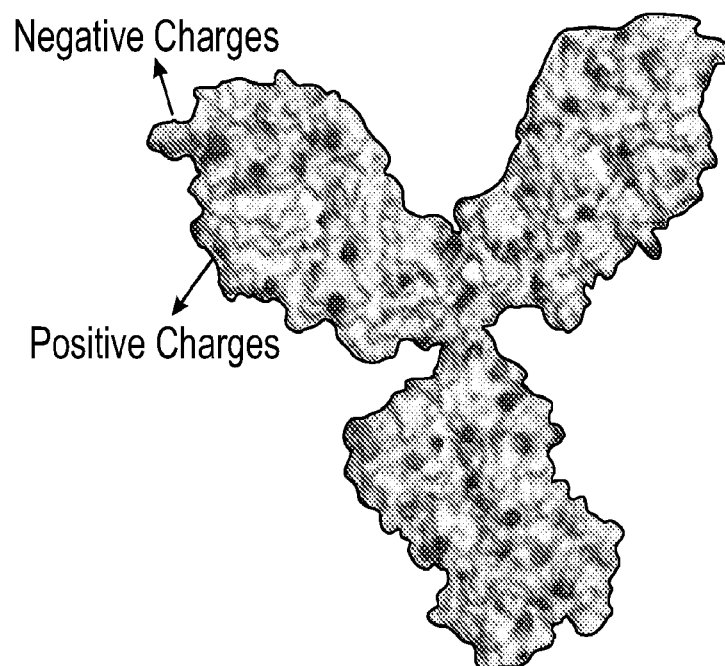
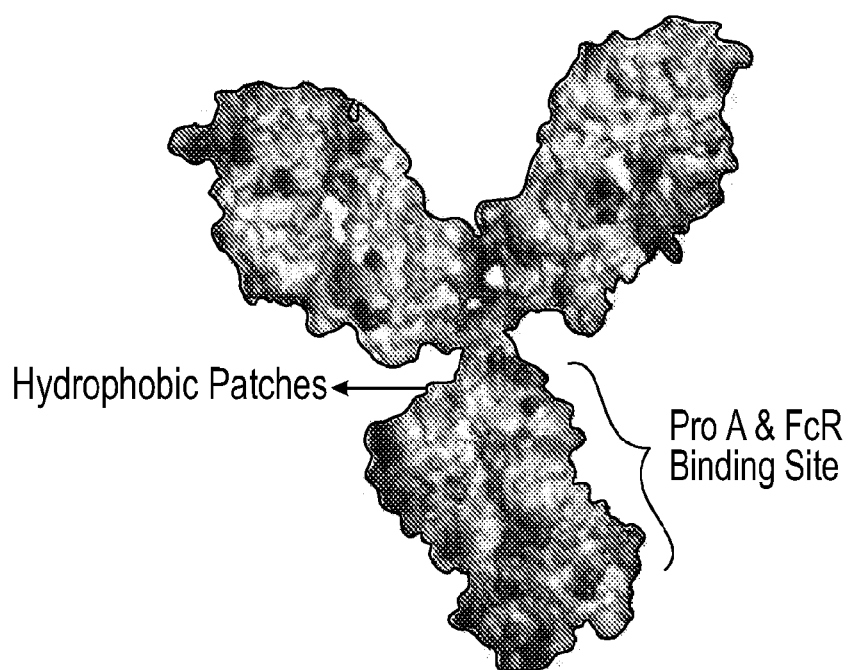




Surface Charge Plot



Surface Hydrophobicity Plot

FIG. 1

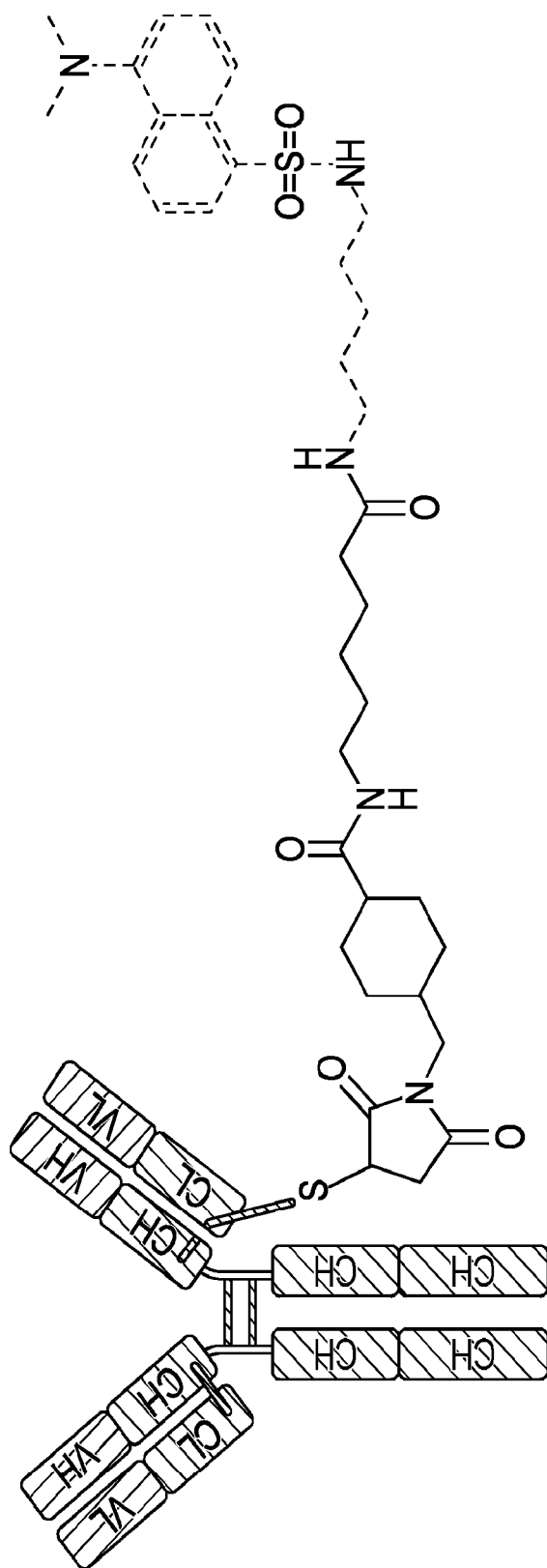
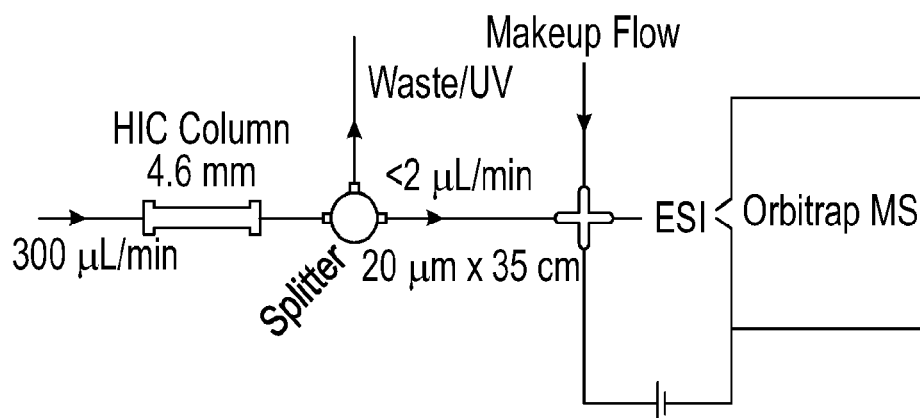


