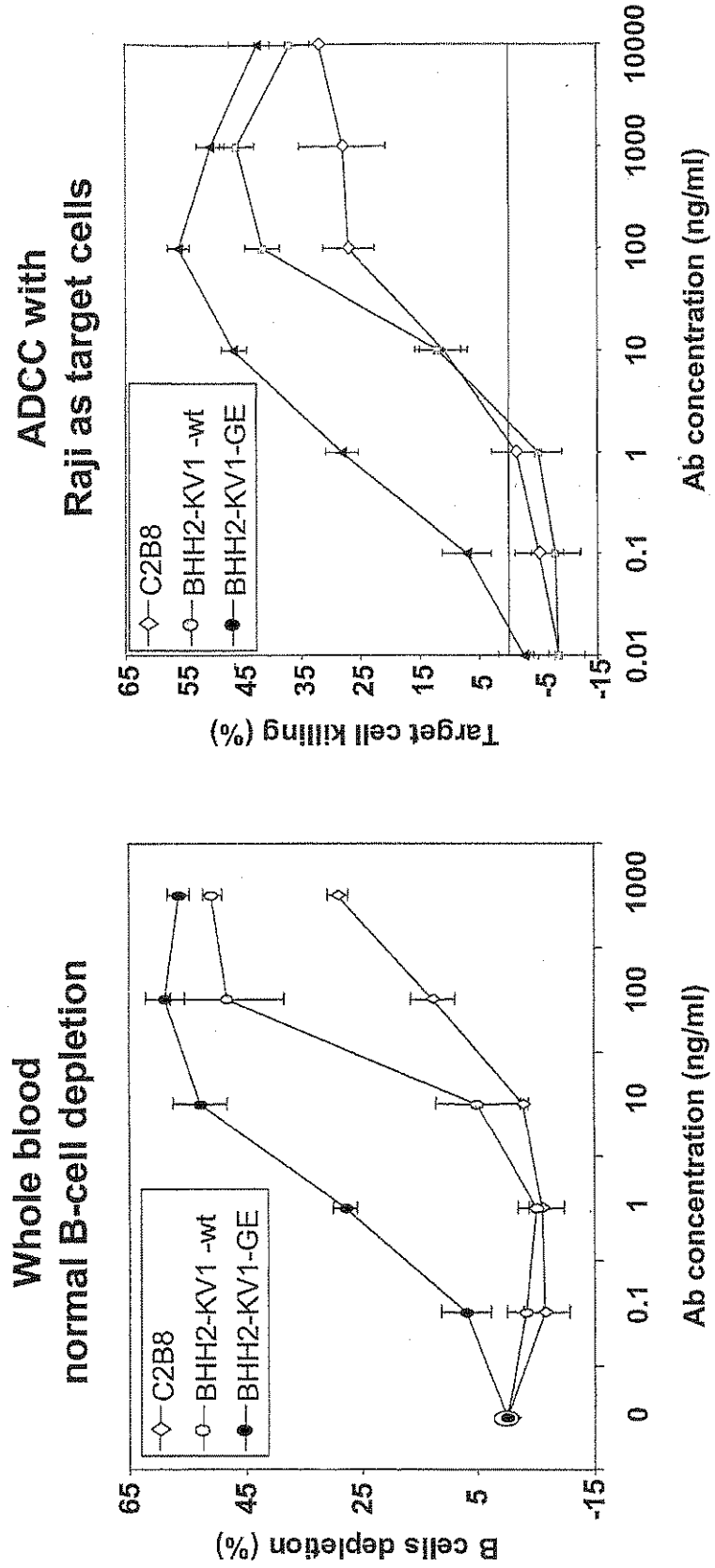

Whole blood
normal B-cell depletion
B cells depletion (%)
65
45
25
5
-15
0
0.1
1
10
100
1000
Ab concentration (ng/ml)
C2B8
BHH2-KV1 -wt
BHH2-KV1-GE
ADCC with
Raji as target cells
Target cell killing (%)
65
55
45
35
25
15
5
-5
-15
0.01
0.1
1
10
100
1000
10000
Ab concentration (ng/ml)
C2B8
BHH2-KV1 -wt
BHH2-KV1-GE

