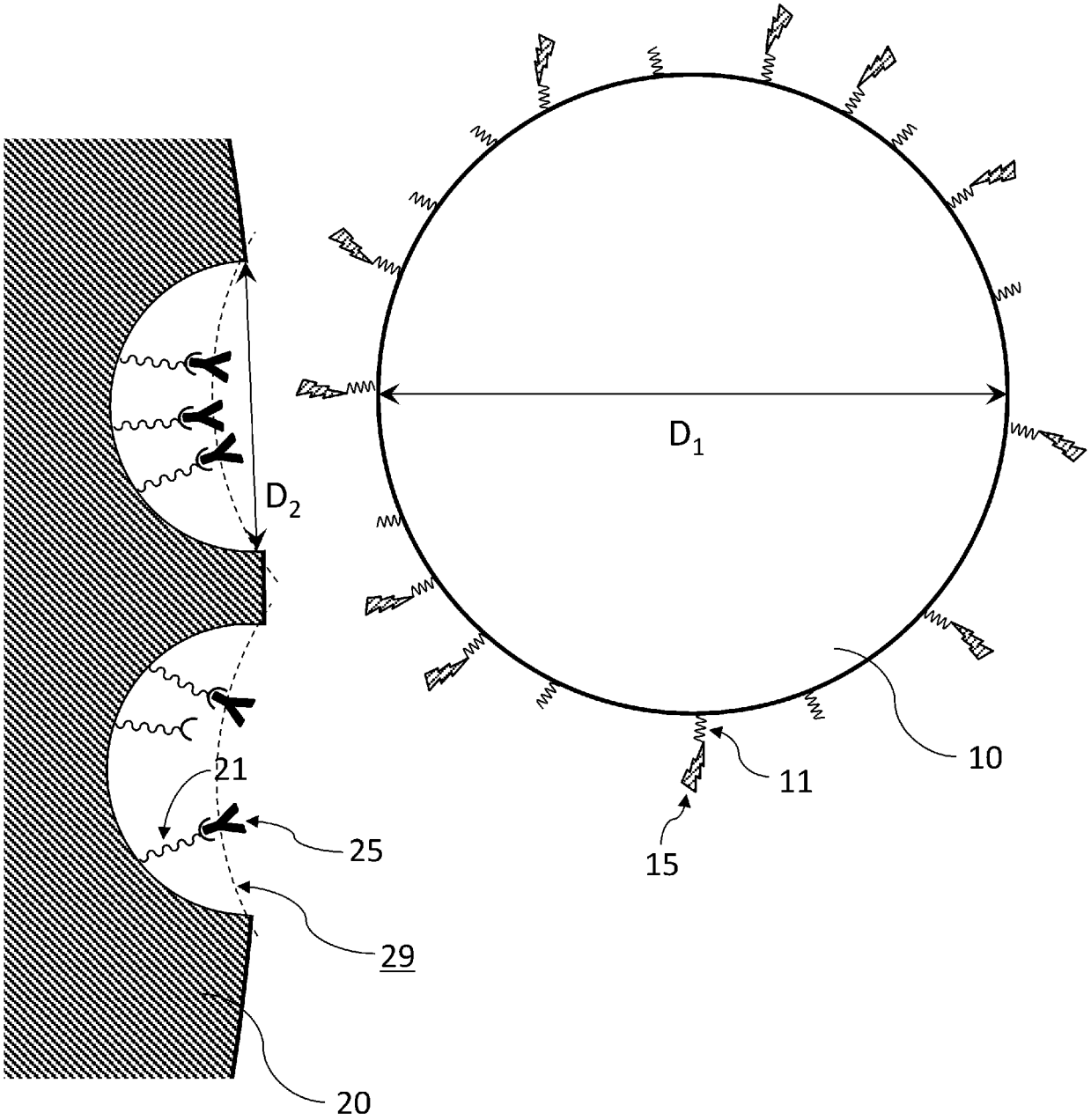
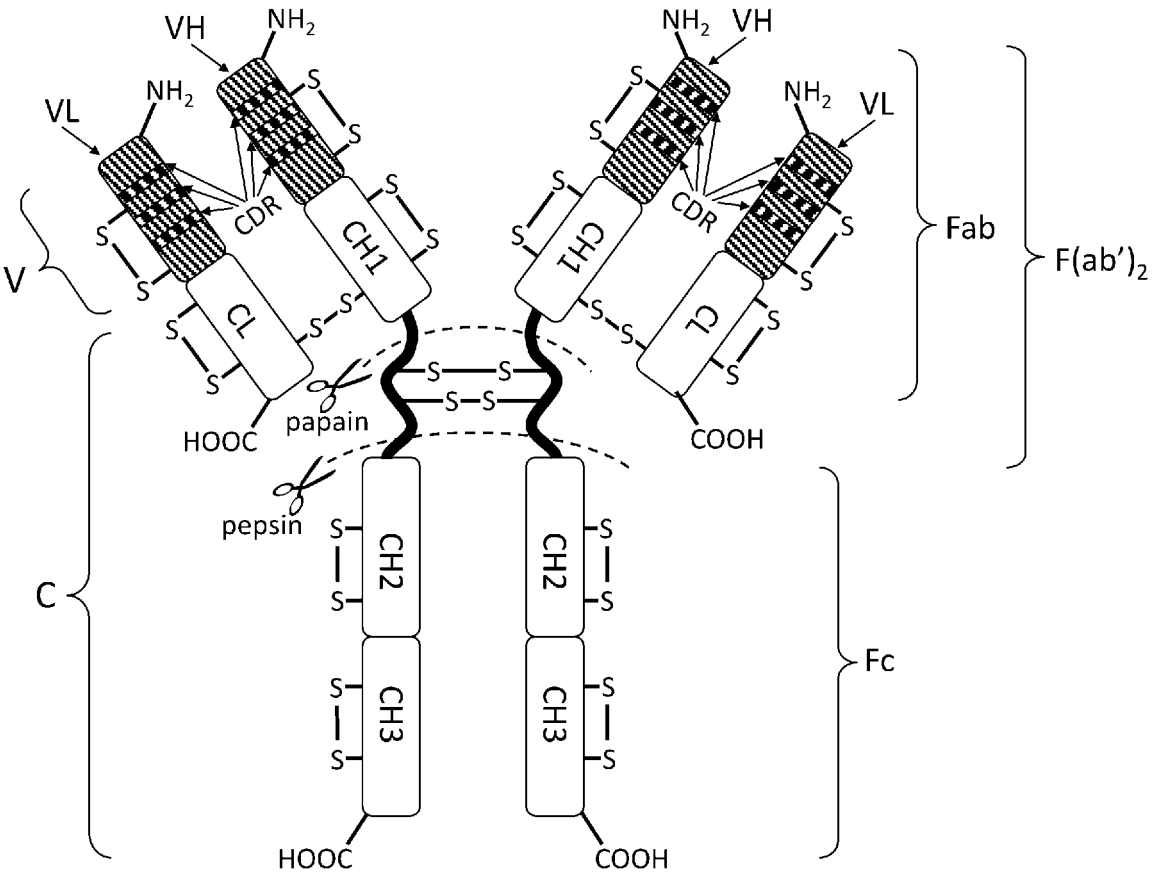
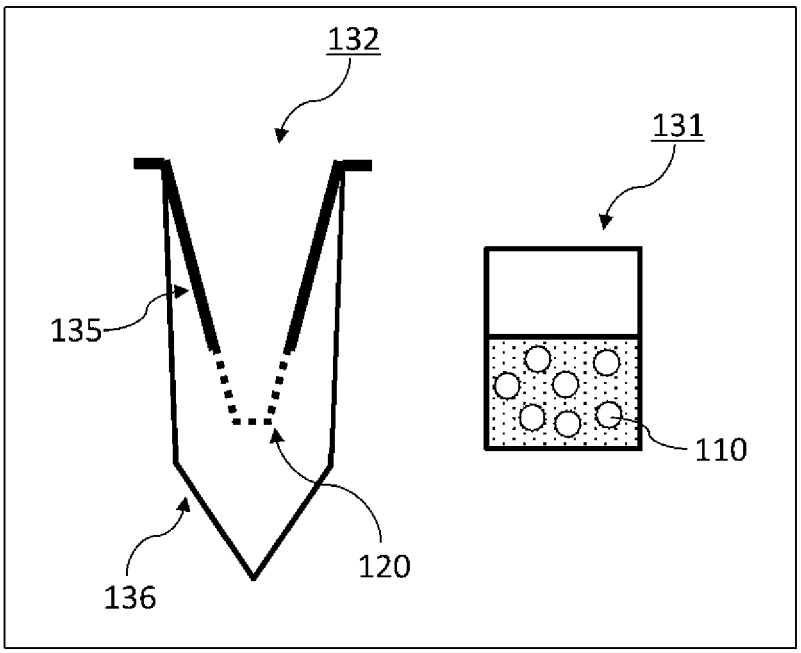
[図1]