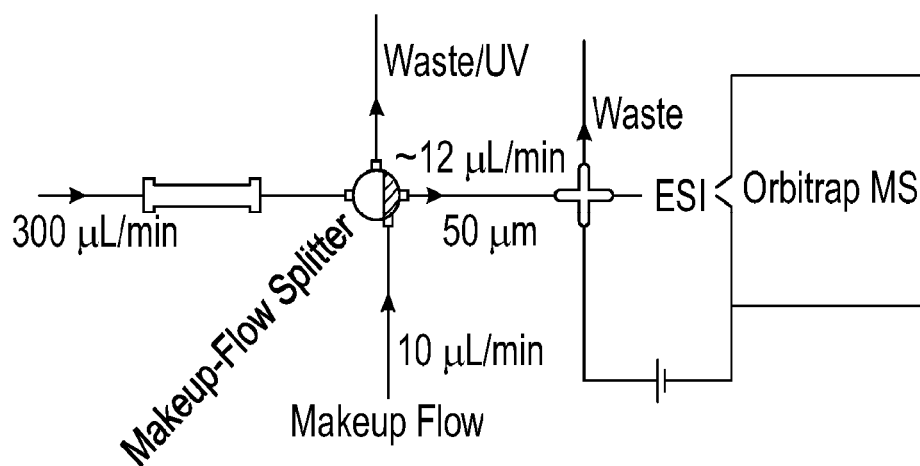
FIG. 2

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Flow Path Design A:



Flow Path Design B:



Flow Path Design C:

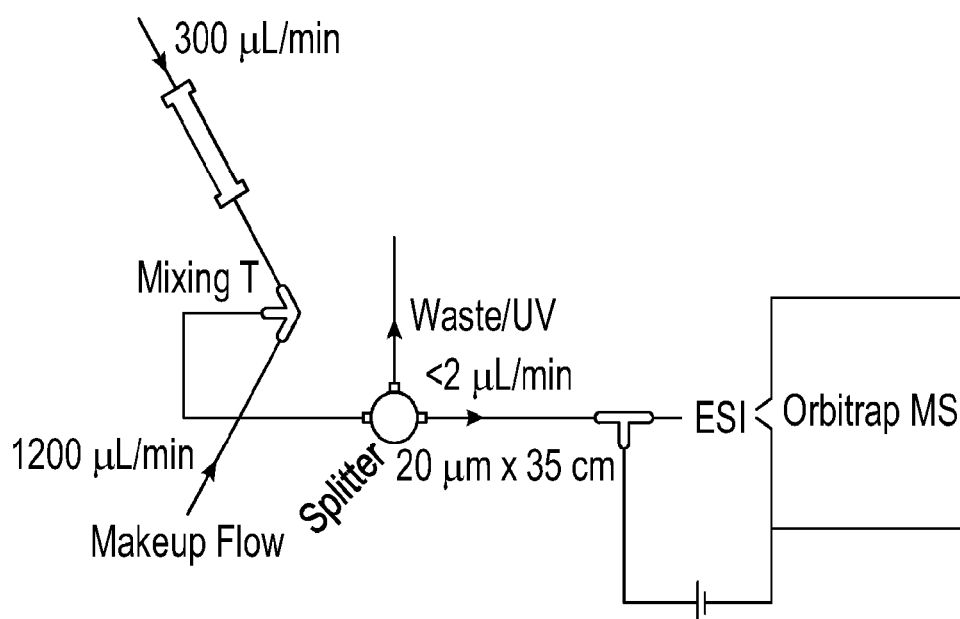
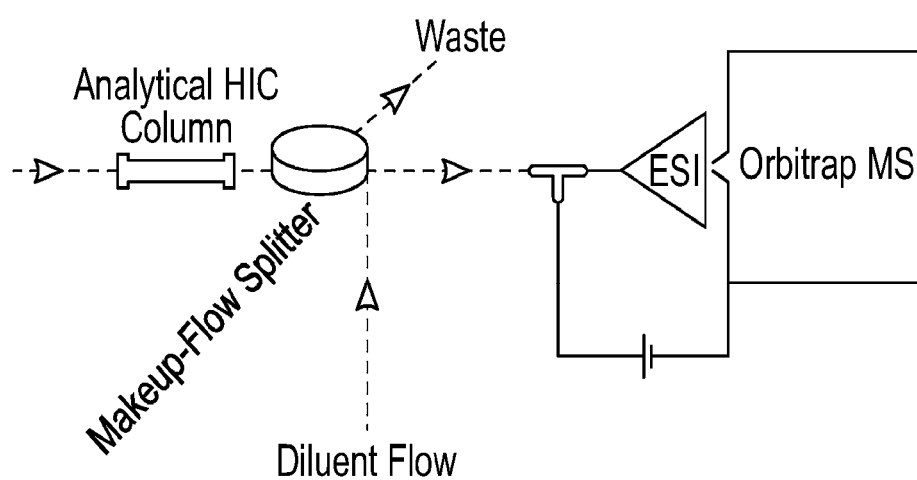
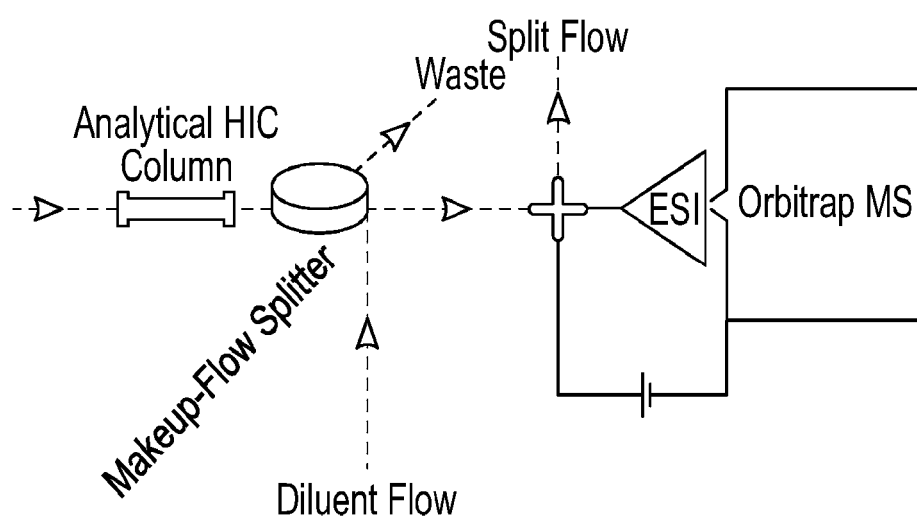


