FIG. 1

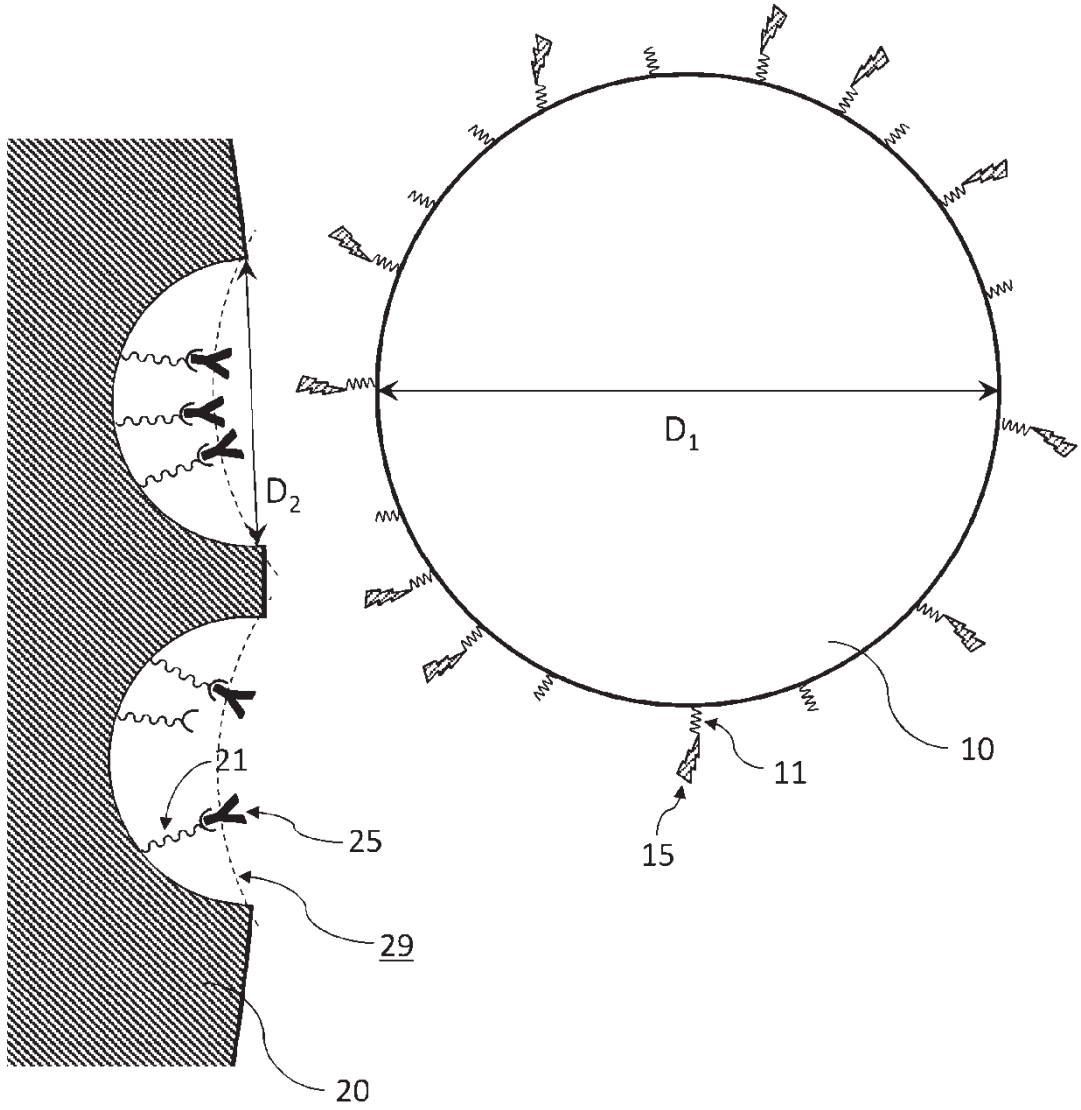


FIG. 2

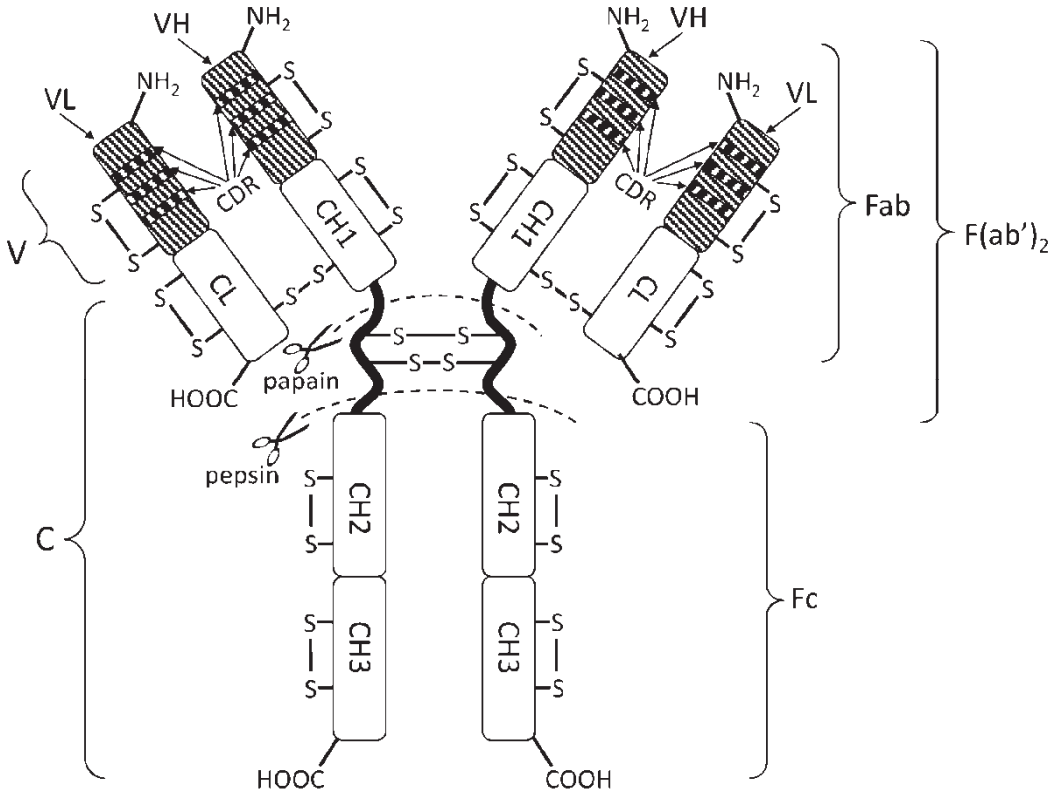

VH
NH2
VL
NH2
CDR
V
CL
CH1
papain
HOOC
pepsin
C
CH2