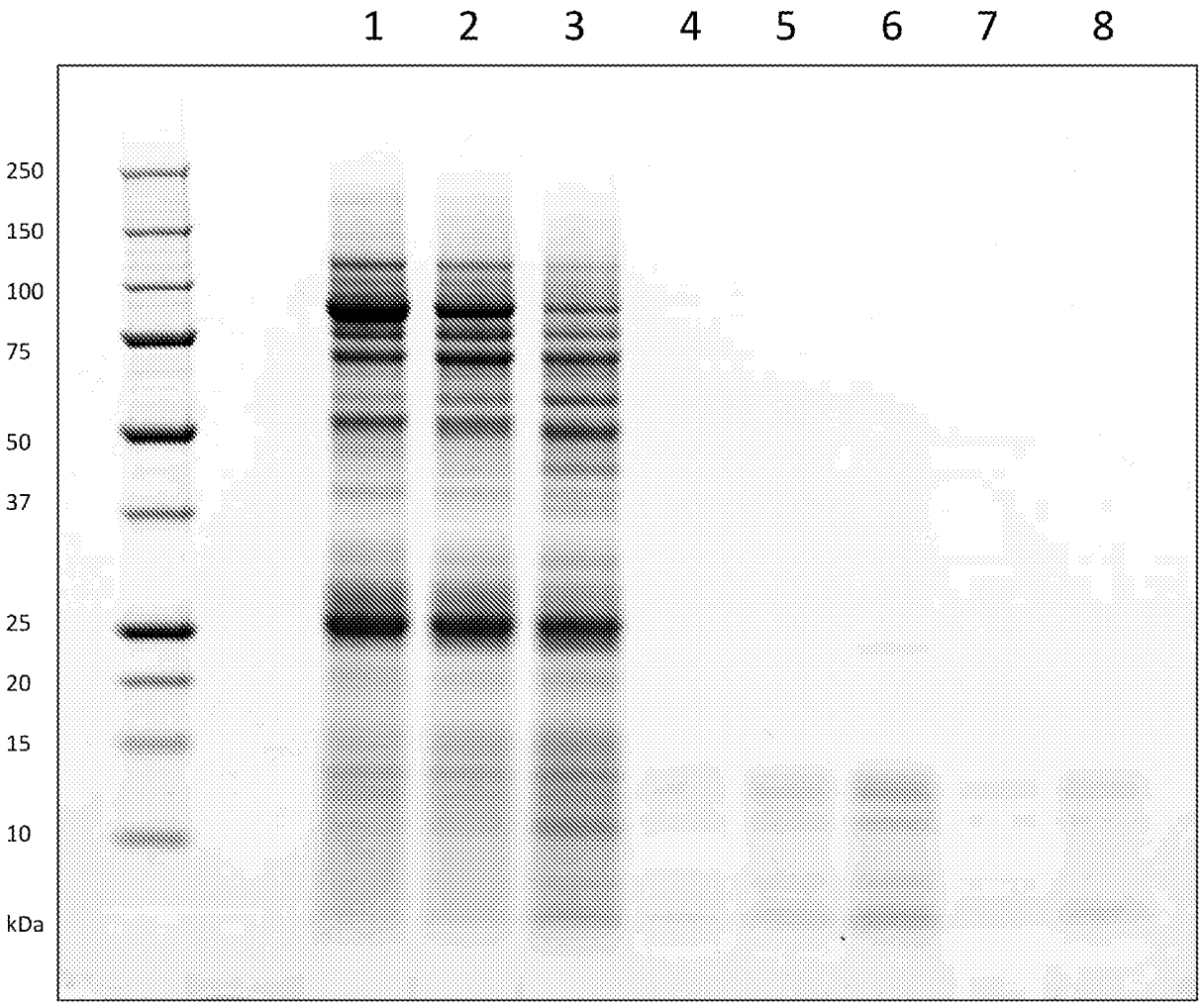
[図2]


