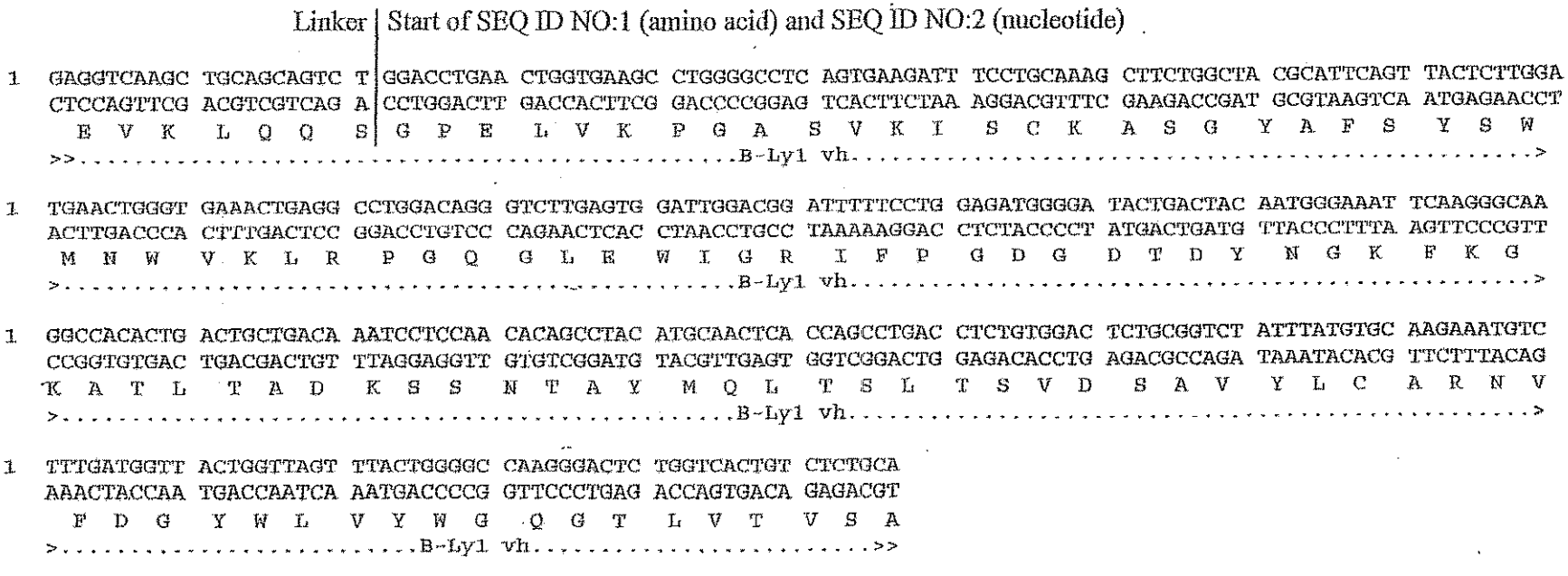

Linker
Start of SEQ ID NO:1 (amino acid) and SEQ ID NO:2 (nucleotide)
1 GAGGTCAAGC TGCAGCAGTC T GGACCTGAA CTGGTGAAGC CTGGGGCCTC AGTGAAGATT TCCTGCAAAG CTTCTGGCTA CGCATTCAGT TACTCTTGGA
CTCCAGTTCG ACGTCGTCAG A CCTGGACTT GACCACTTCG GACCCCGGAG TCACTTCTAA AGGACGTTTC GAAGACCGAT GCGTAAGTCA ATGAGAACCT
E V K L 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.....>
1 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.....>
1 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.....>
1 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

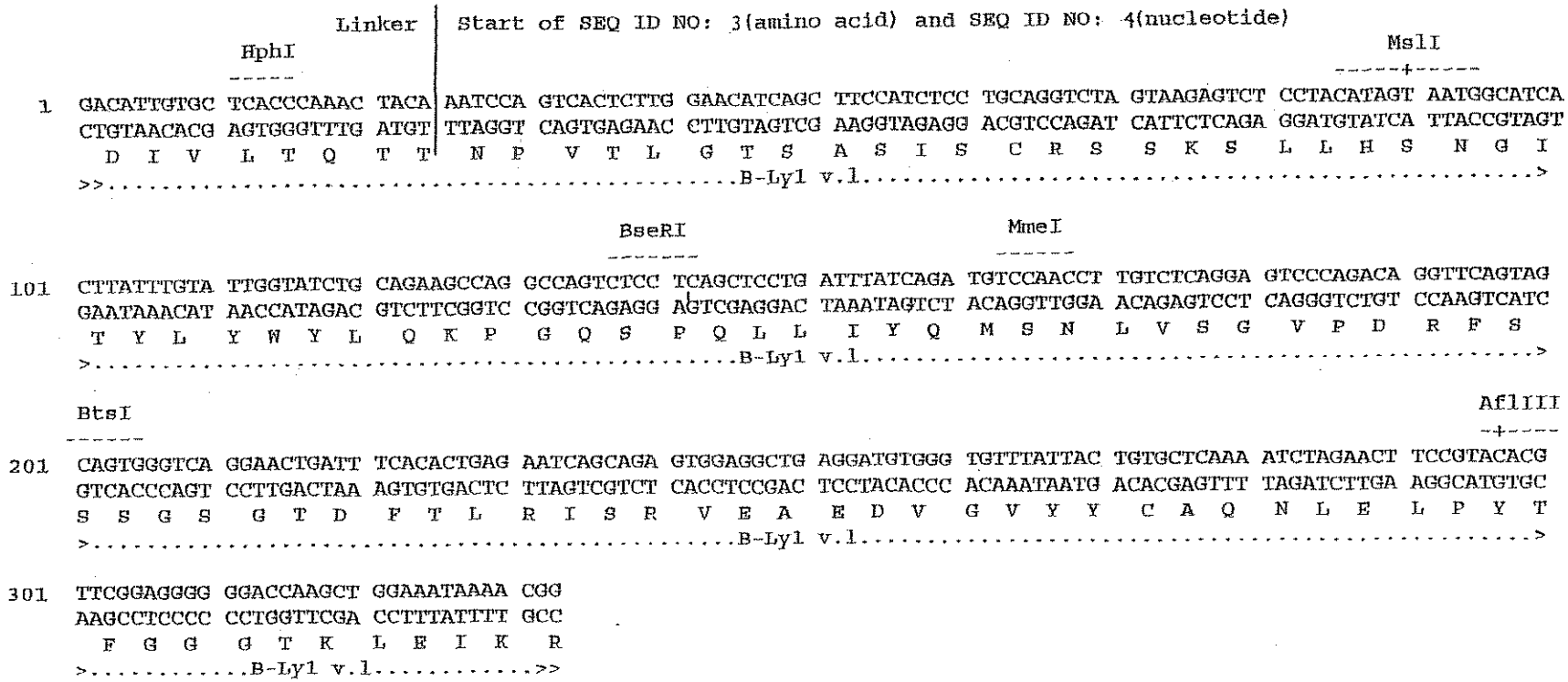

Linker
Start of SEQ ID NO: 3(amino acid) and SEQ ID NO: 4(nucleotide)
HphI
MslI
1 GACATTGTGC TCACCCAAAC TACA AATCCA GTCACTCTTG GAACATCAGC TTCCATCTCC TGCAGGTCTA GTAAGAGTCT CCTACATAGT AATGGCATCA
CTGTAACACG AGTGGGTTTG ATGT TTAGGT CAGTGAGAAC CTTGTAGTCG AAGGTAGAGG ACGTCCAGAT CATTCTCAGA GGATGTATCA TTACCGTAGT
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

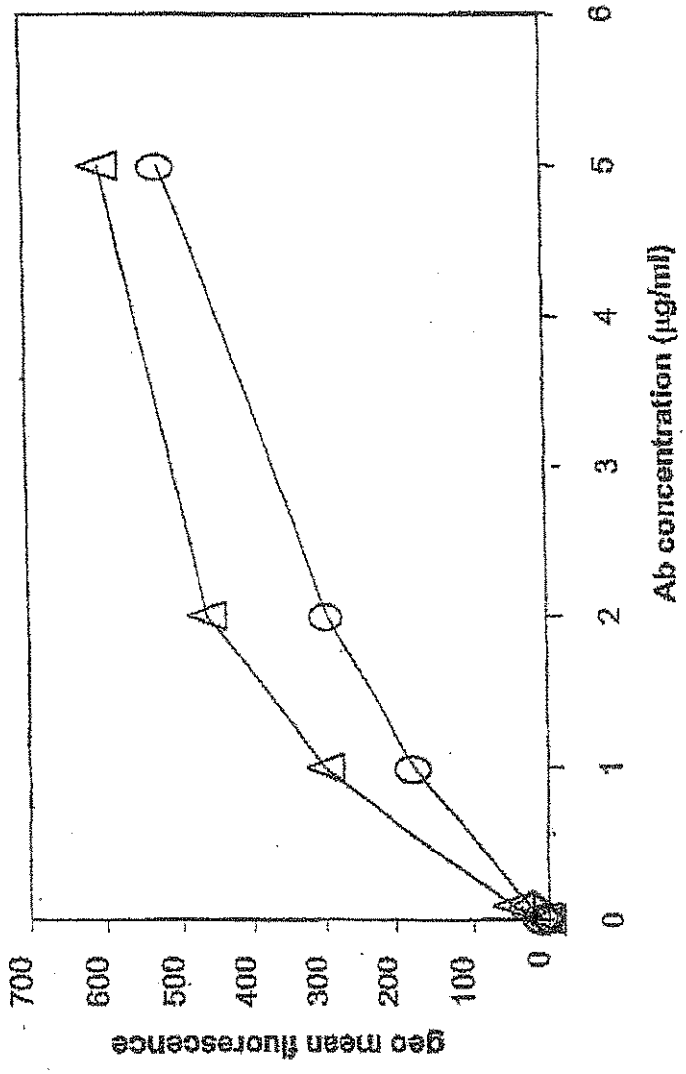

geo mean fluorescence
700
600
500
400
300
200
100
0
0
1
2
3
4
5
6
Ab concentration (µg/ml)

