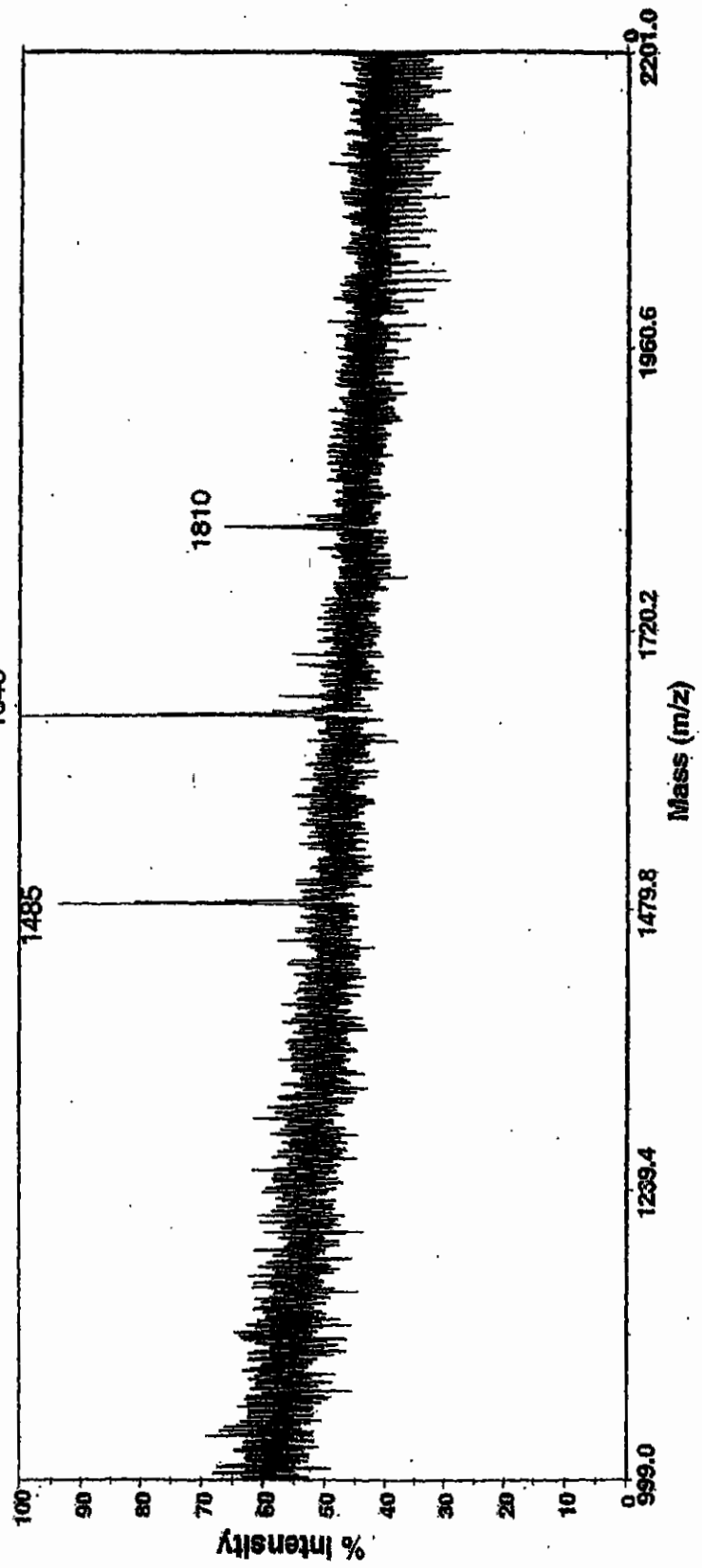

% Intensity
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
Mass (m/z)
1485
1648
1810

Figure 1

Figure 2

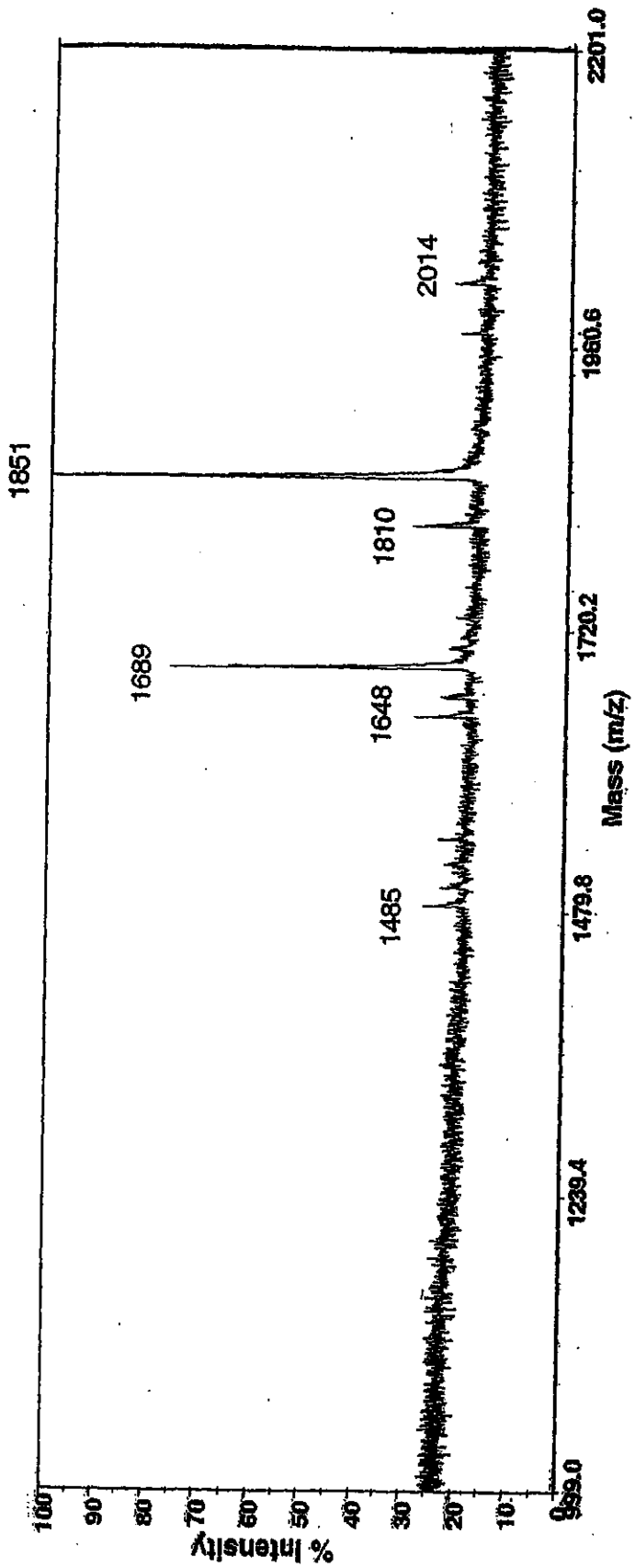

1851
2014
1810
1689
1648
1485
% Intensity
Mass (m/z)
2201.0
1960.6
1720.2
1479.8
1239.4
999.0
100
90
80
70
60
50
40
30
20
10
0

Figure 3

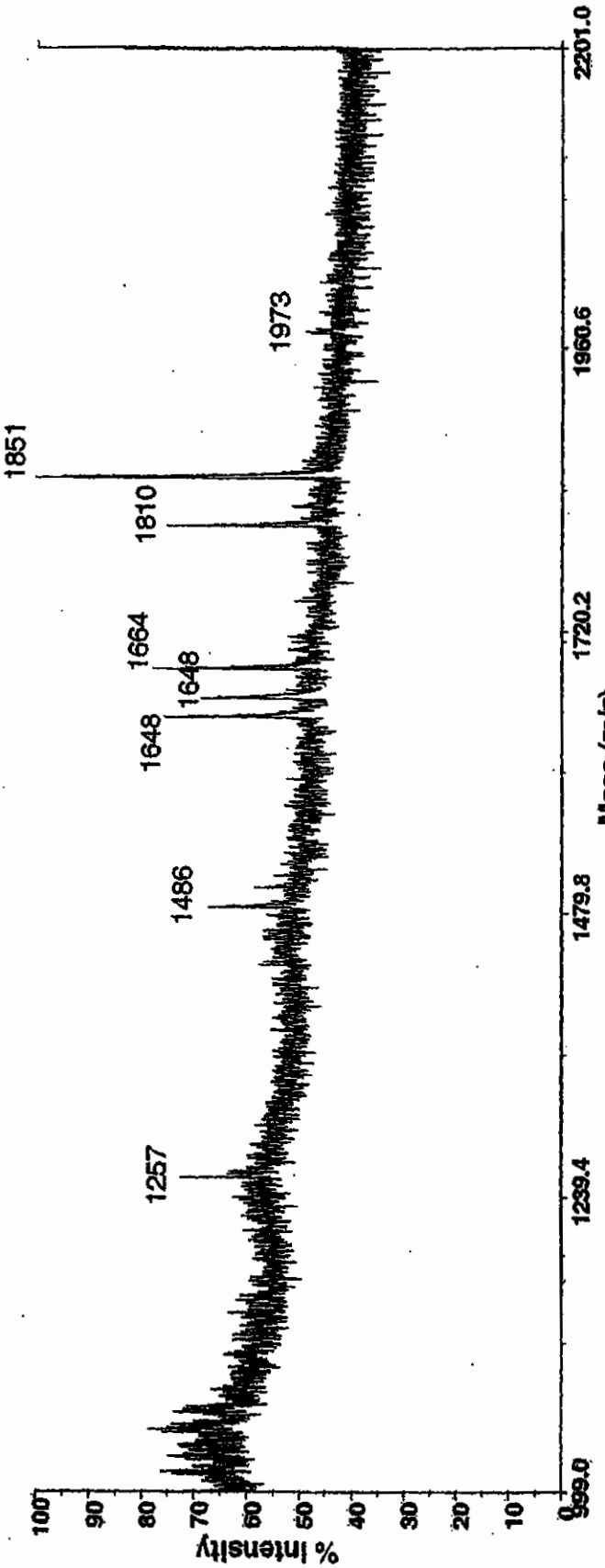

% Intensity
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
Mass (m/z)
1257
1486
1648
1648
1664
1810
1851
1973

Figure 4

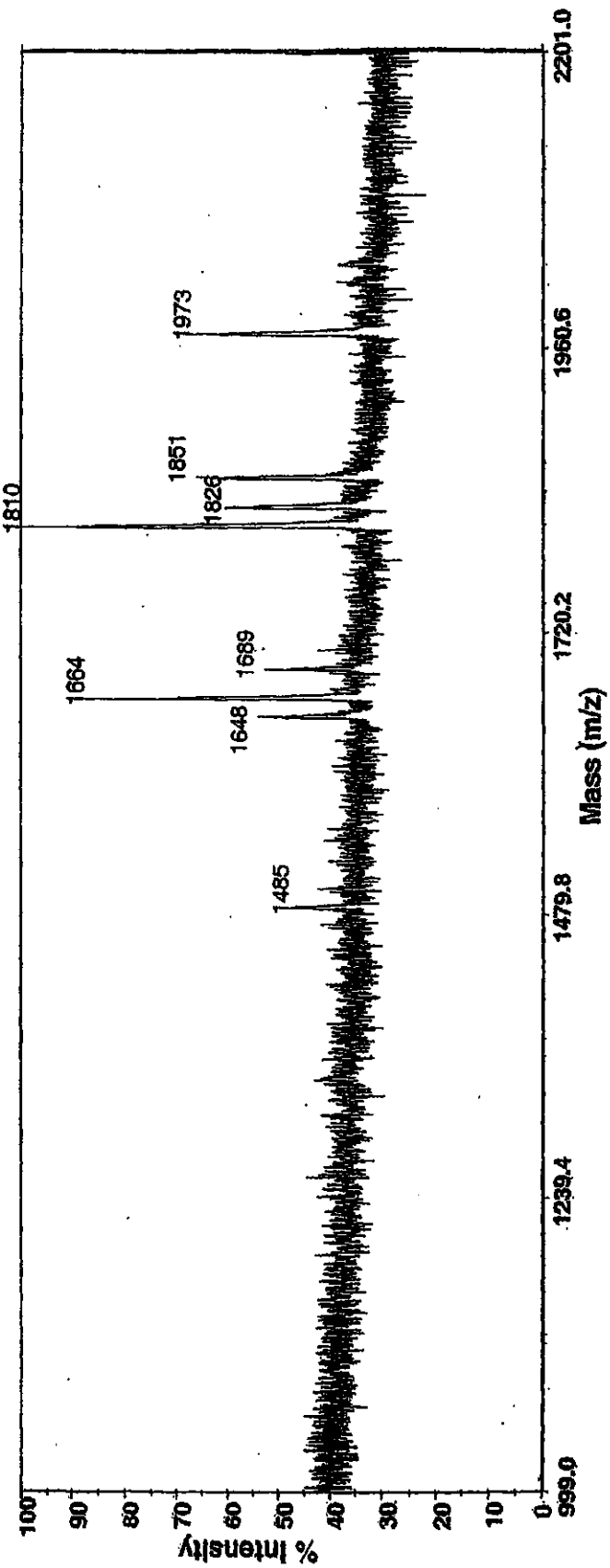

% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
1810
1851
1826
1973
1664
1689
1648
1485

Figure 5

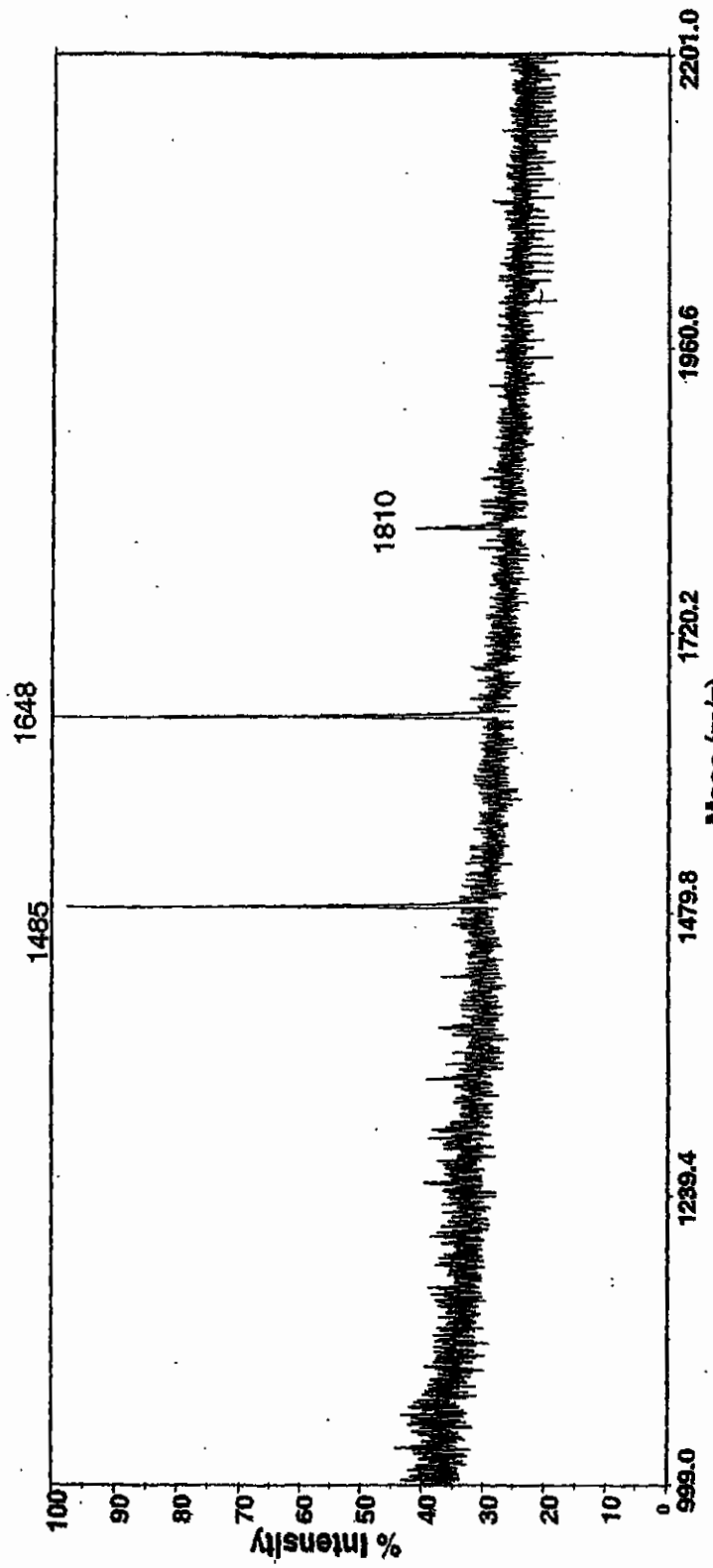

1485
1648
1810
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0

Figure 6

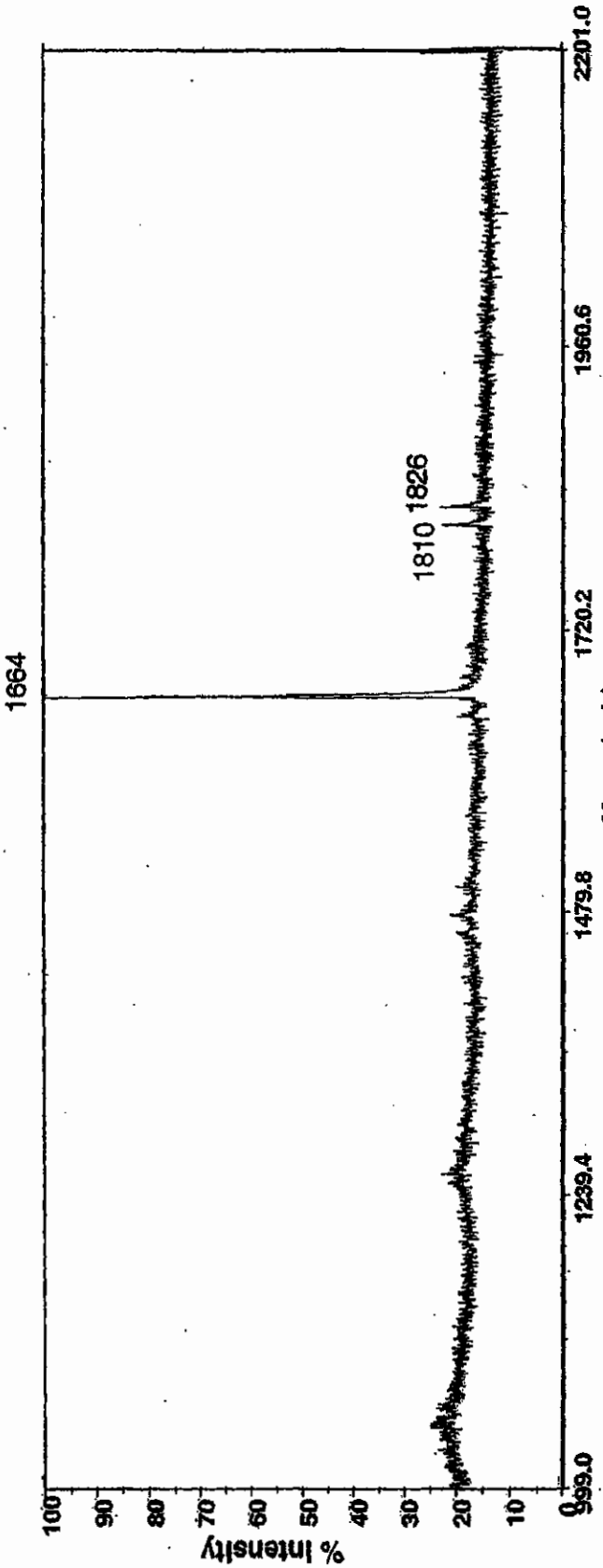
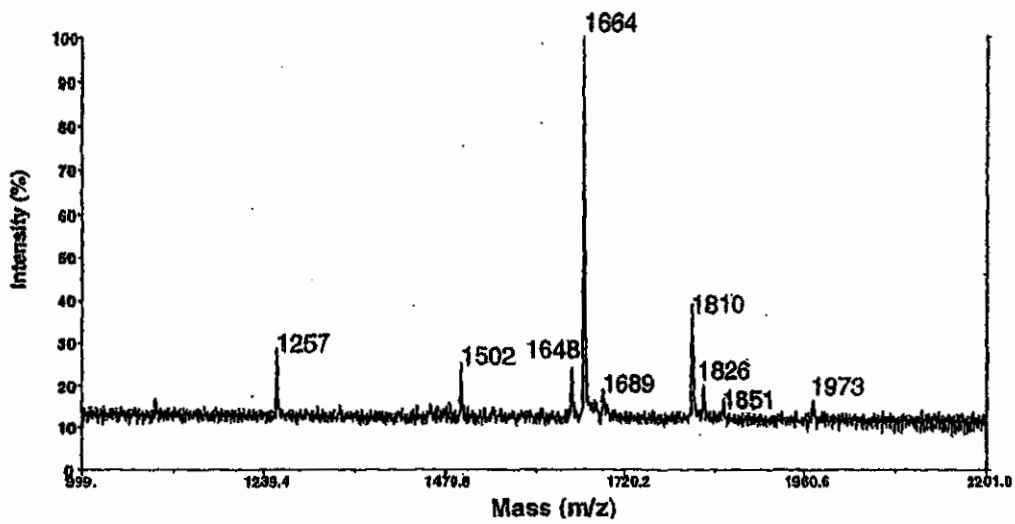

1664
1810
1826
100
90
80
70
60
50
40
30
20
10
0
% Intensity
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
Mass (m/z)

Figure 7

(a)


1664
1810
1257
1502
1648
1689
1826
1851
1973
Intensity (%)
Mass (m/z)

(b)