FIG. 3

Design B1:**Design B2:****FIG. 4**

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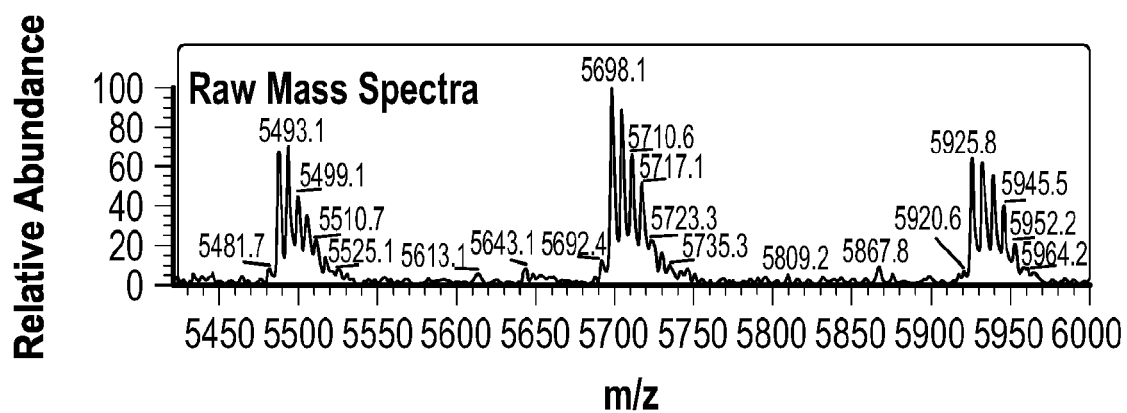
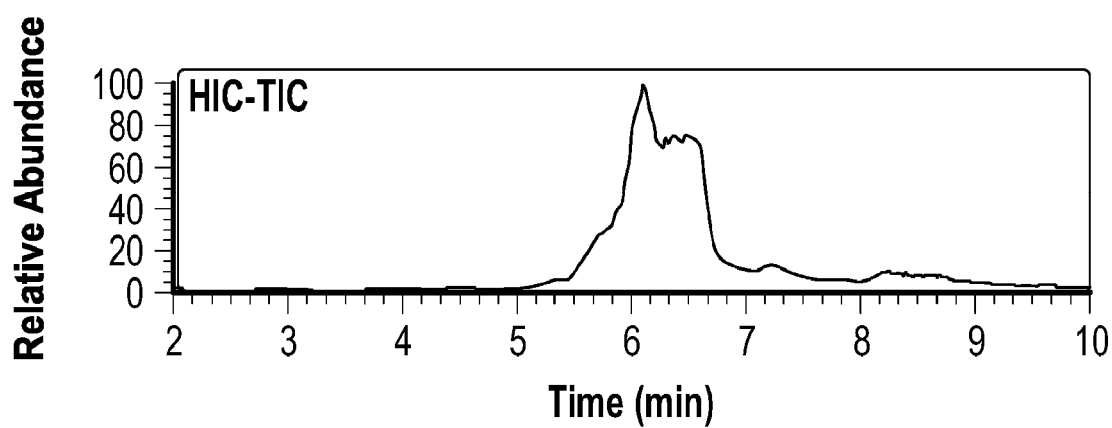
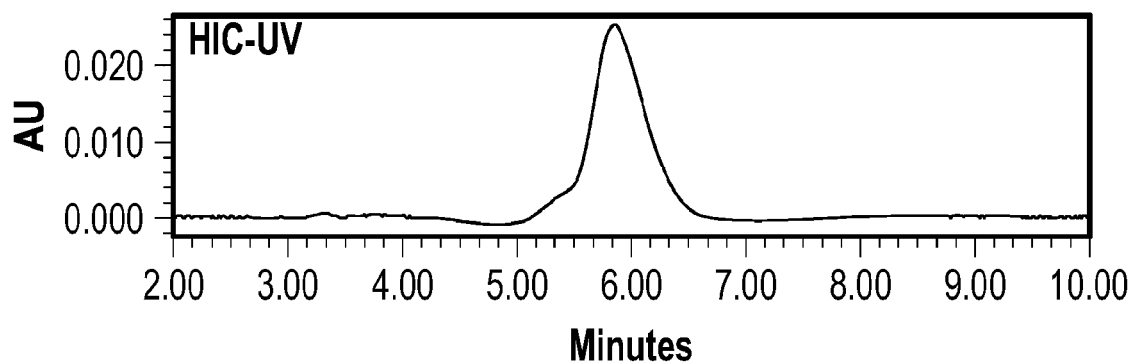