Figure 17

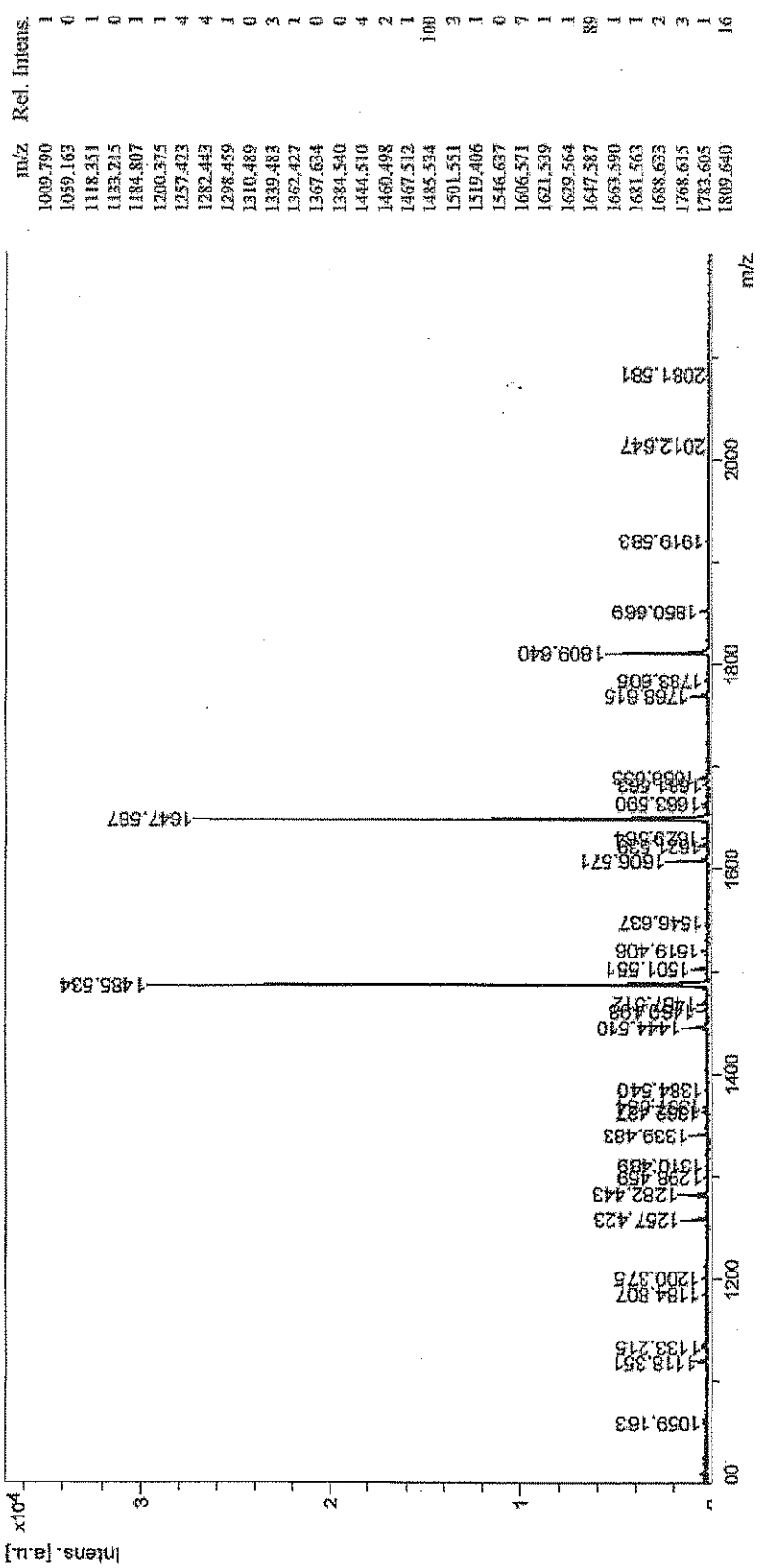

m/z
Rel. Intens.
1009.790 1
1059.163 0
1118.351 1
1133.215 0
1184.807 1
1200.375 1
1257.423 4
1282.443 4
1298.459 1
1310.489 0
1339.483 3
1362.427 1
1367.634 0
1384.540 0
1444.510 4
1460.498 2
1467.512 1
1485.534 100
1501.551 3
1519.406 1
1546.637 0
1606.571 7
1621.539 1
1629.564 1
1647.587 89
1663.590 1
1681.563 1
1688.623 2
1768.615 3
1783.605 1
1809.640 16
Intens. [a.u.]
x10⁴
m/z
1059.163
1118.351
1133.215
1184.807
1200.375
1257.423
1282.443
1298.459
1310.489
1339.483
1384.540
1444.510
1485.534
1501.551
1519.406
1546.637
1606.571
1647.587
1663.590
1768.615
1809.640
1850.669
1919.583
2012.547
2081.581