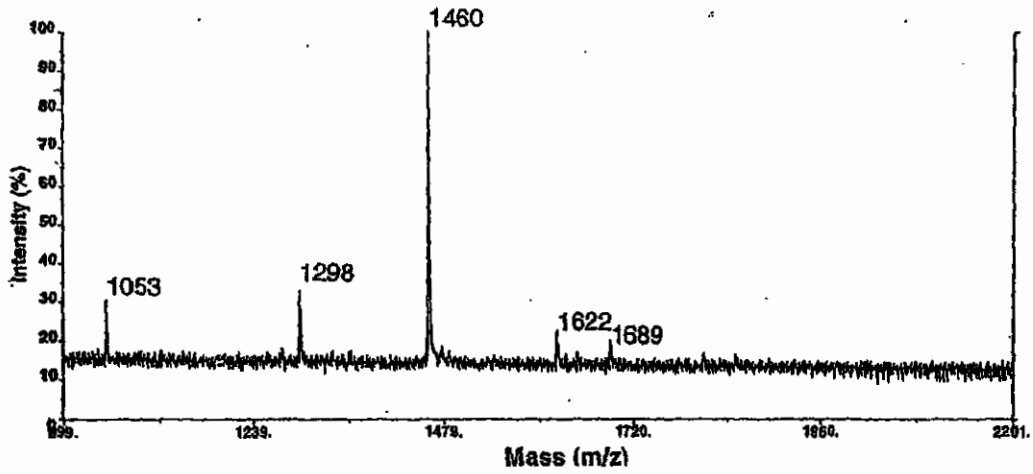
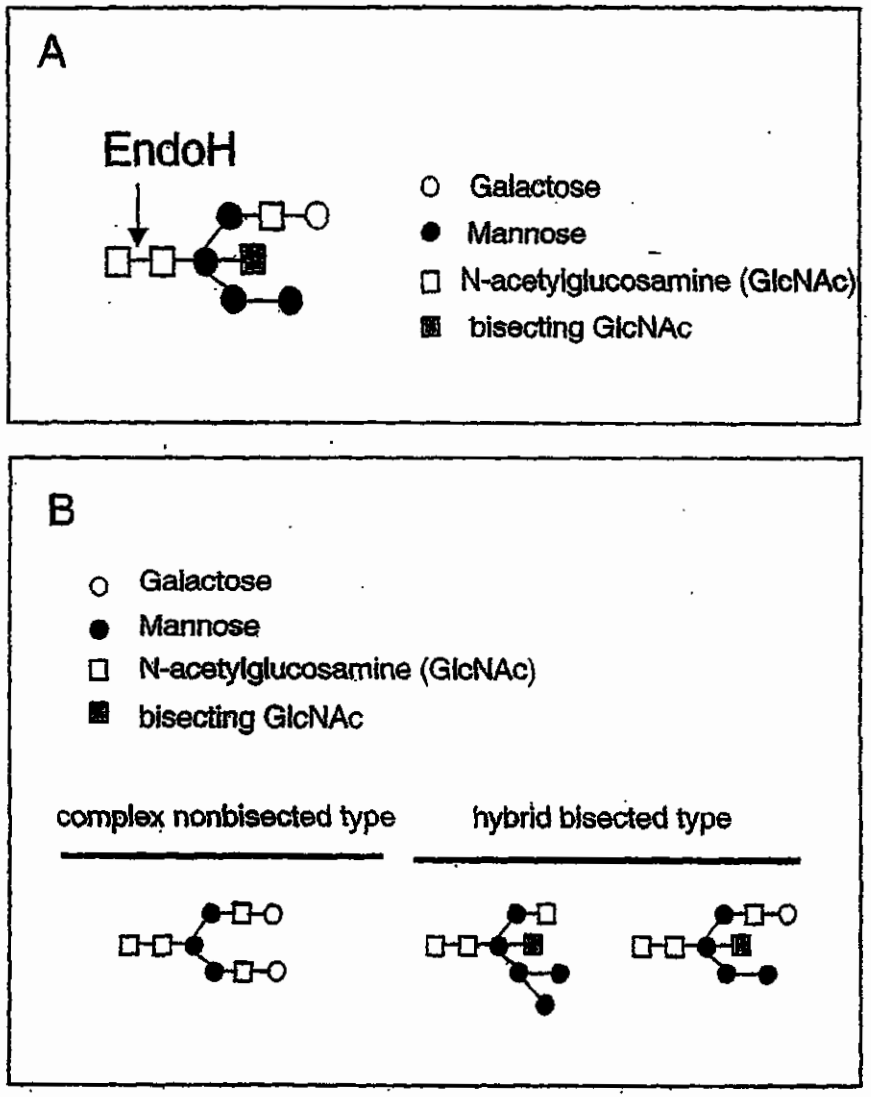

1460
1053
1298
1622
1689
Intensity (%)
Mass (m/z)

Figure 8


A
EndoH
Galactose
Mannose
N-acetylglucosamine (GlcNAc)
bisecting GlcNAc
B
Galactose
Mannose
N-acetylglucosamine (GlcNAc)
bisecting GlcNAc
complex nonbisected type
hybrid bisected type

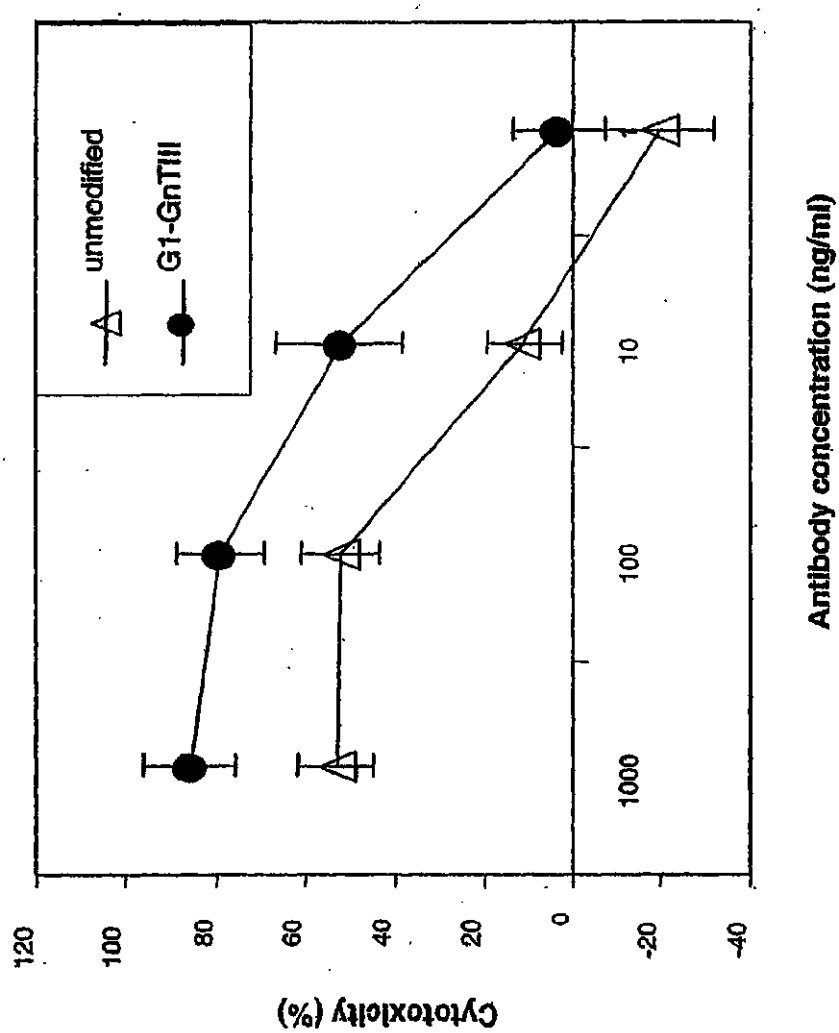

unmodified
G1-GnTIII
120
100
80
60
40
20
0
-20
-40
Cytotoxicity (%)
1000
100
10
Antibody concentration (ng/ml)

Figure 9

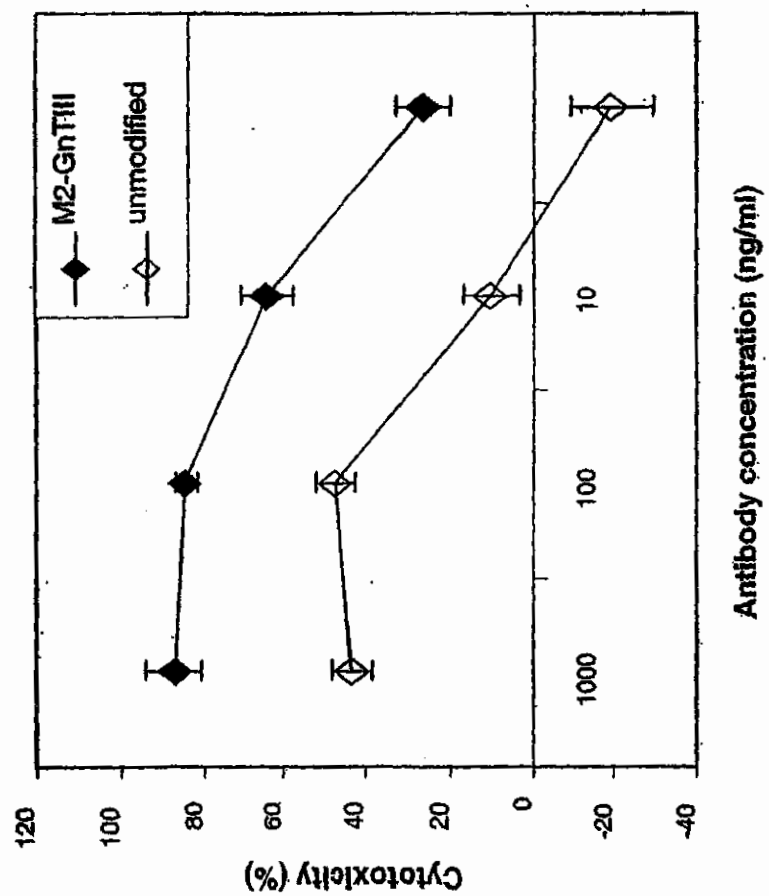

M2-GnTIII
unmodified
Cytotoxicity (%)
120
100
80
60
40
20
0
-20
-40
1000
100
10
Antibody concentration (ng/ml)

Figure 10

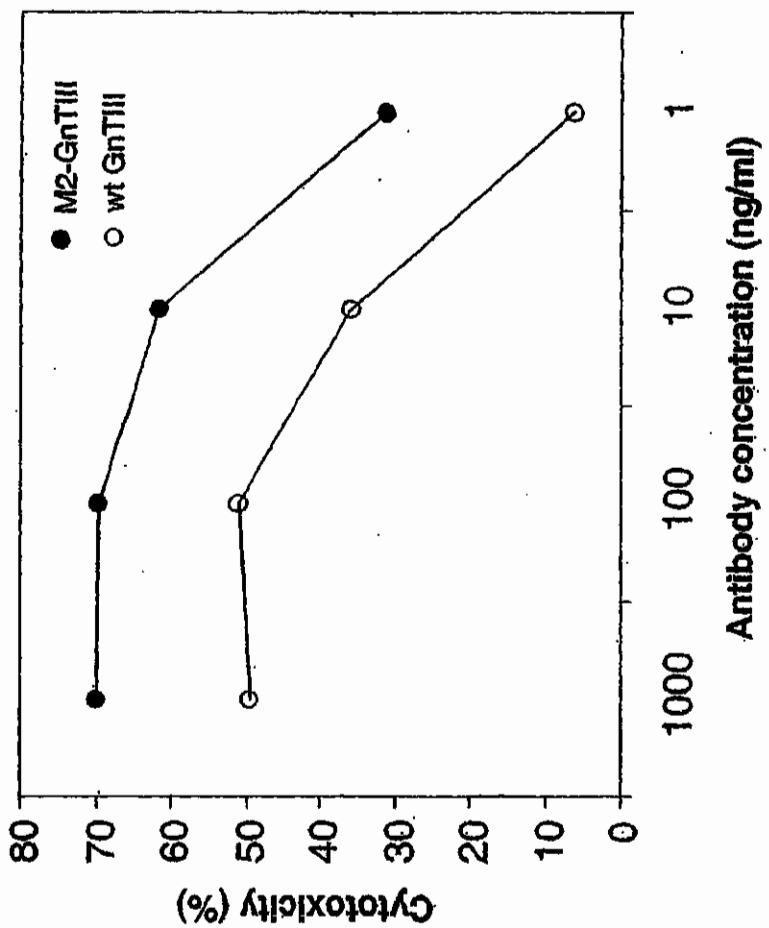

M2-GnTIII
wt GnTIII
Cytotoxicity (%)
0
10
20
30
40
50
60
70
80
1000
100
10
1
Antibody concentration (ng/ml)

Figure 11

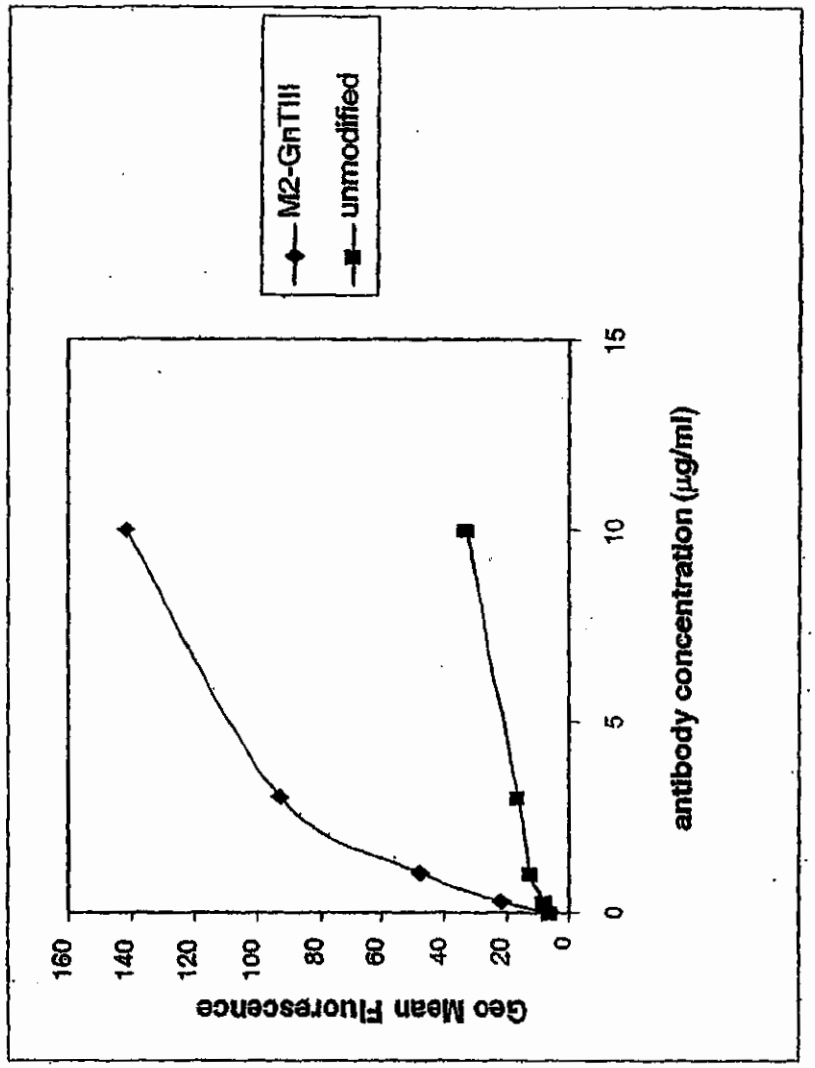

M2-GnTIII
unmodified
Geo Mean Fluorescence
0
20
40
60
80
100
120
140
160
0
5
10
15
antibody concentration (µg/ml)

Figure 12

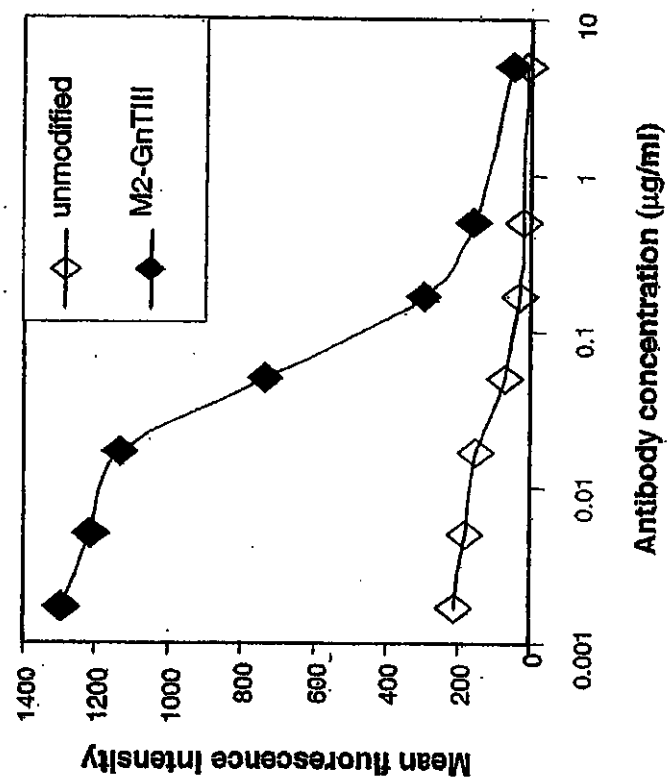
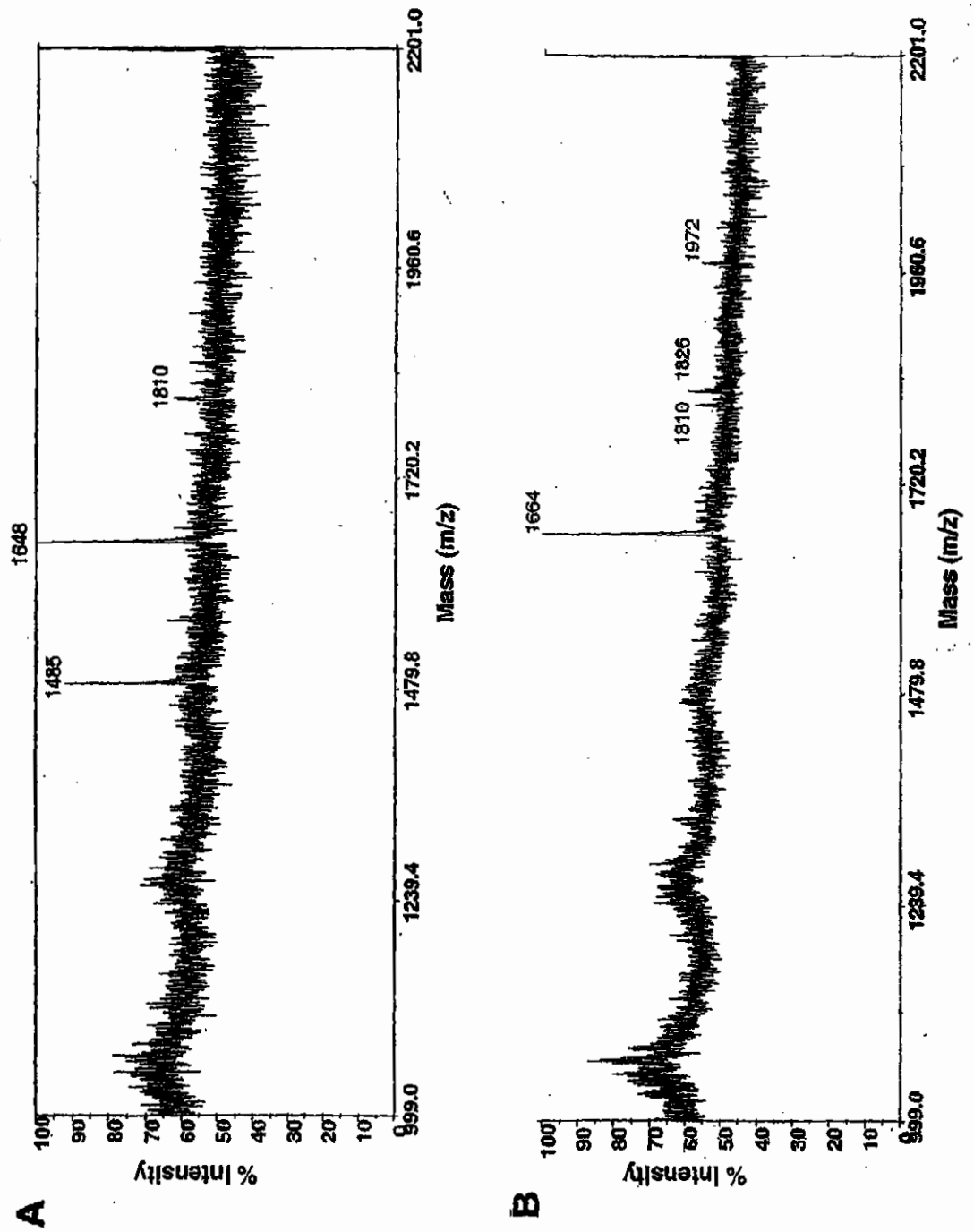

unmodified
M2-GnTIII
Mean fluorescence intensity
1400
1200
1000
800
600
400
200
0
0.001
0.01
0.1
1
10
Antibody concentration (µg/ml)

Figure 13

Figure 14


A
% Intensity
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)
1485
1648
1810
B
% Intensity
1664
1810
1826
1972
Mass (m/z)

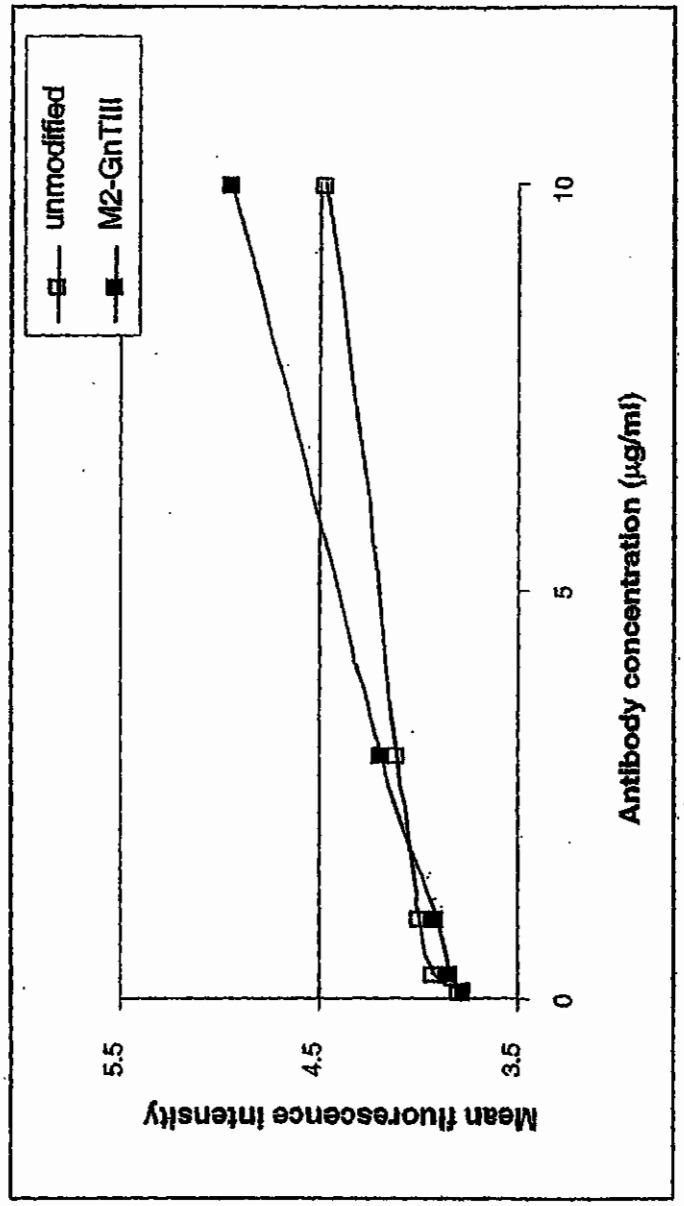

unmodified
M2-GnTIII
Mean fluorescence intensity
5.5
4.5
3.5
0
5
10
Antibody concentration (µg/ml)