CH3
HOOC
NH2
VH
NH2
VL
CDR
CH1
CL
COOH
Fab
F(ab')2
Fc
COOH

FIG. 3

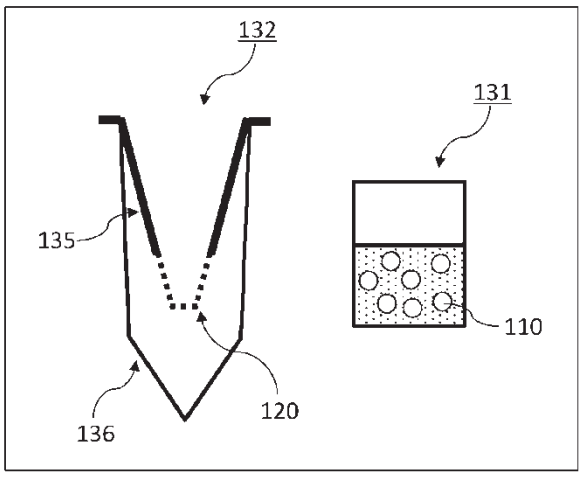
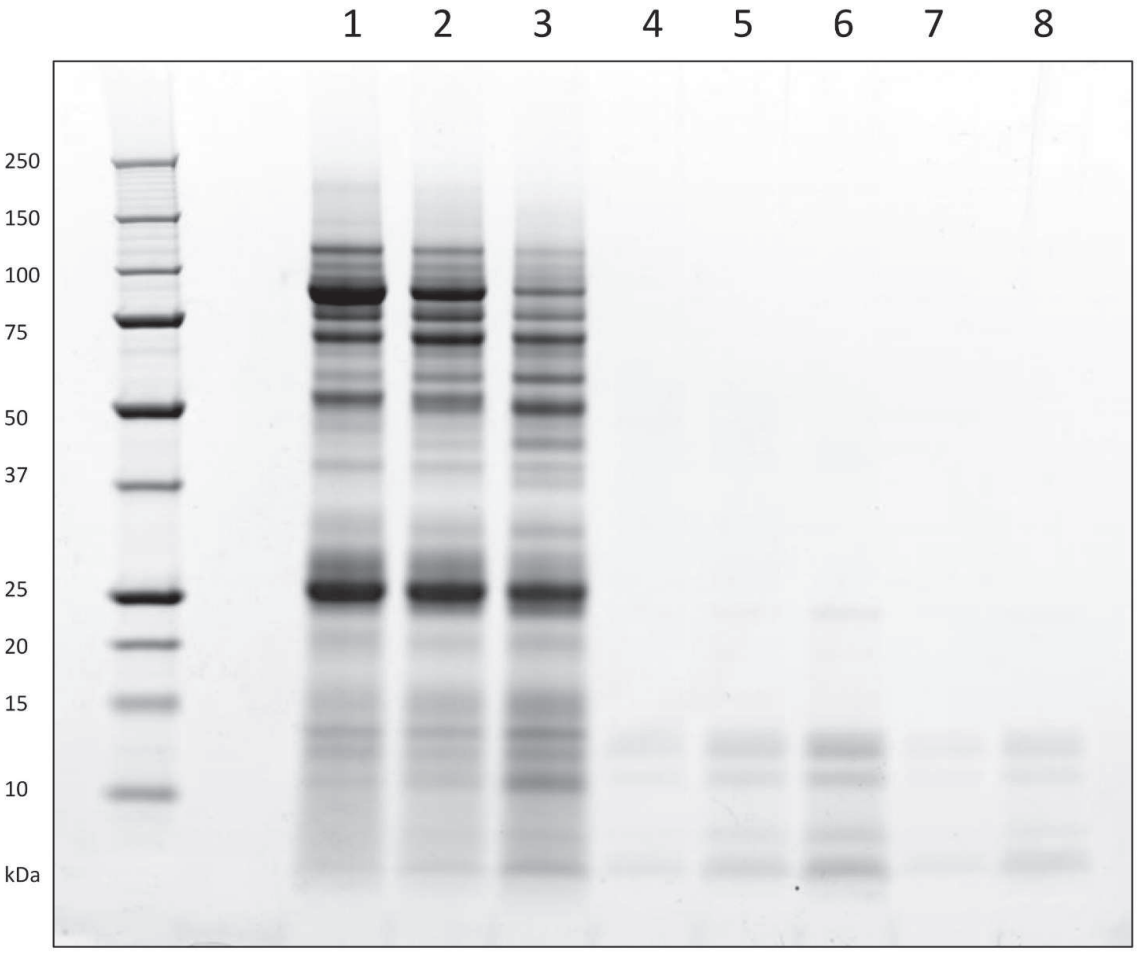