FIG. 5

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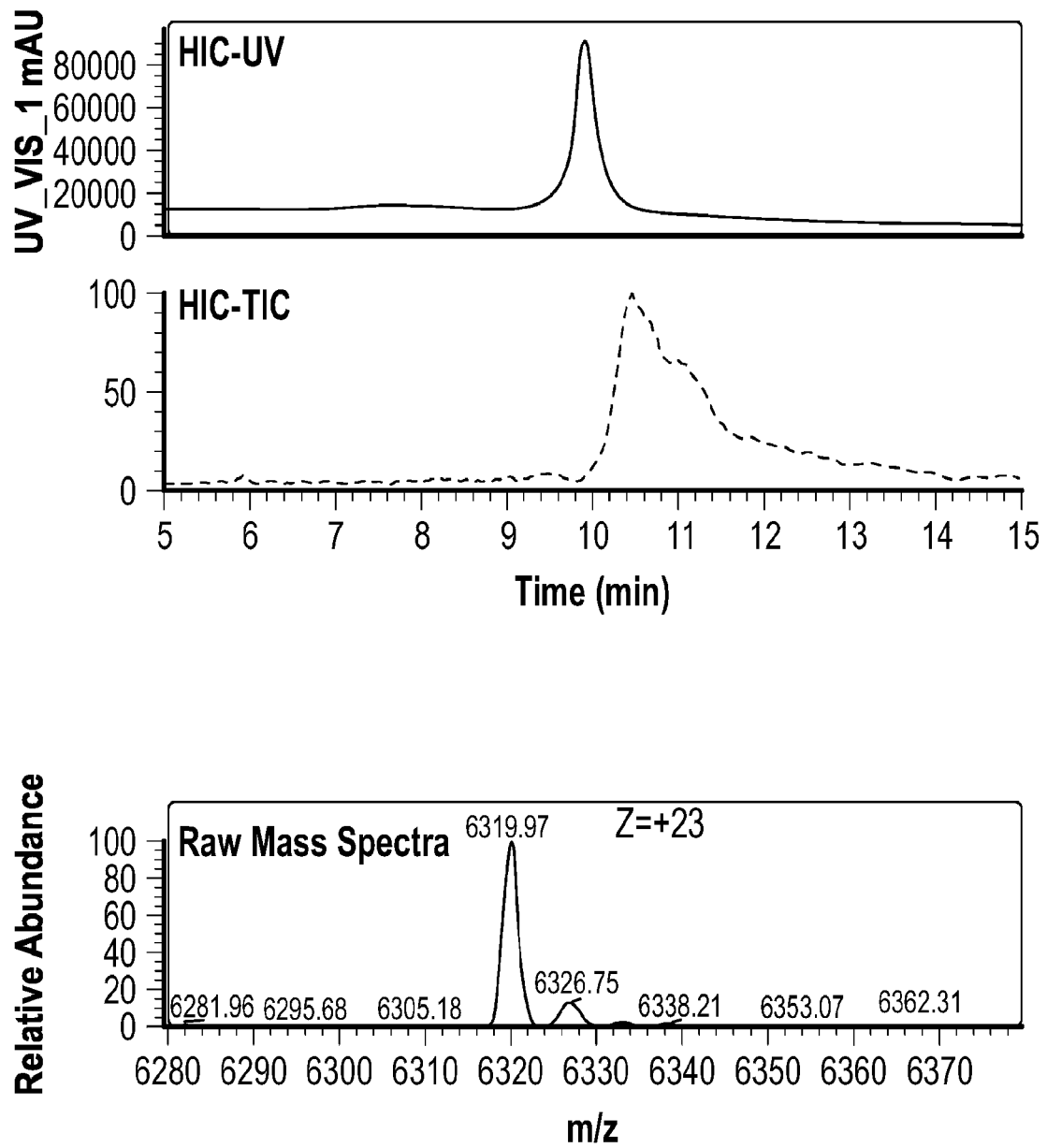