Figure 15

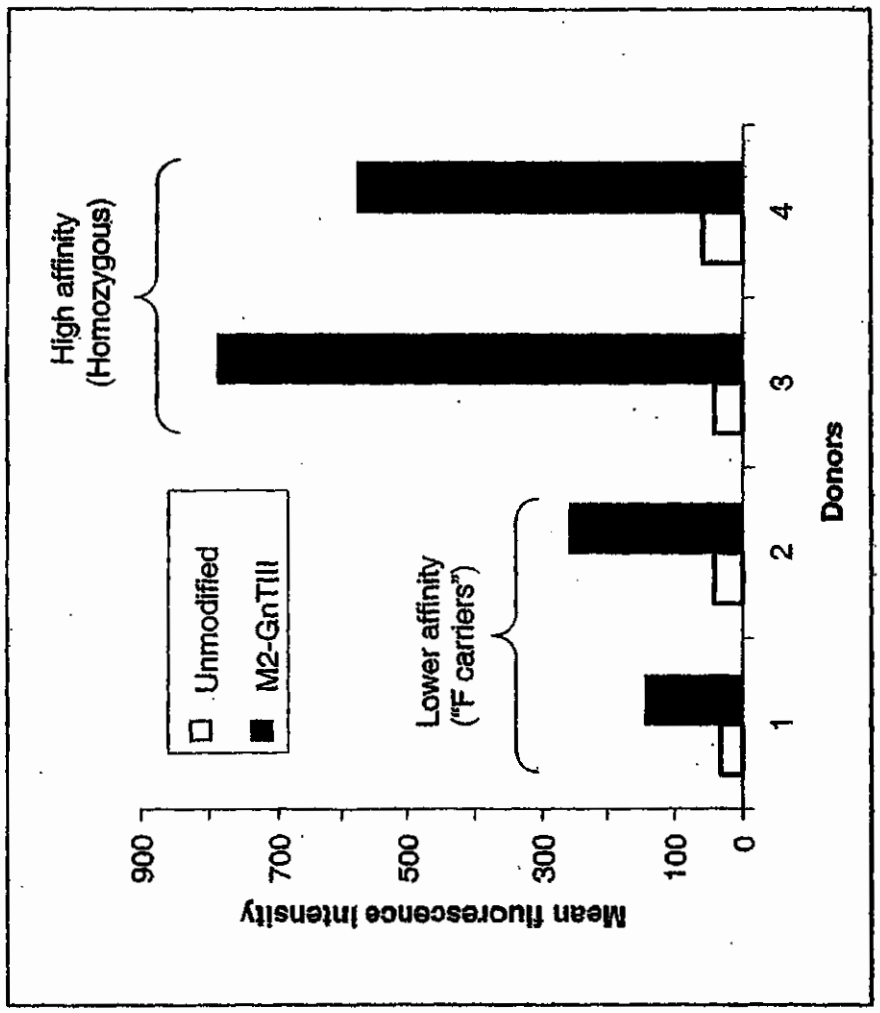

Mean fluorescence intensity
900
700
500
300
100
0
Unmodified
M2-GnTIII
High affinity
(Homozygous)
Lower affinity
("F carriers")
1
2
3
4
Donors

Figure 16

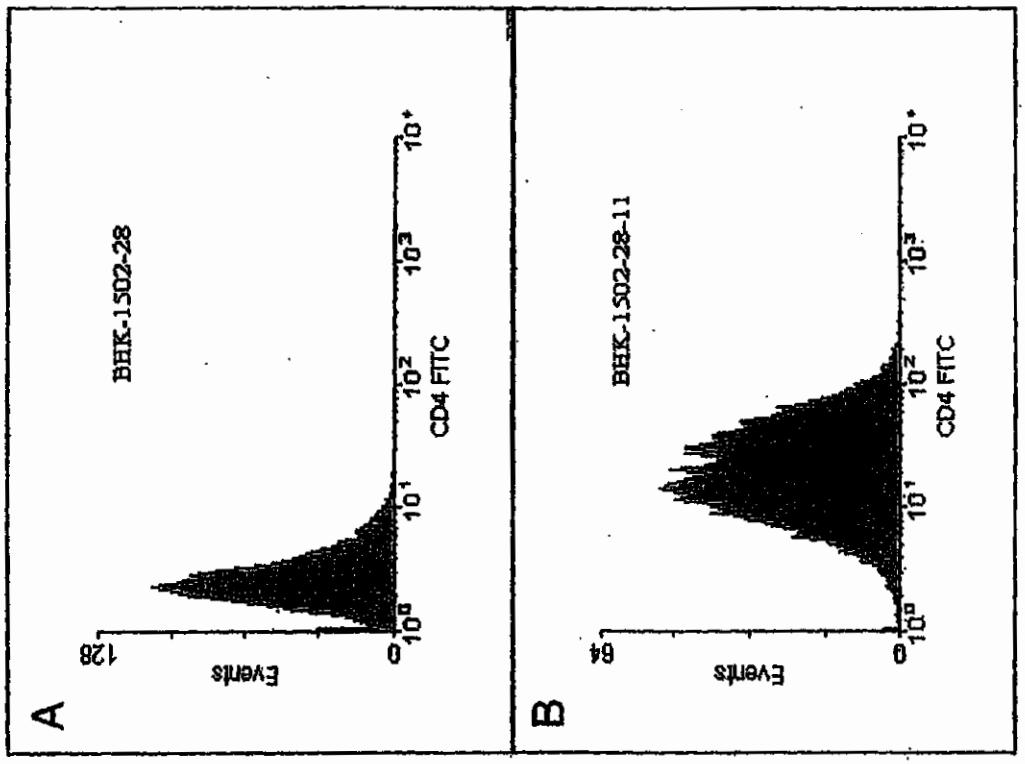

A
BHK-1502-28
Events
128
0
10^0
10^1
10^2
10^3
10^4
CD4 FITC
B
BHK-1502-28-11
Events
64
0
10^0
10^1
10^2
10^3
10^4
CD4 FITC

Figure 17

Figure 18

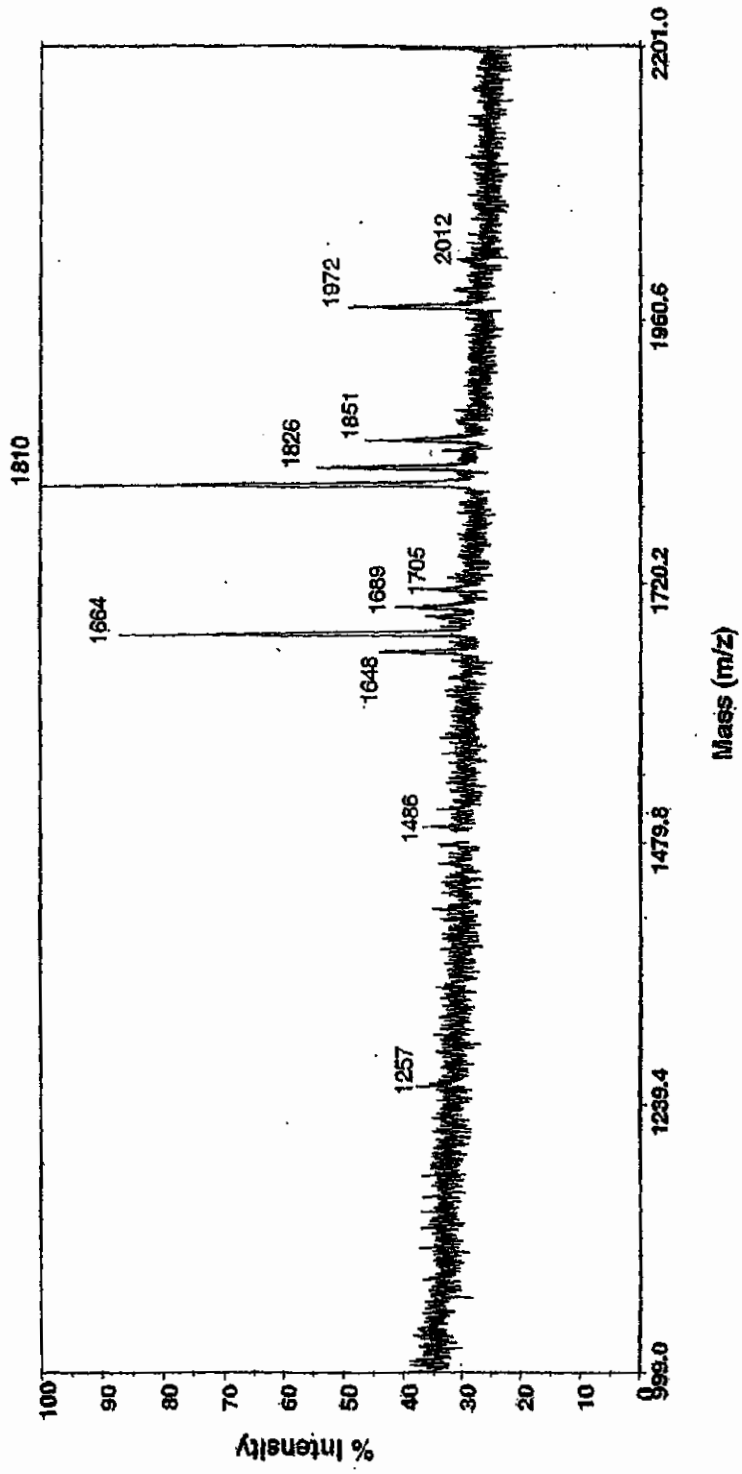
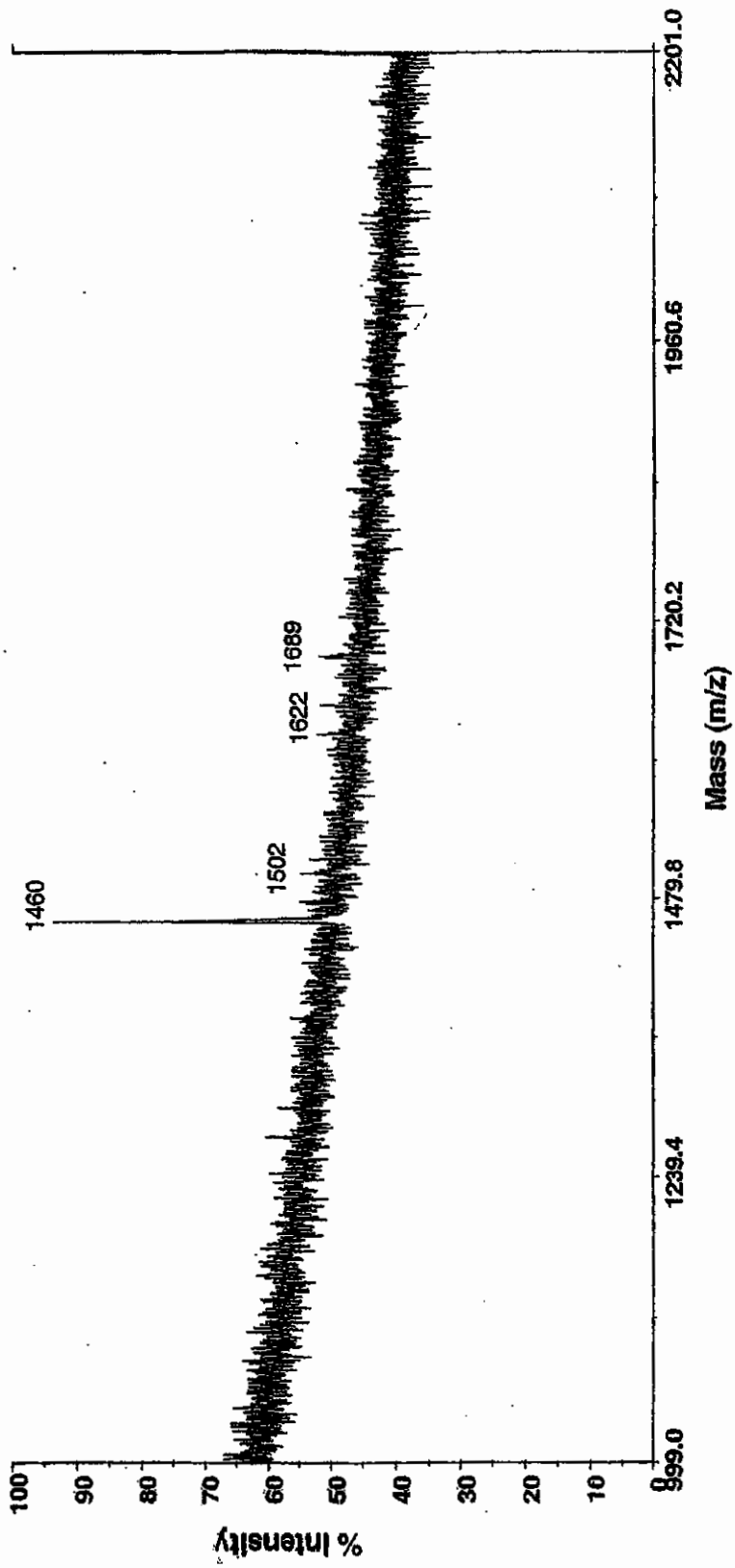

% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
1810
1826
1851
1972
2012
1664
1689
1705
1648
1486
1257

Figure 19


% Intensity
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)
1460
1502
1622
1689

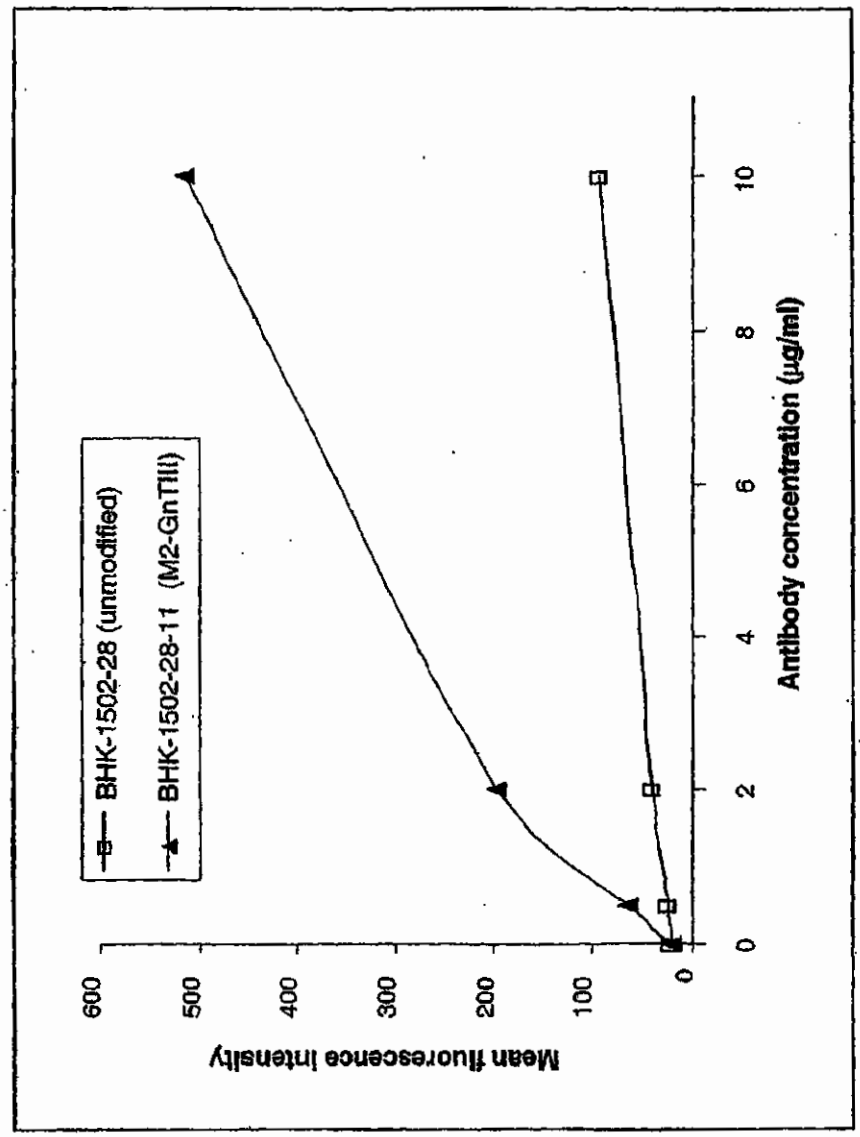

BHK-1502-28 (unmodified)
BHK-1502-28-11 (M2-GnTIII)
Mean fluorescence intensity
600
500
400
300
200
100
0
0
2
4
6
8
10
Antibody concentration (µg/ml)

Figure 20

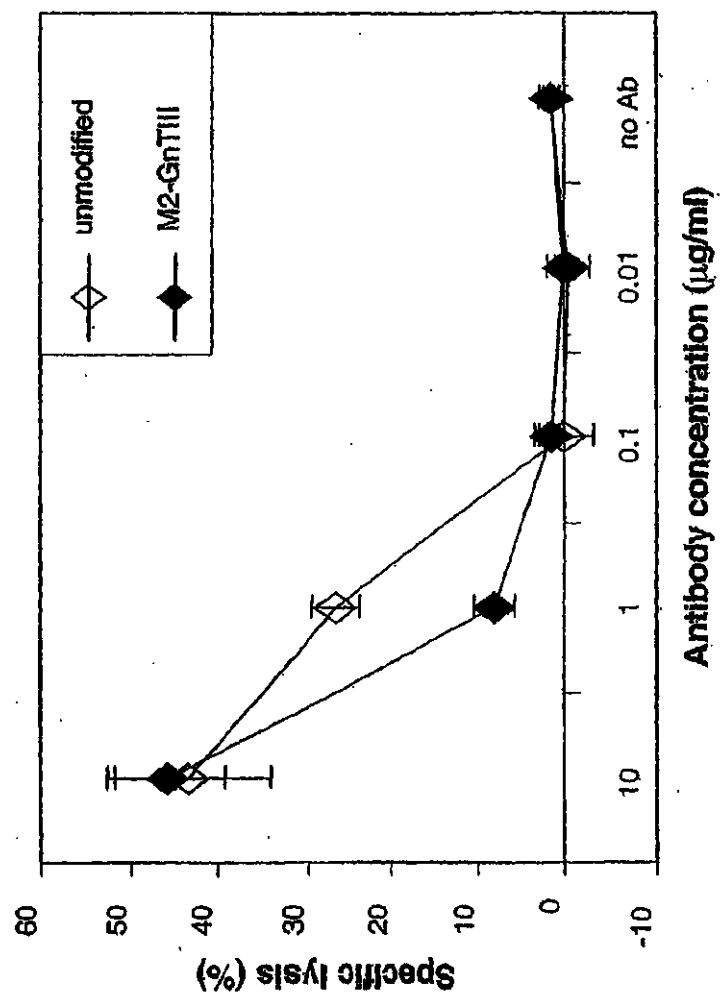
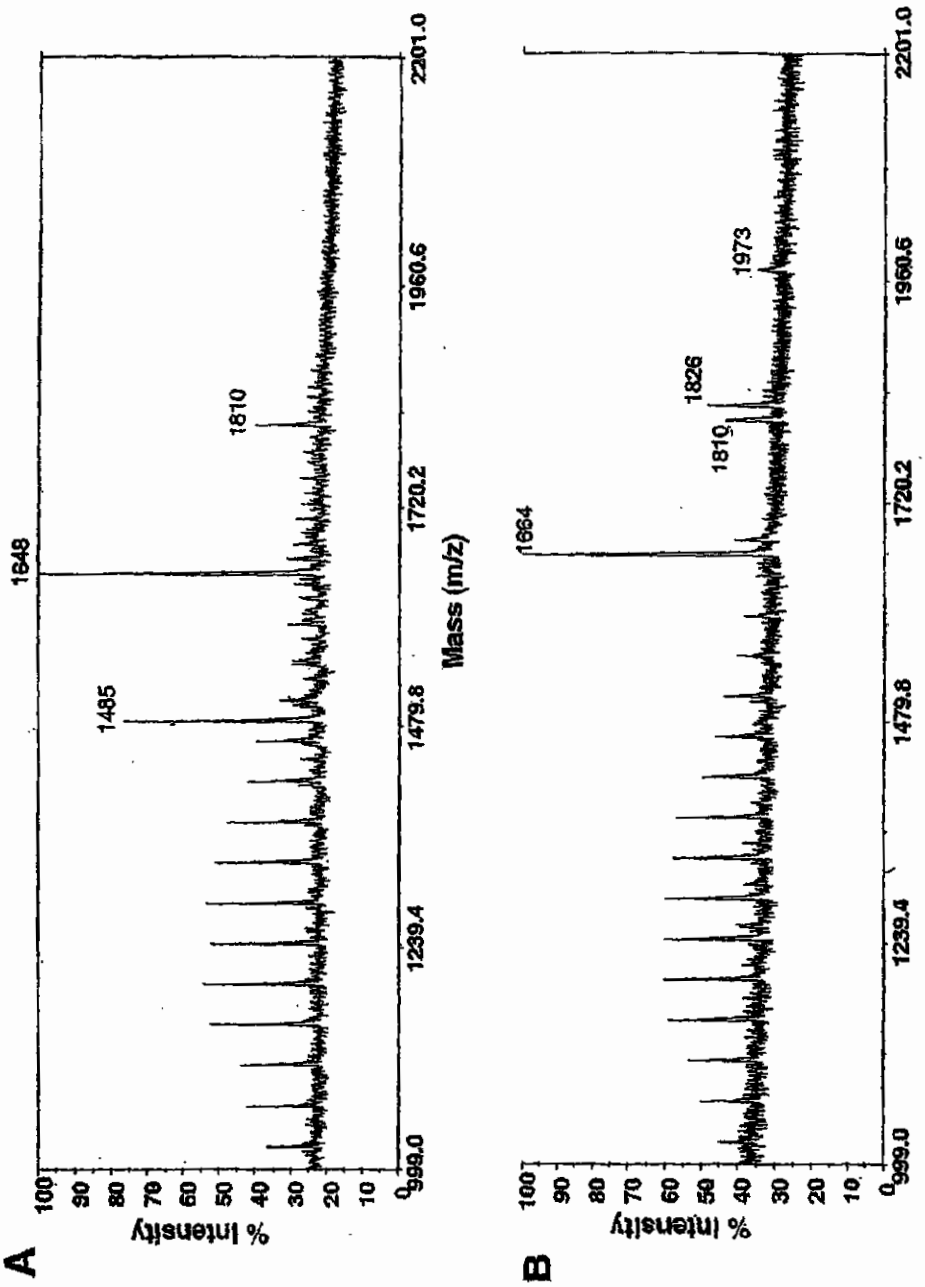

unmodified
M2-GnTIII
Specific lysis (%)
60
50
40
30
20
10
0
-10
10
1
0.1
0.01
no Ab
Antibody concentration (µg/ml)