FIG. 3

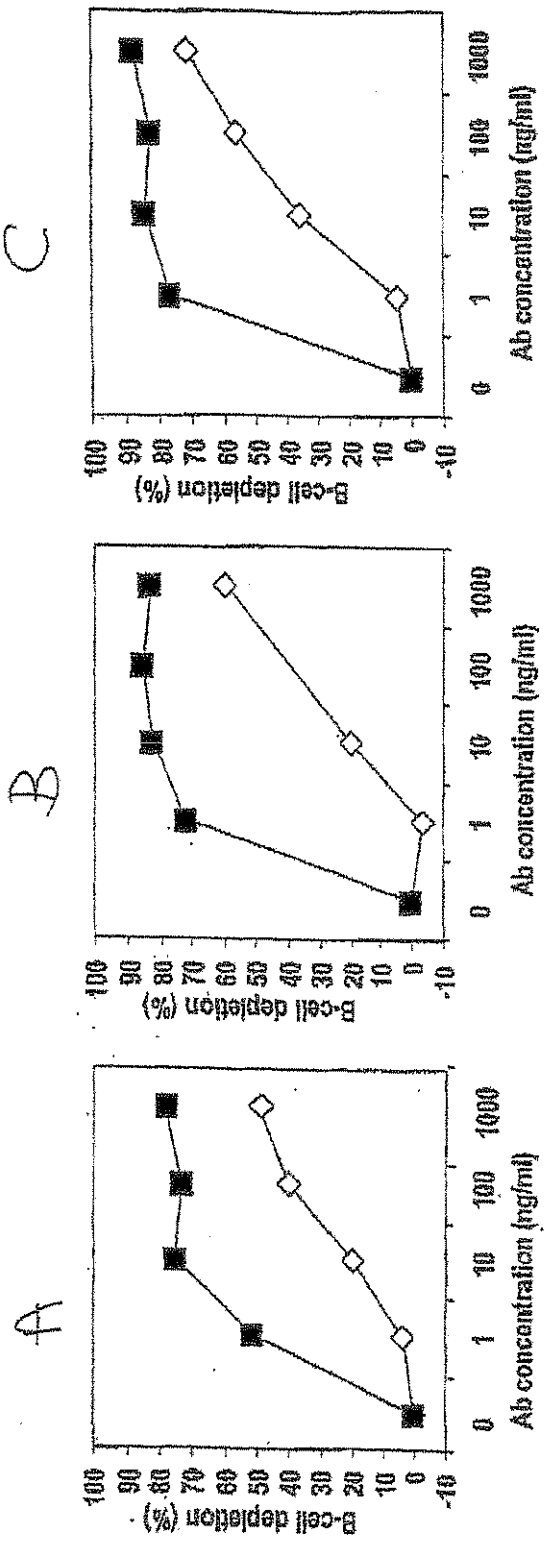
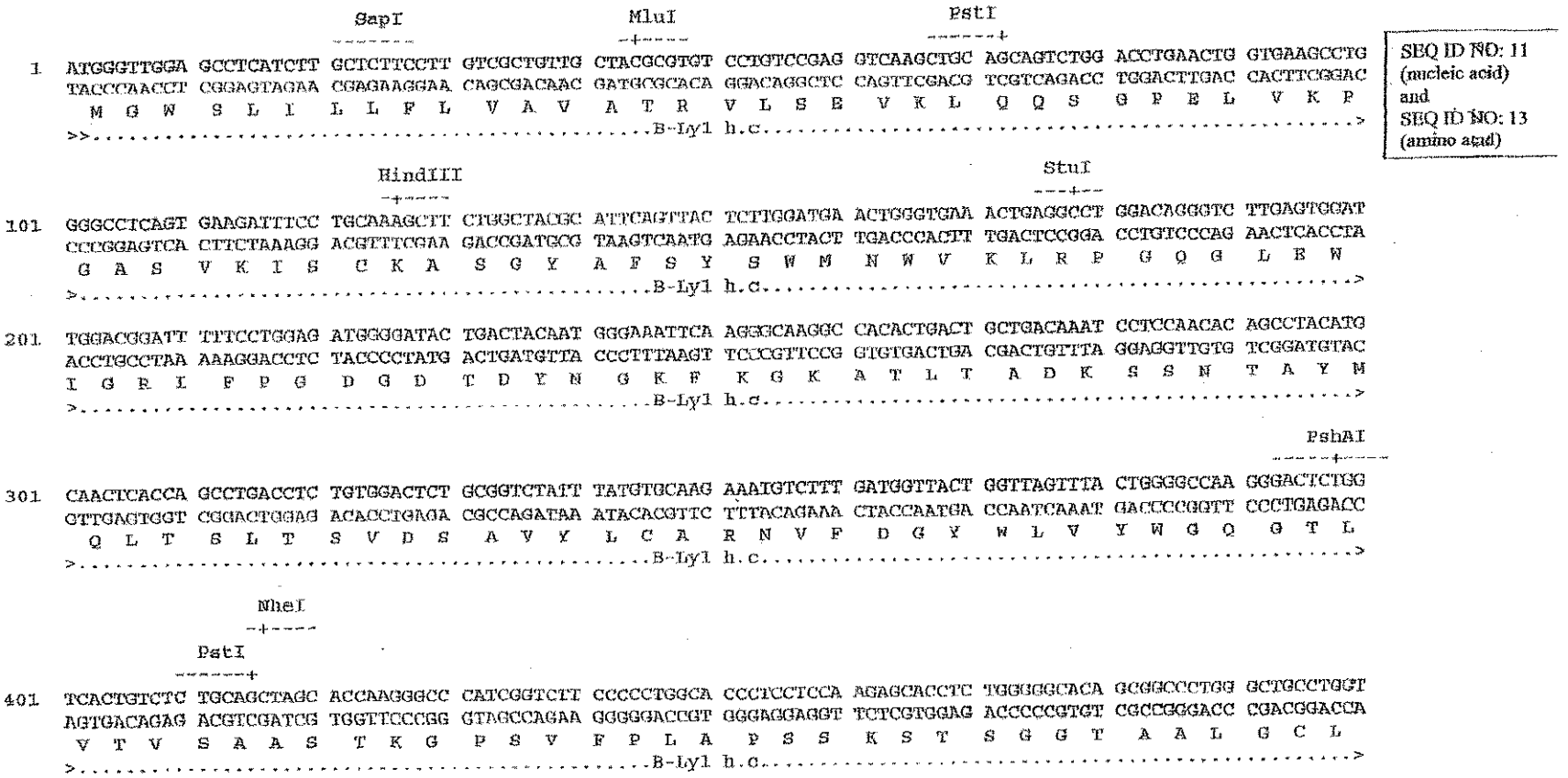
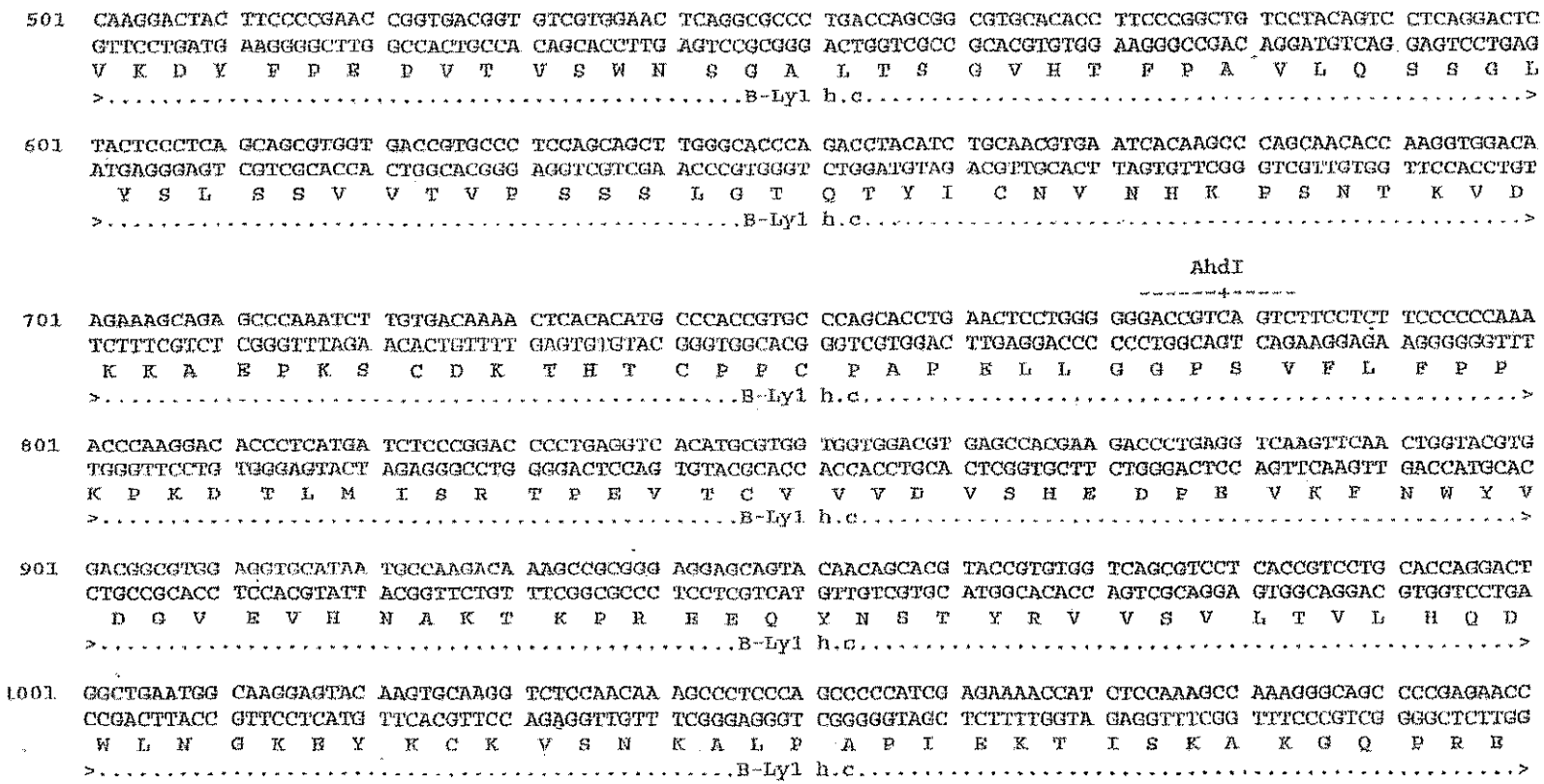

A
B
C
B-cell depletion (%)
Ab concentration (ng/ml)
100
90
80
70
60
50
40
30
20
10
0
-10
0
1
10
100
1000

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.....................................................>