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

[図3]

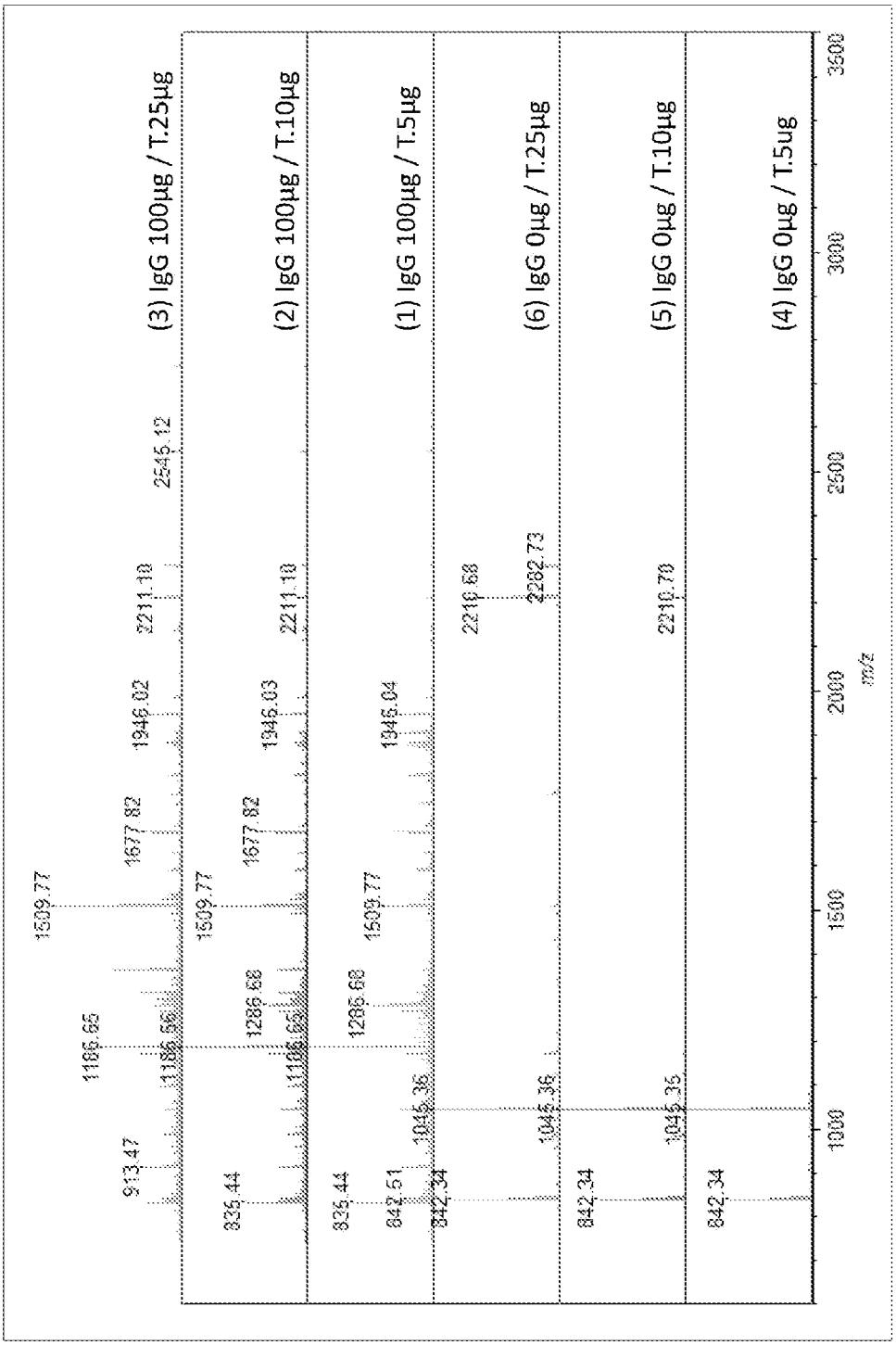

132
131
135
110
120
136

[図4]