Figure 21

Figure 22


A
% Intensity
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)
1648
1485
1810
B
% Intensity
1664
1810
1826
1973
Mass (m/z)

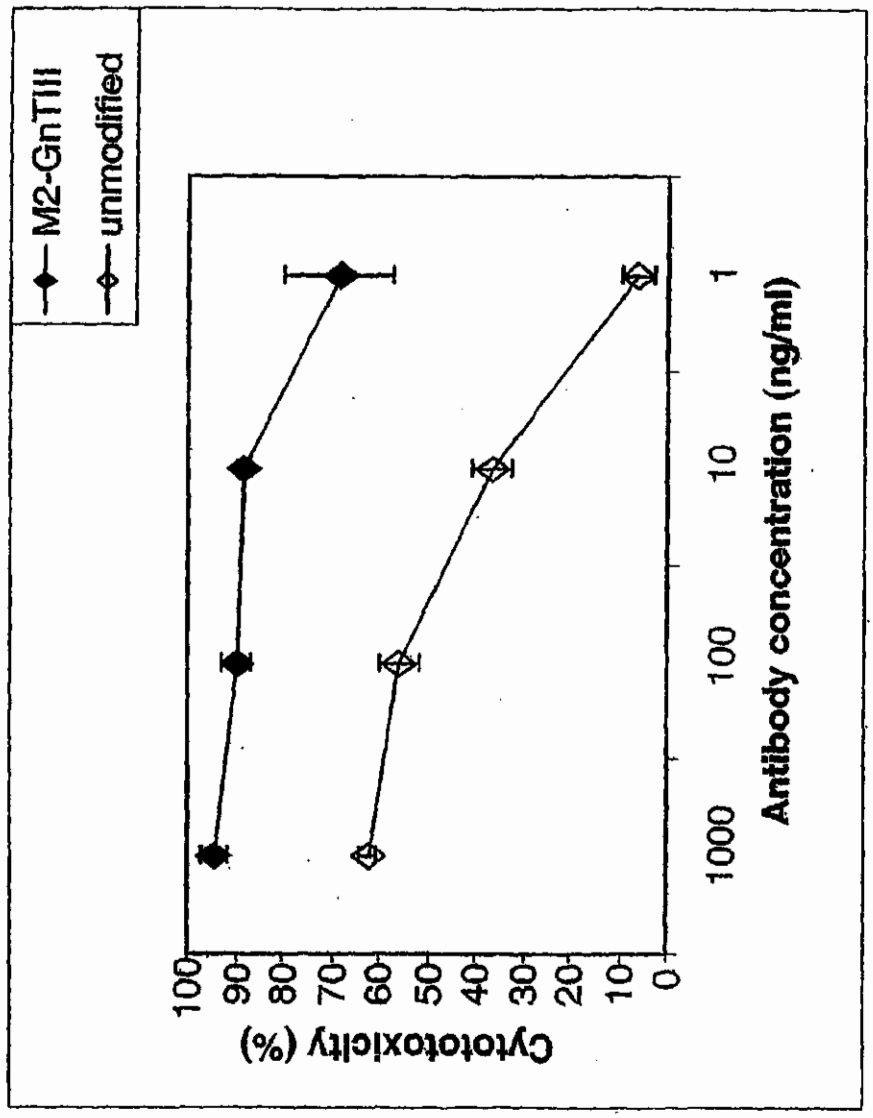

M2-GnTIII
unmodified
Cytotoxicity (%)
100
90
80
70
60
50
40
30
20
10
0
1000
100
10
1
Antibody concentration (ng/ml)

Figure 23

ManII-GnTIII:

Bold: ManII localization domain (cytoplasmic tail + transmembrane region + stem region)

ATGAAGTTAAGCCGCCAGTTCACCGTGTTCGGCAGTGCGATCTTCTGTGTGGTGATTTTC
TCGCTCTACCTGATGCTGGACCGGGGTCACTTAGACTACCCCAGGAACCCGCGCCGCGAG
GGCTCCTTCCCTCAGGGCCAGCTCTCAATGTTGCAAGAAAAAATAGACCATTTGGAGCGT
TTGCTAGCTGAGAATAATGAGATCATCTCAAATATTAGAGACTCAGTCATCAATTTGAGT
GAGTCTGTGGAGGATGGTCCGAAAAGTTCACAAAGCAATTTCAGCCAAGGTGCTGGCTCA
CCCCTGCTCCAGCCACTGTCCCCTAGCAAGGCCACCGAAGAACTGCACCGGGTGGACTTC
GTGTTGCCGGAGGACACCACAGAGTATTTTGTGCGCACCAAAGCTGGCGGTGTGTGCTTC
AAACCAGGTACCAGGATGCTGGAGAAACCTTCTCCAGGGCGGACAGAGGAGAAGACCAAG
GTGGCTGAGGGGTCCTCGGTCCGGGGTCCTGCTCGGAGGCCTATGCGGCATGTGTTGAGT
GCACGGGAGCGCCTGGGAGGCCGGGGCACTAGGCGCAAGTGGGTTGAGTGTGTGTGCCTG
CCAGGCTGGCACGGGCCCAGCTGCGGGGTGCCCACTGTGGTCCAGTATTCCAACCTGCCC
ACCAAGGAGCGCCTGGTACCCAGGGAGGTGCCGAGGCGGGTTATCAACGCCATCAACATC
AACCATGAGTTCGACCTGCTGGATGTGCGCTTCCATGAGCTGGGCGATGTTGTGGACGCC
TTTGTGGTCTGCGAATCCAATTTCACCGCCTACGGGGAGCCTCGGCCGCTCAAGTTCCGA
GAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTACGTCTTCCTG
GACCACTTCCCACCTGGTGGCCGTCAGGACGGCTGGATTGCAGACGACTACCTGCGTACC
TTCCTCACCCAGGATGGTGTCTCCCGCCTGCGCAACCTGCGACCTGATGACGTCTTTATC
ATCGACGACGCGGACGAGATCCCTGCGCGTGATGGTGTGCTGTTCCTCAAGCTCTACGAT
GGCTGGACAGAGCCCTTCGCCTTCCATATGCGCAAGTCCCTGTATGGTTTCTTTTGGAAG
CAACCAGGCACACTGGAGGTGGTGTCAGGCTGCACCATTGACATGCTGCAGGCTGTGTAT
GGGCTGGACGGCATCCGCCTGCGCCGCCGTCAGTACTACACCATGCCCAACTTTCGACAG
TATGAGAACCGCACCGGCCACATCCTAGTGCAGTGGTCTCTCGGCAGCCCCCTGCACTTC
GCGGGCTGGCACTGCTCCTGGTGCTTCACACCCGAGGGCATCTACTTCAAACTCGTGTCG
GCCCAGAATGGTGACTTCCCCCGCTGGGGTGACTACGAGGACAAGAGGGACCTCAATTAC
ATCCGAAGCTTGATTCGCACTGGGGGATGGTTCGACGGCACGCAGCAGGAGTACCCTCCT
GCAGACCCCAGTGAACACATGTATGCTCCTAAGTACCTGCTCAAGAACTATGACCAGTTC
CGCTACTTGCTCGAAAATCCCTACCGGGAGCCCAAGAGCACTGTAGAGGGTGGGCGCCGG
AACCAGGGCTCAGACGGAAGGTCATCTGCTGTCAGGGGCAAGTTGGATACAACGGAGGGC
CCGGAACAGAAACTGATCTCTGAAGAGGACCTGTAG

MKLSRQFTVFGSAIFCVVIFSLYLMLDRGHLDYPRNPRREGSFPQGQLSMLQEKIDHLER
LLAENNETISNIRDSVINLSESVEDGPKSSQSNFSQGAGSPLLQPLSPSKATEELHRVDF
VLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSPGRTEEKTKVAEGSSVRGPARRPMRHVLS
ARERLGGRGTRRKWVECVCLPGWHGPSCGVPTVVQYSNLPTKERLVPREVPRRVINAINI
NHEFDLLDVRFHELGDVVDAFVVCESNFTAYGEPRPLKFREMLTNGTFEYIRHKVLYVFL
DHFPPGGRQDGWIADDYLRTFLTQDGVSRLRNLRPDDVFIIDDADEIPARDGVLFLKLYD
GWTEPFAFHMRKSLYGFFWKQPGTLEVVSGCTIDMLQAVYGLDGIRLRRRQYYTMPNFRQ
YENRTGHILVQWSLGSPLHFAGWHCSWCFTPEGIYFKLVSAQNGDFPRWGDYEDKRDLNY
IRSLIRTGGWFDGTQQEYPPADPSEHMYAPKYLLKNYDQFRYLLENPYREPKSTVEGGRR
NQGSDGRSSAVRGKLDTTEGPEQKLISEEDL

Figure 24

GnTI-GnTIII

Bold: GnTI ManII localization domain (cytoplasmic tail + transmembrane region + stem region)

ATGCTGAAGAAGCAGTCTGCAGGGCTTGTGCTGTGGGGCGCTATCCTCTTTGTGGCCTGG
AATGCCCTGCTGCTCCTCTTCTTCTGGACGCGCCCAGCACCTGGCAGGCCACCCTCAGTC
AGCGCTCTCGATGGCGACCCCGCCAGCCTCACCCGGGAAGTGATTCGCCTGGCCCAAGAC
GCCGAGGTGGAGCTGGAGCGGCAGCGTGGGCTGCTGCAGCAGATCGGGGATGCCCTGTCG
AGCCAGCGGGGGAGGGTGCCCACCGCGGCCCCTCCCGCCCAGCCGCGTGTGCCTGTGACC
CCCGCGCCCCTGCTCCAGCCACTGTCCCCTAGCAAGGCCACCGAAGAACTGCACCGGGTG
GACTTCGTGTTGCCGGAGGACACCACAGAGTATTTTGTGCGCACCAAAGCTGGCGGTGTG
TGCTTCAAACCAGGTACCAGGATGCTGGAGAAACCTTCTCCAGGGCGGACAGAGGAGAAG
ACCAAGGTGGCTGAGGGGTCCTCGGTCCGGGGTCCTGCTCGGAGGCCTATGCGGCATGTG
TTGAGTGCACGGGAGCGCCTGGGAGGCCGGGGCACTAGGCGCAAGTGGGTTGAGTGTGTG
TGCCTGCCAGGCTGGCACGGGCCCAGCTGCGGGGTGCCCACTGTGGTCCAGTATTCCAAC
CTGCCCACCAAGGAGCGCCTGGTACCCAGGGAGGTGCCGAGGCGGGTTATCAACGCCATC
AACATCAACCATGAGTTCGACCTGCTGGATGTGCGCTTCCATGAGCTGGGCGATGTTGTG
GACGCCTTTGTGGTCTGCGAATCCAATTTCACCGCCTACGGGGAGCCTCGGCCGCTCAAG
TTCCGAGAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTACGTC
TTCCTGGACCACTTCCCACCTGGTGGCCGTCAGGACGGCTGGATTGCAGACGACTACCTG
CGTACCTTCCTCACCCAGGATGGTGTCTCCCGCCTGCGCAACCTGCGACCTGATGACGTC
TTTATCATCGACGACGCGGACGAGATCCCTGCGCGTGATGGTGTGCTGTTCCTCAAGCTC
TACGATGGCTGGACAGAGCCCTTCGCCTTCCATATGCGCAAGTCCCTGTATGGTTTCTTT
TGGAAGCAACCAGGCACACTGGAGGTGGTGTCAGGCTGCACCATTGACATGCTGCAGGCT
GTGTATGGGCTGGACGGCATCCGCCTGCGCCGCCGTCAGTACTACACCATGCCCAACTTT
CGACAGTATGAGAACCGCACCGGCCACATCCTAGTGCAGTGGTCTCTCGGCAGCCCCCTG
CACTTCGCGGGCTGGCACTGCTCCTGGTGCTTCACACCCGAGGGCATCTACTTCAAACTC
GTGTCGGCCCAGAATGGTGACTTCCCCCGCTGGGGTGACTACGAGGACAAGAGGGACCTC
AATTACATCCGAAGCTTGATTCGCACTGGGGGATGGTTCGACGGCACGCAGCAGGAGTAC
CCTCCTGCAGACCCCAGTGAACACATGTATGCTCCTAAGTACCTGCTCAAGAACTATGAC
CAGTTCCGCTACTTGCTCGAAAATCCCTACCGGGAGCCCAAGAGCACTGTAGAGGGTGGG
CGCCGGAACCAGGGCTCAGACGGAAGGTCATCTGCTGTCAGGGGCAAGTTGGATACAACG
GAGGGCCCGGAACAGAAACTGATCTCTGAAGAGGACCTGTAG

MLKKQSAGLVLWGAILFVAWNALLLLFFWTRPAPGRPPSVSALDGDPASLTREVIRLAQD
AEVELERQRGLLQQIGDALSSQRGRVPTAAPPAQPRVPVTPAPLLQPLSPSKATEELHRV
DFVLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSPGRTEEKTKVAEGSSVRGPARRPMRHV
LSARERLGGRGTRRKWVECVCLPGWHGPSCGVPTVVQYSNLPTKERLVPREVPRRVINAI
NINHEFDLLDVRFHELGDVVDAFVVCESNFTAYGEPRPLKFREMLTNGTFEYIRHKVLYV
FLDHFPPGGRQDGWIADDYLRTFLTQDGVSRLRNLRPDDVFIIDDADEIPARDGVLFLKL
YDGWTEPFAFHMRKSLYGFFWKQPGTLEVVSGCTIDMLQAVYGLDGIRLRRRQYYTMPNF
RQYENRTGHILVQWSLGSPLHFAGWHCSWCFTPEGIYFKLVSAQNGDFPRWGDYEDKRDL
NYIRSLIRTGGWFDGTQQEYPPADPSEHMYAPKYLLKNYDQFRYLLENPYREPKSTVEGG
RRNQGSDGRSSAVRGKLDTTEGPEQKLISEEDL

Figure 25

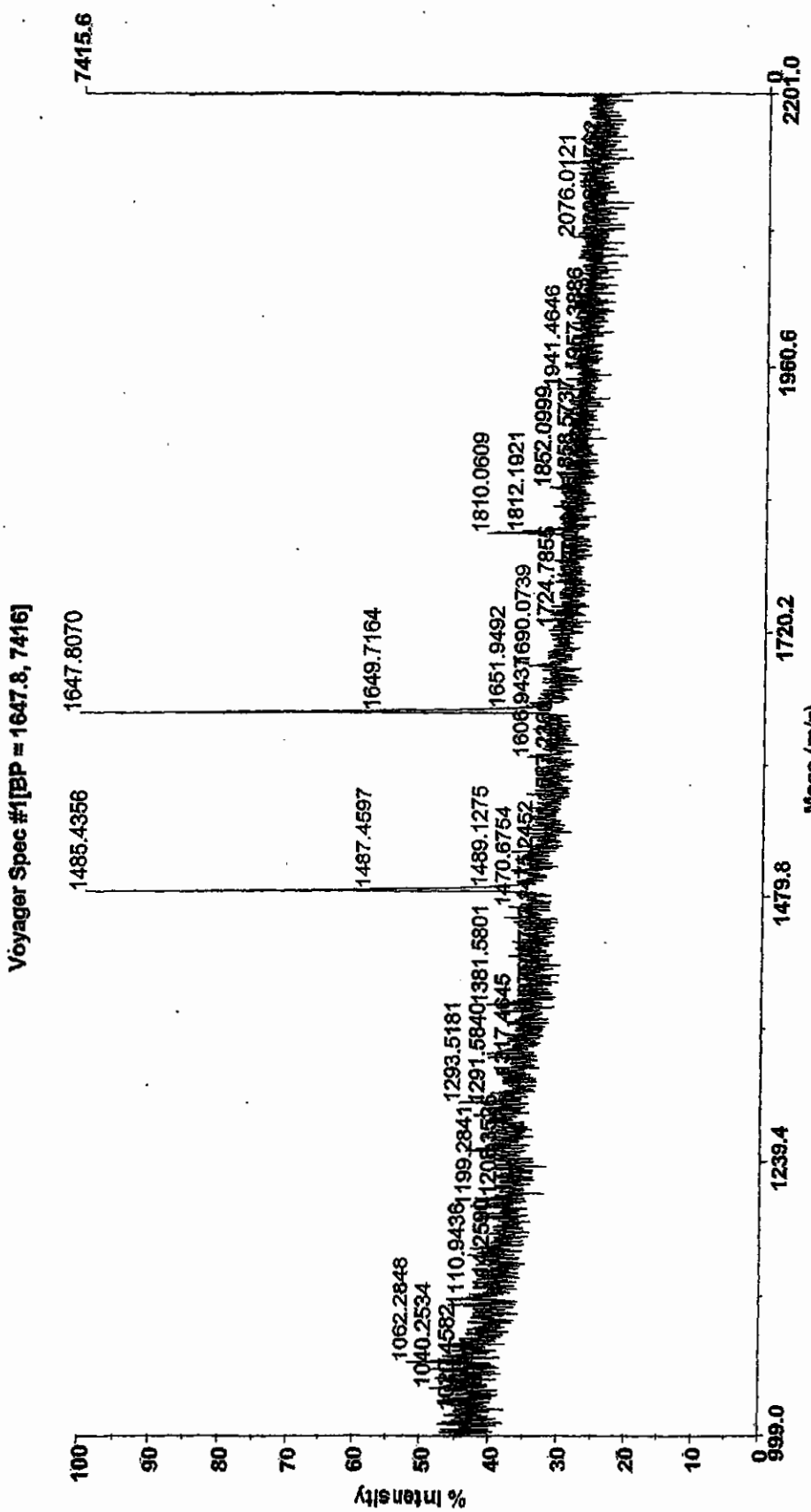

Voyager Spec #1[BP = 1647.8, 7416]
% Intensity
Mass (m/z)
7415.6
1647.8070
1649.7164
1485.4356
1487.4597
1489.1275
1651.9492
1810.0609
1812.1921
1852.0999
1941.4646
2076.0121
1690.0739
1724.7855
1606.9431
1470.6754
1381.5801
1293.5181
1291.5840
1199.2841
1110.9436
1062.2848
1040.2534
999.0
1239.4
1479.8
1720.2
1960.6
2201.0

FIG. 26

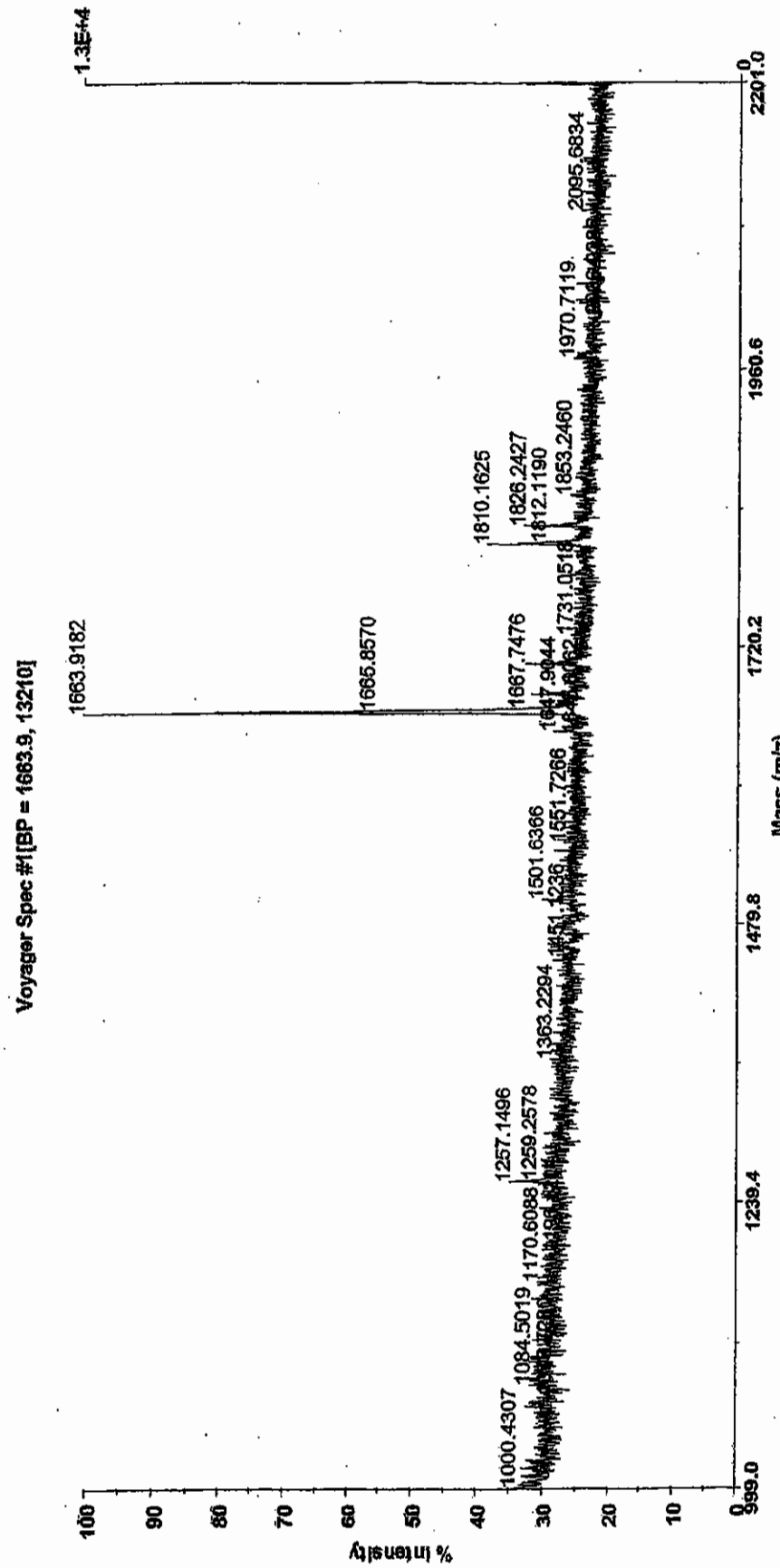

Voyager Spec #1[BP = 1663.9, 13210]
1.3E+4
0
% Intensity
100
90
80
70
60
50
40
30
20
10
0
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
Mass (m/z)
1663.9182
1665.8570
1667.7476
1810.1625
1826.2427
1812.1190
1853.2460
1970.7119
2095.6834
1501.6366
1551.7266
1363.2294
1257.1496
1259.2578
1170.6088
1084.5019
1000.4307