Figure 18

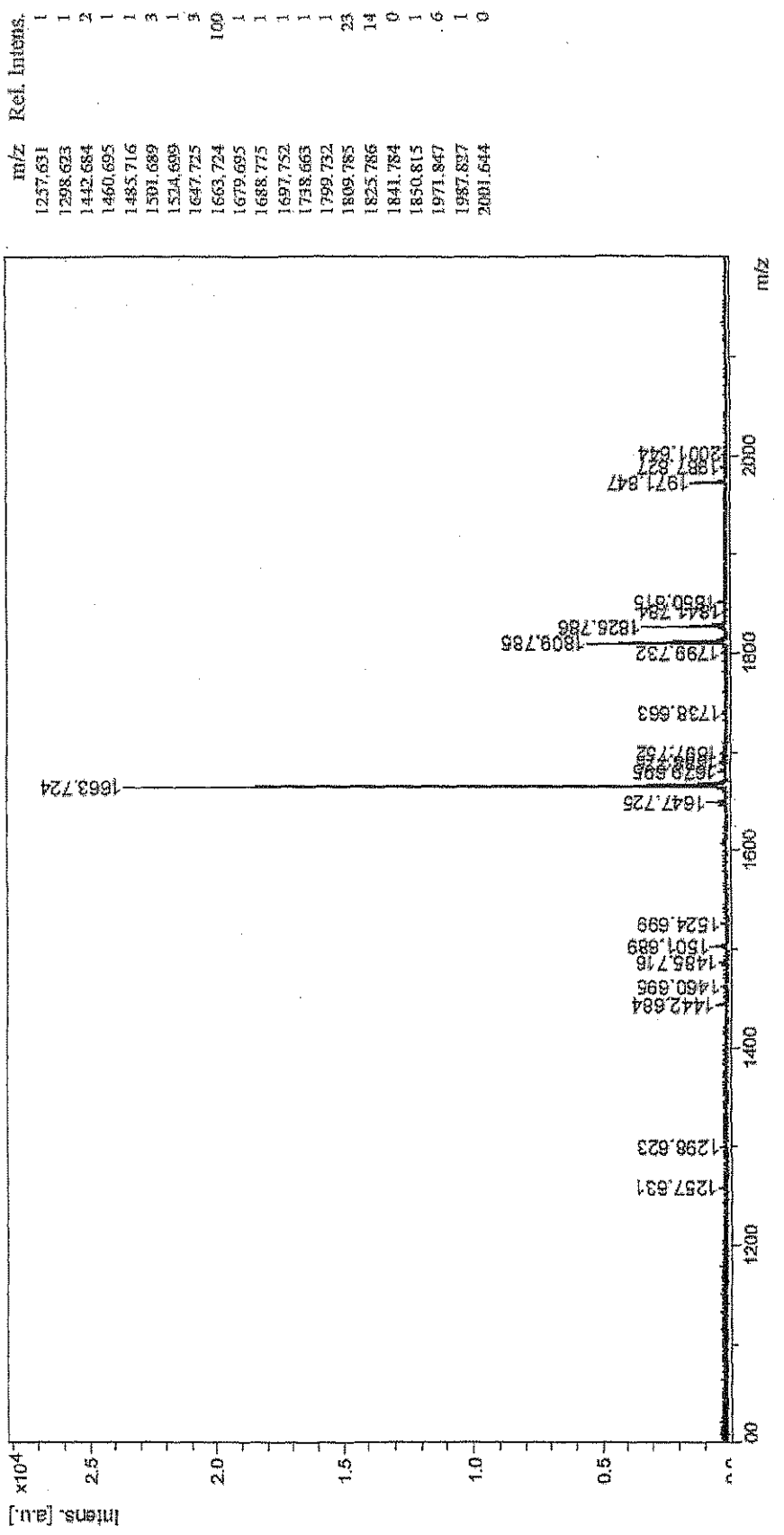