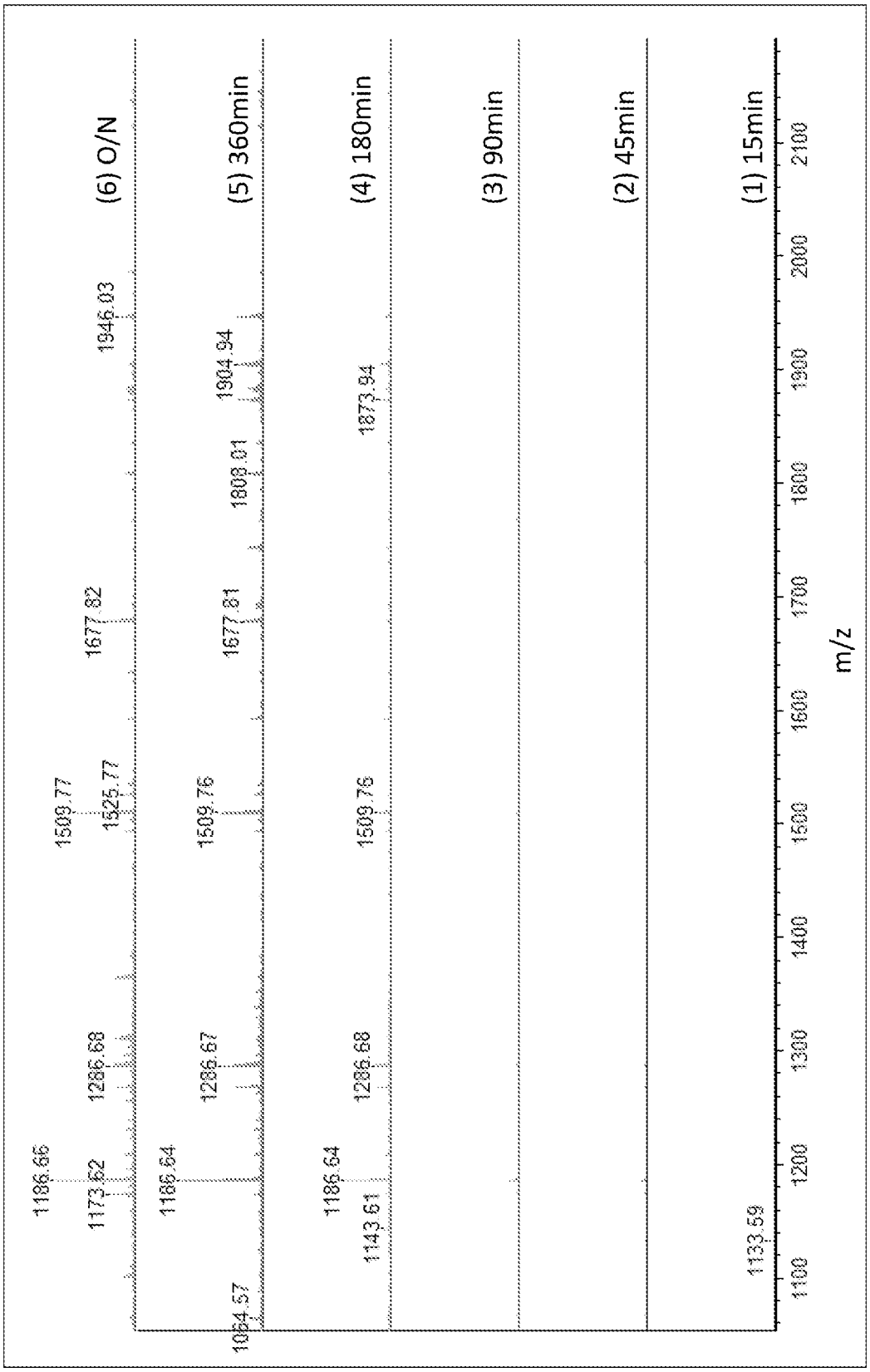


1. ProteinG-IgG / FG beads-Trypsin 5μg
2. ProteinG-IgG / FG beads-Trypsin 10μg
3. ProteinG-IgG / FG beads-Trypsin 25μg
4. ProteinG / FG beads-Trypsin 5μg
5. ProteinG / FG beads-Trypsin 10μg
6. ProteinG / FG beads-Trypsin 25μg
7. FG beads-Trypsin 5ug
8. FG beads-Trypsin 10ug

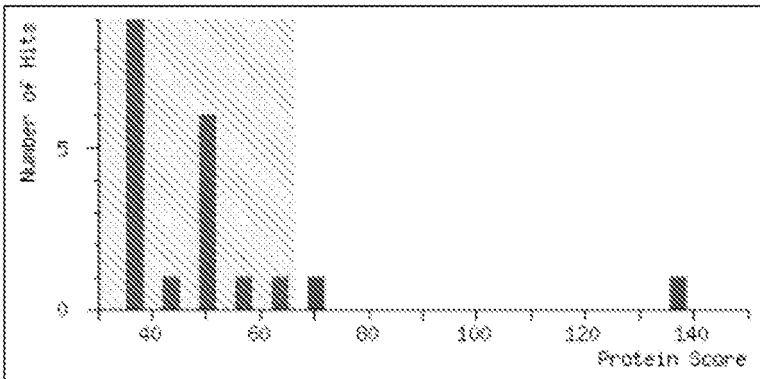
[図5]


(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
2211.18
2545.12
1186.65
1286.68
913.47
835.44
842.51
1045.36
842.34
2210.68
2282.73
2210.78
1000
1500
2000
2500
3000
3500
m/z

[図6]