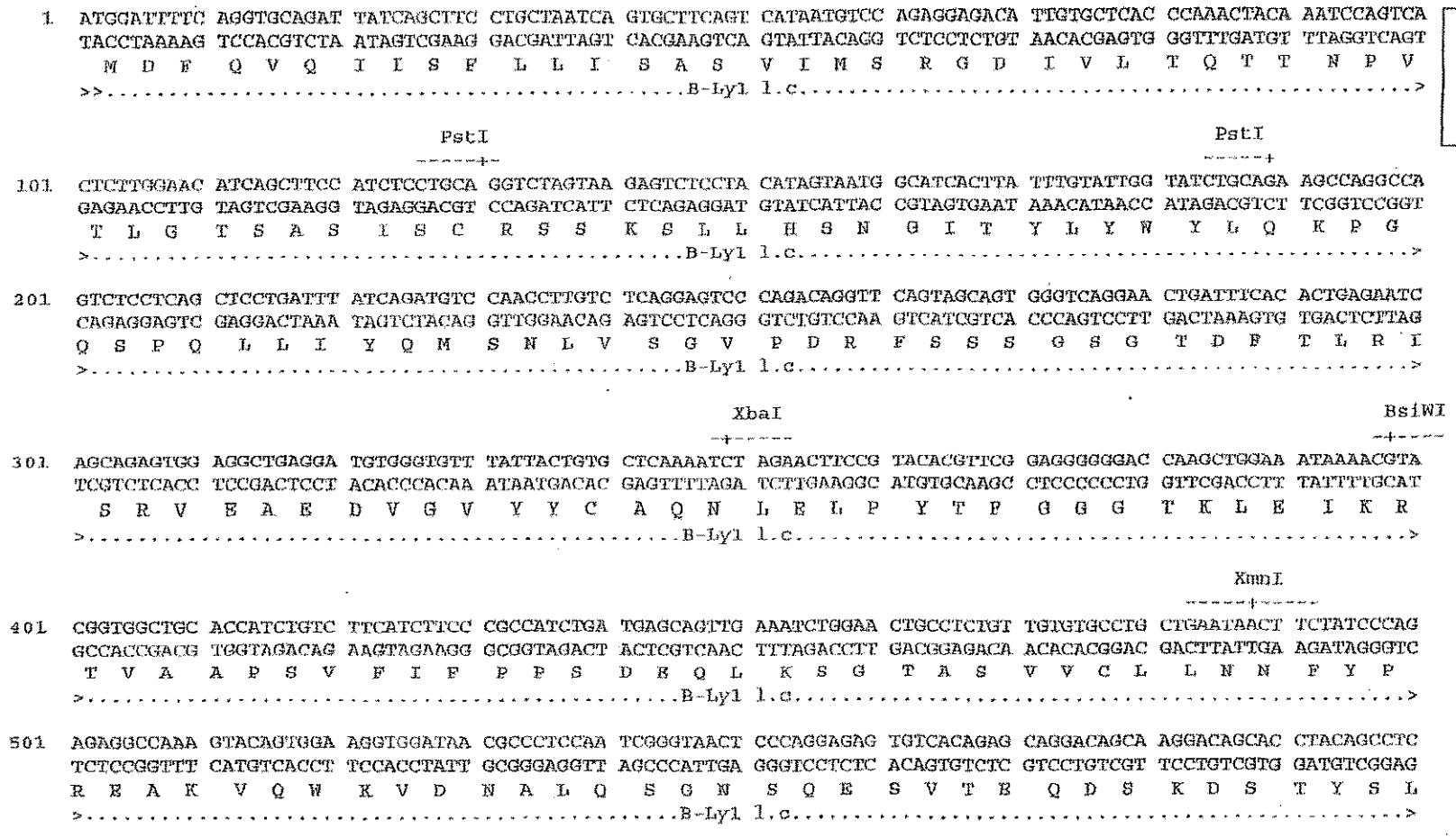
                                                                                                  SapI
                                                                                                  --------
1301  ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG
      TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTTGGTGAT 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)

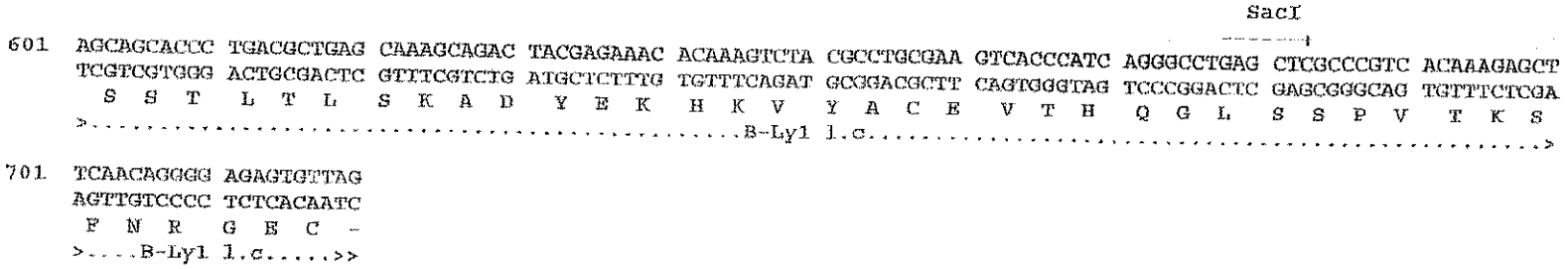
126

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):
'ACTCTTGGATGAAC — SEQ ID NO: 5
TyrSerTrpMetAsn — SEQ ID NO: 15

CDR1(Chothia):
GCTACGCATTCAGTTAC — SEQ ID NO: 6
GlyTyrAlaPheSerTyr — SEQ ID NO: 16

CDR1(AbM):
GCTACGCATTCAGTTACTCTTGGATGAAC — SEQ ID NO: 7
GlyTyrAlaPheSerTyrSerTrpMetAsn — SEQ ID NO: 17

CDR2(Kabat):
GGATTTTTCCTGGAGATGGGGATACTGACTACAATGGGAAATTCAAGGGC — SEQ ID NO: 21
ArgIlePheProGlyAspGlyAspThrAspTyrAsnGlyLysPheLysGly — SEQ ID NO: 25

CDR2(Chothia):
TTCCTGGAGATGGGGATACTGAC — SEQ ID NO: 22
PheProGlyAspGlyAspThrAsp — SEQ ID NO: 26

CDR2(AbM):
GGATTTTTCCTGGAGATGGGGATACTGAC — SEQ ID NO: 23
ArgIlePheProGlyAspGlyAspThrAsp — SEQ ID NO: 27

CDR3(Kabat, Chothia, AbM):
ATGTCTTTGATGGTTACTGGTTAGTTTAC — SEQ ID NO: 24
AsnValPheAspGlyTyrTrpLeuValTyr — SEQ ID NO: 28

B

CDR1(Kabat):
GGTCTAGTAAGAGTCTCCTACATAGTAATGGCATCACTTATTTGTAT — 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

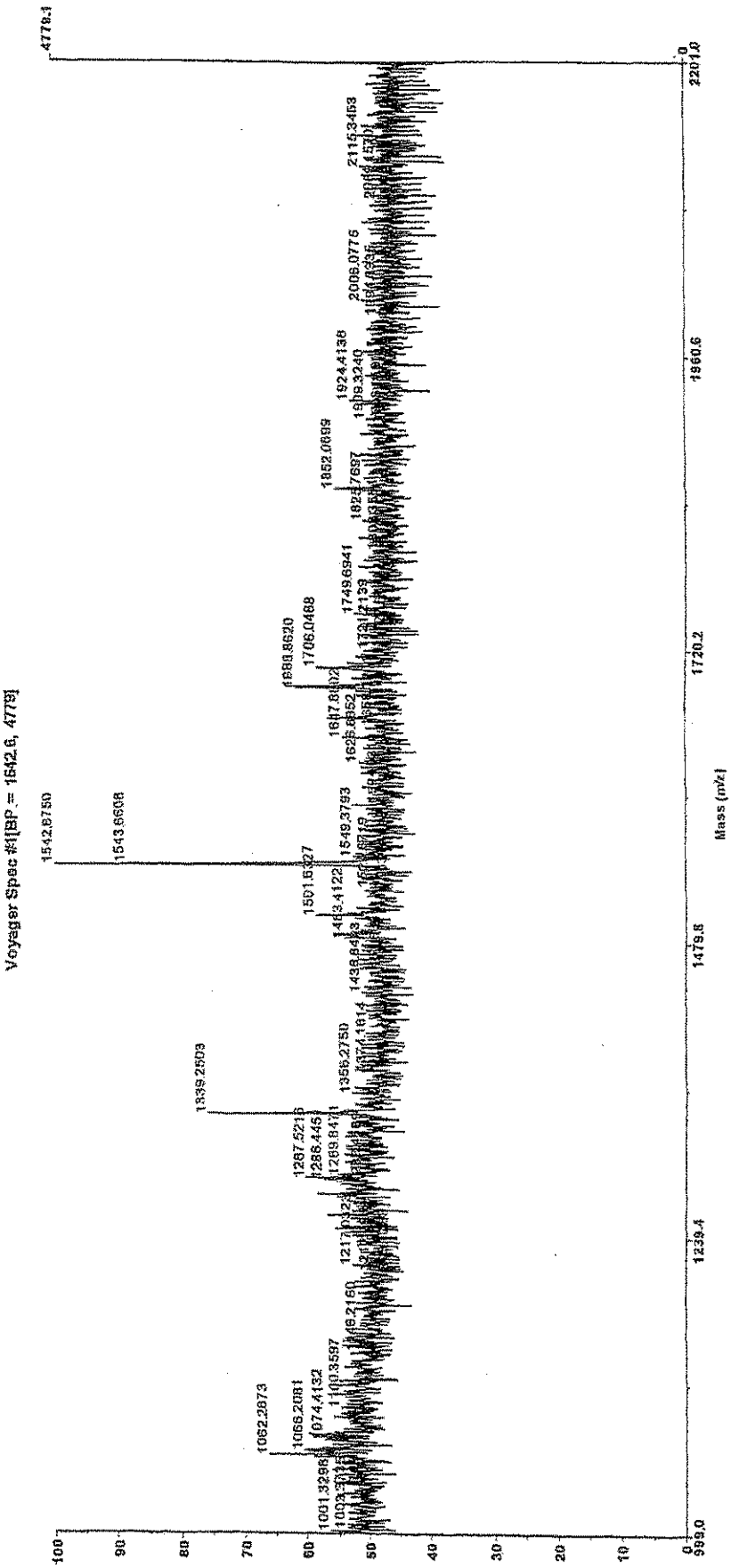

Voyager Spec #1[BP = 1642.6, 4778]
4778.1
1542.8750
1543.8608
1339.2503
1062.2873
1066.2081
1074.4132
1100.3597
1356.2750
1501.8327
1706.0468
1749.6941
1852.0699
1924.4138
2008.0776
2116.3453
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
Mass (m/z)