FIG. 6

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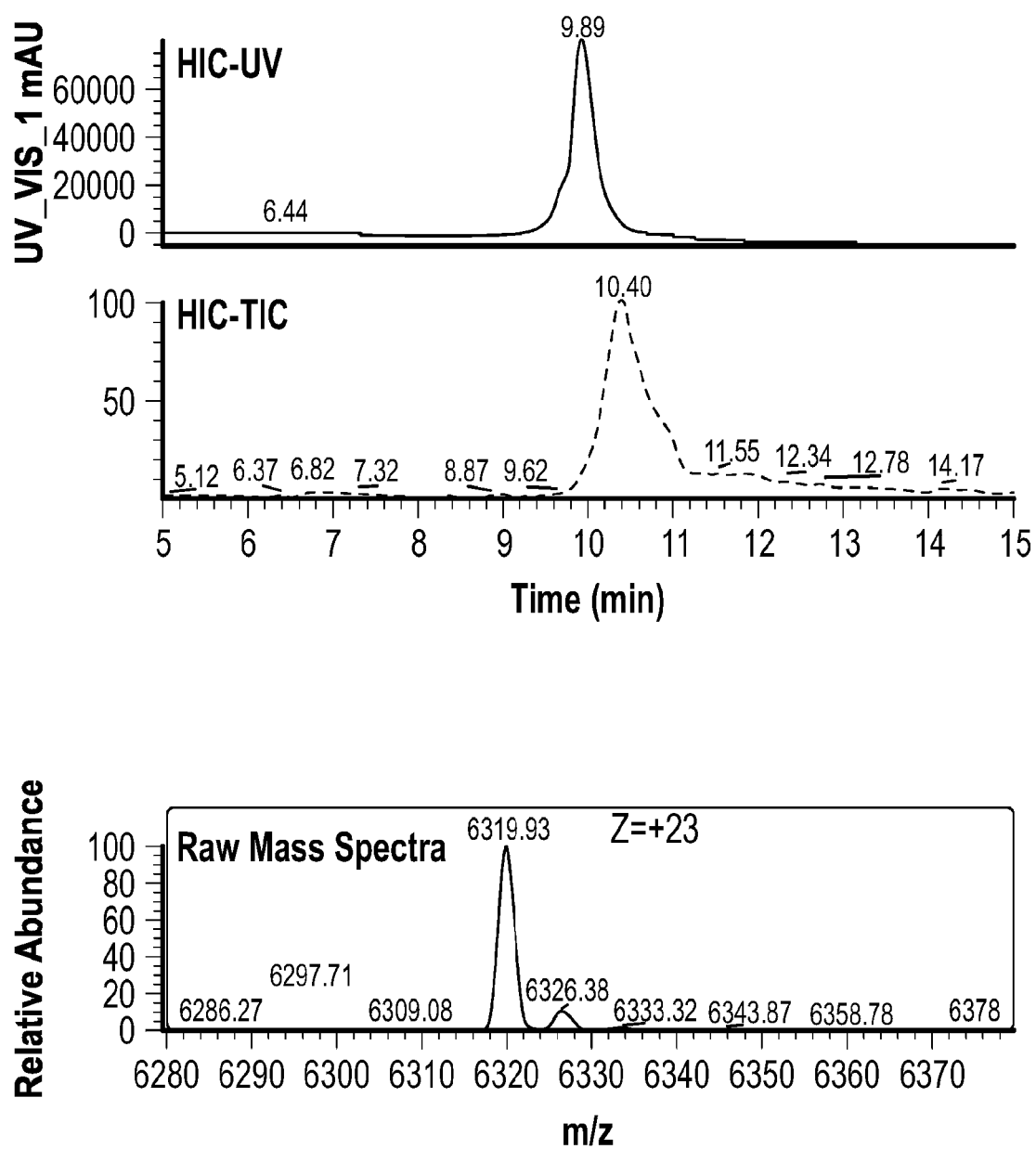


FIG. 7

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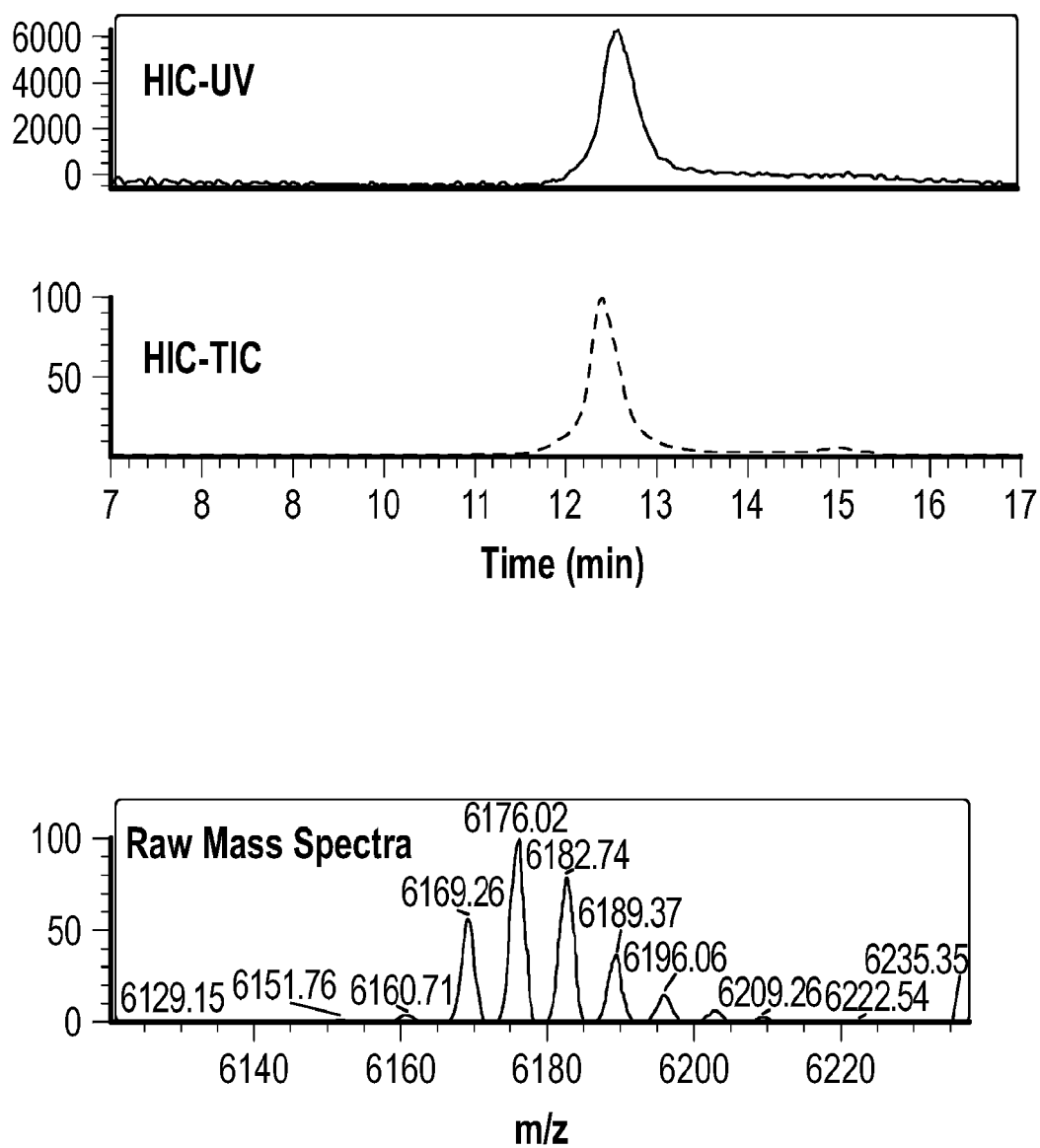