FIG. 27A

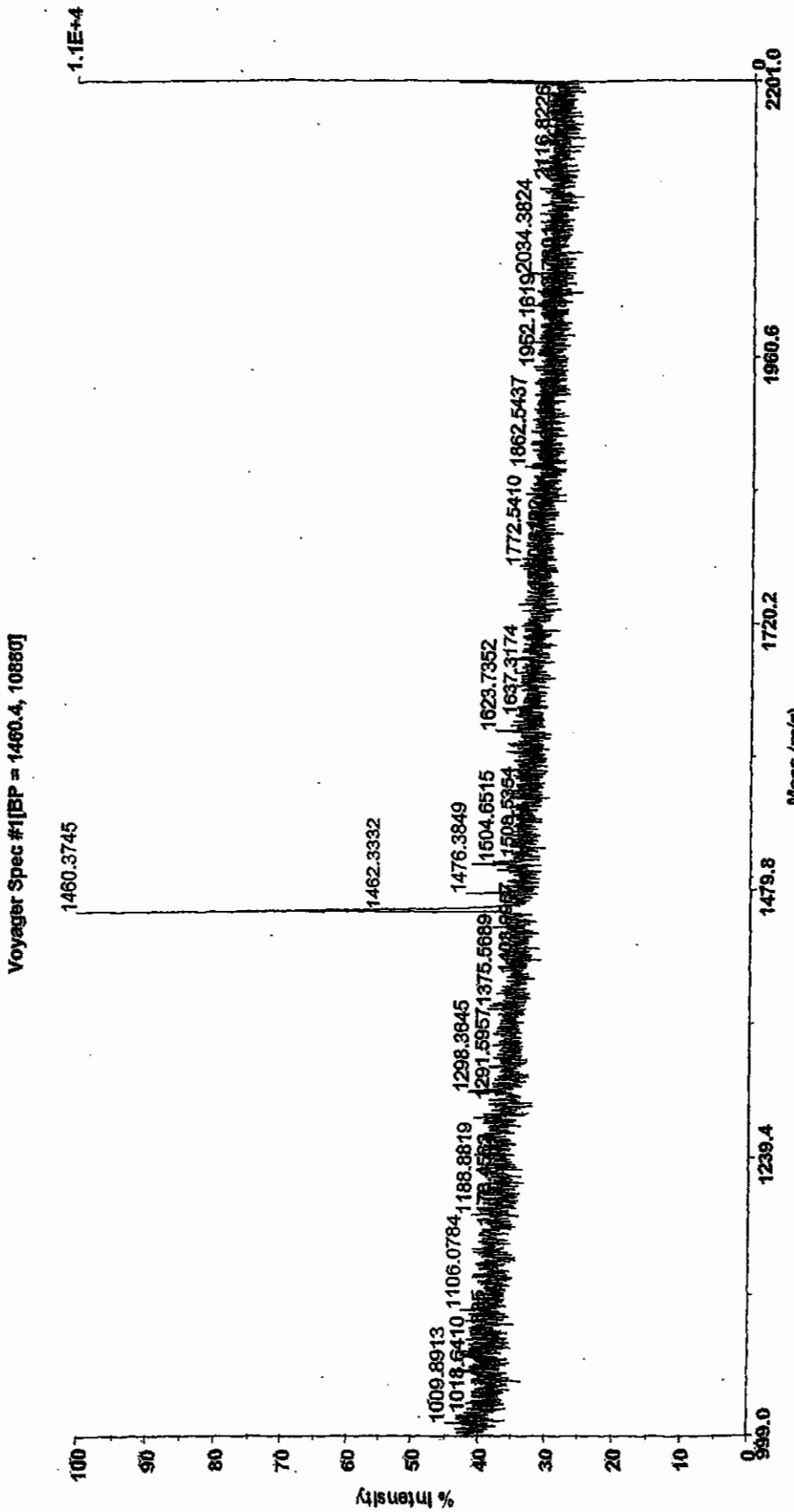

Voyager Spec #1[BP = 1460.4, 10880]
1.1E+4
% Intensity
Mass (m/z)
999.0
1239.4
1479.8
1720.2
1960.6
2201.0
1460.3745
1462.3332
1476.3849
1604.6515
1623.7352
1637.3174
1772.5410
1862.5437
1952.1619
2034.3824
1298.3845
1291.5957
1375.5669
1188.8819
1106.0784
1009.8913
1018.6410

FIG. 27B

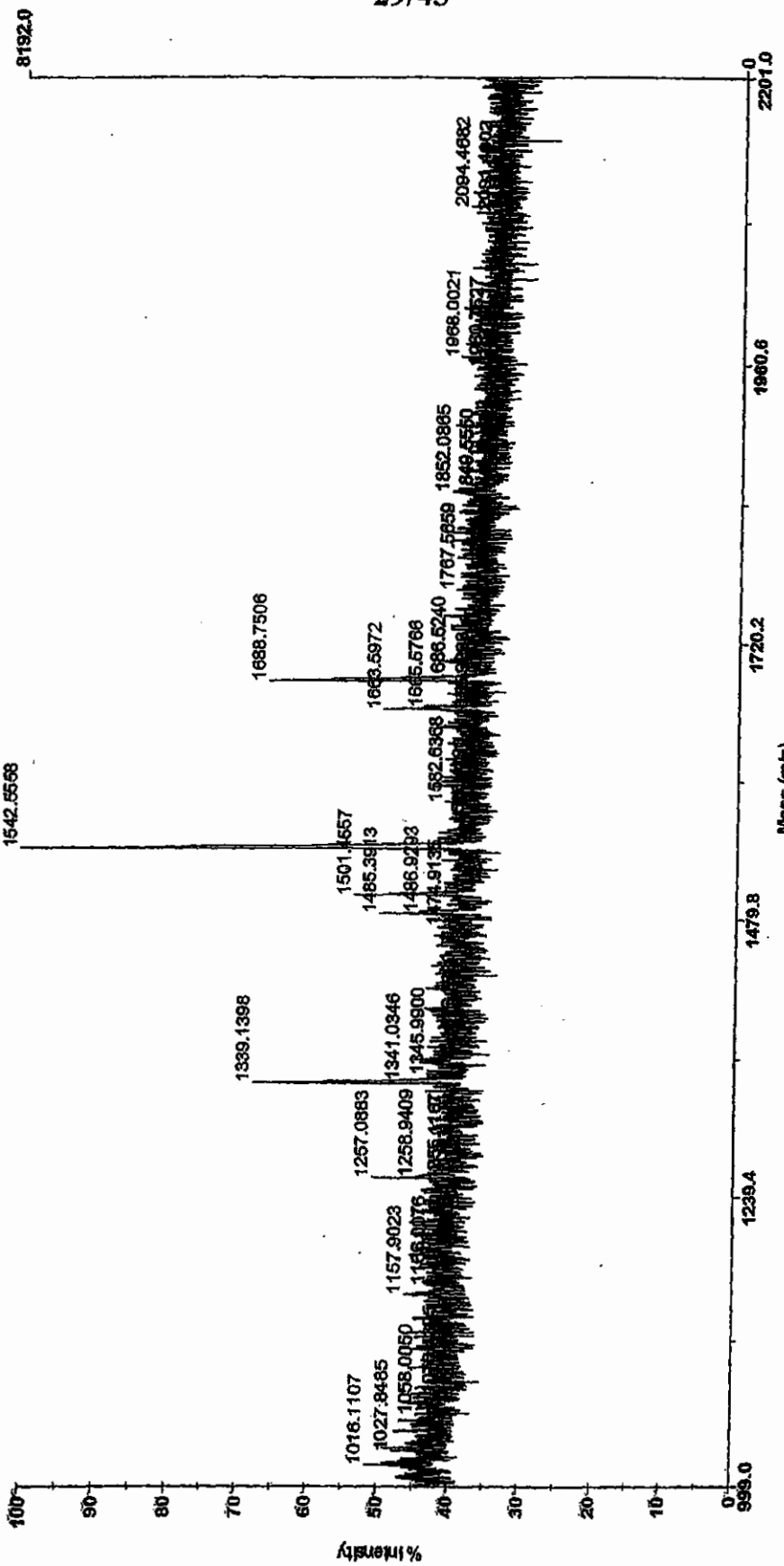

Voyager Spec #1[BP = 1542.6, 8192]
% Intensity
Mass (m/z)
8192.0
0
2201.0
1960.6
1720.2
1479.8
1239.4
999.0
100
90
80
70
60
50
40
30
20
10
0
1542.5568
1688.7506
1663.5972
1685.5766
1686.6240
1787.5859
1852.0865
1968.0021
2094.4682
1501.7657
1485.3913
1486.9263
1582.6368
1339.1398
1341.0346
1345.9900
1257.0883
1258.9409
1157.9023
1016.1107
1027.8485
1058.0050

FIG. 28A

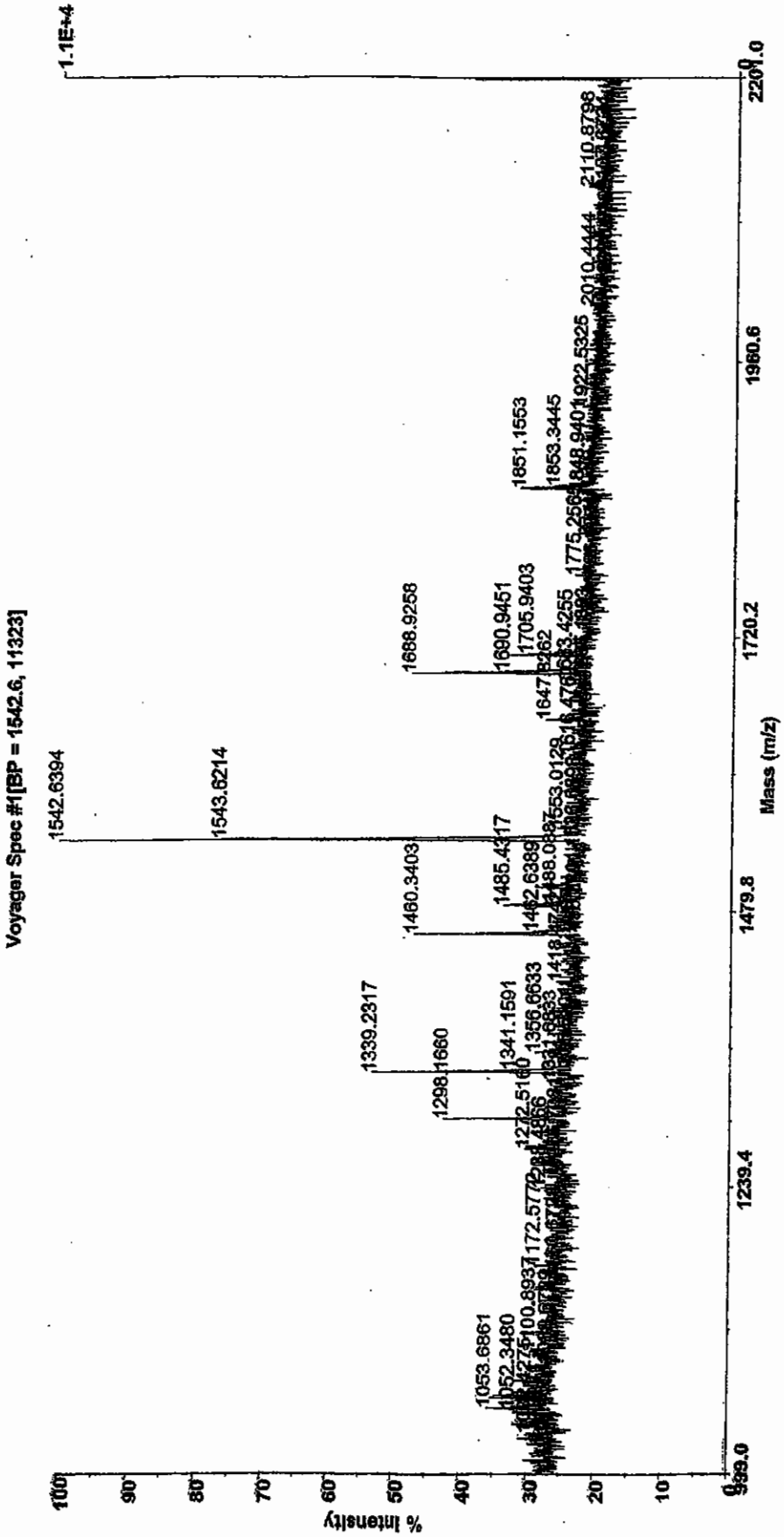

Voyager Spec #1[BP = 1542.6, 11323]
1.1E+4
% Intensity
Mass (m/z)
1542.6394
1543.6214
1688.9258
1690.9451
1705.9403
1851.1553
1853.3445
1460.3403
1485.4317
1462.6389
1339.2317
1341.1591
1298.1660
1053.6861
1239.4
1479.8
1720.2
1960.6
2201.0

FIG. 28B

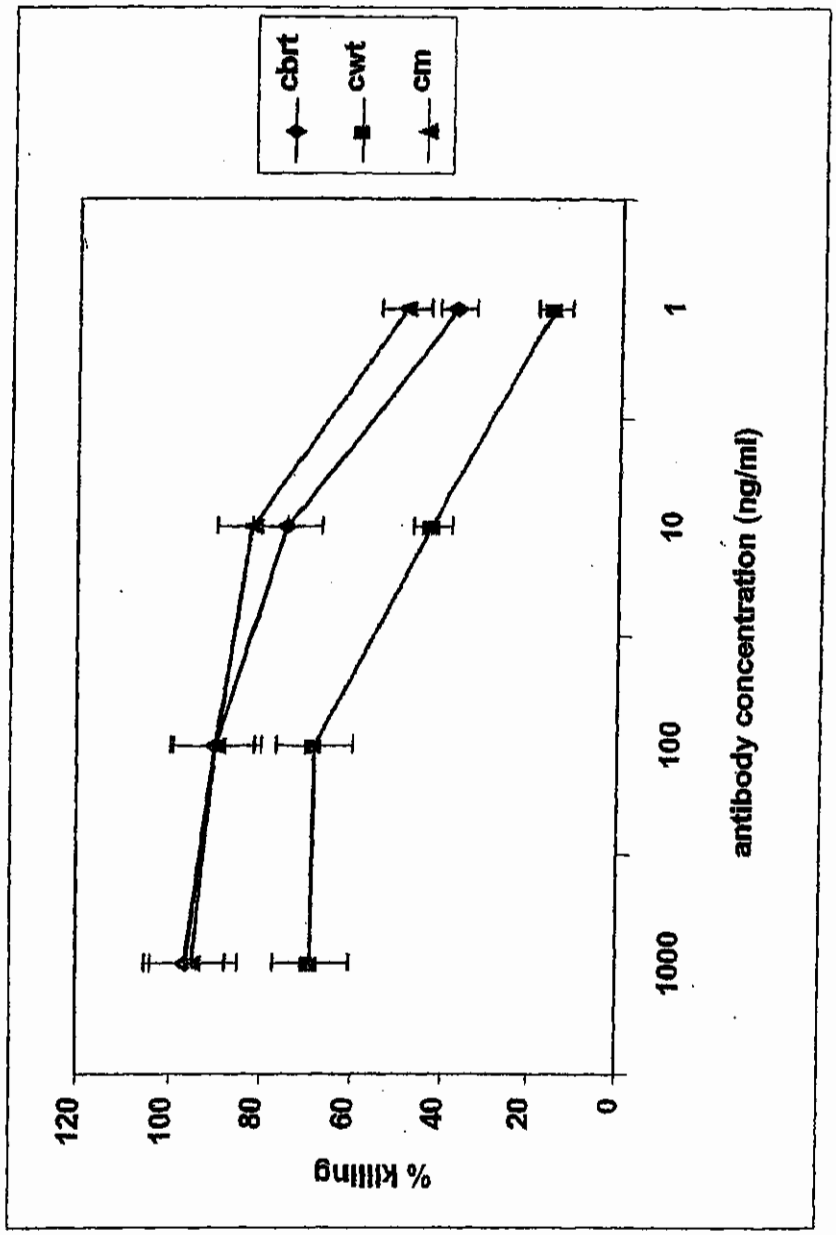

cbrt
cwt
cm
% killing
120
100
80
60
40
20
0
1000
100
10
1
antibody concentration (ng/ml)

FIG. 29

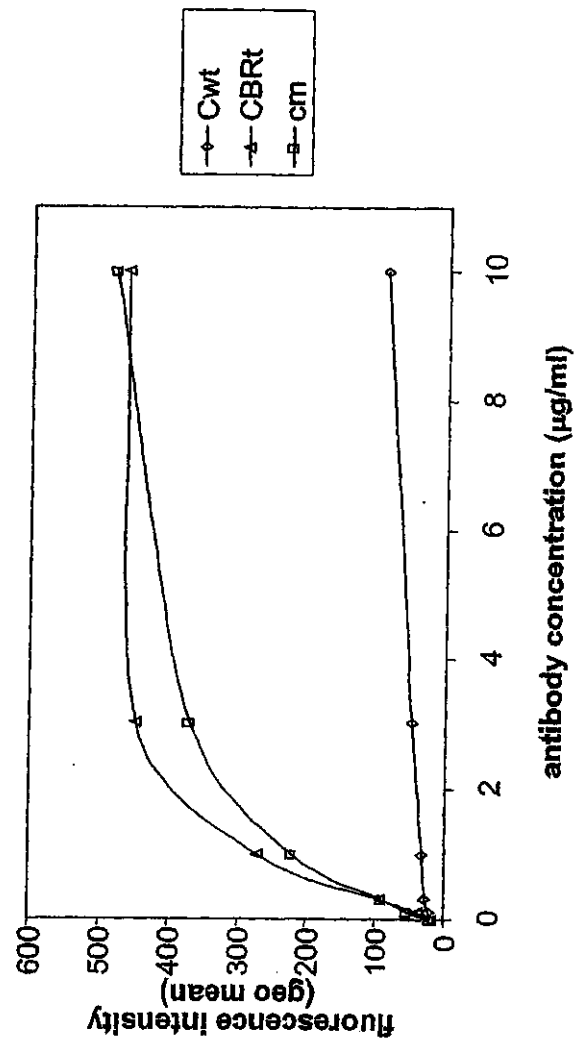

Cwt
CBRt
cm
Fluorescence intensity
(geo mean)
600
500
400
300
200
100
0
0
2
4
6
8
10
antibody concentration (µg/ml)

FIG. 30

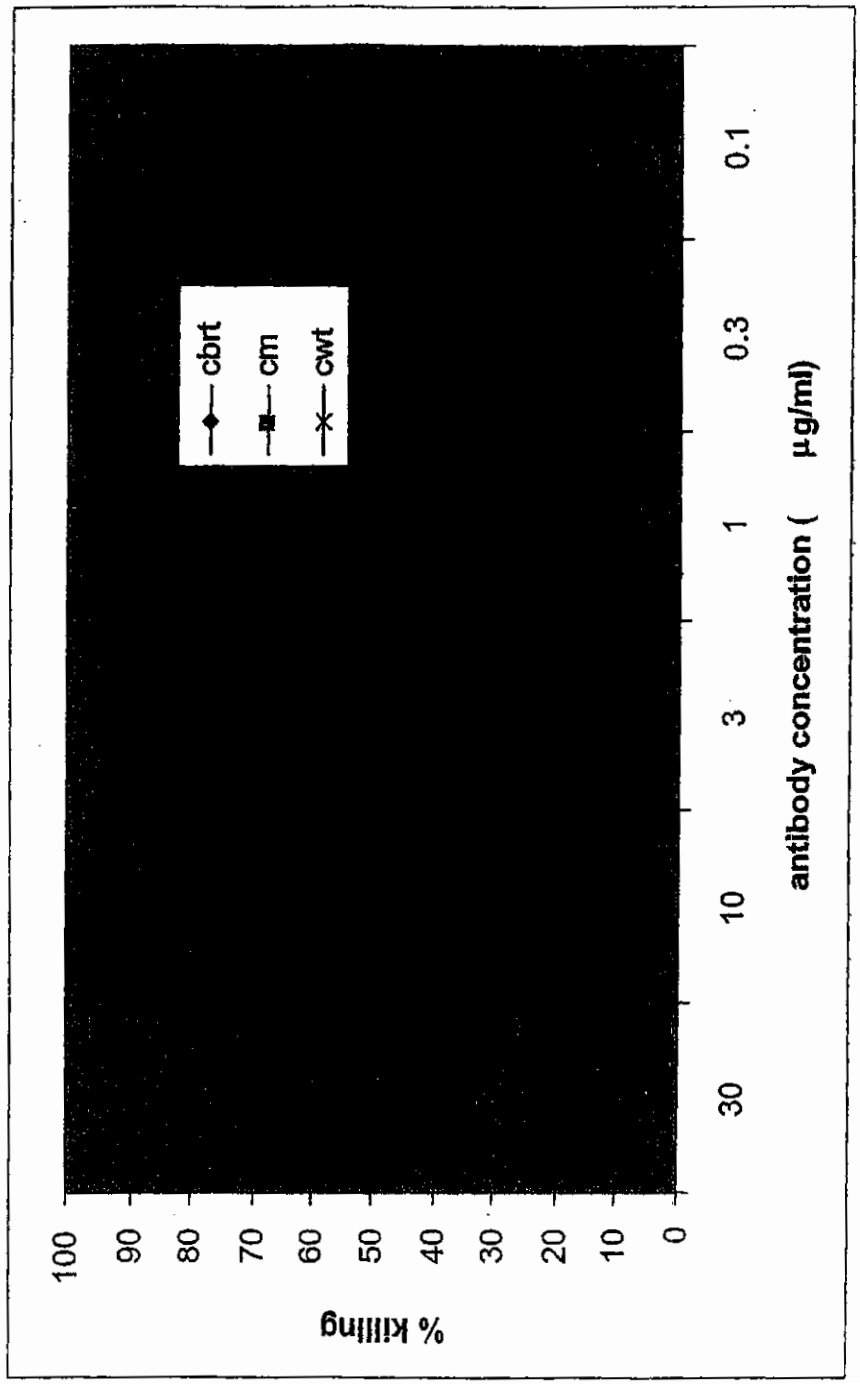

% killing
100
90
80
70
60
50
40
30
20
10
0
30
10
3
1
0.3
0.1
antibody concentration (µg/ml)
cbrt
cm
cwt