FIG. 8B

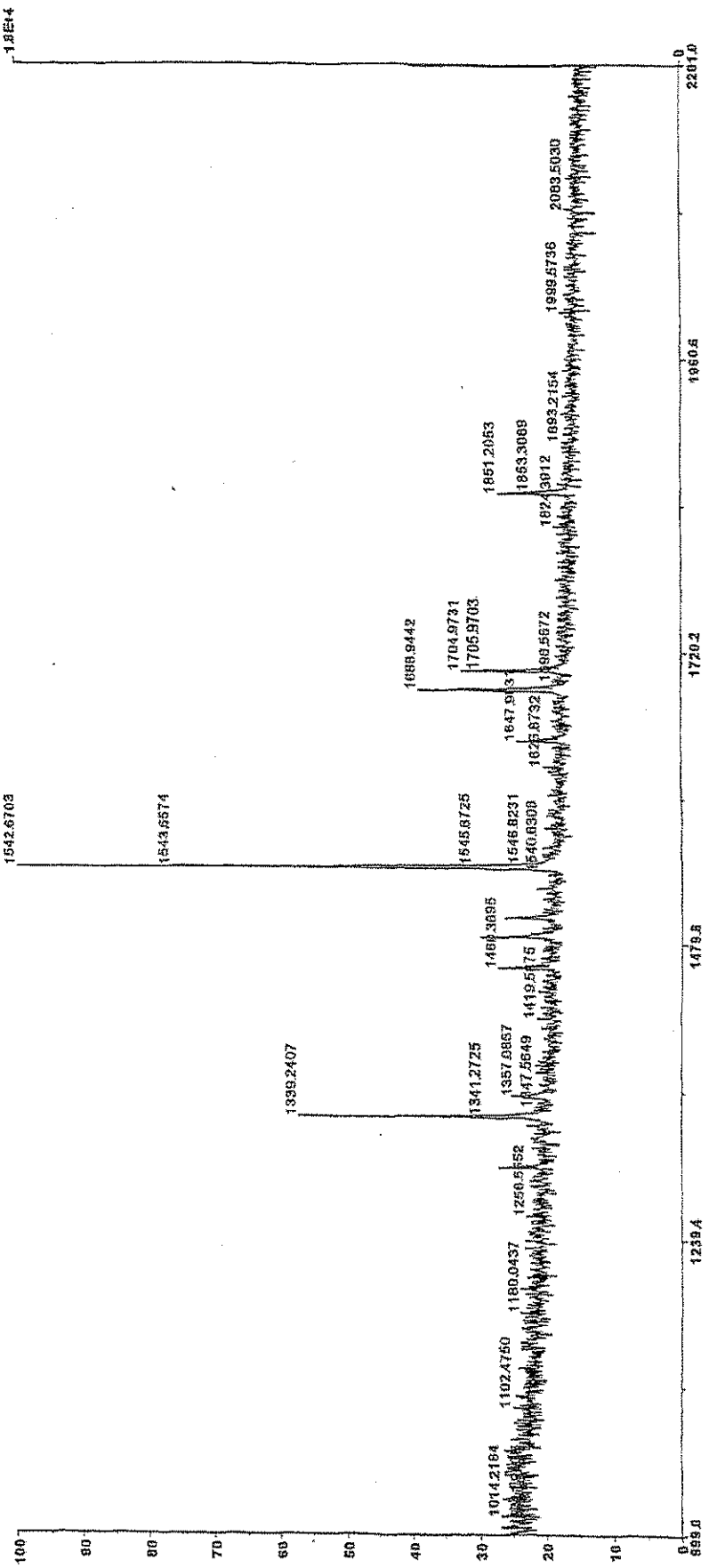

Voyager Spec #1[BP = 1542.6, 18358]
1542.6703
1543.6574
1545.6725
1546.6231
1688.9442
1704.9731
1705.9703
1851.2053
1863.3069
1339.2407
1341.2725
1357.2857
1419.5675
1466.3695
1250.5552
1180.0437
1102.4750
1014.2164
100
90
80
70
60
50
40
30
20
10
0
899.8
1239.4
1579.8
1720.2
1960.6
2201.0
Mass (m/z)

FIG. 8C

Figure 9

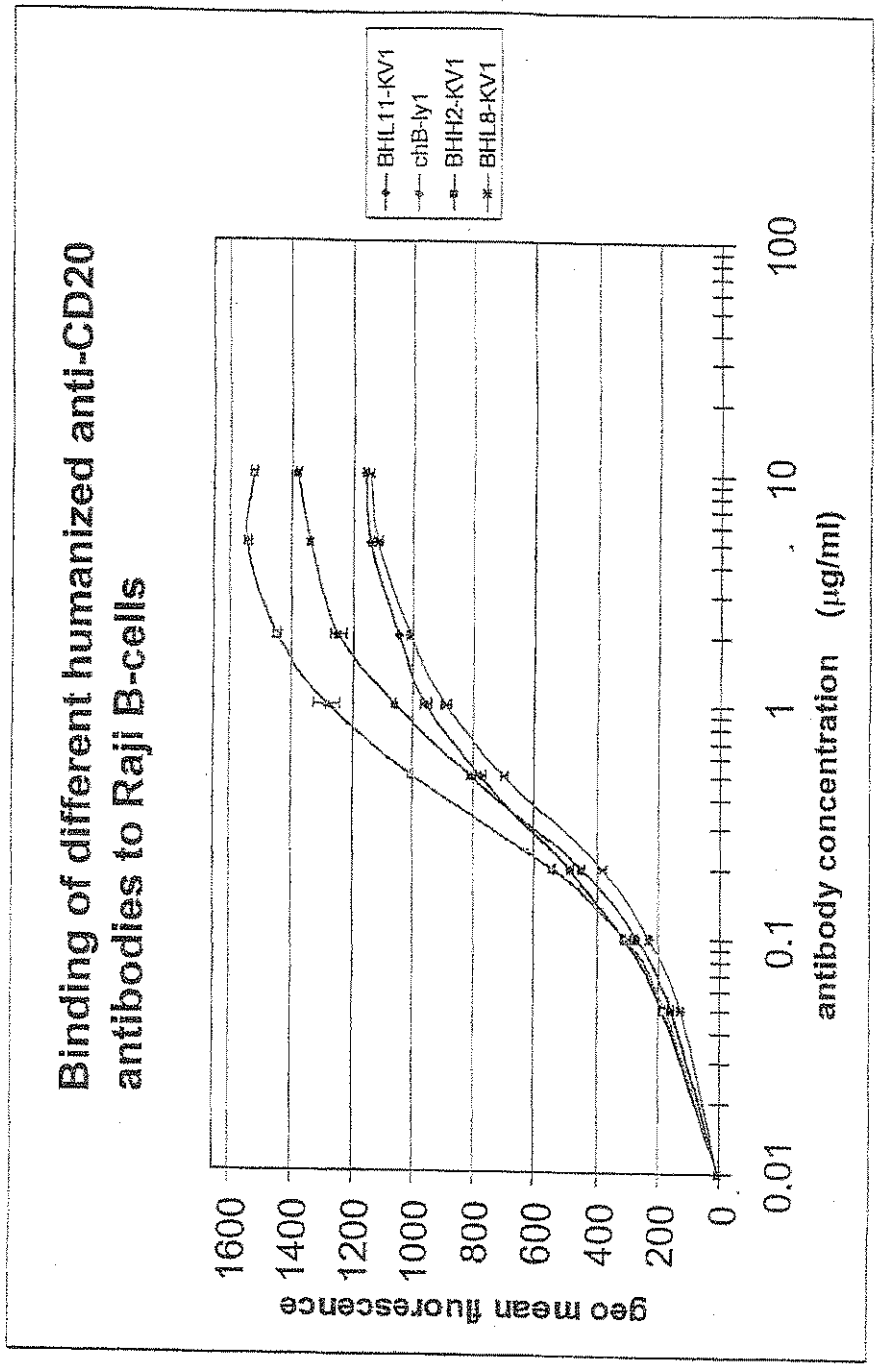

Binding of different humanized anti-CD20 antibodies to Raji B-cells
BHL11-KV1
chiB-ly1
BHH2-KV1
BHL8-KV1
geo mean fluorescence
1600
1400
1200
1000
800
600
400
200
0
0.01
0.1
1
10
100
antibody concentration (µg/ml)

Figure 10

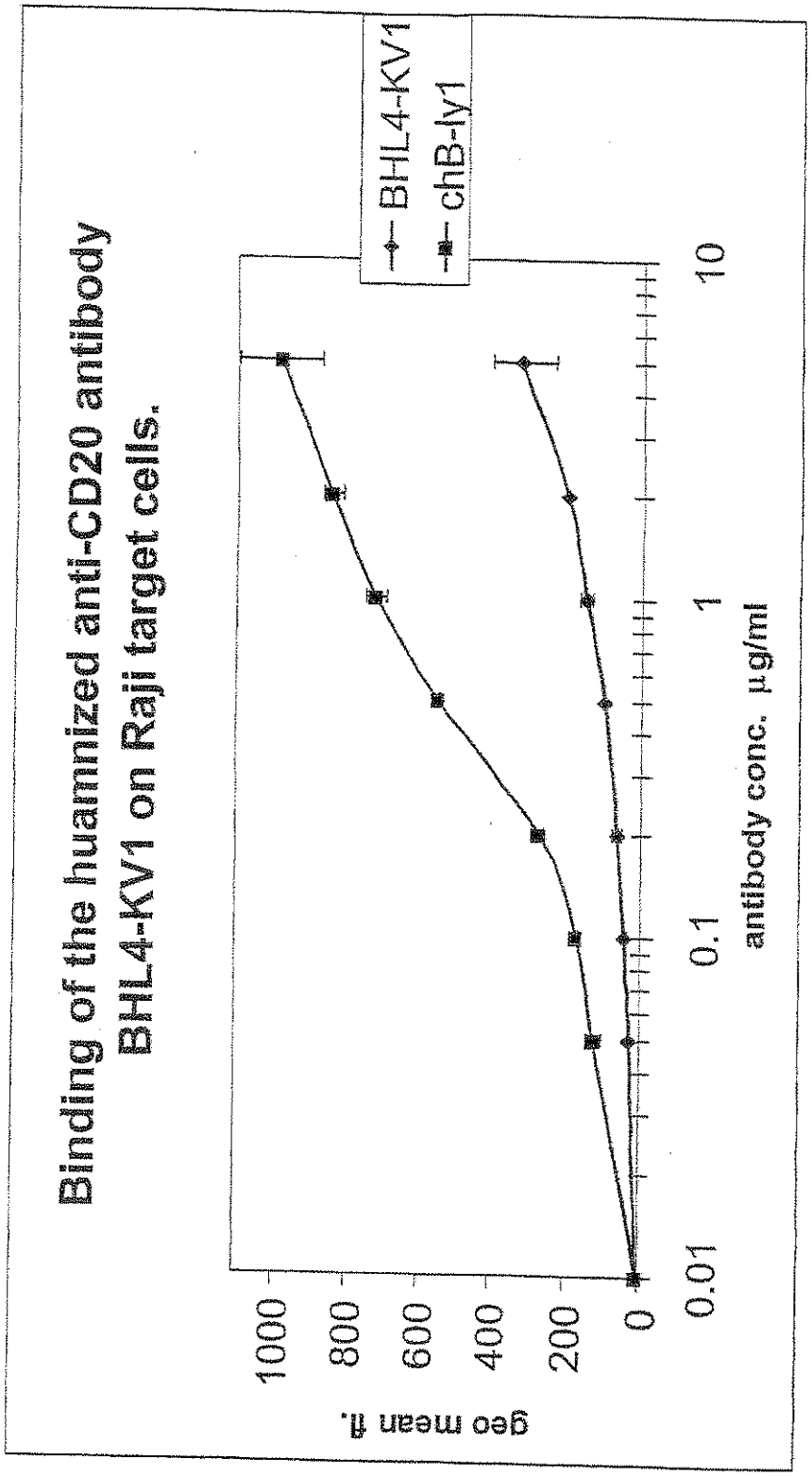

Binding of the huamnized anti-CD20 antibody
BHL4-KV1 on Raji target cells.
BHL4-KV1
chB-lv1
geo mean fl.
1000
800
600
400
200
0
0.01
0.1
1
10
antibody conc. µg/ml