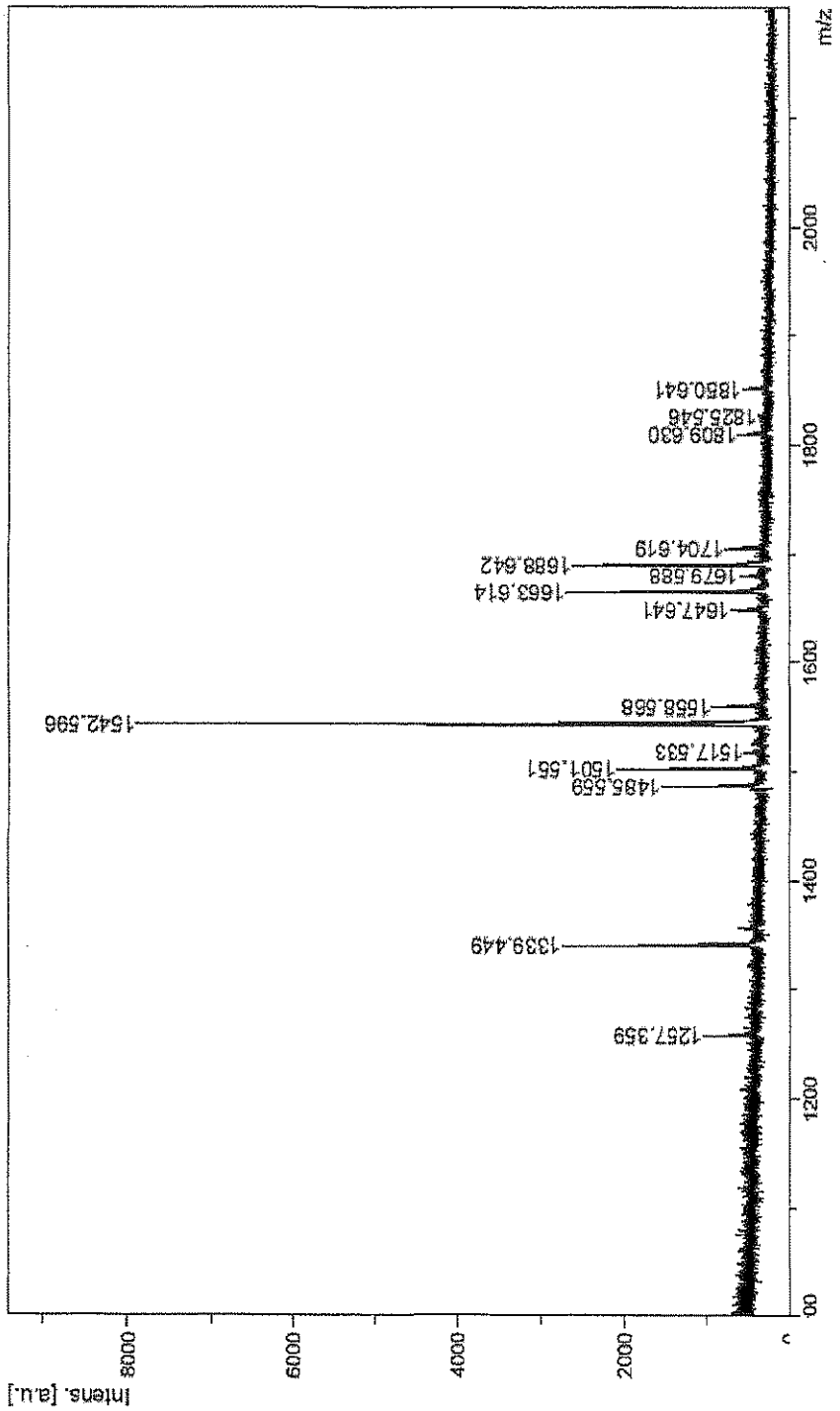