FIG. 31

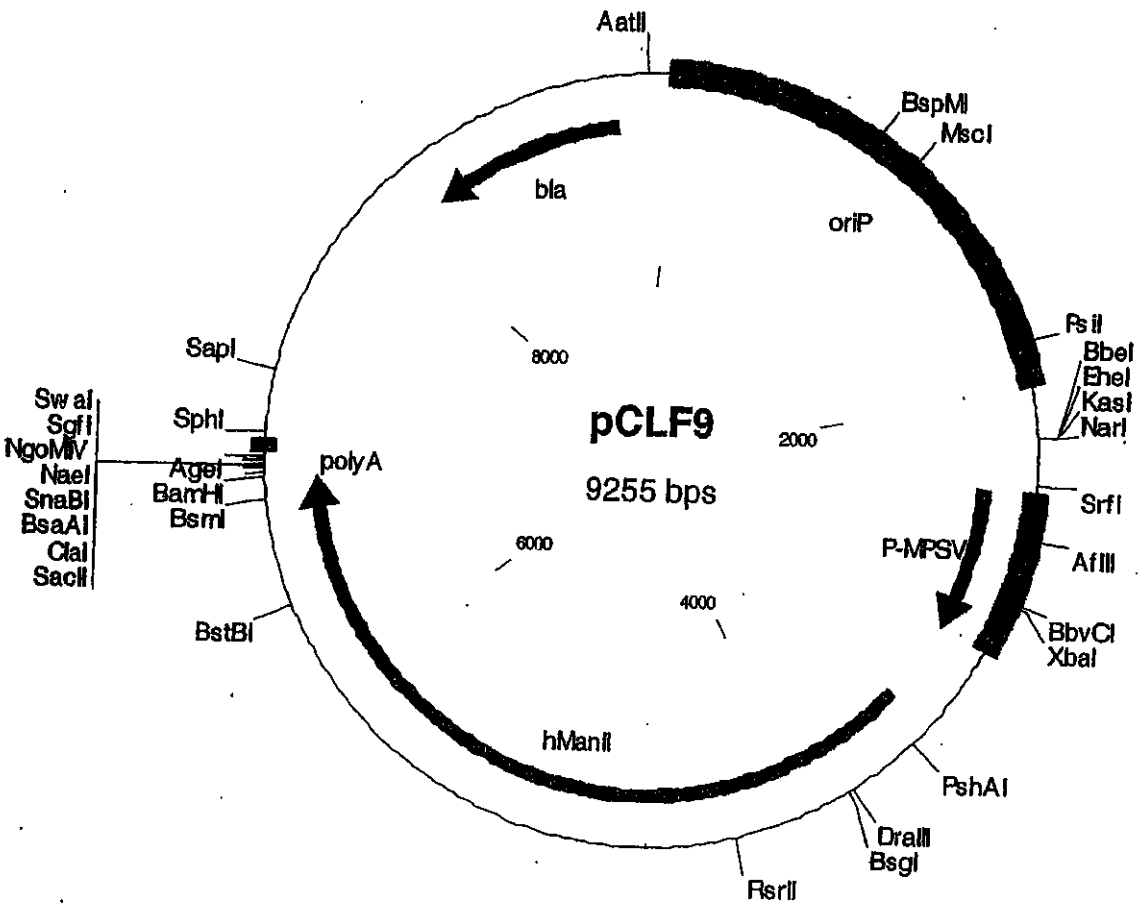

AatII
BspMI
MscI
bla
oriP
PsiI
BbeI
EheI
KasI
NarI
SrfI
AflII
BbvCI
XbaI
PshAI
DraIII
BsgI
RsrII
hManII
P-MPSV
BstBI
polyA
SapI
SphI
AgeI
BamHI
BsmI
SwaI
SgfI
NgoMIV
NaeI
SnaBI
BsaAI
ClaI
SacII
8000
2000
6000
4000
pCLF9
9255 bps

FIG. 32A

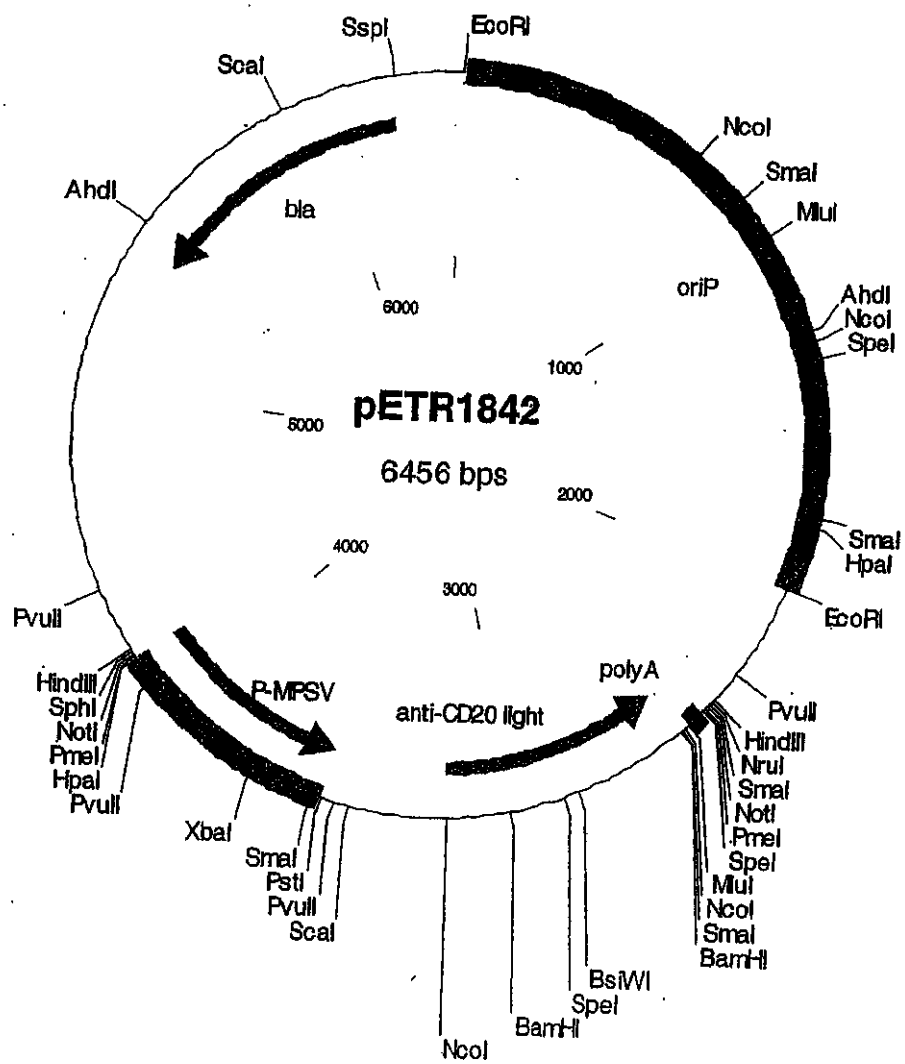

pETR1842
6456 bps
1000
2000
3000
4000
5000
6000
SspI
EcoRI
ScaI
NcoI
SmaI
MluI
AhdI
bla
oriP
AhdI
NcoI
SpeI
SmaI
HpaI
EcoRI
PvuII
HindIII
SphI
NotI
PmeI
HpaI
PvuII
P-MPSV
anti-CD20 light
polyA
PvuII
HindIII
NruI
SmaI
NotI
PmeI
SpeI
MluI
NcoI
SmaI
BamHI
XbaI
SmaI
PstI
PvuII
ScaI
NcoI
BamHI
SpeI
BsiWI

FIG. 32B

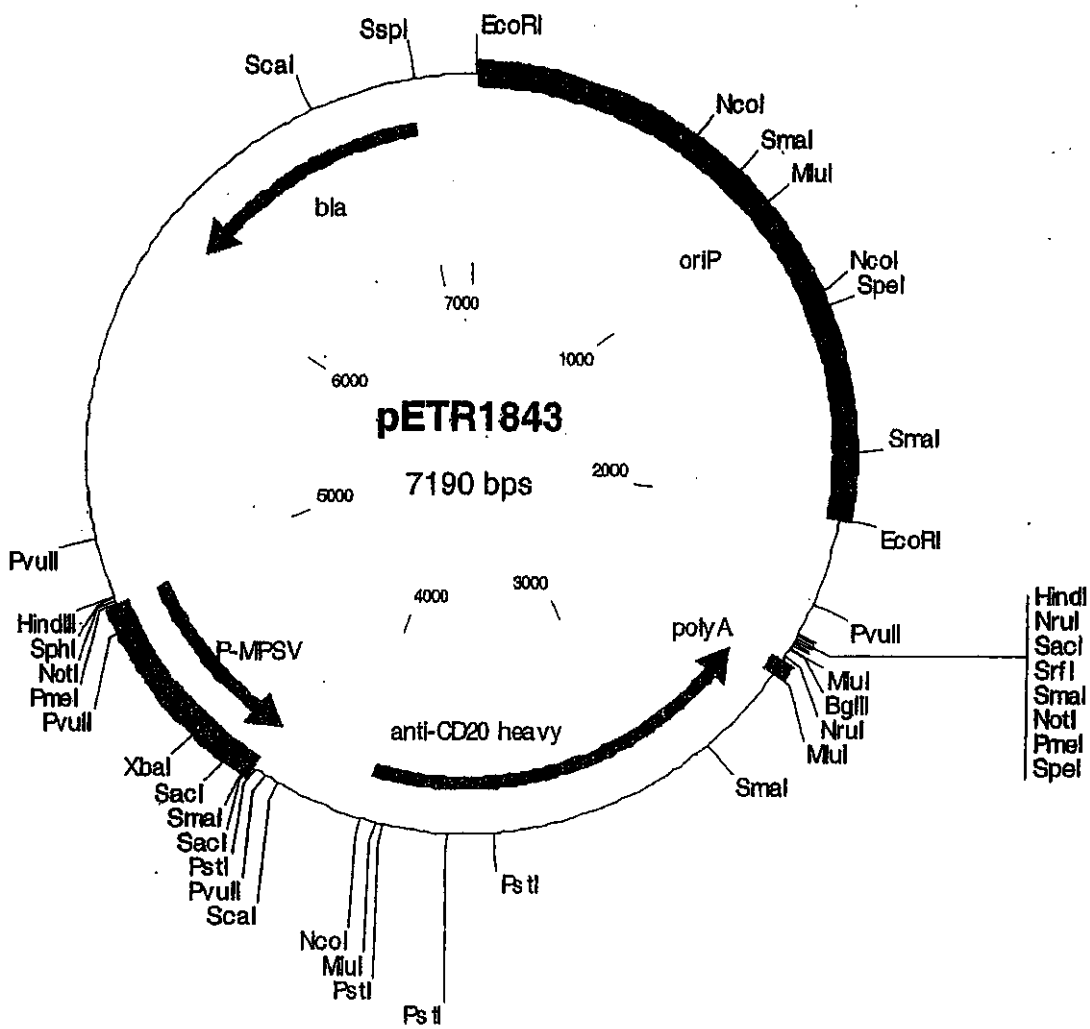

pETR1843
7190 bps
1000
2000
3000
4000
5000
6000
7000
bla
oriP
P-MPSV
anti-CD20 heavy
polyA
SspI
EcoRI
ScaI
NcoI
SmaI
MluI
NcoI
SpeI
SmaI
EcoRI
PvuII
HindIII
NruI
SacI
SrfI
SmaI
NotI
PmeI
SpeI
MluI
BglII
NruI
MluI
SmaI
PstI
NcoI
MluI
PstI
PstI
XbaI
SacI
SmaI
SacI
PstI
PvuII
ScaI
HindIII
SphI
NotI
PmeI
PvuII

FIG. 32C

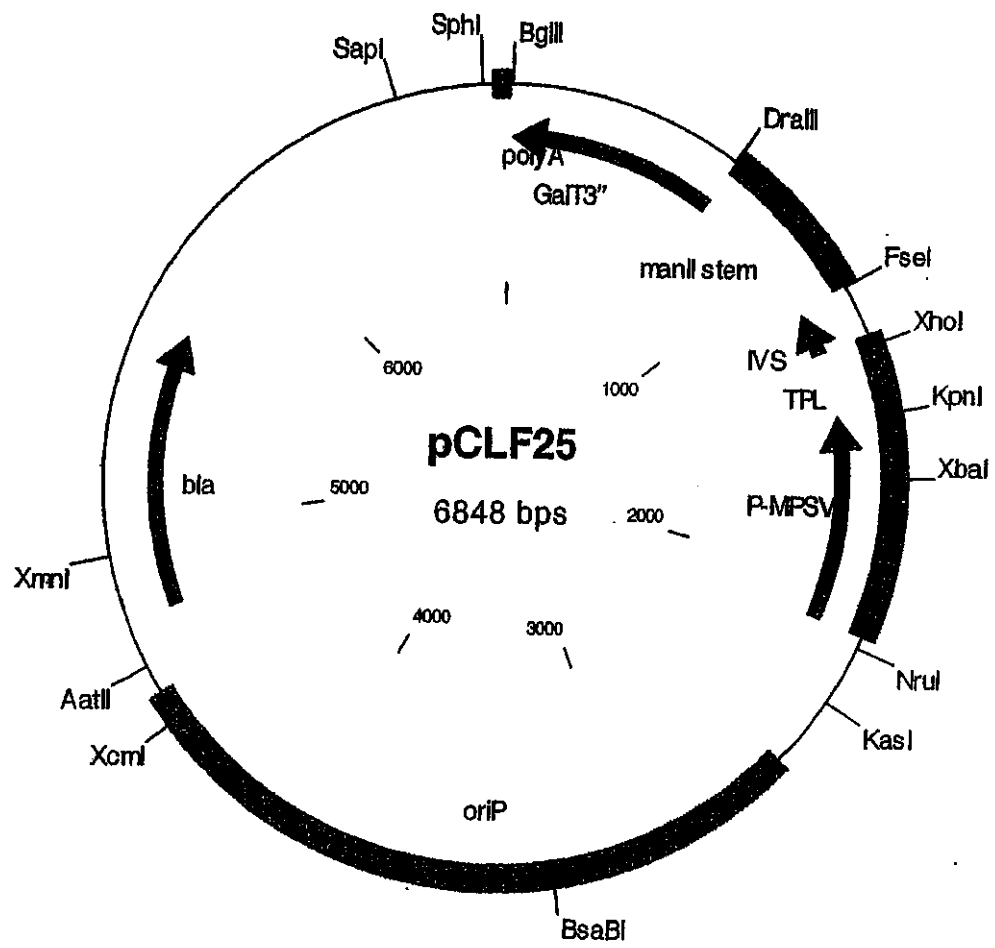

SapI
SphI
BglII
DraIII
polyA
GalT3"
manII stem
FseI
XhoI
IVS
TPL
KpnI
XbaI
P-MPSV
NruI
KasI
BsaBI
oriP
AatII
XcmI
XmnI
bla
pCLF25
6848 bps
1000
2000
3000
4000
5000
6000

FIG. 33A

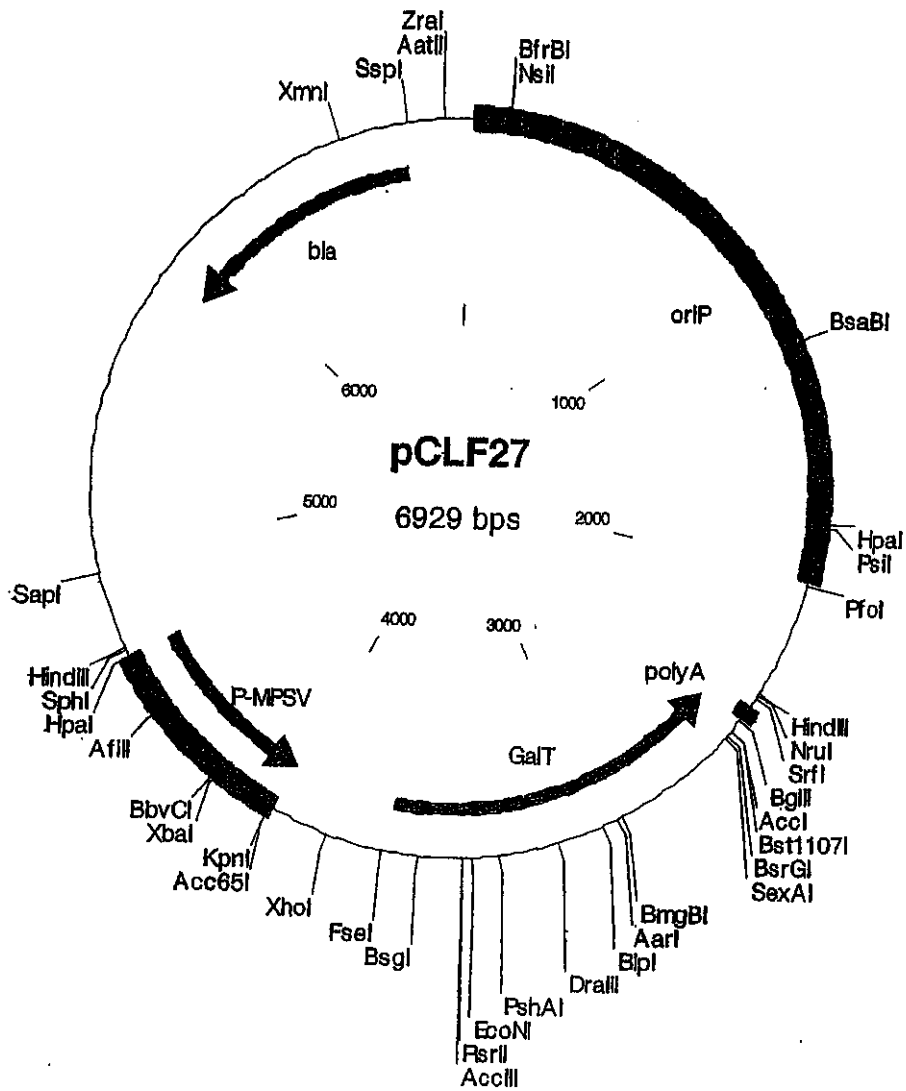
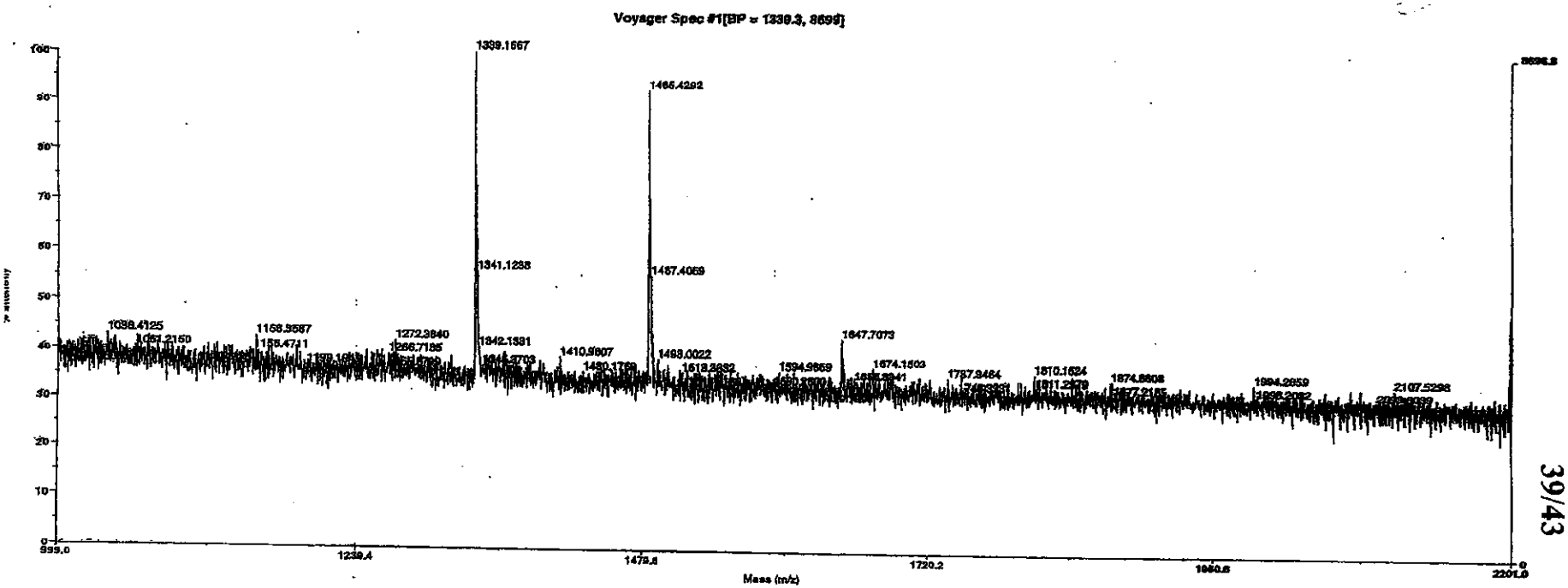