Figure 11

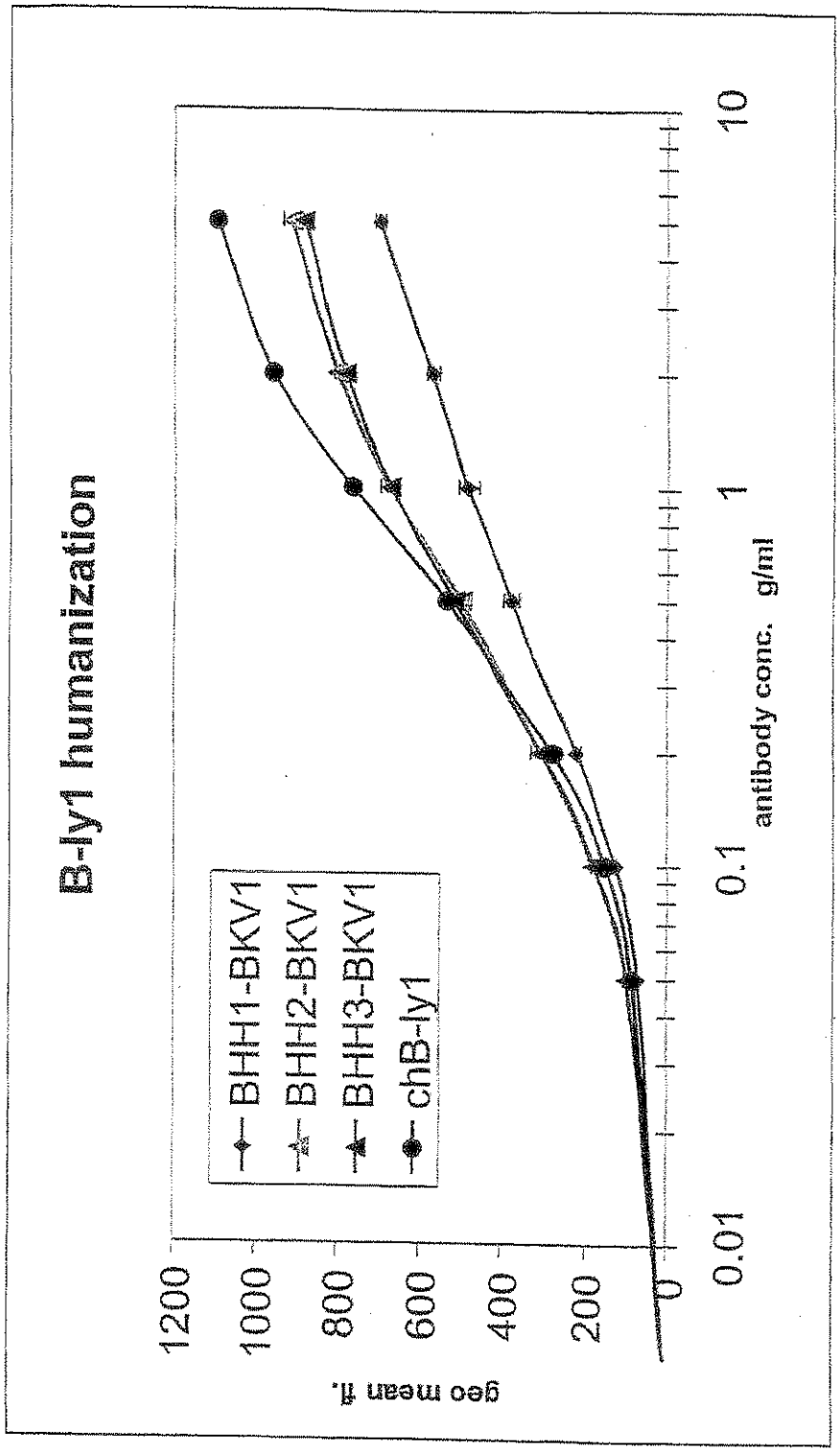

B-ly1 humanization
BHH1-BKV1
BHH2-BKV1
BHH3-BKV1
chB-ly1
geo mean fl.
1200
1000
800
600
400
200
0
0.01
0.1
1
10
antibody conc. g/ml

Figure 12

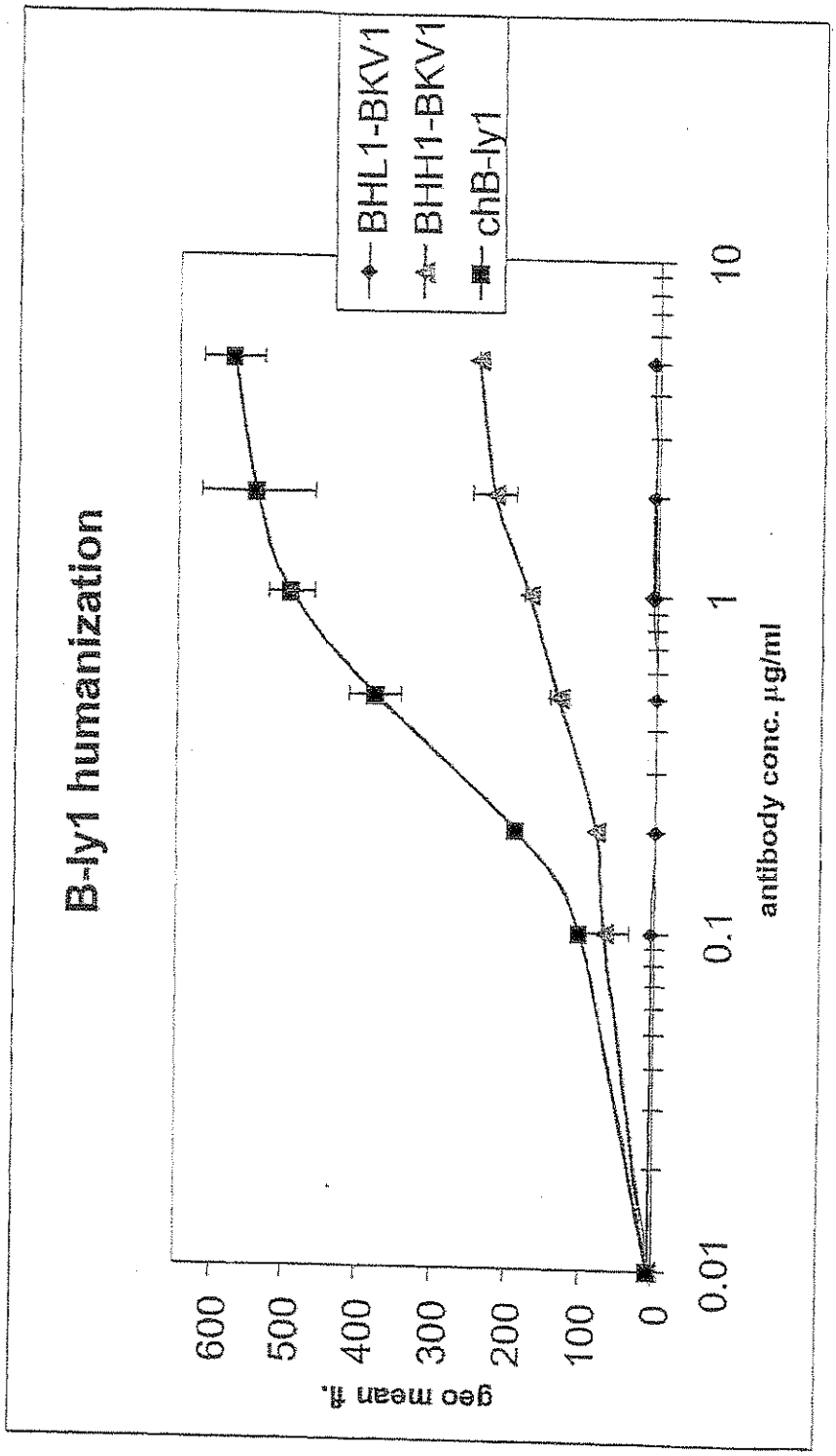

B-ly1 humanization
BHL1-BKV1
BHH1-BKV1
chB-ly1
geo mean fl.
600
500
400
300
200
100
0
0.01
0.1
1
10
antibody conc. µg/ml