FIG. 8

HIC-UV/MS Analysis of NISTmAb using flow path design C:

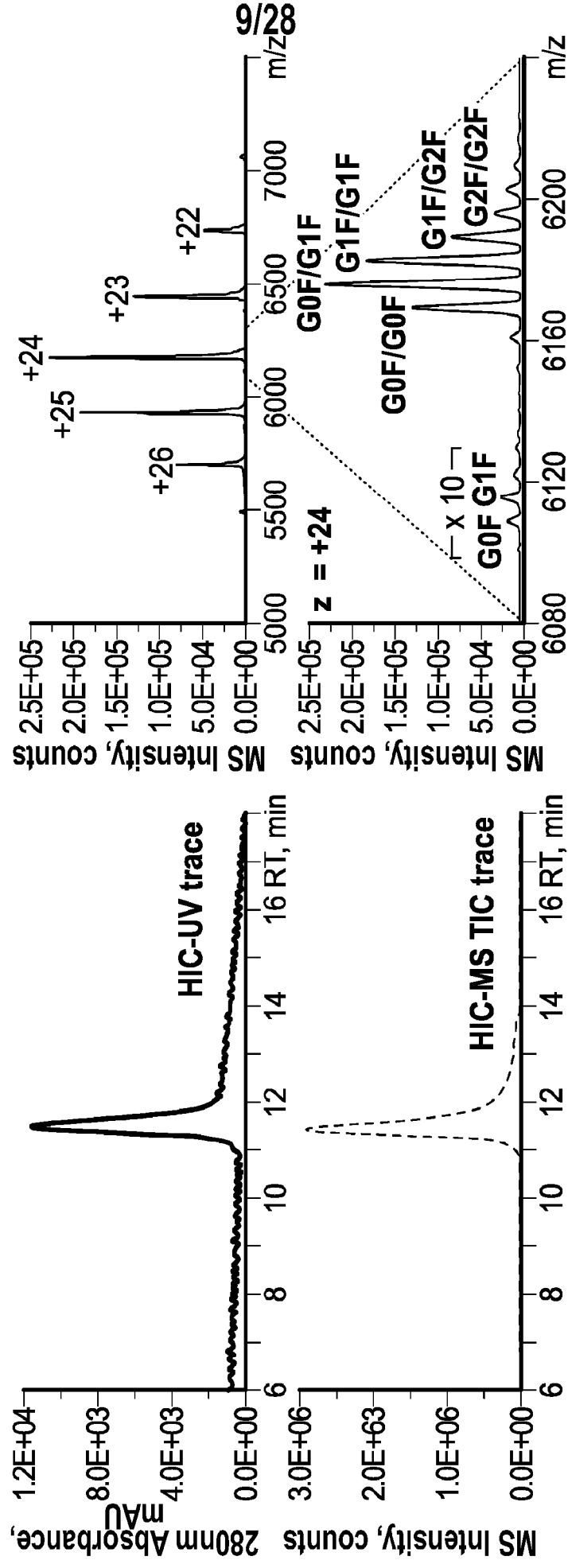


FIG. 9

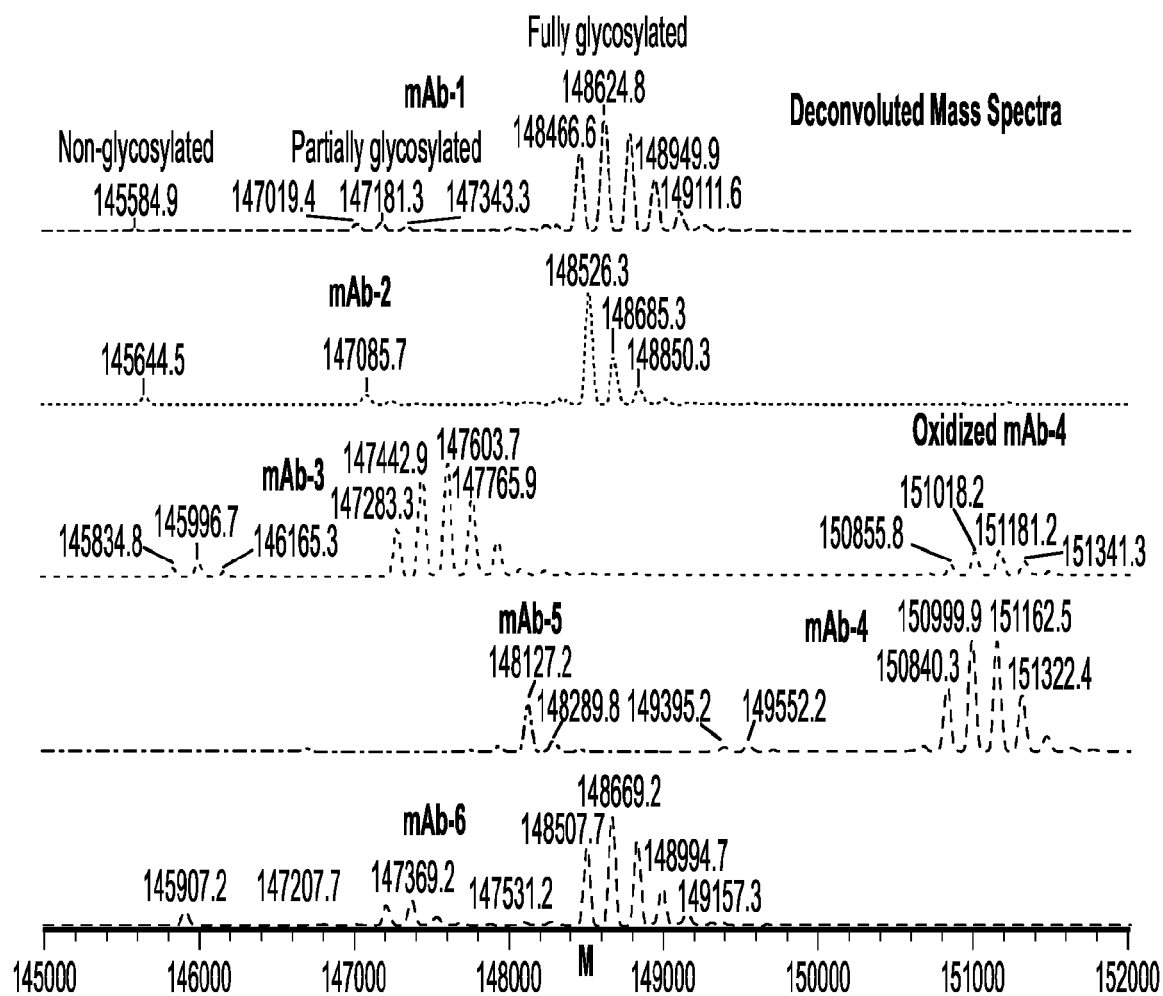
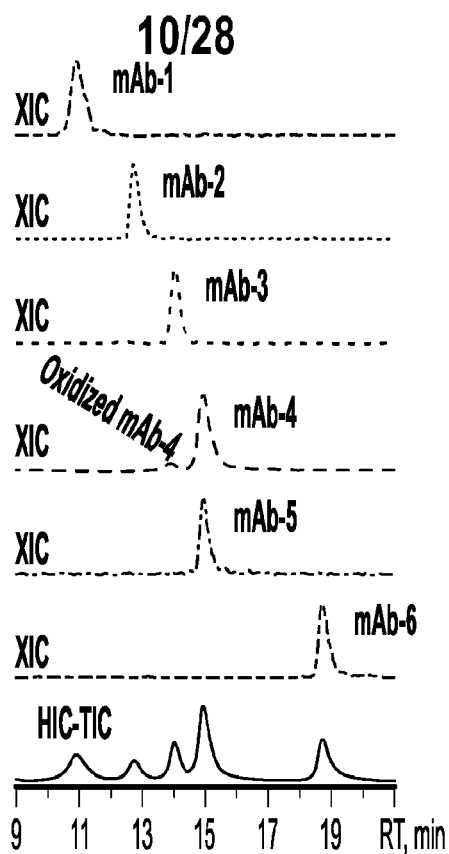