(6) O/N
(5) 360min
(4) 180min
(3) 90min
(2) 45min
(1) 15min
1946.03
1904.94
1677.82
1677.81
1525.77
1509.77
1509.76
1509.76
1808.01
1873.94
1286.68
1286.67
1286.68
1186.66
1186.64
1186.64
1173.62
1143.61
1133.59
1084.57
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
2100
m/z

[図7]



Concise Protein Summary Report

Format As | Concise Protein Summary | Help

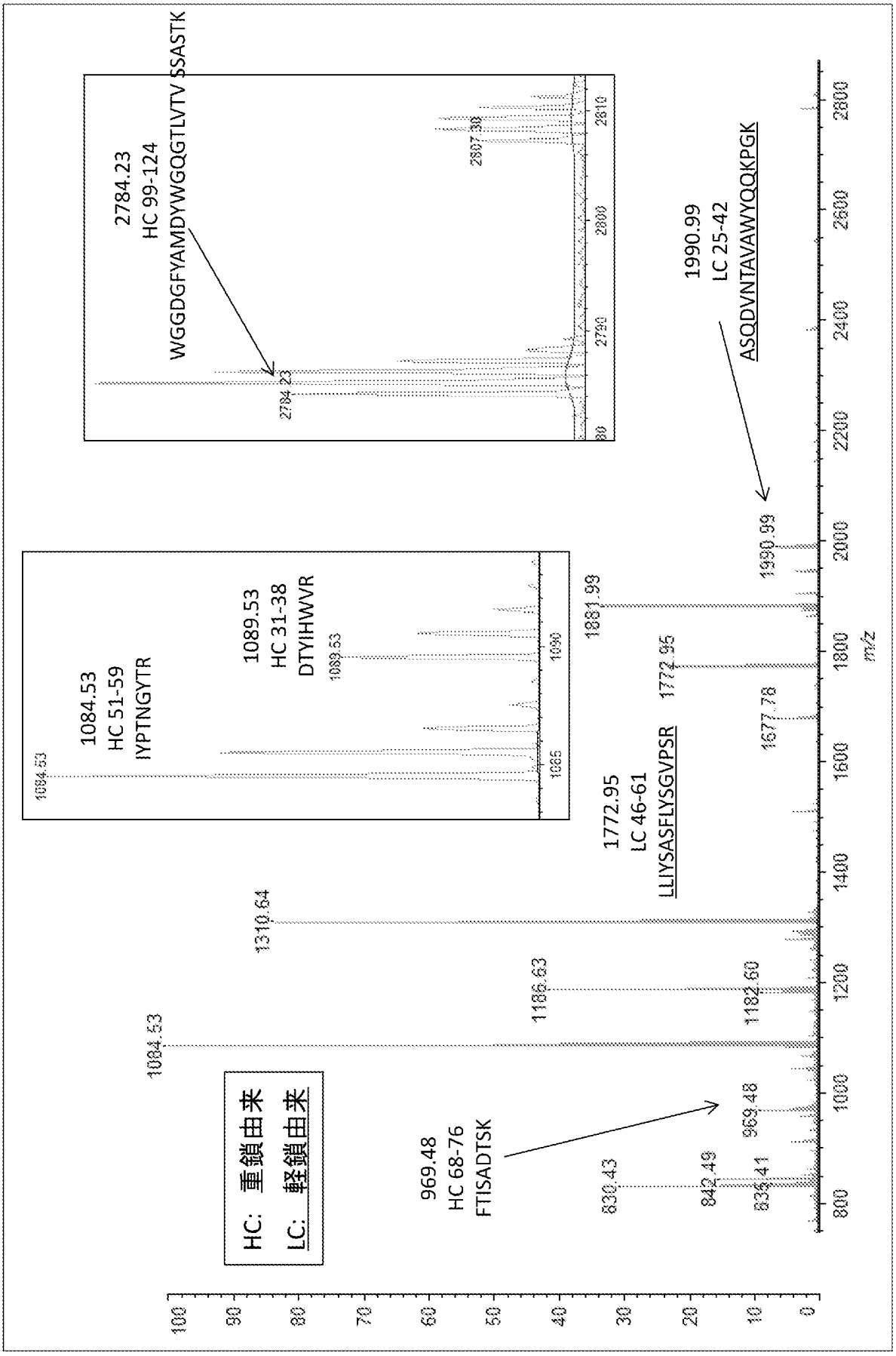
Significance threshold p< 0.05 | Max. number of hits AUTO