Figure 13

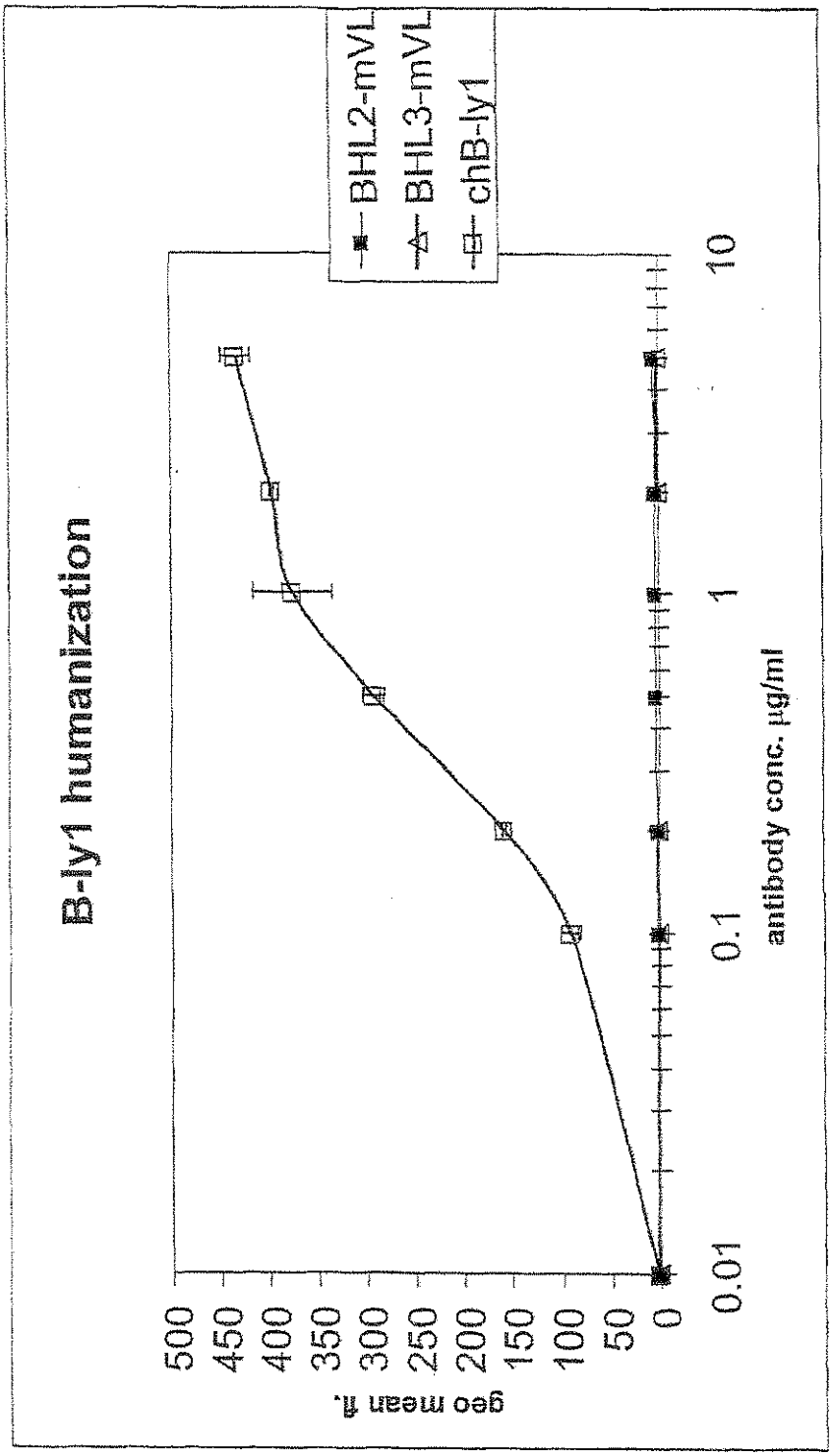

B-ly1 humanization
BHL2-mVL
BHL3-mVL
chB-ly1
geo mean ñ.
500
450
400
350
300
250
200
150
100
50
0
0.01
0.1
1
10
antibody conc. µg/ml

Figure 14

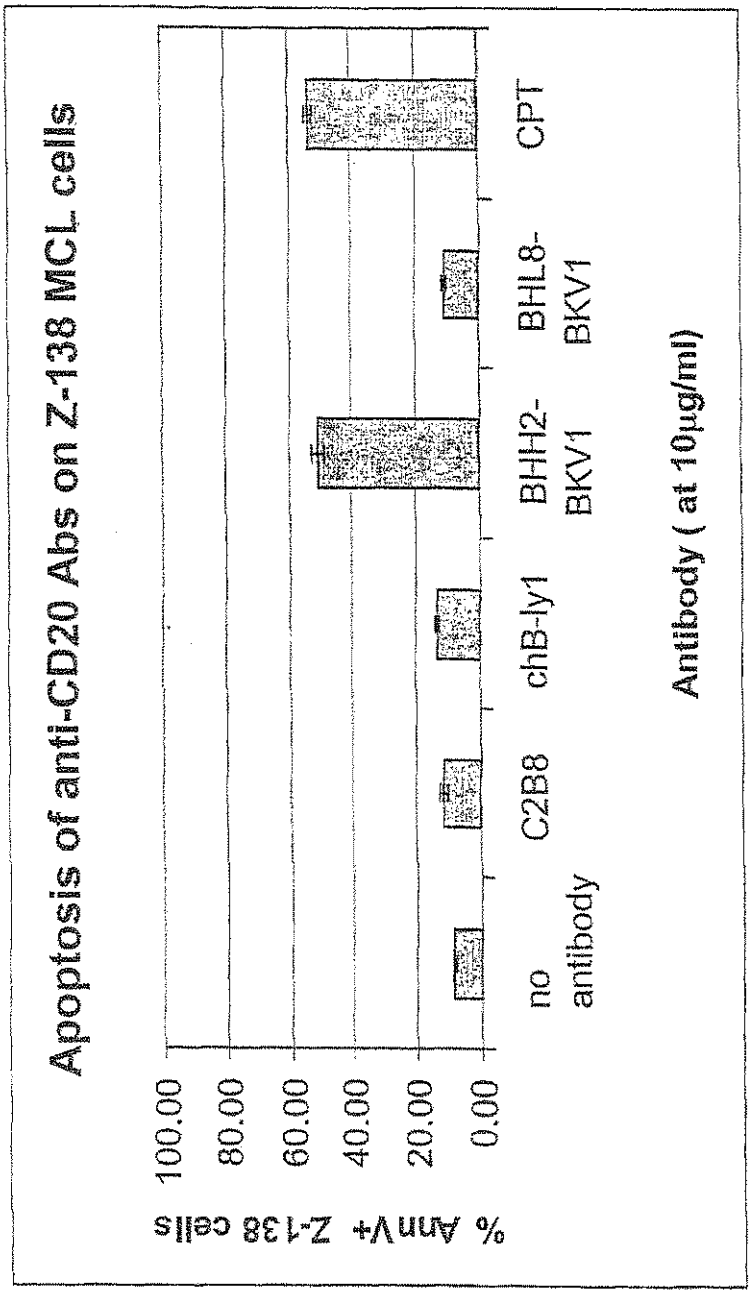

Apoptosis of anti-CD20 Abs on Z-138 MCL cells
% AnnV+ Z-138 cells
100.00
80.00
60.00
40.00
20.00
0.00
no antibody
C2B8
chB-ly1
BHH2-BKV1
BHL8-BKV1
CPT
Antibody (at 10µg/ml)

Figure15

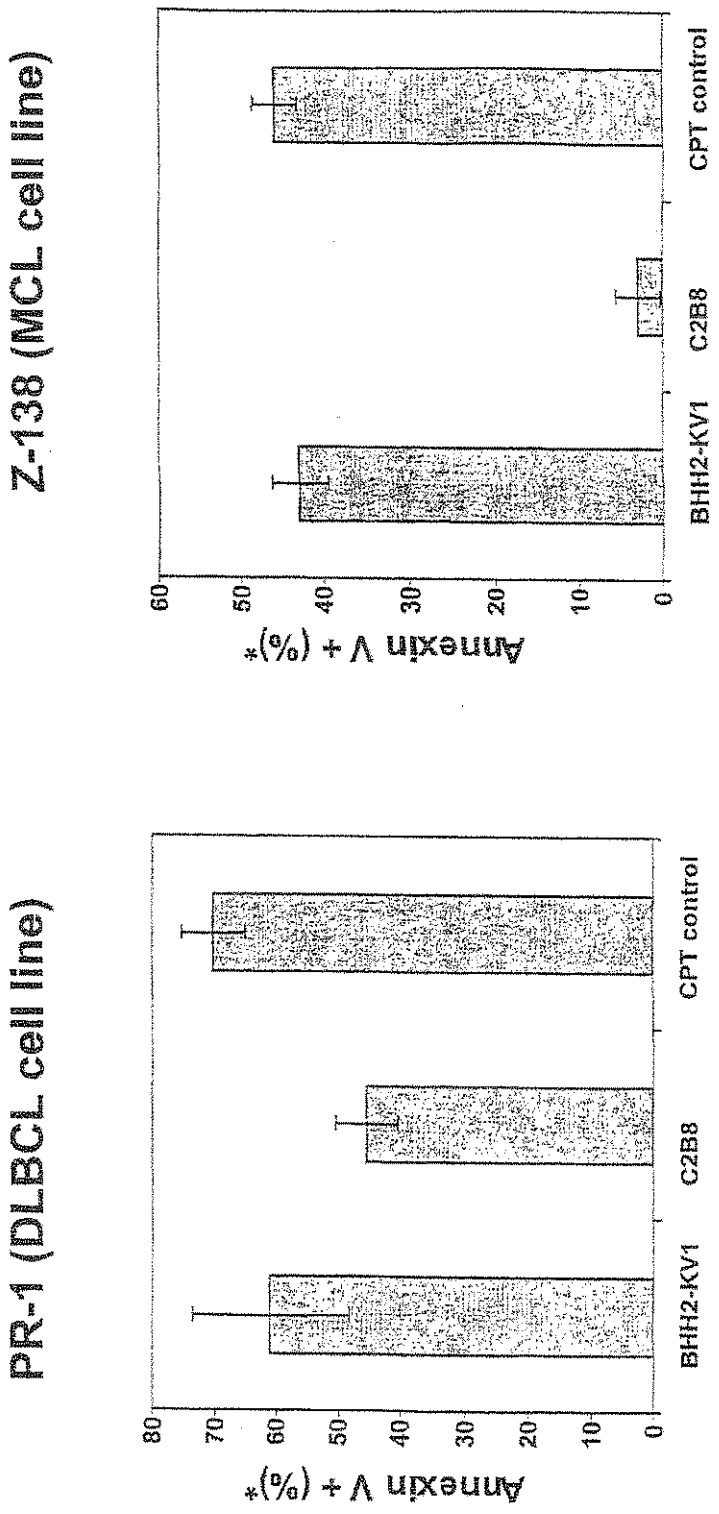

Z-138 (MCL cell line)
Annexin V + (%)*
0
10
20
30
40
50
60
BHH2-KV1
C2B8
CPT control
PR-1 (DLBCL cell line)
Annexin V + (%)*
0
10
20
30
40
50
60
70
80
BHH2-KV1
C2B8
CPT control