132
131
135
110
120
136

FIG. 4



1. ProteinG-IgG / FG beads-Trypsin 5μg
2. ProteinG-IgG / FG beads-Trypsin 10μg
3. ProteinG-IgG / FG beads-Trypsin 25μg
4. ProteinG / FG beads-Trypsin 5μg
5. ProteinG / FG beads-Trypsin 10μg
6. ProteinG / FG beads-Trypsin 25μg
7. FG beads-Trypsin 5ug
8. FG beads-Trypsin 10ug

FIG. 5

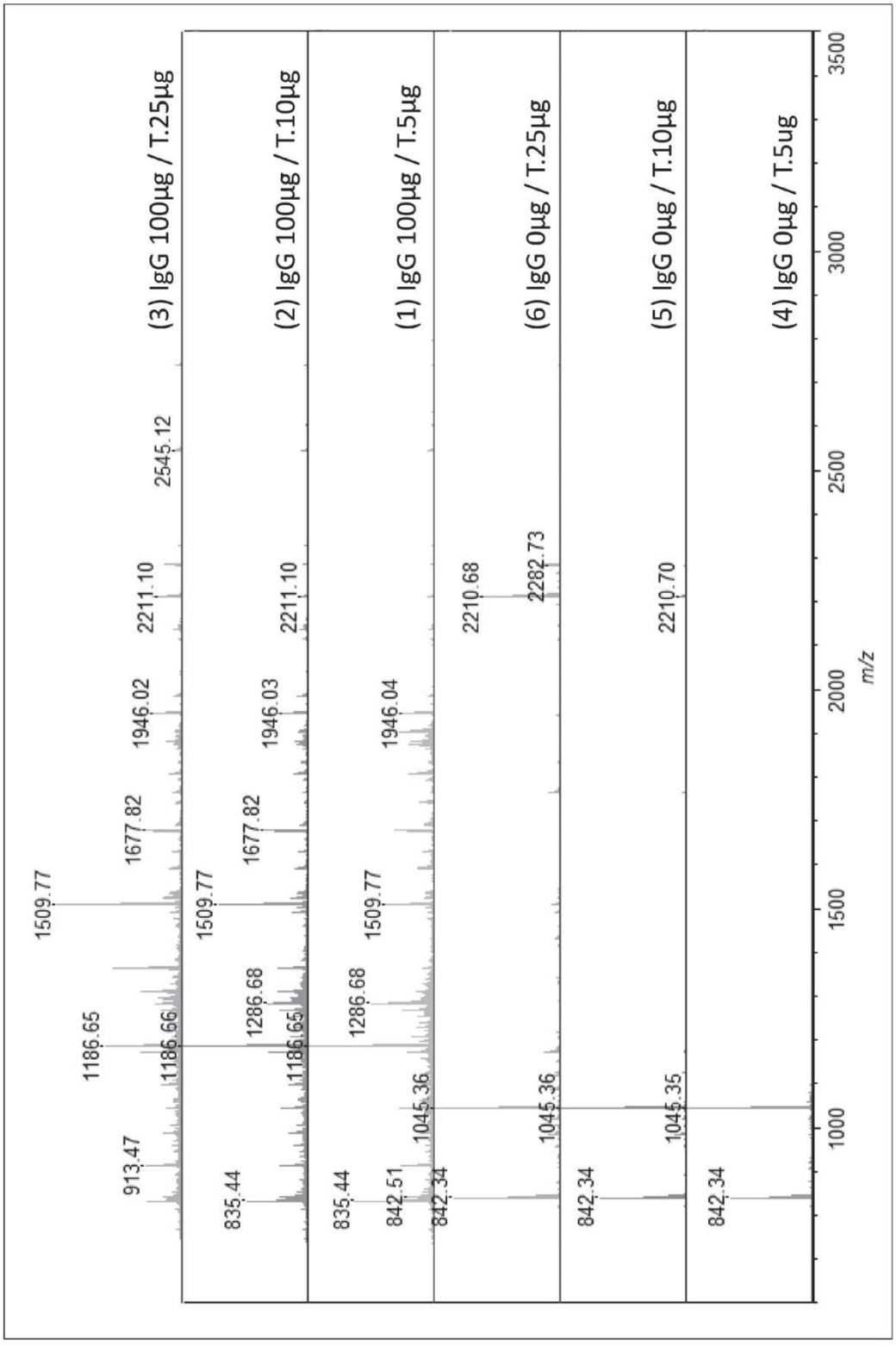

(3) IgG 100μg / T.25μg
(2) IgG 100μg / T.10μg
(1) IgG 100μg / T.5μg
(6) IgG 0μg / T.25μg
(5) IgG 0μg / T.10μg
(4) IgG 0μg / T.5ug
1509.77
1677.82
1946.02
2211.10
2545.12
1186.65
1286.68
913.47
835.44
842.51
1045.36
842.34
1946.03
1946.04
2210.68
2282.73
2210.70
1045.35
1000
1500
2000
2500
3000
3500
m/z