Preferred taxonomy | All entries

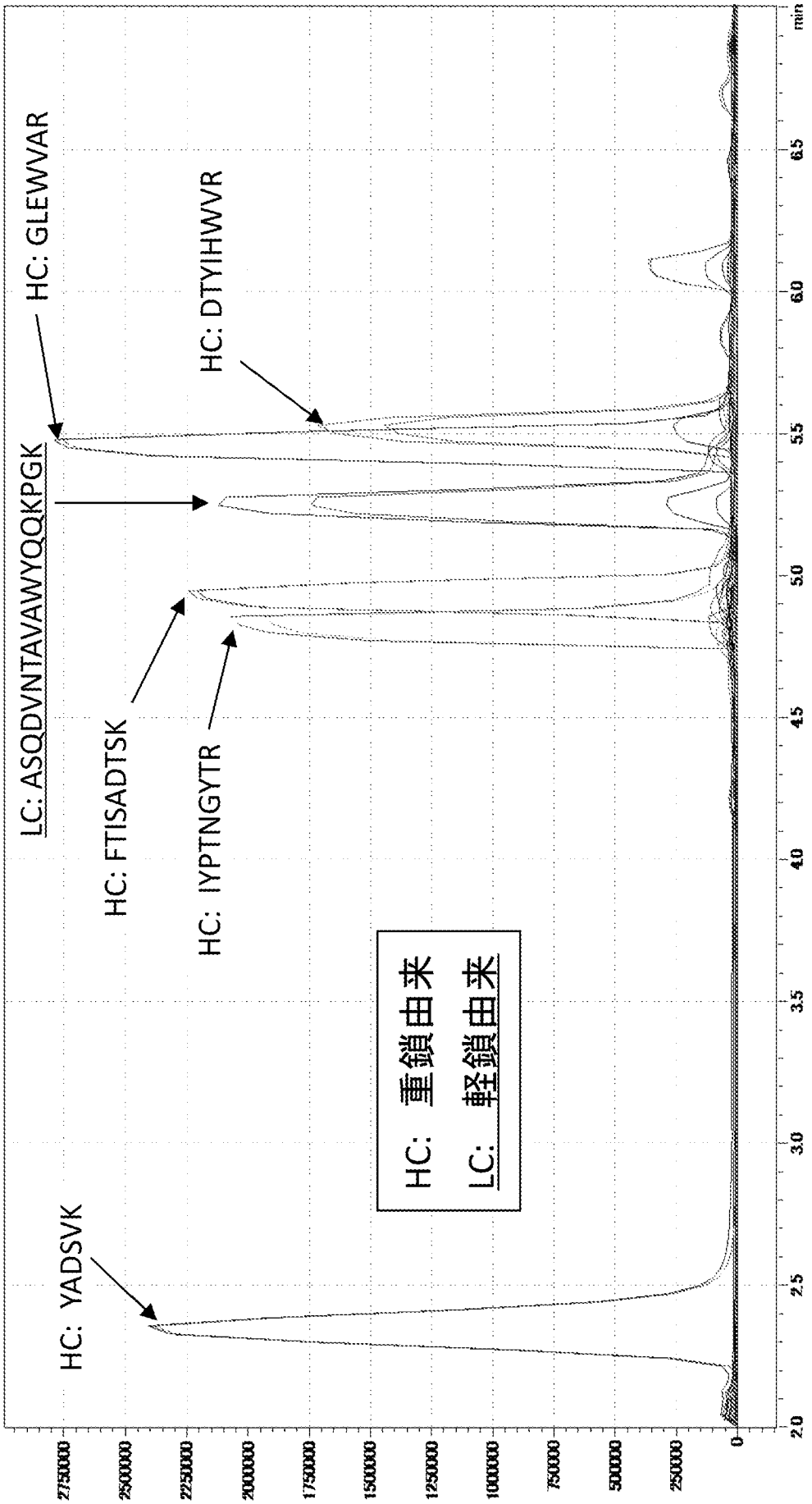
Re-Search All | Search Unmatched

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 Bhl 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

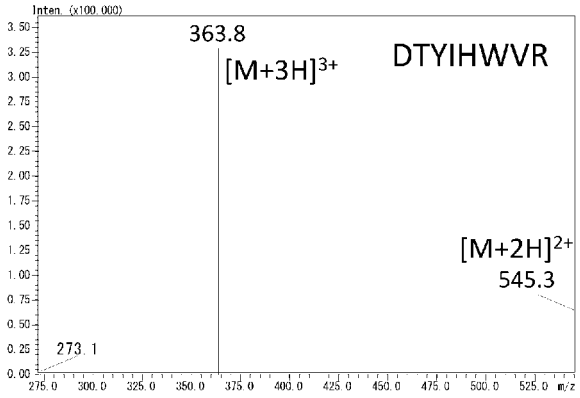
[図8]

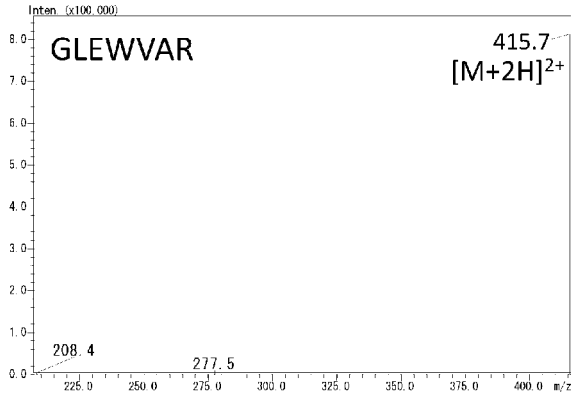

HC: 重鎖由来
LC: 軽鎖由来
1084.53
HC 51-59
IYPTNGYTR
1089.53
HC 31-38
DTYIHWVR
2784.23
HC 99-124
WGGDGFYAMDYWGQGTLVTV
SASTK
1772.95
LC 46-61
LLIYSASFLYSGVPSR
1990.99
LC 25-42
ASQDVNTAVAWYQQKPGK
969.48
HC 68-76
FTISADTSK
m/z

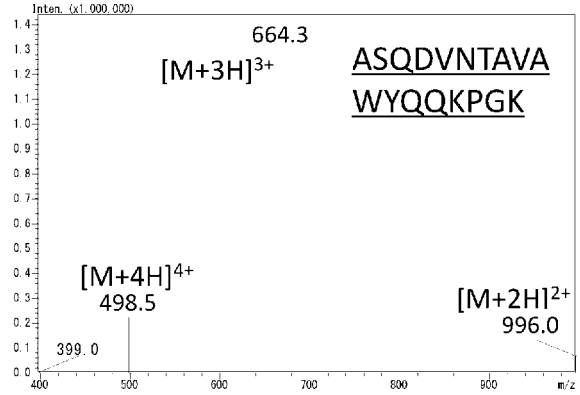
[図9]