FIG. 10



FIG. 11

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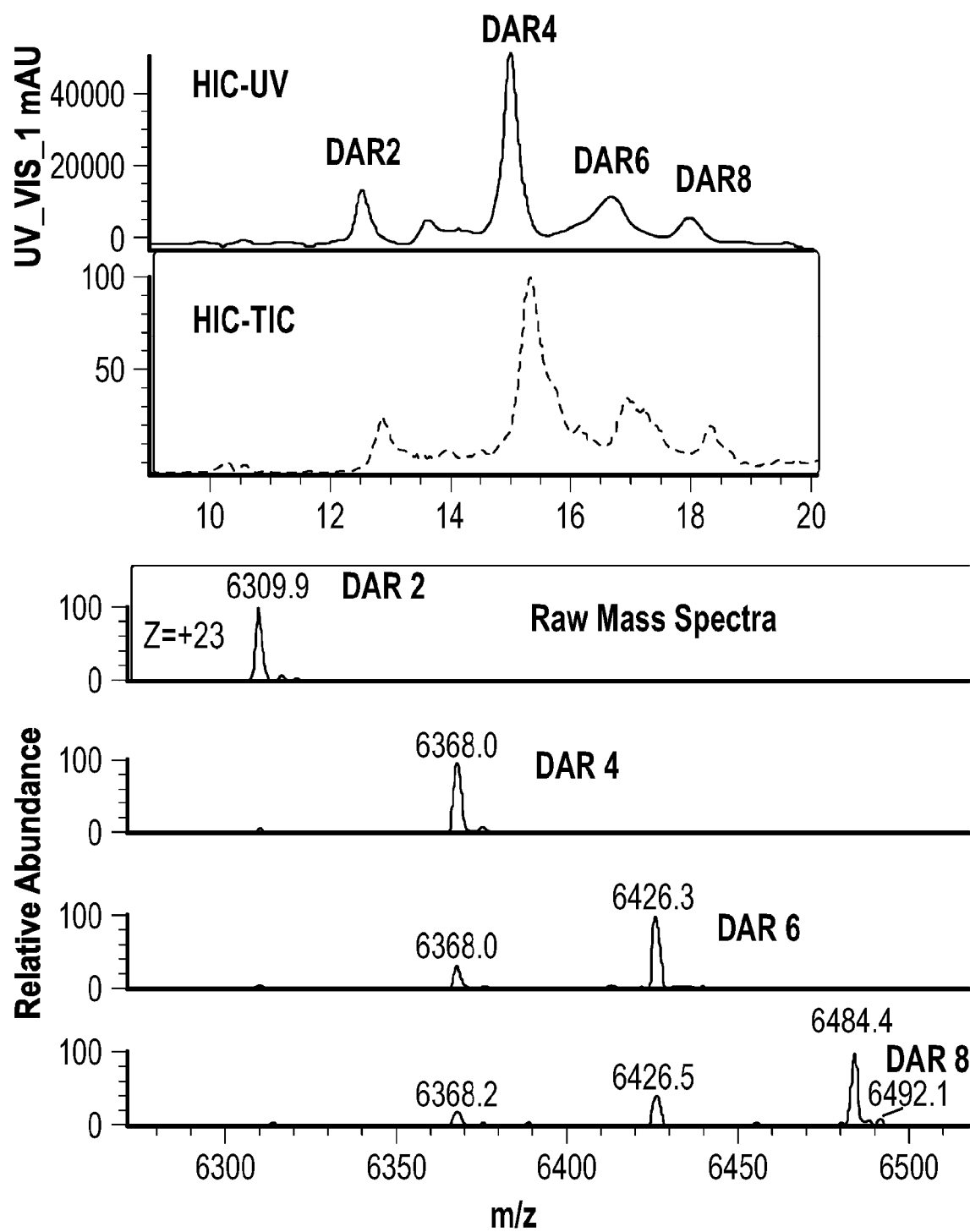
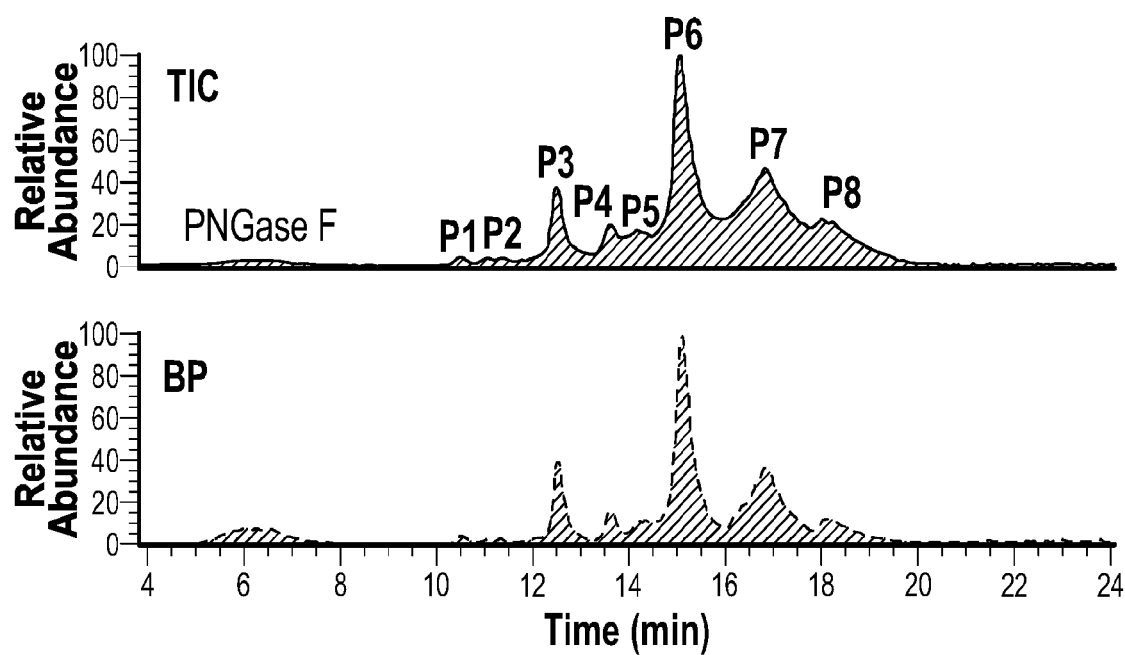