FIG. 6

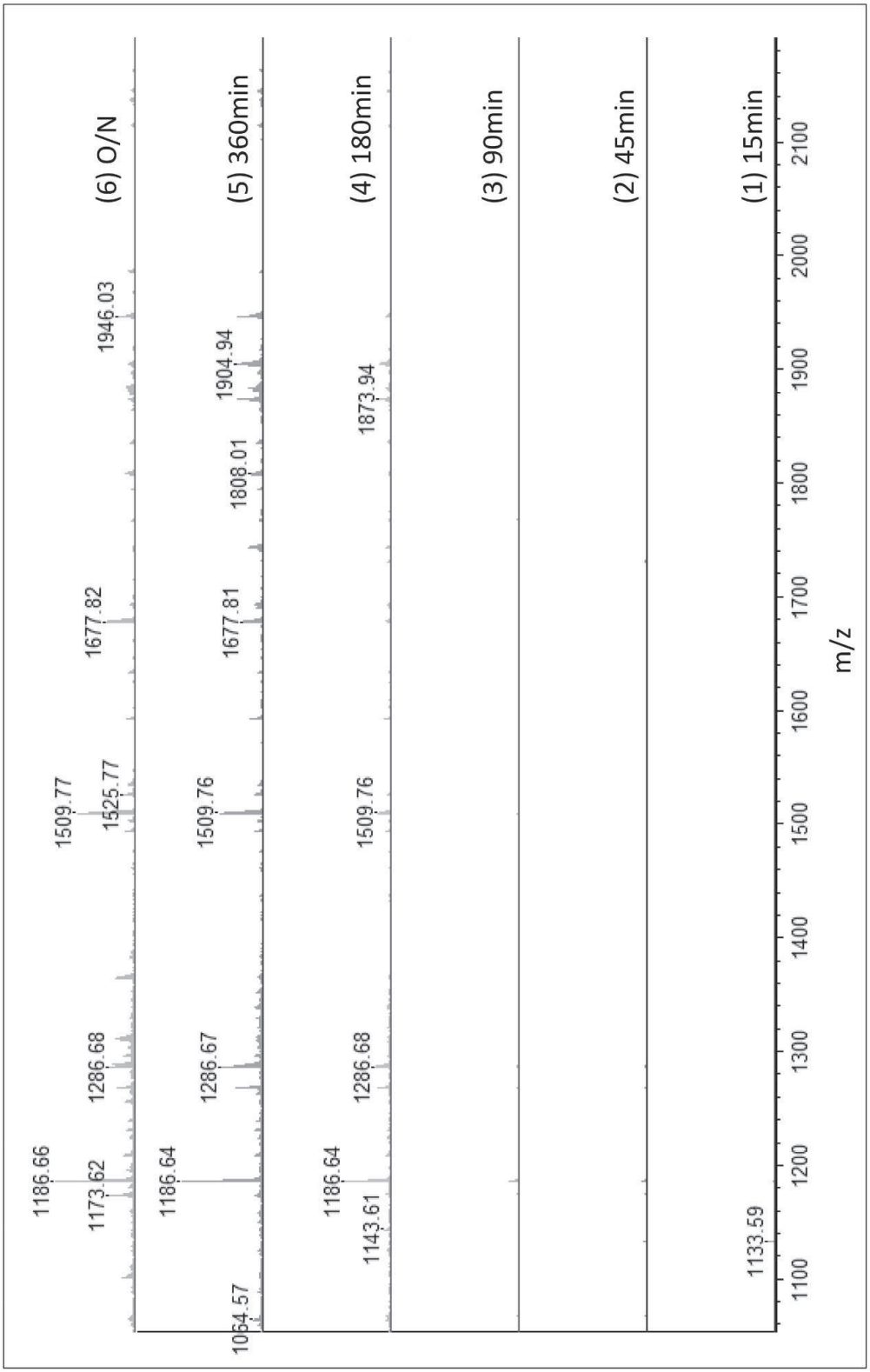

(6) O/N
(5) 360min
(4) 180min
(3) 90min
(2) 45min
(1) 15min
1186.66
1173.62
1286.68
1509.77
1525.77
1677.82
1946.03
1186.64
1286.67
1509.76
1677.81
1808.01
1904.94
1064.57
1186.64
1143.61
1286.68
1509.76
1873.94
1133.59
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
2100
m/z