ZraI
AatII
BfrBI
NsiI
SspI
XmnI
bla
oriP
BsaBI
6000
1000
pCLF27
6929 bps
5000
2000
HpaI
PsiI
PfoI
SapI
4000
3000
polyA
HindIII
SphI
HpaI
AflII
P-MPSV
GalT
HindIII
NruI
SrfI
BglII
AccI
Bst1107I
BsrGI
SexAI
BbvCI
XbaI
KpnI
Acc65I
XhoI
FseI
BsgI
BmgBI
AarI
BlpI
DraIII
PshAI
EcoNI
PsrII
AccIII

FIG. 33B



	ManII
1339	48.40%
1486	43.30%
1647	8.30%

tot complex	100.00%
non-fuc, complex	48.40%

FIG. 34

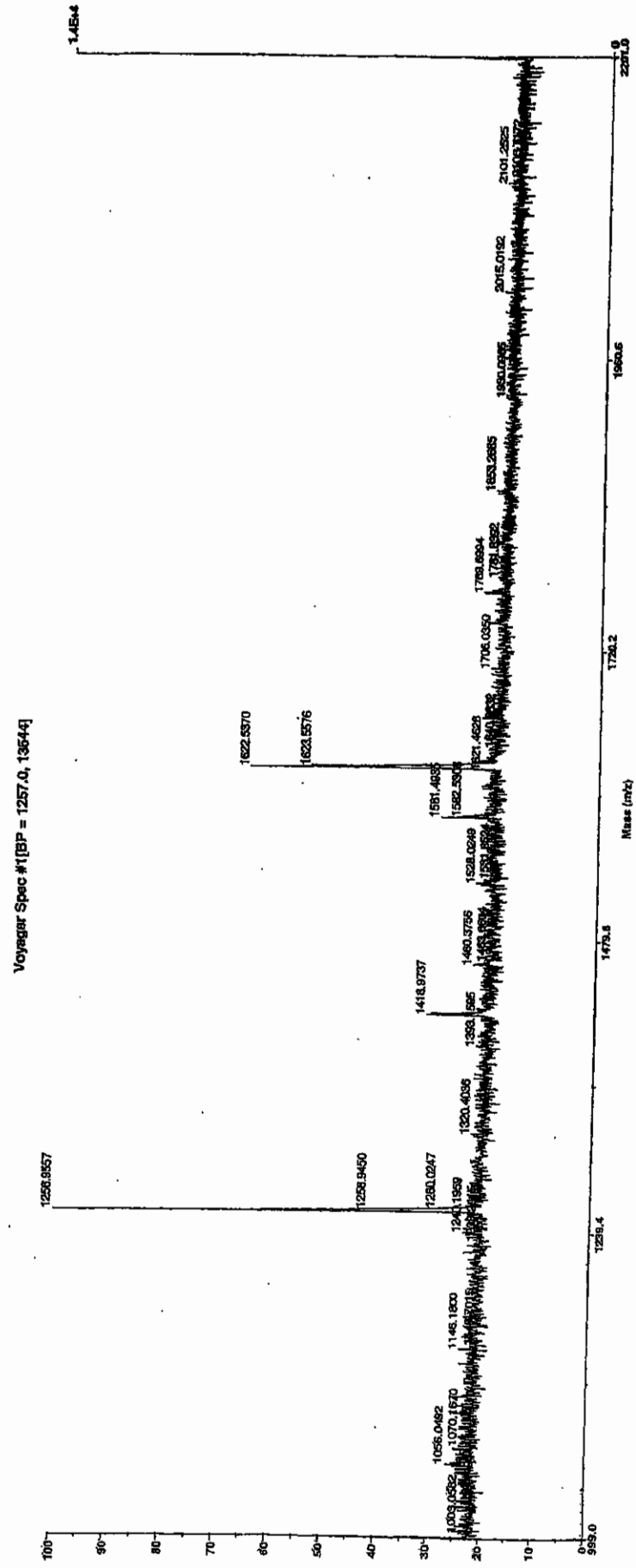
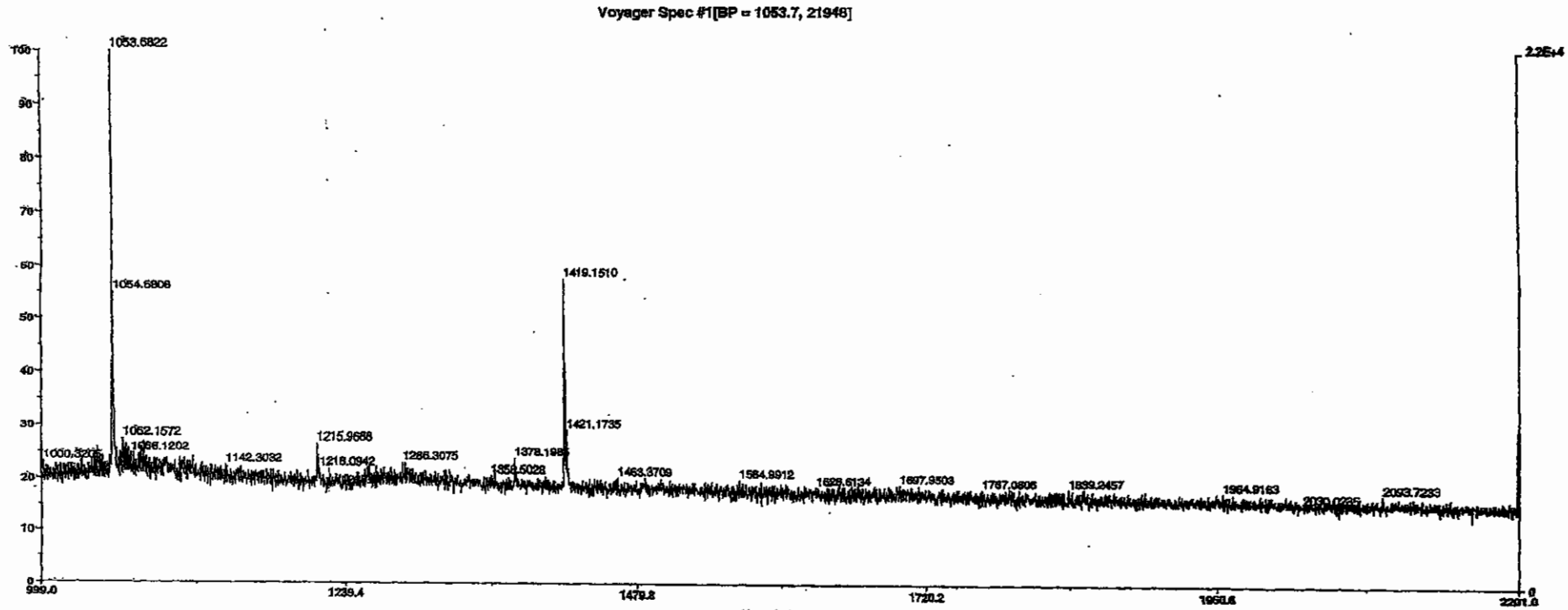

Voyager Spec #1[BP = 1257.0, 13644]
1454
1622.5370
1623.5576
1256.8557
1258.9450
1418.9737
1146.1800
1056.0482
1070.1670
Mass (m/z)

FIG. 35A



	pManII-GalT	+EndoH
1053		66.50%
1256	51.90%	
1419	8.20%	33.50%
1581	7.00%	
1622	30.00%	
1769	2.90%	
	100.00%	100.00%

FIG. 35B

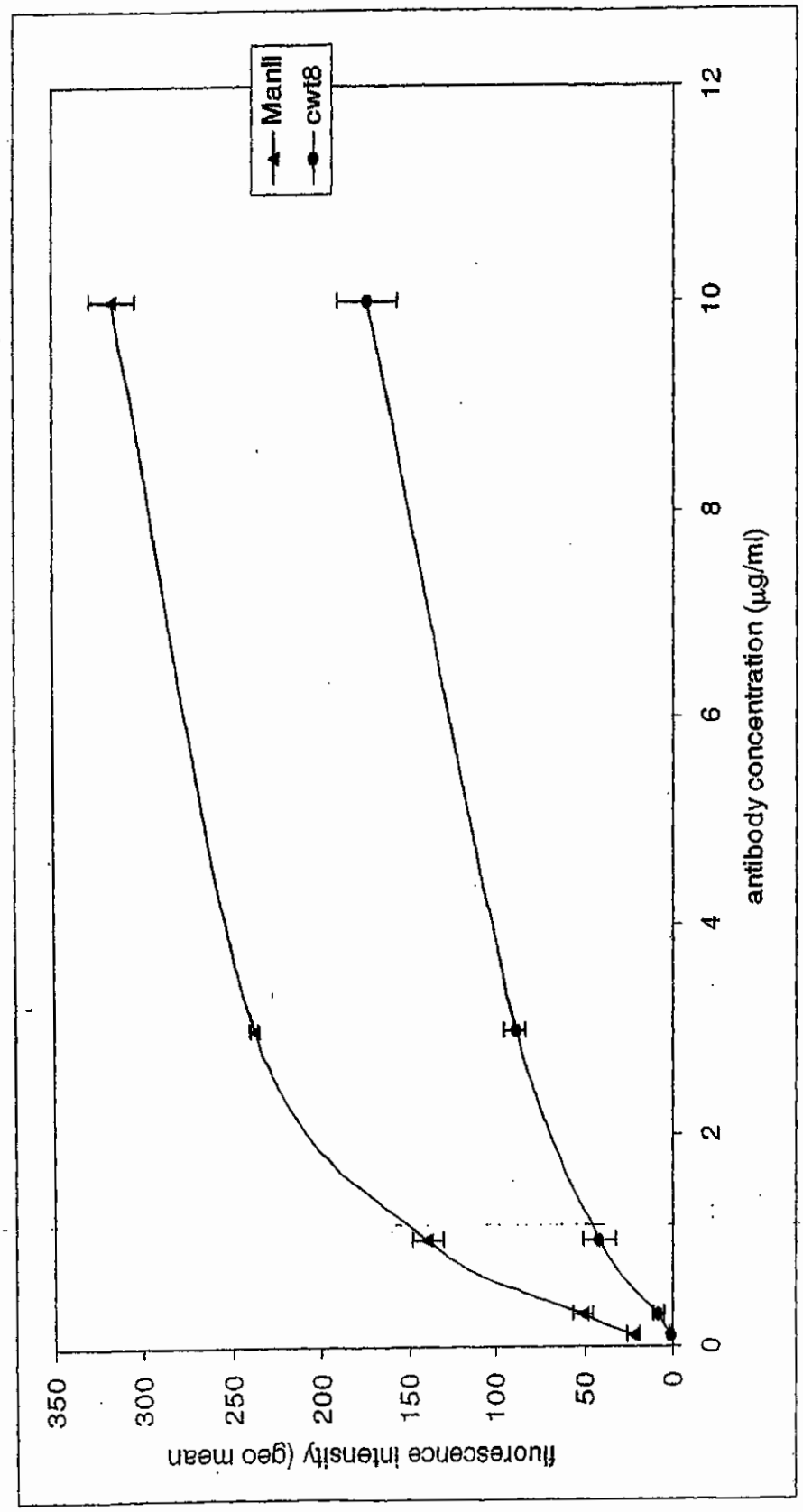

ManII
cwt8
fluorescence intensity (geo mean
350
300
250
200
150
100
50
0
0
2
4
6
8
10
12
antibody concentration (µg/ml)

FIG. 36

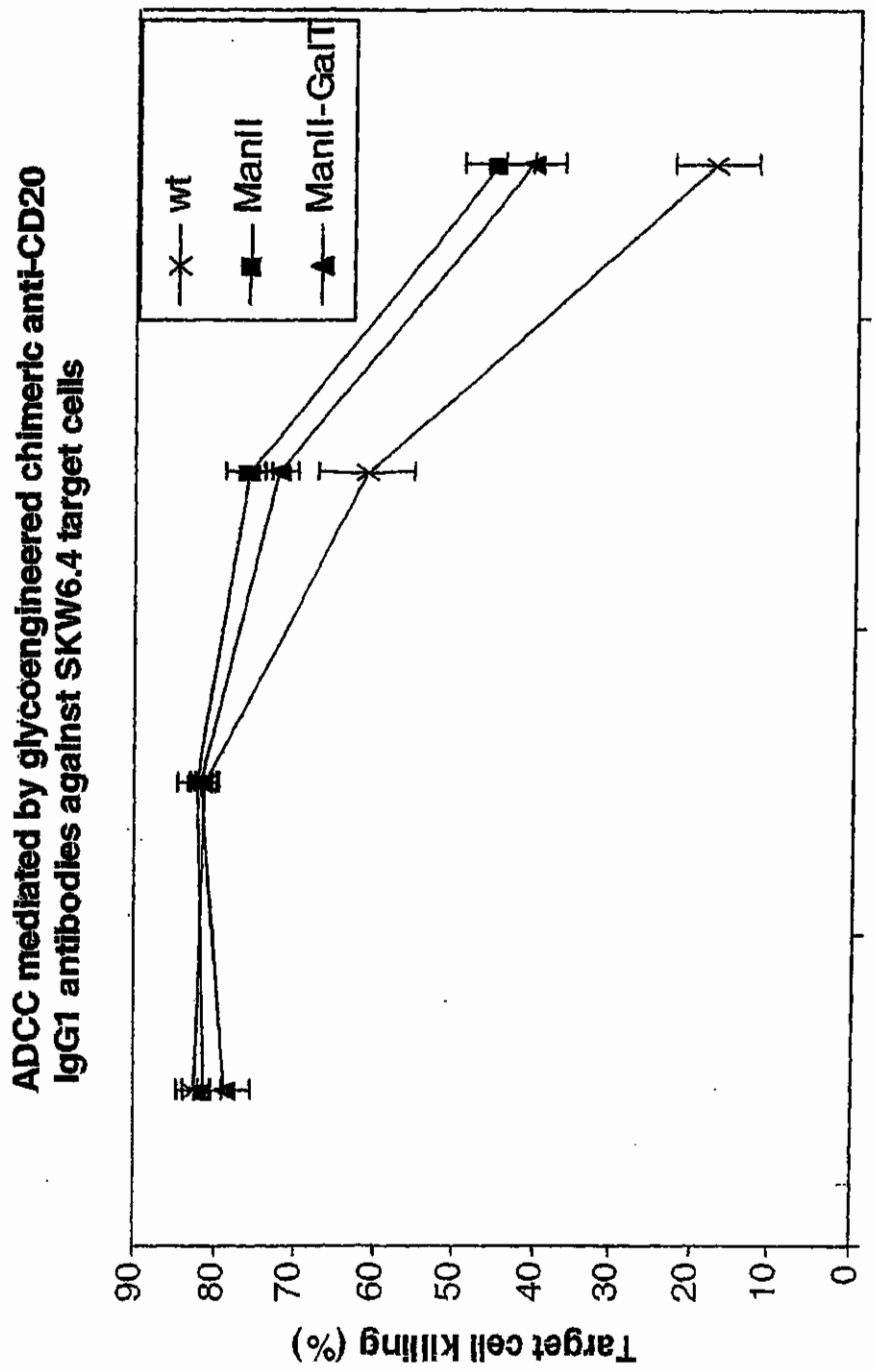

ADCC mediated by glycoengineered chimeric anti-CD20
IgG1 antibodies against SKW6.4 target cells
wt
ManII
ManII-GalT
Target cell killing (%)
0
10
20
30
40
50
60
70
80
90
1
10
100
1000
Antibody concentration (ng/ml)

FIG. 37

SEQUENCE LISTING

<110> GlycArt Biotechnology AG
Umana, Pablo
Bruenker, Peter
Ferrara, Claudia
Suter, Tobias

<120> Fusion Constructs and Use of Same to Produce Antibodies with Increased Fc Receptor Binding Affinity and Effector Function

<130> 1975.018PC04

<150> US 60/441,307
<151> 2003-01-22

<150> US 60/491,254
<151> 2003-07-31

<150> US 60/495,142
<151> 2003-08-15

<160> 20

<170> PatentIn version 3.2

<210> 1
<211> 11
<212> PRT
<213> Unknown

<220>
<223> c-myc epitope tag

<400> 1

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-177 PCR primer

<400> 2
gcgtgtgcct gtgacccccg cgcccctgct ccagccactg tcccc 45

<210> 3
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-178 PCR primer

<400> 3
gaaggtttct ccagcatcct ggtacc 26

<210> 4
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-179 PCR primer

<400> 4
ctgaggcgcg ccgccaccat gctgaagaag cagtctgcag ggc 43

<210> 5
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-180 PCR primer

<400> 5
ggggacagtg gctggagcag gggcgcgggg gtcacaggca cacgcggc 48

<210> 6
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-252 PCR primer

<400> 6
gctaggccgg ccgccaccat gaagttaagc cgccagttca ccgtgttcgg 50

<210> 7
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-253 PCR primer

<400> 7
ggggacagtg gctggagcag gggtgagcca gcaccttggc tgaaattgct ttgtgaactt 60

ttcgg 65

<210> 8
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-254 PCR primer

<400> 8
tccgaaaagt tcacaaagca atttcagcca aggtgctggc tcacccctgc tccagccact 60

gtcccc 66

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-255 PCR primer

<400> 9
atgccgcata ggcctccgag caggacccc 29

<210> 10
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-261 PCR primer

<400> 10
gctaaatatt gaattccctt tatgtgtaac tcttggctga agc 43

<210> 11
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-262 PCR primer

<400> 11
tagcaatatt gaattcgcag gaaaaggaca agcagcgaaa attcacgc 48

<210> 12
<211> 1715
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of GnTI-GnTIII

<400> 12
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60

tcgctctacc tgatgctgga ccggggtcac ttagactacc ccaggaaccc gcgccgcgag 120

ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180

ttgctagctg agaataatga gatcatctca aatattagag actcagtcat caatttgagt 240

gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300

cccctgctcc agccactgtc ccctagcaag gccaccgaag aactgcaccg ggtggacttc 360

gtgttgccgg aggacaccac agagtatttt gtgcgcacca aagctggcgg tgtgtgcttc 420

aaaccaggta ccaggatgct ggagaaacct tctccagggc ggacagagga gaagaccaag 480

gtggctgagg ggtcctcggt ccggggtcct gctcggaggc ctatgcggca tgtgttgagt 540

gcacgggagc gcctgggagg ccggggcact aggcgcaagt gggttgagtg tgtgtgcctg 600

ccaggctggc acgggcccag ctgcggggtg cccactgtgg tccagtattc caacctgccc 660

accaaggagc gcctggtacc cagggaggtg ccgaggcggg ttatcaacgc catcaacatc 720

aaccatgagt tcgacctgct ggatgtgcgc ttccatgagc tgggcgatgt tgtggacgcc 780

tttgtggtct gcgaatccaa tttcaccgcc tacggggagc ctcggccgct caagttccga 840

gagatgctga ccaatggcac cttcgagtac atccgccaca aggtgctcta cgtcttcctg 900

gaccacttcc cacctggtgg ccgtcaggac ggctggattg cagacgacta cctgcgtacc 960

ttcctcaccc aggatggtgt ctcccgcctg cgcaacctgc gacctgatga cgtctttatc 1020

atcgacgacg cggacgagat ccctgcgcgt gatggtgtgc tgttcctcaa gctctacgat 1080

ggctggacag agcccttcgc cttccatatg cgcaagtccc tgtatggttt cttttggaag 1140

caaccaggca cacggaggtg gtgtcaggct gcaccattga catgctgcag gctgtgtatg 1200

ggctggacgg catccgcctg cgccgccgtc agtactacac catgcccaac tttcgacagt 1260

atgagaaccg caccggccac atcctagtgc agtggtctct cggcagcccc ctgcacttcg 1320

cgggctggca ctgctcctgg tgcttcacac ccgagggcat ctacttcaaa ctcgtgtcgg 1380

cccagaatgg tgacttcccc cgctggggtg actacgagga caagagggac ctcaattaca 1440

tccgaagctt gattcgcact gggggatggt tcgacggcac gcagcaggag taccctcctg 1500

cagaccccag tgaacacatg tatgctccta agtacctgct caagaactat gaccagttcc 1560

gctacttgct cgaaaatccc taccgggagc ccaagagcac tgtagagggt gggcgccgga 1620

accagggctc agacggaagg tcatctgctg tcaggggcaa gttggataca acggagggcc 1680

cggaacagaa actgatctct gaagaggacc tgtag 1715

<210> 13
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GnTI-GnTIII

<400> 13

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

```
Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
        35                  40                  45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
    50                  55                  60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65                  70                  75                  80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
                85                  90                  95

Gly Ala Gly Ser Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys Ala Thr
            100                 105                 110

Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr Thr Glu
        115                 120                 125

Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro Gly Thr
    130                 135                 140

Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys Thr Lys
145                 150                 155                 160

Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro Met Arg
                165                 170                 175

His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr Arg Arg
            180                 185                 190

Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro Ser Cys
        195                 200                 205

Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys Glu Arg
    210                 215                 220

Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile Asn Ile
225                 230                 235                 240

Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu Gly Asp
                245                 250                 255

Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala Tyr Gly
            260                 265                 270

Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly Thr Phe
        275                 280                 285
```

```
Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His Phe Pro
    290                 295                 300

Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu Arg Thr
305                 310                 315                 320

Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg Pro Asp
                325                 330                 335

Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg Asp Gly
            340                 345                 350

Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe Ala Phe
        355                 360                 365

His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro Gly Thr
    370                 375                 380

Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala Val Tyr
385                 390                 395                 400

Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr Met Pro
                405                 410                 415

Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val Gln Trp
            420                 425                 430

Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser Trp Cys
        435                 440                 445

Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln Asn Gly
    450                 455                 460

Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu Asn Tyr
465                 470                 475                 480

Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr Gln Gln
                485                 490                 495

Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro Lys Tyr
            500                 505                 510

Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn Pro Tyr
        515                 520                 525

Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln Gly Ser
```