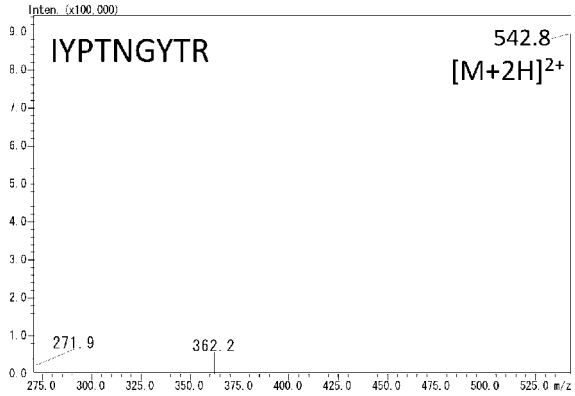

HC: YADSVK
HC: FTISADTSK
HC: IYPTNGYTR
LC: ASQDVNTAVAWYQQKPGK
HC: DTYIHWVR
HC: GLEWVAR
HC: 重鎖由来
LC: 軽鎖由来
min

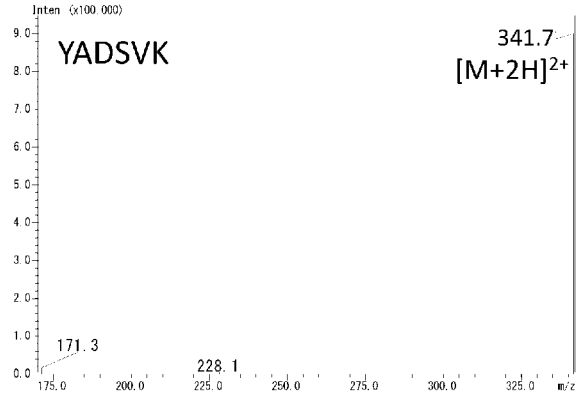
[図10]

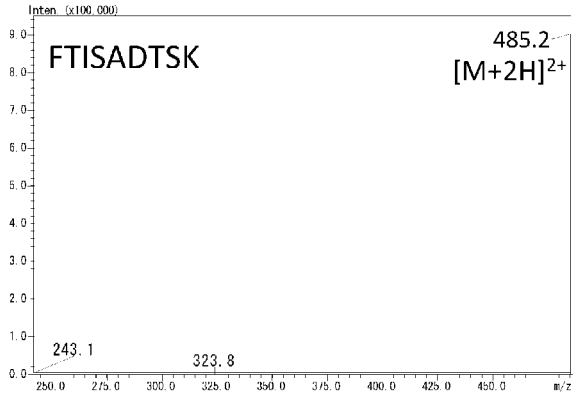

Inten. (x100,000)
363.8
[M+3H]3+
DTYIHWVR
[M+2H]2+
545.3
273.1
m/z


Inten. (x100,000)
GLEWVAR
415.7
[M+2H]2+
208.4
277.5
m/z


Inten. (x1,000,000)
664.3
[M+3H]3+
ASQDVNTAVA
WYQQKPGK
[M+4H]4+
498.5
[M+2H]2+
996.0
399.0
m/z


Inten. (x100,000)
IYPTNGYTR
542.8
[M+2H]2+
271.9
362.2
m/z


Inten. (x100,000)
YADSVK
341.7
[M+2H]2+
171.3
228.1
m/z


Inten. (x100,000)
FTISADTSK
485.2
[M+2H]2+
243.1
323.8
m/z

[図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

(B) Herceptin H-Chain

CDR1 CDR2

DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS

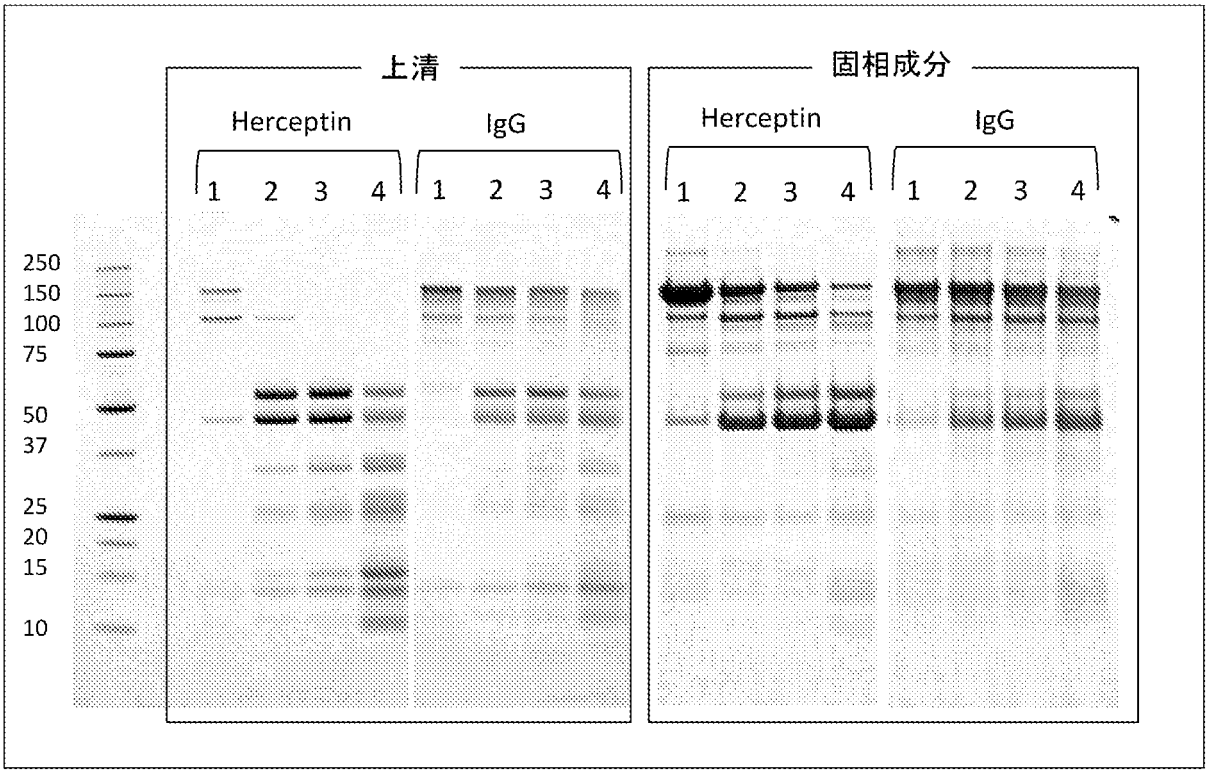
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ GTKVEIKRTV AAPSVFIFPP