FIG. 7

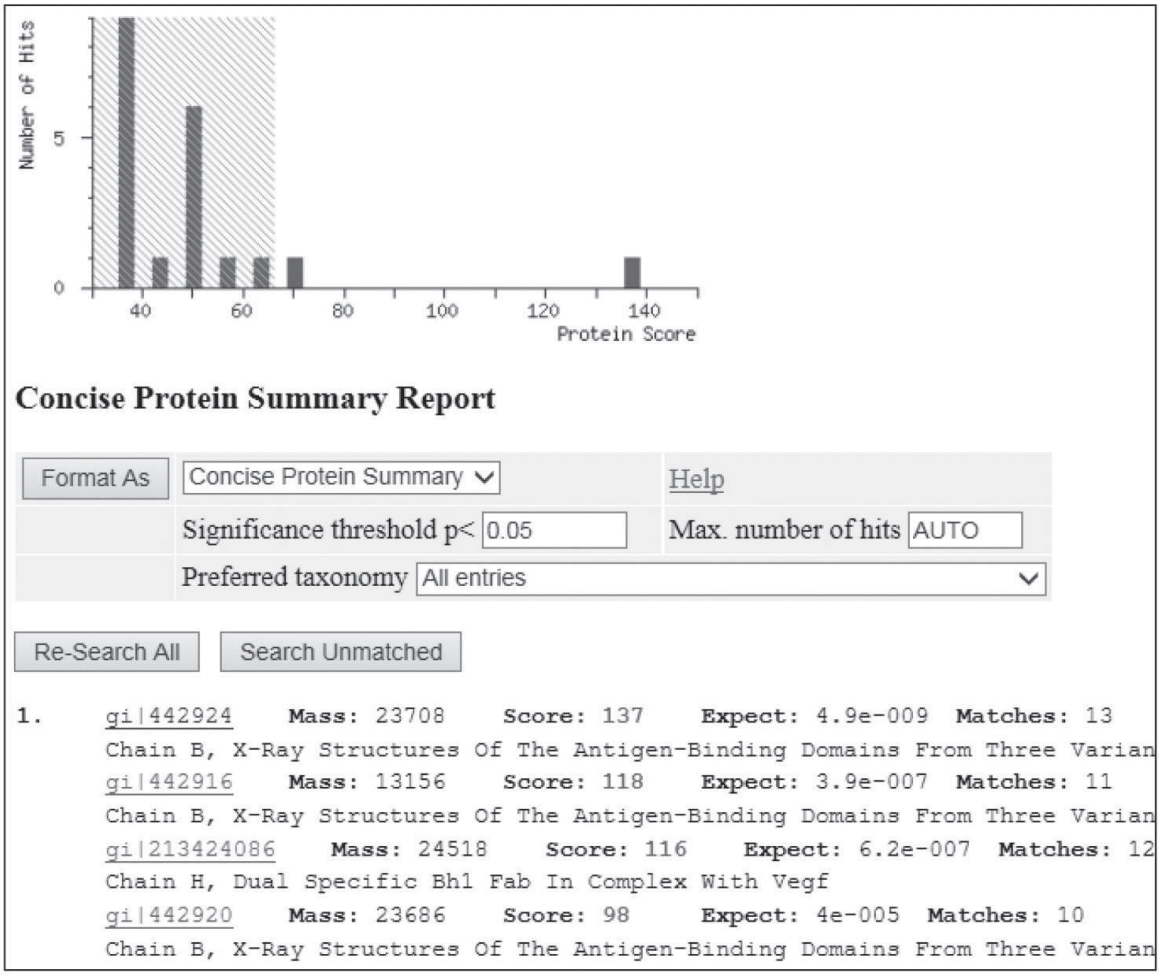

Number of Hits
0
5
40
60
80
100
120
140
Protein Score
Concise Protein Summary Report
Format As
Concise Protein Summary
Help
Significance threshold p< 0.05
Max. number of hits AUTO
Preferred taxonomy All entries
Re-Search All
Search Unmatched
1. gi|442924 Mass: 23708 Score: 137 Expect: 4.9e-009 Matches: 13
Chain B, X-Ray Structures Of The Antigen-Binding Domains From Three Varian
gi|442916 Mass: 13156 Score: 118 Expect: 3.9e-007 Matches: 11
Chain B, X-Ray Structures Of The Antigen-Binding Domains From Three Varian
gi|213424086 Mass: 24518 Score: 116 Expect: 6.2e-007 Matches: 12
Chain H, Dual Specific Bh1 Fab In Complex With Vegf
gi|442920 Mass: 23686 Score: 98 Expect: 4e-005 Matches: 10
Chain B, X-Ray Structures Of The Antigen-Binding Domains From Three Varian