530 535 540

Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr Glu Gly
545 550 555 560

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
565 570

<210> 14
<211> 1722
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GnTIII

<400> 14
atgctgaaga agcagtctgc agggcttgtg ctgtggggcg ctatcctctt tgtggcctgg 60

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agcgctctcg atggcgaccc cgccagcctc acccgggaag tgattcgcct ggcccaagac 180

gccgaggtgg agctggagcg gcagcgtggg ctgctgcagc agatcgggga tgccctgtcg 240

agccagcggg ggagggtgcc caccgcggcc cctcccgccc agccgcgtgt gcctgtgacc 300

cccgcgcccc tgctccagcc actgtccctt agcaaggcca ccgaagaact gcaccgggtg 360

gacttcgtgt tgccggagga caccacagag tattttgtgc gcaccaaagc tggcggtgtg 420

tgcttcaaac caggtaccag gatgctggag aaaccttctc cagggcggac agaggagaag 480

accaaggtgg ctgaggggtc ctcggtccgg ggtcctgctc ggaggcctat gcggcatgtg 540

ttgagtgcac gggagcgcct gggaggccgg ggcactaggc gcaagtgggt tgagtgtgtg 600

tgcctgccag gctggcacgg gcccagctgc ggggtgccca ctgtggtcca gtattccaac 660

ctgcccacca aggagcgcct ggtacccagg gaggtgccga ggcgggttat caacgccatc 720

aacatcaacc atgagttcga cctgctggat gtgcgcttcc atgagctggg cgatgttgtg 780

gacgcctttg tggtctgcga atccaatttc accgcctacg gggagcctcg gccgctcaag 840

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tggaagcaac caggcacact ggaggtggtg tcaggctgca ccattgacat gctgcaggct 1200

gtgtatgggc tggacggcat ccgcctgcgc cgccgtcagt actacaccat gcccaacttt 1260

cgacagtatg agaaccgcac cggccacatc ctagtgcagt ggtctctcgg cagccccctg 1320

cacttcgcgg gctggcactg ctcctggtgc ttcacacccg agggcatcta cttcaaactc 1380

gtgtcggccc agaatggtga cttcccccgc tggggtgact acgaggacaa gagggacctc 1440

aattacatcc gaagcttgat tcgcactggg ggatggttcg acggcacgca gcaggagtac 1500

cctcctgcag accccagtga acacatgtat gctcctaagt acctgctcaa gaactatgac 1560

cagttccgct acttgctcga aaatccctac cgggagccca agagcactgt agagggtggg 1620

cgccggaacc agggctcaga cggaaggtca tctgctgtca ggggcaagtt ggatacaacg 1680

gagggcccgg aacagaaact gatctctgaa gaggacctgt ag 1722

<210> 15
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GnTIII fusion

<400> 15

Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
1 5 10 15

Phe Val Ala Trp Asn Ala Leu Leu Leu Leu Phe Phe Trp Thr Arg Pro
20 25 30

Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser
65 70 75 80

Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg
85 90 95

Val Pro Val Thr Pro Ala Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys
100 105 110

Ala Thr Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr
115 120 125

Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro
130 135 140

```
Gly Thr Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys
145                 150                 155                 160

Thr Lys Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro
                165                 170                 175

Met Arg His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr
            180                 185                 190

Arg Arg Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro
        195                 200                 205

Ser Cys Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys
    210                 215                 220

Glu Arg Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile
225                 230                 235                 240

Asn Ile Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu
                245                 250                 255

Gly Asp Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala
            260                 265                 270

Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly
        275                 280                 285

Thr Phe Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His
    290                 295                 300

Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu
305                 310                 315                 320

Arg Thr Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg
                325                 330                 335

Pro Asp Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg
            340                 345                 350

Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe
        355                 360                 365

Ala Phe His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro
    370                 375                 380

Gly Thr Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala
385                 390                 395                 400
```

```
Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr
                405                 410                 415

Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val
            420                 425                 430

Gln Trp Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser
        435                 440                 445

Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln
    450                 455                 460

Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu
465                 470                 475                 480

Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr
                485                 490                 495

Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro
            500                 505                 510

Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn
        515                 520                 525

Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln
    530                 535                 540

Gly Ser Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr
545                 550                 555                 560

Glu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
                565                 570
```

<210> 16
<211> 398
<212> PRT
<213> Unknown

<220>
<223> GalT amino acid sequence from pBlueGalT

<400> 16

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Met Arg Leu Arg Glu Pro Leu Leu Ser Gly Ser Ala Ala Met Pro Gly
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Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
            20                  25                  30
```

```
His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Ser
        35                  40                  45

Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln Gly Gly Ser
    50                  55                  60

Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu Arg Thr Gly
65                  70                  75                  80

Gly Ala Arg Pro Pro Pro Pro Leu Gly Ala Ser Ser Gln Pro Arg Pro
                85                  90                  95

Gly Gly Asp Ser Ser Pro Val Val Asp Ser Gly Pro Gly Pro Ala Ser
            100                 105                 110

Asn Leu Thr Ser Val Pro Val Pro His Thr Thr Ala Leu Ser Leu Pro
        115                 120                 125

Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro Met Leu Ile Glu
    130                 135                 140

Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala Lys Gln Asn Pro Asn
145                 150                 155                 160

Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp Cys Val Ser Pro His
                165                 170                 175

Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg Gln Glu His Leu Lys
            180                 185                 190

Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln Arg Gln Gln Leu Asp
        195                 200                 205

Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp Thr Ile Phe Asn Arg
    210                 215                 220

Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala Leu Lys Asp Tyr Asp
225                 230                 235                 240

Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro Met Asn Asp
                245                 250                 255

His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile Ser Val Ala
            260                 265                 270

Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr Phe Gly Gly
        275                 280                 285
```

Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn Gly Phe Pro
290 295 300

Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile Phe Asn Arg
305 310 315 320

Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala Val Val Gly
325 330 335

Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn Glu Pro Asn
340 345 350

Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr Met Leu Ser
355 360 365

Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val Gln Arg Tyr
370 375 380

Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro Ser
385 390 395

<210> 17
<211> 3435
<212> DNA
<213> Homo sapiens

<400> 17
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tcgctctacc tgatgctgga ccggggtcac ttagactacc ccaggaaccc gcgccgcgag 120

ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180

ttgctagctg agaataatga gatcatctca aatattagag actcagtcat caatttgagt 240

gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300

catcttctgc cctcacaatt atcctctcca gttgacactg cagactgtct gtttgcttca 360

caaagtggaa gtcacaattc agatgtgcag atgttggatg tttacagtct aatttctttt 420

gacaatccag atggtggagt ttggaagcaa ggatttgaca ttacttatga atctaatgaa 480

tgggacactg aacccttca agtctttgtg gtgcctcatt cccataacga cccaggttgg 540

ttgaagactt tcaatgacta ctttagagac aagactcagt atatttttaa taacatggtc 600

ctaaagctga aagaagactc acggaggaag tttatttggt ctgagatctc ttacctttca 660

aagtggtggg atattataga tattcagaag aaggatgctg ttaaaagttt aatagaaaat 720

ggtcagcttg aaattgtgac aggtggctgg gttatgcctg atgaagctac tccacattat 780

tttgccttaa ttgatcaact aattgaagga catcagtggc tggaaaataa tataggagtg 840

aaacctcggt ccggctgggc tattgatccc tttggacact caccaacaat ggcttatctt 900

ctaaaccgtg ctggactttc tcacatgctt atccagagag ttcattatgc agttaaaaaa 960

cactttgcac tgcataaaac attggagttt ttttggagac agaattggga tctgggatct 1020

gtcacagata ttttatgcca catgatgccc ttctacagct atgacatccc tcacacttgt 1080

ggacctgatc ctaaaatatg ctgccagttt gattttaaac gtcttcctgg aggcagattt 1140

ggttgtccct ggggagtccc cccagaaaca atacatcctg gaaatgtcca aagcagggct 1200

cggatgctac tagatcagta ccgaaagaag tcaaagcttt ttcgtaccaa agttctcctg 1260

gctccactag gagatgattt ccgctactgt gaatacacgg aatgggattt acagtttaag 1320

aattatcagc agctttttga ttatatgaat tctcagtcca agtttaaagt taagatacag 1380

tttggaactt tatcagattt ttttgatgcg ctggataaag cagatgaaac tcagagagac 1440

aagggccagt cgatgttccc tgttttaagt ggagattttt tcacttatgc cgatcgagat 1500

gatcattact ggagtggcta ttttacatcc agacccttt acaaacgaat ggacagaatc 1560

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gttgtggatt atggtaccag acttttttcat tcgttaatgg ttttggagaa gataattgga 1800

aattctgcat ttcttcttat tttgaaggac aaactcacat acgactctta ctctcctgat 1860

accttcctgg agatggattt gaaacaaaaa tcacaagatt ctctgccaca aaaaaatata 1920

ataaggctga gtgcggagcc aaggtacctt gtggtctata atcctttaga acaagaccga 1980

atctcgttgg tctcagtcta tgtgagttcc ccgacagtgc aagtgttctc tgcttcagga 2040

aaacctgtgg aagttcaagt cagcgcagtt tgggatacag caaatactat ttcagaaaca 2100

gcctatgaga tctcttttcg agcacatata ccgccattgg gactgaaagt gtataagatt 2160

ttggaatcag caagttcaaa ttcacattta gctgattatg tcttgtataa gaataaagta 2220

gaagatagcg gaattttcac cataaagaat atgataaata ctgaagaagg tataacacta 2280

gagaactcct ttgttttact tcggtttgat caaactggac ttatgaagca aatgatgact 2340

aaagaagatg gtaaacacca tgaagtaaat gtgcaatttt catggtatgg aaccacaatt 2400

aaaagagaca aaagtggtgc ctacctcttc ttacctgatg gtaatgccaa gccttatgtt 2460

tacacaacac cgccctttgt cagagtgaca catggaagga tttattcgga agtgacttgc 2520

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acaatggcct atatccagga tgccaaacat cgtttgacac tgctctctgc tcagtcttta 2820

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cgaatactac tagaaaaaag aagtgctgtt aatacggaag aagaaaagaa gtcggtcagt 3000

tatccttctc tccttagcca cataacttct tctctcatga atcatccagt cattccaatg 3060

gcaaataagt tcttctcacc tacccttgag ctgcaaggtg aattctctcc attacagtca 3120

tctttgcctt gtgacattca tctggttaat ttgagaacaa tacagtcaaa ggtgggcaat 3180

gggcactcca atgaggcagc cttgatcctc cacagaaaag ggtttgattg tcggttctct 3240

agcaaaggca cagggctgtt ttgttctact actcagggaa agatattggt acagaaactt 3300

ttaaacaagt ttattgtcga aagtctcaca ccttcatcac tatccttgat gcattcacct 3360

cccggcactc agaatataag tgagatcaac ttgagtccaa tggaaatcag cacattccga 3420

atccagttga ggtga 3435

<210> 18
<211> 1144
<212> PRT
<213> Homo sapiens

<400> 18

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser His Leu Leu Pro Ser Gln Leu Ser Leu Ser Val Asp
100 105 110

```
Thr Ala Asp Cys Leu Phe Ala Ser Gln Ser Gly Ser His Asn Ser Asp
        115                 120                 125

Val Gln Met Leu Asp Val Tyr Ser Leu Ile Ser Phe Asp Asn Pro Asp
    130                 135                 140

Gly Gly Val Trp Lys Gln Gly Phe Asp Ile Thr Tyr Glu Ser Asn Glu
145                 150                 155                 160

Trp Asp Thr Glu Pro Leu Gln Val Phe Val Val Pro His Ser His Asn
                165                 170                 175

Asp Pro Gly Trp Leu Lys Thr Phe Asn Asp Tyr Phe Arg Asp Lys Thr
            180                 185                 190

Gln Tyr Ile Phe Asn Asn Met Val Leu Lys Leu Lys Glu Asp Ser Arg
        195                 200                 205

Arg Lys Phe Ile Trp Ser Glu Ile Ser Tyr Leu Ser Lys Trp Trp Asp
    210                 215                 220

Ile Ile Asp Ile Gln Lys Lys Asp Ala Val Lys Ser Leu Ile Glu Asn
225                 230                 235                 240

Gly Gln Leu Glu Ile Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala
                245                 250                 255

Thr Pro His Tyr Phe Ala Leu Ile Asp Gln Leu Ile Glu Gly His Gln
            260                 265                 270

Trp Leu Glu Asn Asn Ile Gly Val Lys Pro Arg Ser Gly Trp Ala Ile
        275                 280                 285

Asp Pro Phe Gly His Ser Pro Thr Met Ala Tyr Leu Leu Asn Arg Ala
    290                 295                 300

Gly Leu Ser His Met Leu Ile Gln Arg Val His Tyr Ala Val Lys Lys
305                 310                 315                 320

His Phe Ala Leu His Lys Thr Leu Glu Phe Phe Trp Arg Gln Asn Trp
                325                 330                 335

Asp Leu Gly Ser Val Thr Asp Ile Leu Cys His Met Met Pro Phe Tyr
            340                 345                 350
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```
Ser Tyr Asp Ile Pro His Thr Cys Gly Pro Asp Pro Lys Ile Cys Cys
        355                 360                 365

Gln Phe Asp Phe Lys Arg Leu Pro Gly Gly Arg Phe Gly Cys Pro Trp
    370                 375                 380

Gly Val Pro Pro Glu Thr Ile His Pro Gly Asn Val Gln Ser Arg Ala
385                 390                 395                 400

Arg Met Leu Leu Asp Gln Tyr Arg Lys Lys Ser Lys Leu Phe Arg Thr
                405                 410                 415

Lys Val Leu Leu Ala Pro Leu Gly Asp Asp Phe Arg Tyr Cys Glu Tyr
            420                 425                 430

Thr Glu Trp Asp Leu Gln Phe Lys Asn Tyr Gln Gln Leu Phe Asp Tyr
        435                 440                 445

Met Asn Ser Gln Ser Lys Phe Lys Val Lys Ile Gln Phe Gly Thr Leu
    450                 455                 460

Ser Asp Phe Phe Asp Ala Leu Asp Lys Ala Asp Glu Thr Gln Arg Asp
465                 470                 475                 480

Lys Gly Gln Ser Met Phe Pro Val Leu Ser Gly Asp Phe Phe Thr Tyr
                485                 490                 495

Ala Asp Arg Asp Asp His Tyr Trp Ser Gly Tyr Phe Thr Ser Arg Pro
            500                 505                 510

Phe Tyr Lys Arg Met Asp Arg Ile Met Glu Ser His Leu Arg Ala Ala
        515                 520                 525

Glu Ile Leu Tyr Tyr Phe Ala Leu Arg Gln Ala His Lys Tyr Lys Ile
    530                 535                 540

Asn Lys Phe Leu Ser Ser Ser Leu Tyr Thr Ala Leu Thr Glu Ala Arg
545                 550                 555                 560

Arg Asn Leu Gly Leu Phe Gln His His Asp Ala Ile Thr Gly Thr Ala
                565                 570                 575

Lys Asp Trp Val Val Val Asp Tyr Gly Thr Arg Leu Phe His Ser Leu
            580                 585                 590

Met Val Leu Glu Lys Ile Ile Gly Asn Ser Ala Phe Leu Leu Ile Leu
        595                 600                 605
```

```
Lys Asp Lys Leu Thr Tyr Asp Ser Tyr Ser Pro Asp Thr Phe Leu Glu
    610                 615                 620

Met Asp Leu Lys Gln Lys Ser Gln Asp Ser Leu Pro Gln Lys Asn Ile
625                 630                 635                 640

Ile Arg Leu Ser Ala Glu Pro Arg Tyr Leu Val Val Tyr Asn Pro Leu
                645                 650                 655

Glu Gln Asp Arg Ile Ser Leu Val Ser Val Tyr Val Ser Ser Pro Thr
            660                 665                 670

Val Gln Val Phe Ser Ala Ser Gly Lys Pro Val Glu Val Gln Val Ser
        675                 680                 685

Ala Val Trp Asp Thr Ala Asn Thr Ile Ser Glu Thr Ala Tyr Glu Ile
    690                 695                 700

Ser Phe Arg Ala His Ile Pro Pro Leu Gly Leu Lys Val Tyr Lys Ile
705                 710                 715                 720

Leu Glu Ser Ala Ser Ser Asn Ser His Leu Ala Asp Tyr Val Leu Tyr
                725                 730                 735

Lys Asn Lys Val Glu Asp Ser Gly Ile Phe Thr Ile Lys Asn Met Ile
            740                 745                 750

Asn Thr Glu Glu Gly Ile Thr Leu Glu Asn Ser Phe Val Leu Leu Arg
        755                 760                 765

Phe Asp Gln Thr Gly Leu Met Lys Gln Met Met Thr Lys Glu Asp Gly
    770                 775                 780

Lys His His Glu Val Asn Val Gln Phe Ser Trp Tyr Gly Thr Thr Ile
785                 790                 795                 800

Lys Arg Asp Lys Ser Gly Ala Tyr Leu Phe Leu Pro Asp Gly Asn Ala
                805                 810                 815

Lys Pro Tyr Val Tyr Thr Thr Pro Pro Phe Val Arg Val Thr His Gly
            820                 825                 830

Arg Ile Tyr Ser Glu Val Thr Cys Phe Phe Asp His Val Thr His Arg
        835                 840                 845
```

```
Val Arg Leu Tyr His Ile Gln Gly Ile Glu Gly Gln Ser Val Glu Val
    850                 855                 860

Ser Asn Ile Val Asp Ile Arg Lys Val Tyr Asn Arg Glu Ile Ala Met
865                 870                 875                 880

Lys Ile Ser Ser Asp Ile Lys Ser Gln Asn Arg Phe Tyr Thr Asp Leu
                885                 890                 895

Asn Gly Tyr Gln Ile Gln Pro Arg Met Thr Leu Ser Lys Leu Pro Leu
            900                 905                 910

Gln Ala Asn Val Tyr Pro Met Thr Thr Met Ala Tyr Ile Gln Asp Ala
        915                 920                 925

Lys His Arg Leu Thr Leu Leu Ser Ala Gln Ser Leu Gly Val Ser Ser
    930                 935                 940

Leu Asn Ser Gly Gln Ile Glu Val Ile Met Asp Arg Arg Leu Met Gln
945                 950                 955                 960

Asp Asp Asn Arg Gly Leu Glu Gln Gly Ile Gln Asp Asn Lys Ile Thr
                965                 970                 975

Ala Asn Leu Phe Arg Ile Leu Leu Glu Lys Arg Ser Ala Val Asn Thr
            980                 985                 990

Glu Glu Glu Lys Lys Ser Val Ser  Tyr Pro Ser Leu Leu  Ser His Ile
        995                 1000                1005

Thr Ser  Ser Leu Met Asn His  Pro Val Ile Pro Met  Ala Asn Lys
    1010                1015                1020

Phe Phe  Ser Pro Thr Leu Glu  Leu Gln Gly Glu Phe  Ser Pro Leu
    1025                1030                1035

Gln Ser  Ser Leu Pro Cys Asp  Ile His Leu Val Asn  Leu Arg Thr
    1040                1045                1050

Ile Gln  Ser Lys Val Gly Asn  Gly His Ser Asn Glu  Ala Ala Leu
    1055                1060                1065

Ile Leu  His Arg Lys Gly Phe  Asp Cys Arg Phe Ser  Ser Lys Gly
    1070                1075                1080

Thr Gly  Leu Phe Cys Ser Thr  Thr Gln Gly Lys Ile  Leu Val Gln
    1085                1090                1095
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Lys Leu Leu Asn Lys Phe Ile Val Glu Ser Leu Thr Pro Ser Ser
1100 1105 1110

Leu Ser Leu Met His Ser Pro Pro Gly Thr Gln Asn Ile Ser Glu
1115 1120 1125

Ile Asn Leu Ser Pro Met Glu Ile Ser Thr Phe Arg Ile Gln Leu
1130 1135 1140

Arg

<210> 19
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GalT

<400> 19
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60

tcgctctacc tgatgctgga ccggggtcac ttagactacc ccaggaaccc gcgccgcgag 120

ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180

ttgctagctg agaataatga gatcatctca aatattagag actcagtcat caatttgagt 240

gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300

cccgcctgcc ctgaggagtc cccgctgctt gtgggcccca tgctgattga gtttaacatg 360

cctgtggacc tggagctcgt ggcaaagcag aacccaaatg tgaagatggg cggccgctat 420

gcccccaggg actgcgtctc tcctcacaag gtggccatca tcattccatt ccgcaaccgg 480

caggagcacc tcaagtactg gctatattat ttgcacccag tcctgcagcg ccagcagctg 540

gactatggca tctatgttat caaccaggcg ggagacacta tattcaatcg tgctaagctc 600

ctcaatgttg gctttcaaga agccttgaag gactatgact acacctgctt tgtgtttagt 660

gacgtggacc tcattccaat gaatgaccat aatgcgtaca ggtgtttttc acagccacgg 720

cacatttccg ttgcaatgga taagtttgga ttcagcctac cttatgttca gtattttgga 780

ggtgtctctg ctctaagtaa acaacagttt ctaaccatca atggatttcc taataattat 840

tggggctggg gaggagaaga tgatgacatt tttaacagat tagtttttag aggcatgtct 900

atatctcgcc caaatgctgt ggtcgggagg tgtcgcatga tccgccactc aagagacaaa 960

aaaaatgaac ccaatcctca gaggtttgac cgaattgcac acacaaagga gacaatgctc 1020

tctgatggtt tgaactcact cacctaccag gtgctggatg tacagagata cccattgtat 1080

acccaaatca cagtggacat cgggacaccg agctag 1116

<210> 20
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GalT

<400> 20

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly
100 105 110

Pro Met Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala
115 120 125

Lys Gln Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp
130 135 140

Cys Val Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg
145 150 155 160

Gln Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln
165 170 175

Arg Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp
180 185 190

Thr Ile Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala

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        195                 200                 205

Leu Lys Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu
    210                 215                 220

Ile Pro Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg
225                 230                 235                 240

His Ile Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val
                245                 250                 255

Gln Tyr Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr
            260                 265                 270

Ile Asn Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp
        275                 280                 285

Asp Ile Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro
    290                 295                 300

Asn Ala Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys
305                 310                 315                 320

Lys Asn Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys
                325                 330                 335

Glu Thr Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu
            340                 345                 350

Asp Val Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly
        355                 360                 365

Thr Pro Ser
    370
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<210> 20
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GalT

<400> 20

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly
100 105 110

Pro Met Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala
115 120 125

Lys Gln Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp
130 135 140

Cys Val Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg
145 150 155 160

Gln Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln
165 170 175

Arg Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp
180 185 190

Thr Ile Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala

```
        195                 200                 205

Leu Lys Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu
    210                 215                 220

Ile Pro Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg
225                 230                 235                 240

His Ile Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val
                245                 250                 255

Gln Tyr Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr
            260                 265                 270

Ile Asn Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp
        275                 280                 285

Asp Ile Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro
    290                 295                 300

Asn Ala Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys
305                 310                 315                 320

Lys Asn Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys
                325                 330                 335

Glu Thr Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu
            340                 345                 350

Asp Val Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly
        355                 360                 365

Thr Pro Ser
    370
```