CDR3

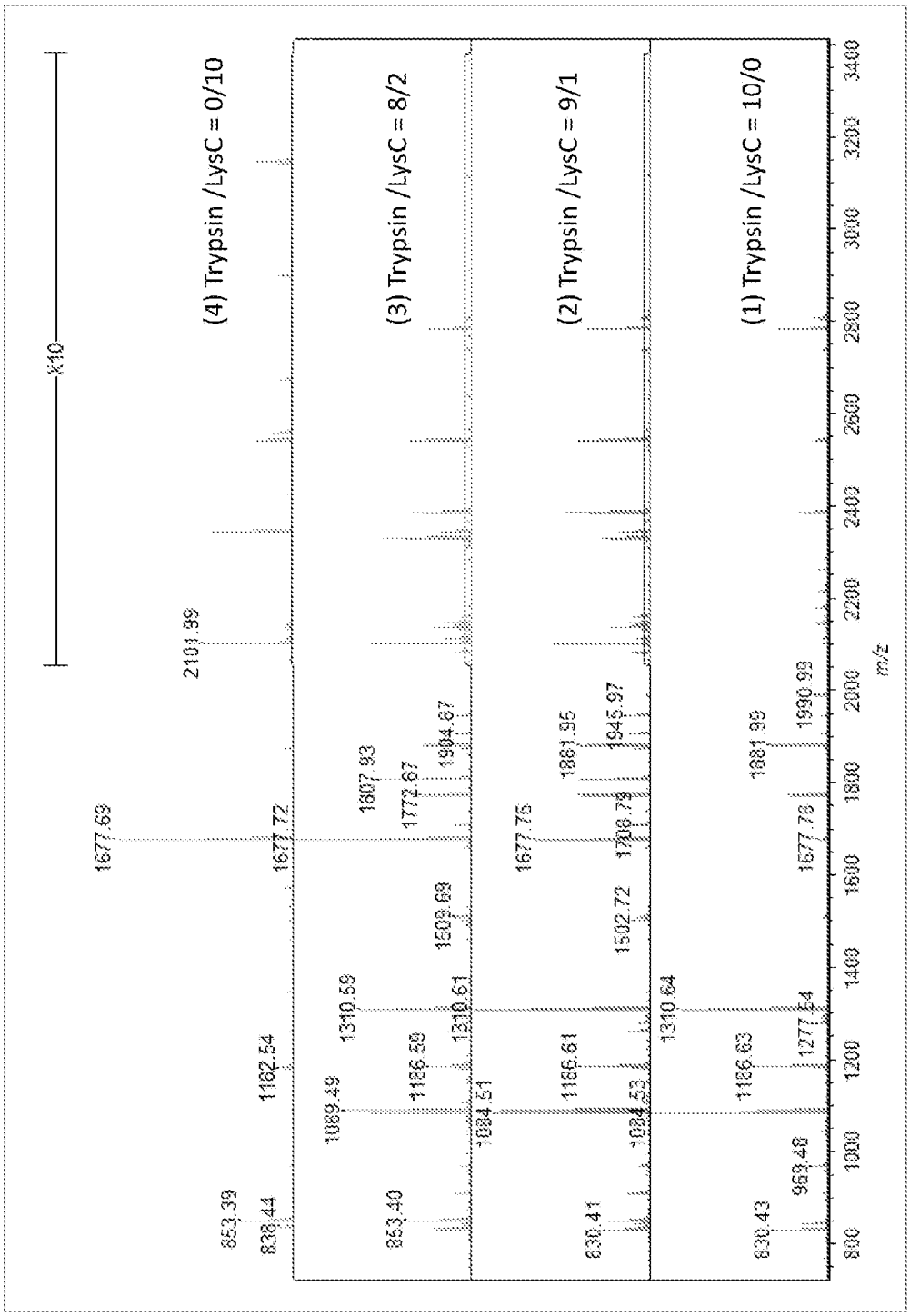
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT

LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC

[図12]



[図13]


(4) Trypsin /LysC = 0/10
(3) Trypsin /LysC = 8/2
(2) Trypsin /LysC = 9/1
(1) Trypsin /LysC = 10/0
x10
m/z
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
2800
3000
3200
3400
1677.69
2101.99
1677.72
1607.93
1772.67
1904.67
1677.75
1881.95
1945.97
1881.99
1990.99
1677.78
1310.59
1310.61
1310.64
1509.69
1502.72
1186.59
1186.61
1186.63
1277.64
1162.54
1089.49
1084.51
1084.53
853.39
838.44
853.40
836.41
836.43
963.48