FIG. 8

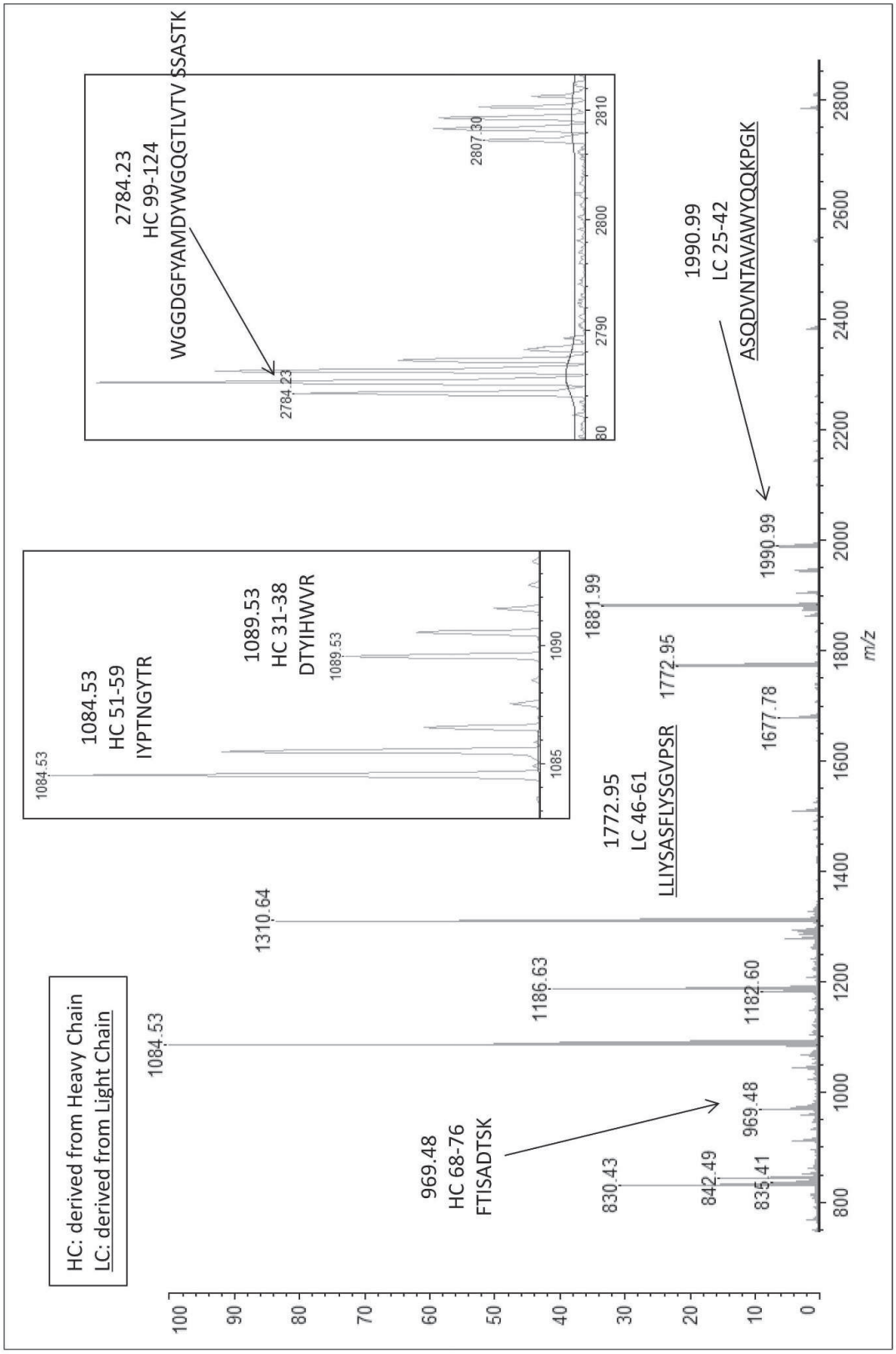

HC: derived from Heavy Chain
LC: derived from Light Chain
1084.53
HC 51-59
IYPTNGYTR
1089.53
HC 31-38
DTYIHWVR
2784.23
HC 99-124
WGGDGFYAMDYWGQGTLVTV SSASTK
969.48
HC 68-76
FTISADTSK
1772.95
LC 46-61
LLIYSASFLYSGVPSR
1990.99
LC 25-42
ASQDVNTAVAWYQQKPGK
m/z

FIG. 9

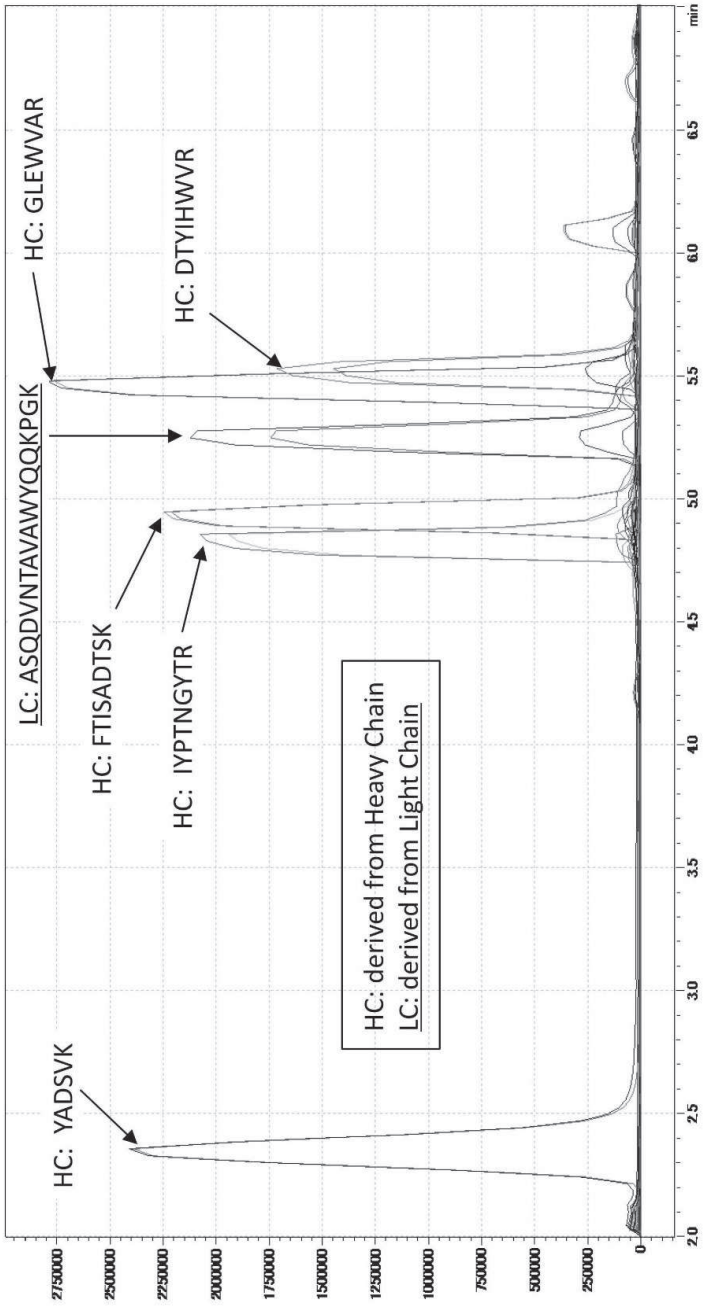

HC: YADSVK
HC: FTISADTSK
HC: IYPTNGYTR
LC: ASQDVNTAVAWYQQKPGK
HC: GLEWVAR
HC: DTYIHWVR
HC: derived from Heavy Chain
LC: derived from Light Chain
min