Figure 16

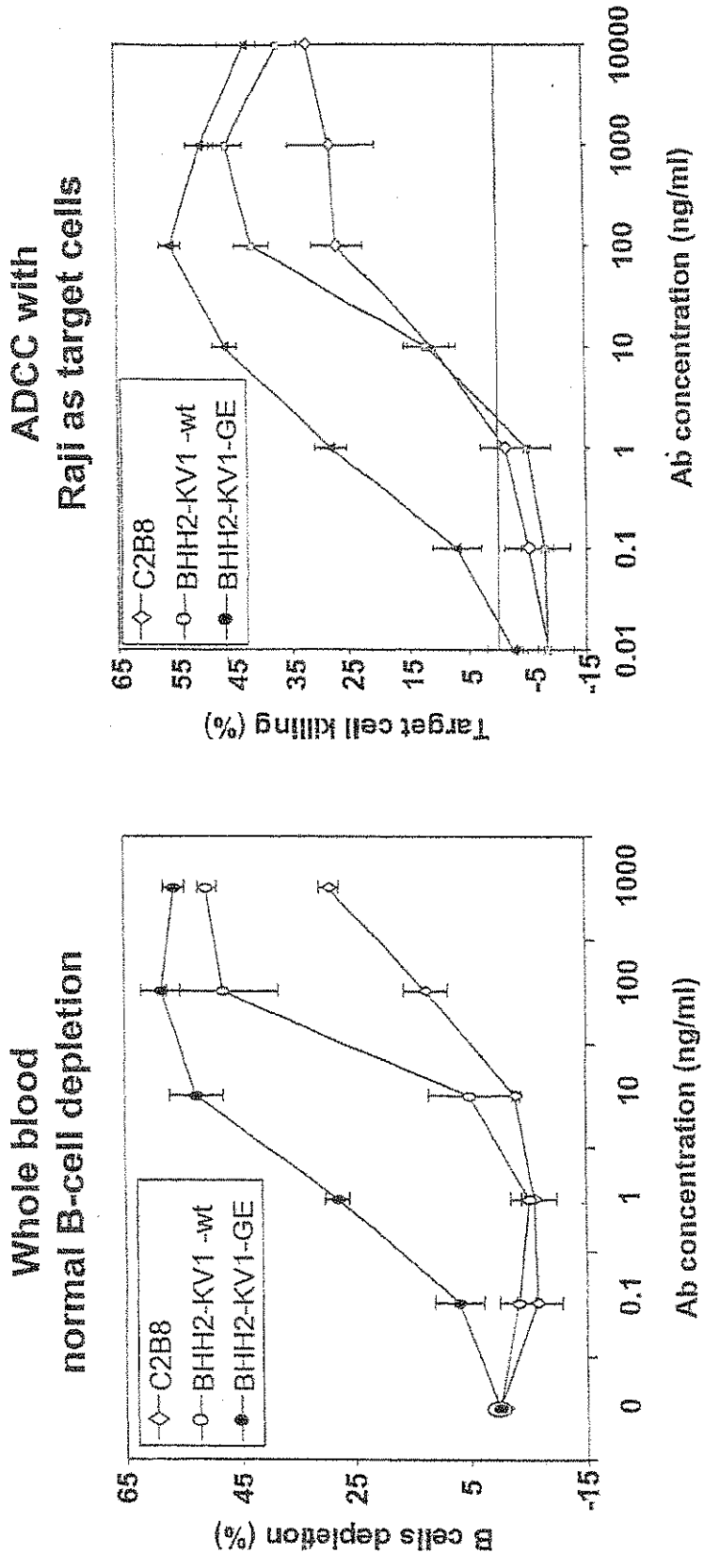

Whole blood
normal B-cell depletion
B cells depletion (%)
65
45
25
5
-15
C2B8
BHH2-KV1 -wt
BHH2-KV1-GE
0
0.1
1
10
100
1000
Ab concentration (ng/ml)
ADCC with
Raji as target cells
Target cell killing (%)
65
55
45
35
25
15
5
-5
-15
C2B8
BHH2-KV1 -wt
BHH2-KV1-GE
0.01
0.1
1
10
100
1000
10000
Ab concentration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

Figure 17

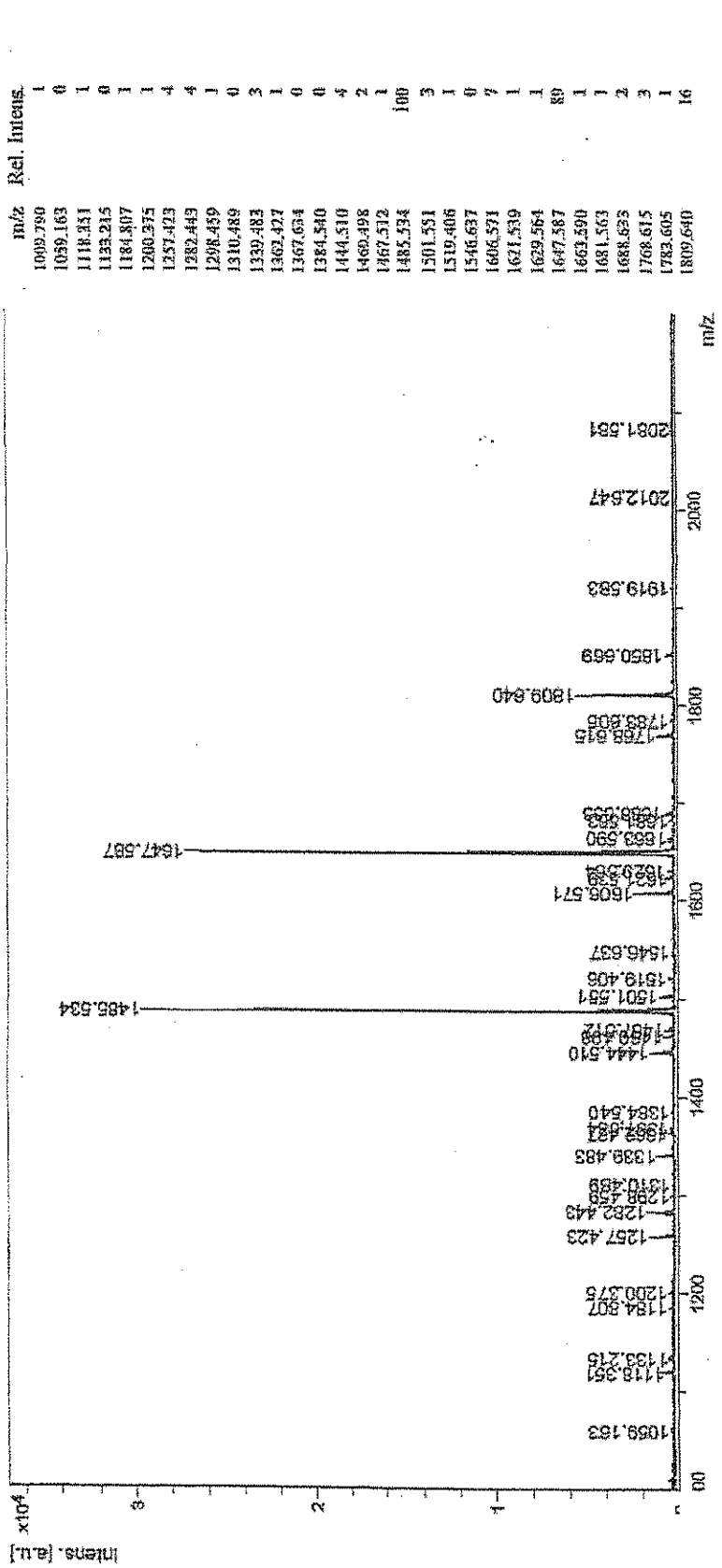

Intens. [a.u.]
x10⁴
m/z
1059.163
1118.351
1133.215
1184.807
1200.375
1257.423
1282.443
1298.459
1310.489
1339.483
1362.427
1367.634
1384.540
1444.510
1469.498
1467.512
1485.534
1501.551
1519.406
1546.637
1606.571
1621.539
1629.564
1647.587
1663.590
1681.563
1688.623
1768.615
1783.605
1809.640
1850.669
1919.583
2012.547
2061.551
m/z Rel. Intens.
1009.790 1
1059.163 0
1118.331 1
1133.215 0
1184.807 1
1260.375 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
1469.498 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