m/z Ref. Intens.
1257.631 1
1298.623 1
1442.684 2
1460.695 1
1485.716 1
1501.689 3
1524.699 1
1647.725 3
1663.724 100
1679.695 1
1688.775 1
1697.752 1
1738.663 1
1799.732 1
1809.785 23
1825.786 14
1841.784 0
1850.815 1
1971.847 6
1987.827 1
2001.644 0
Intens. [a.u.]
x10^4
2.5
2.0
1.5
1.0
0.5
0.0
1200
1400
1600
1800
2000
m/z
1257.631
1298.623
1442.684
1460.695
1485.716
1501.689
1524.699
1647.725
1663.724
1738.663
1799.732
1809.785
1825.786
1841.784
1850.815
1971.847
1987.827
2001.644

Figure 19



m/z	Rel. Intens.
1257.359	8
1339.449	31
1485.559	16
1501.551	23
1517.533	2
1542.596	100
1558.568	8
1647.641	5
1663.614	32
1679.588	4
1688.642	31
1704.619	6
1809.630	5
1825.546	1
1850.641	4

Figure 20

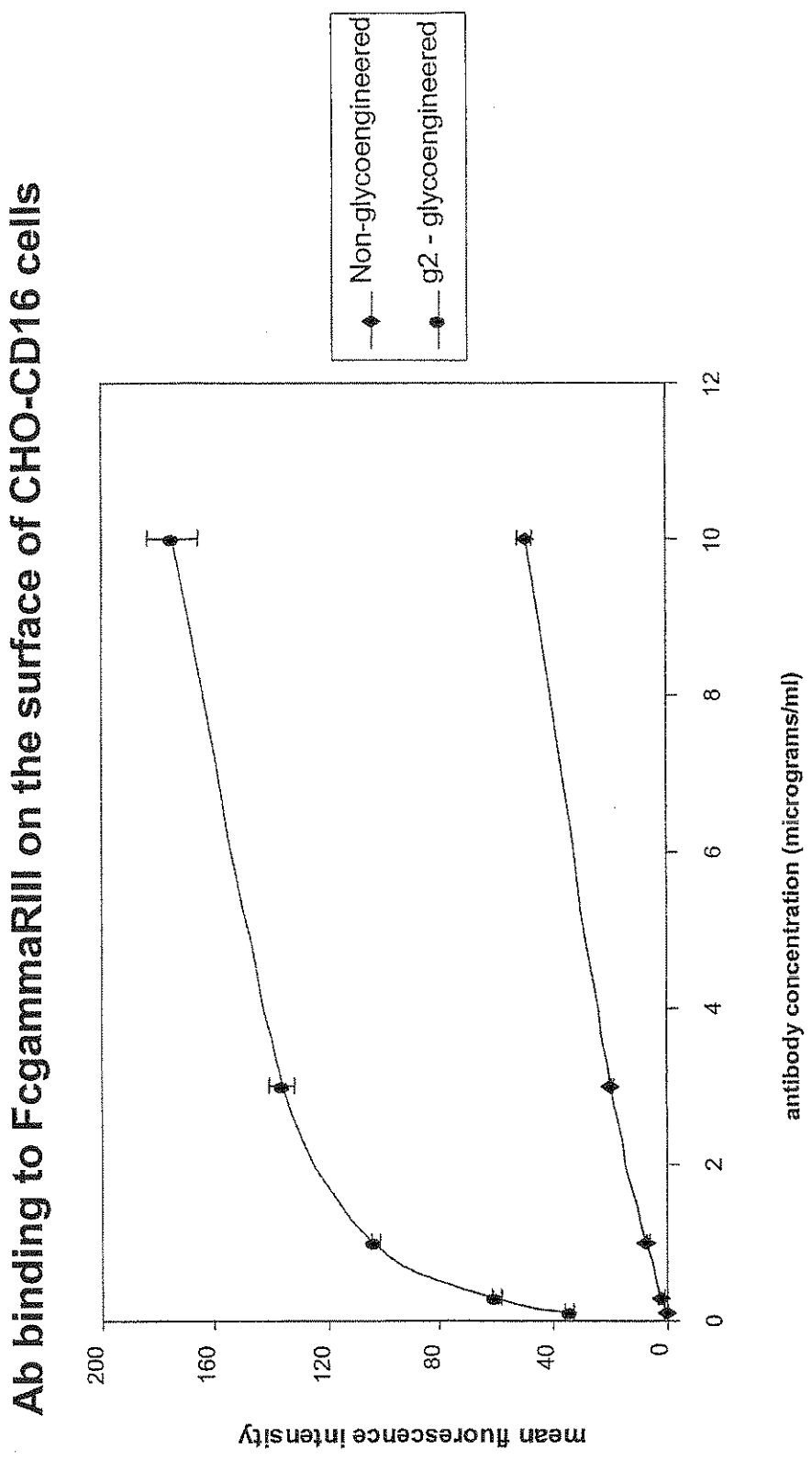
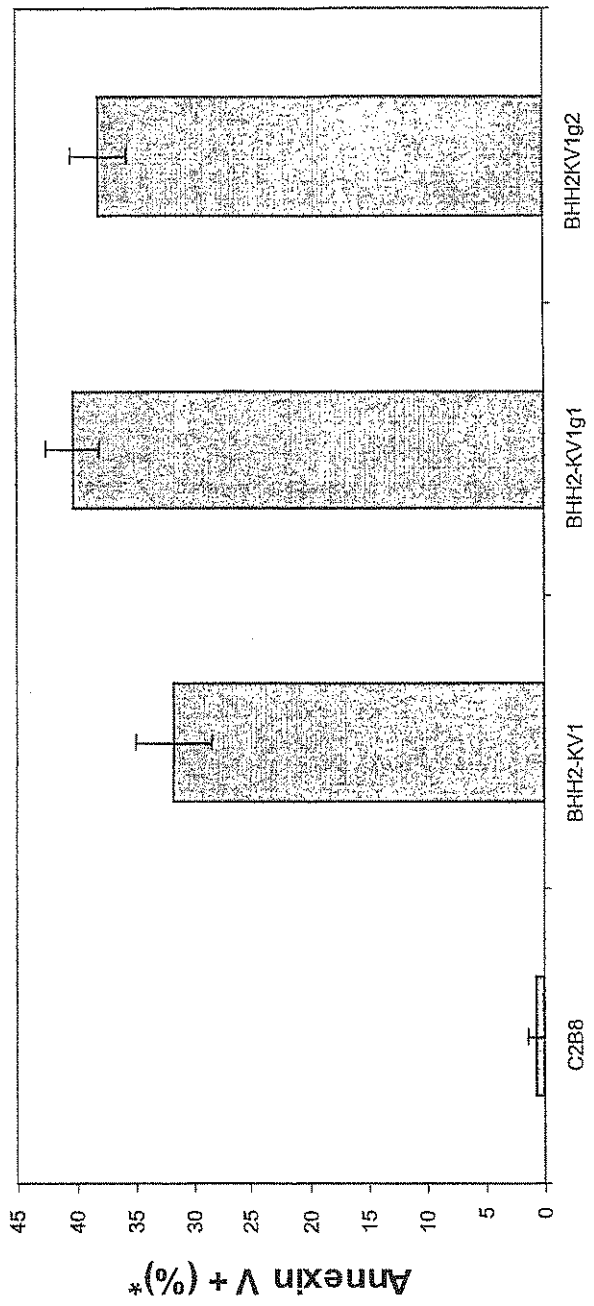

Ab binding to FcgammaRIII on the surface of CHO-CD16 cells
Non-glycoengineered
g2 - glycoengineered
mean fluorescence intensity
0
40
80
120
160
200
0
2
4
6
8
10
12
antibody concentration (micrograms/ml)

Figure 21


Apoptosis by anti-CD20 Abs
Z-138 mantle cell lymphoma cell line
Annexin V + (%)*
45
40
35
30
25
20
15
10
5
0
C2B8
BHH2-KV1
BHH2-KV1g1
BHH2KV1g2