FIG. 10

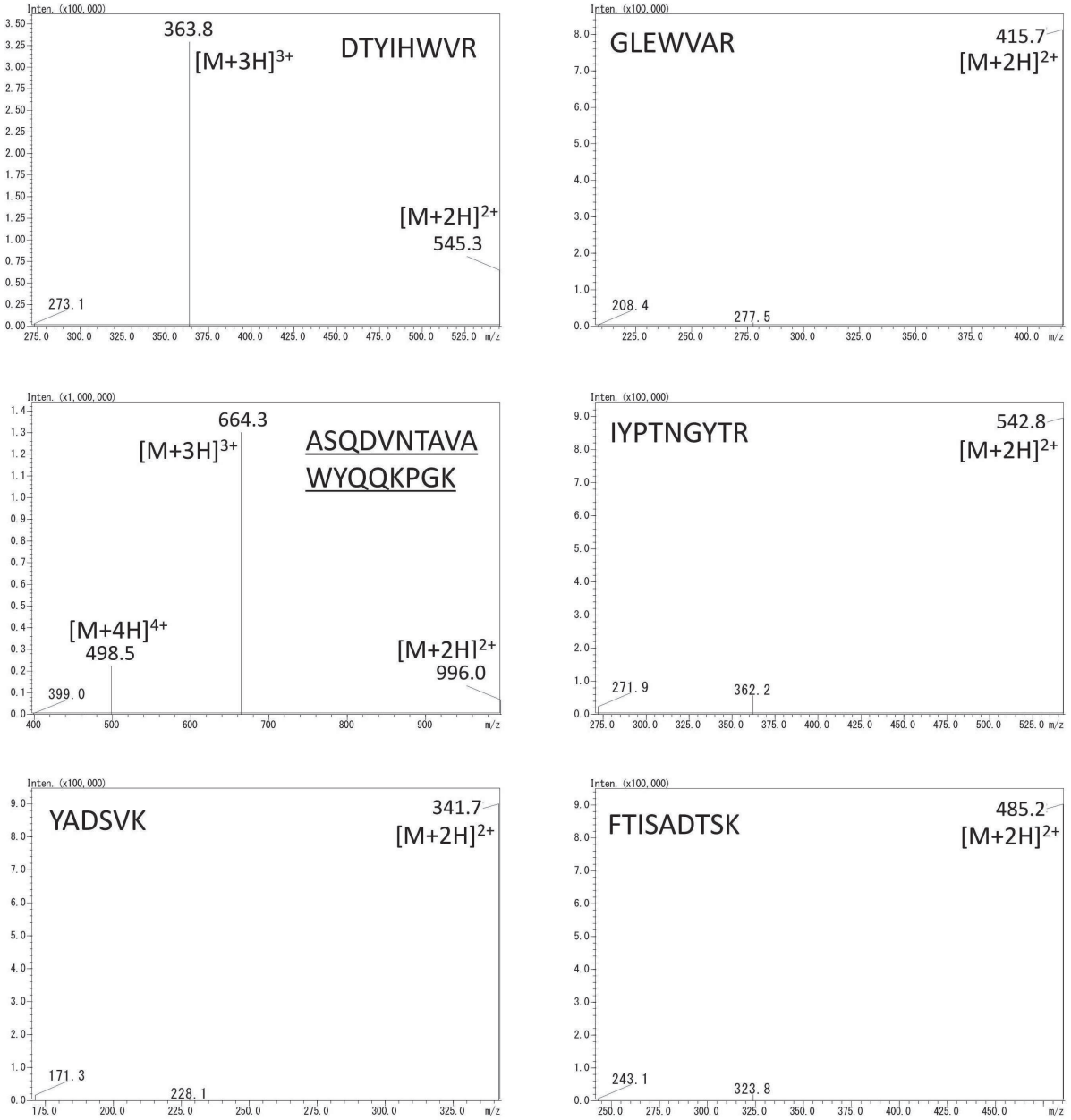

Inten. (x100,000)
363.8
[M+3H]3+
DTYIHWVR
[M+2H]2+
545.3
273.1
Inten. (x100,000)
GLEWVAR
415.7
[M+2H]2+
208.4
277.5
Inten. (x1,000,000)
664.3
[M+3H]3+
ASQDVNTAVA
WYQQKPGK
[M+4H]4+
498.5
[M+2H]2+
996.0
399.0
Inten. (x100,000)
IYPTNGYTR
542.8
[M+2H]2+
271.9
362.2
Inten. (x100,000)
YADSVK
341.7
[M+2H]2+
171.3
228.1
Inten. (x100,000)
FTISADTSK
485.2
[M+2H]2+
243.1
323.8

FIG. 11

FIG. 11(A)

Herceptin H-Chain

CDR1 CDR2

EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR IYPTNGYTRY

ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG GDGFYAMDYW GQGTLVTVSS

CDR3

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS

GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSC

FIG. 11(B)