Figure 18

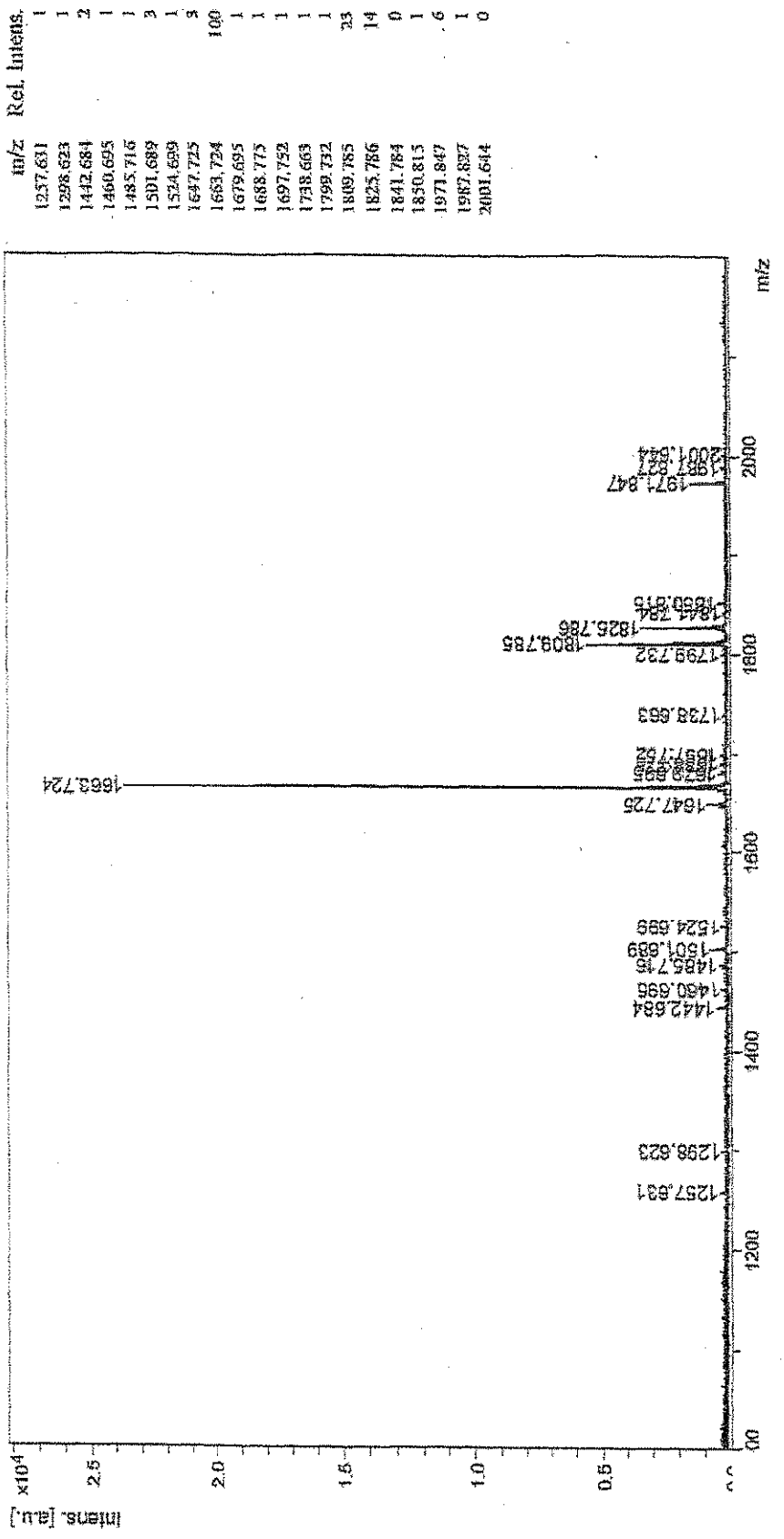
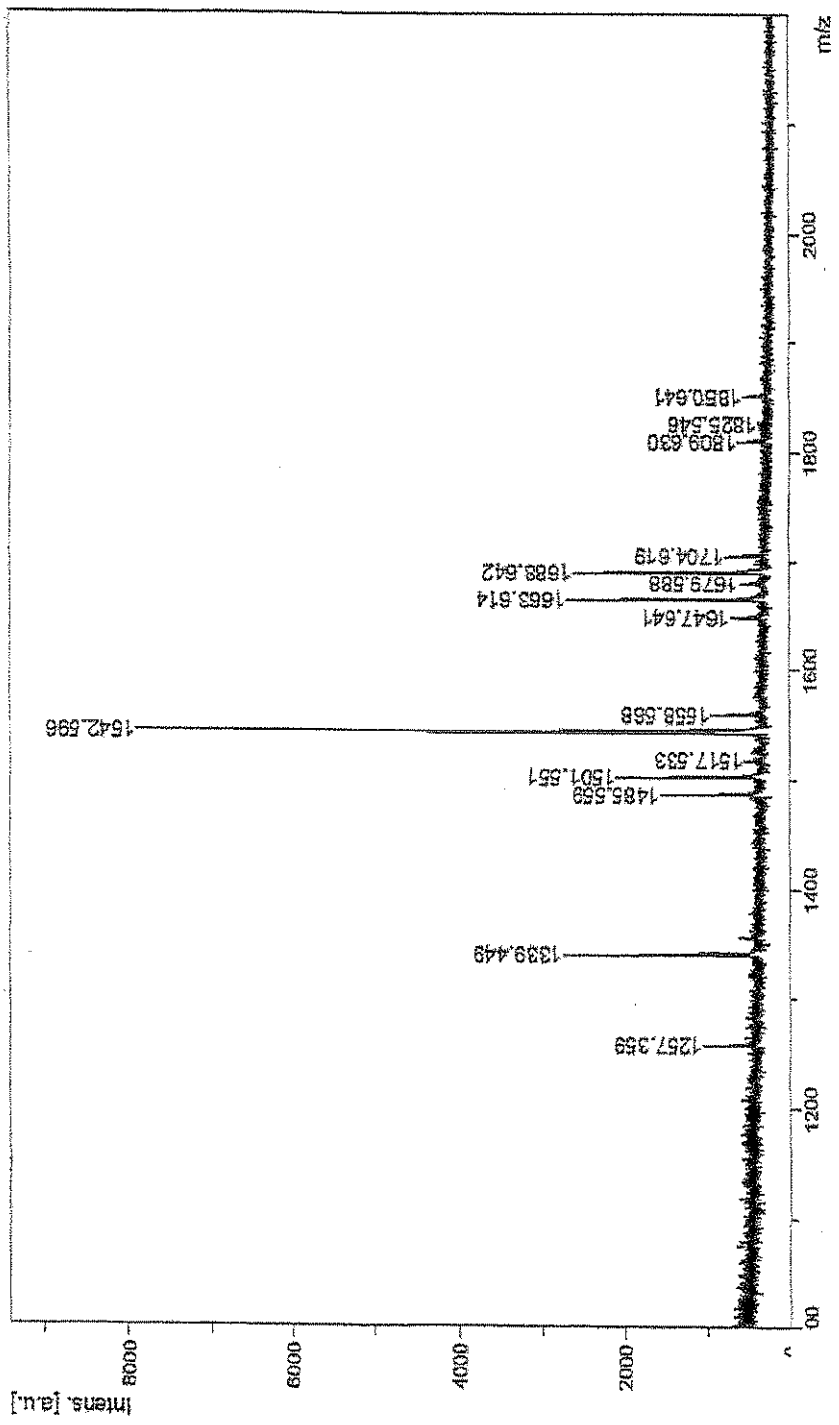

m/z Rel. Intens.
1257.631 1
1298.623 1
1442.684 2
1460.695 1
1485.716 1
1501.689 3
1524.699 1
1647.725 3
1663.724 100
1679.695 1
1688.775 1
1697.752 1
1738.663 1
1799.732 1
1809.785 23
1825.786 14
1841.784 0
1850.815 1
1971.847 6
1987.827 1
2001.644 0
Intens. [a.u.]
x10^4
2.5
2.0
1.5
1.0
0.5
0.0
1200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

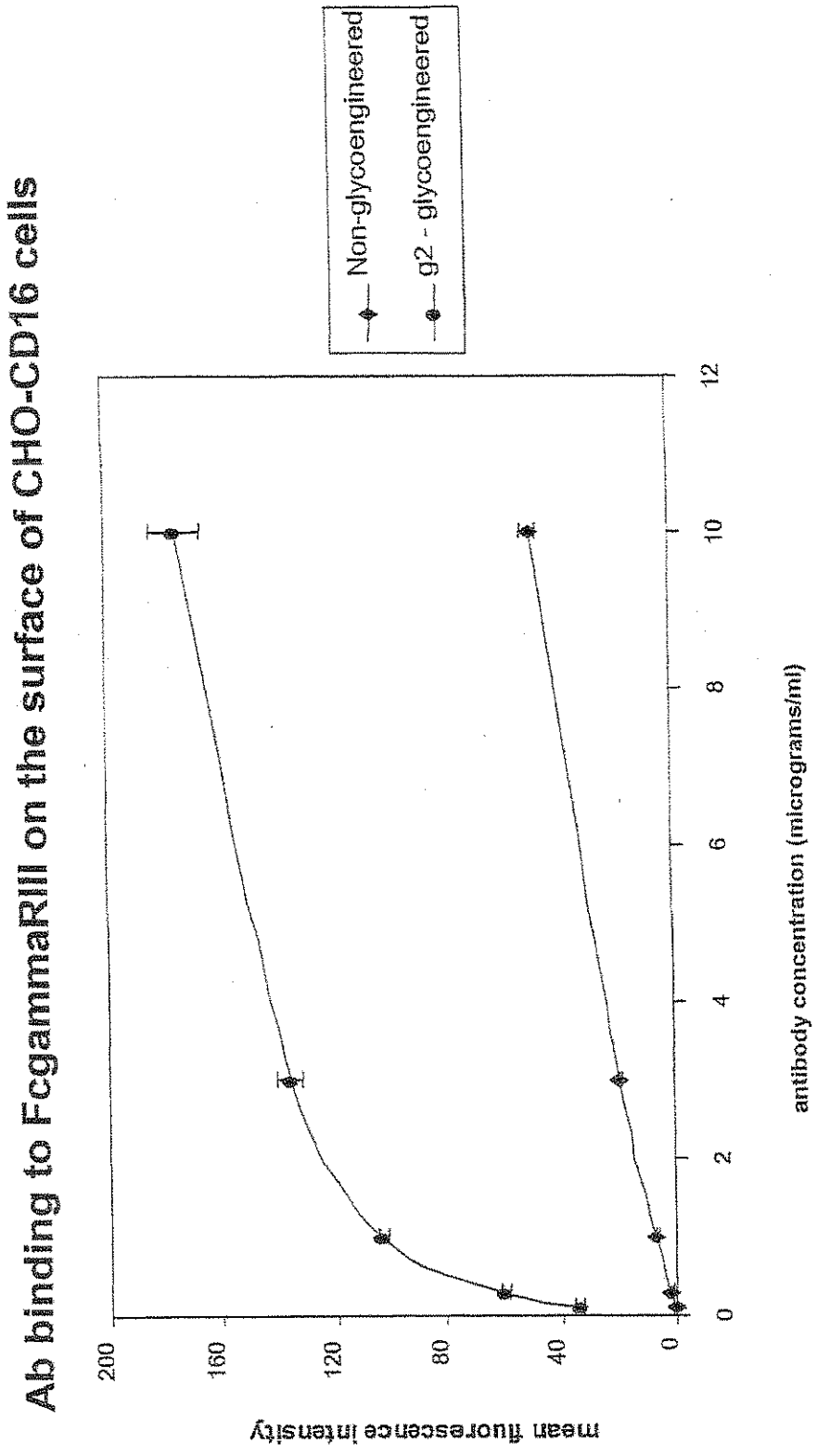
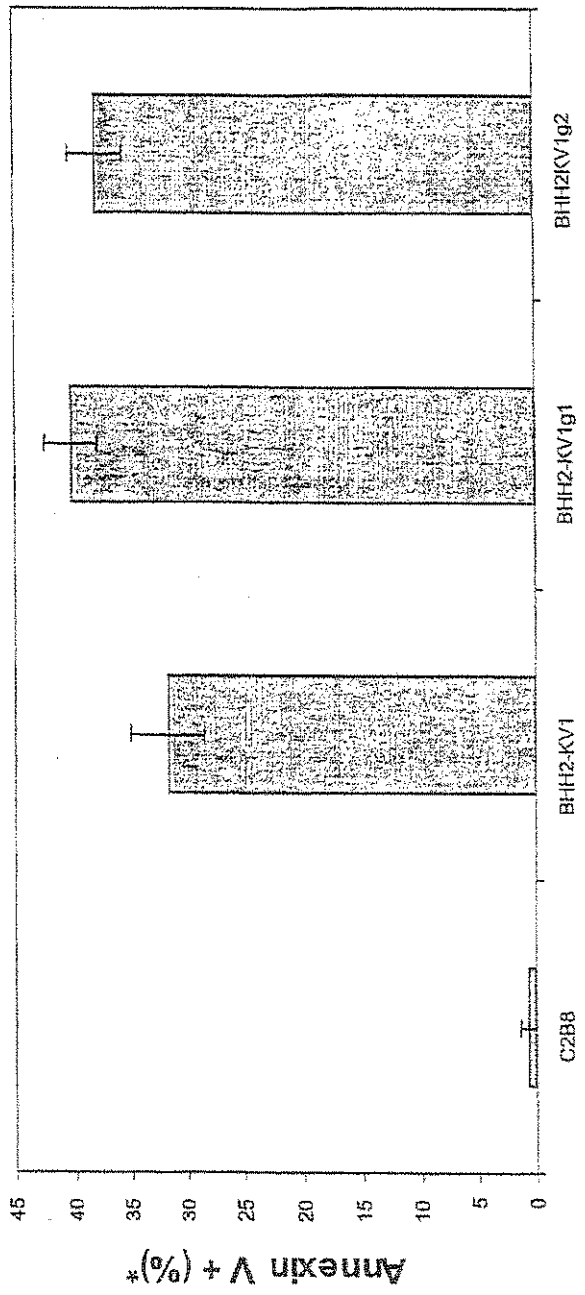

Ab binding to FcgammaRIII on the surface of CHO-CD16 cells
Non-glycoengineered
g2 - glycoengineered
mean fluorescence intensity
antibody concentration (micrograms/ml)
0
40
80
120
160
200
0
2
4
6
8
10
12

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