Herceptin L-Chain

CDR1 CDR2

DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS

RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ GTKVEIKRTV AAPSVFIFPP

CDR3

SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT

LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC

FIG. 12

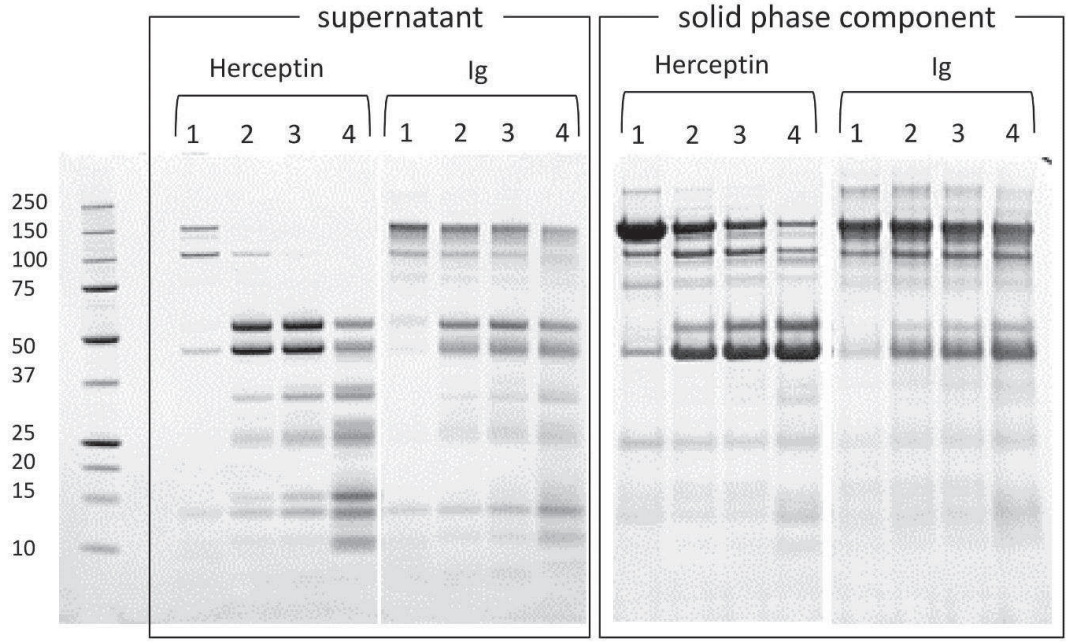
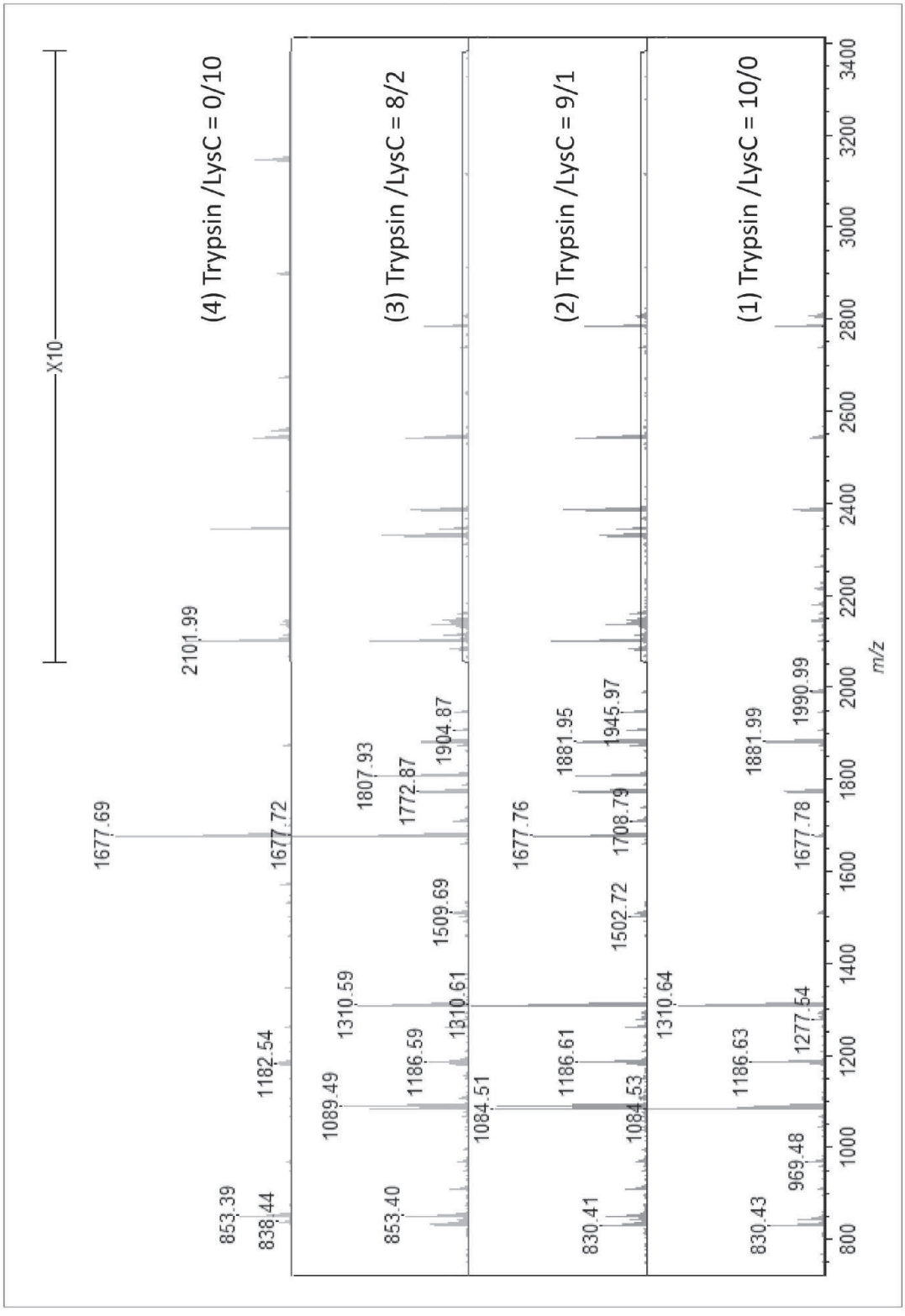


FIG. 13


X10
(4) Trypsin /LysC = 0/10
(3) Trypsin /LysC = 8/2
(2) Trypsin /LysC = 9/1
(1) Trypsin /LysC = 10/0
m/z
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
2800
3000
3200
3400
1677.69
1677.72
2101.99
1807.93
1772.87
1904.87
1509.69
1310.61
1310.59
1186.59
1089.49
1084.51
1182.54
853.40
838.44
853.39
1677.76
1881.95
1945.97
1708.79
1502.72
1186.61
1084.53
1310.64
830.41
1881.99
1990.99
1677.78
1186.63
1277.64
969.48
830.43