FIG. 12

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HIC profile from Sigma

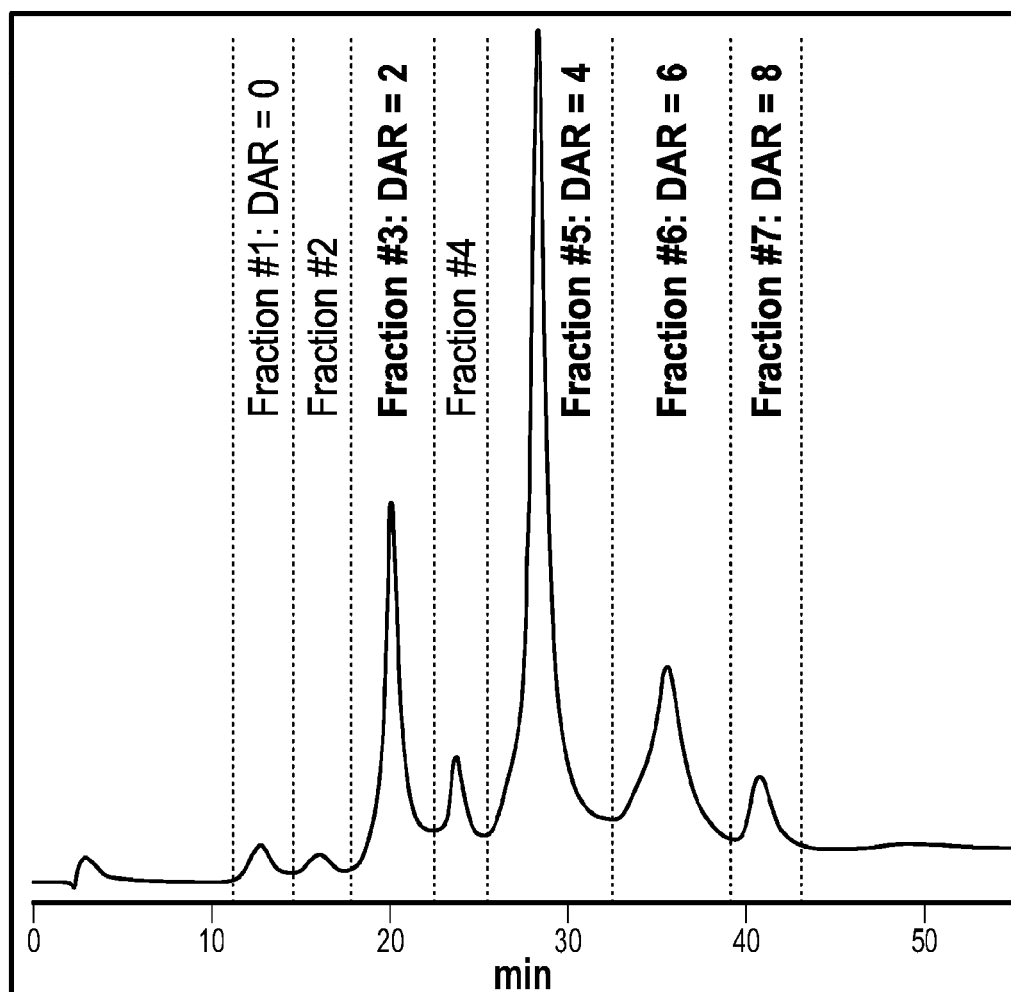


FIG. 13

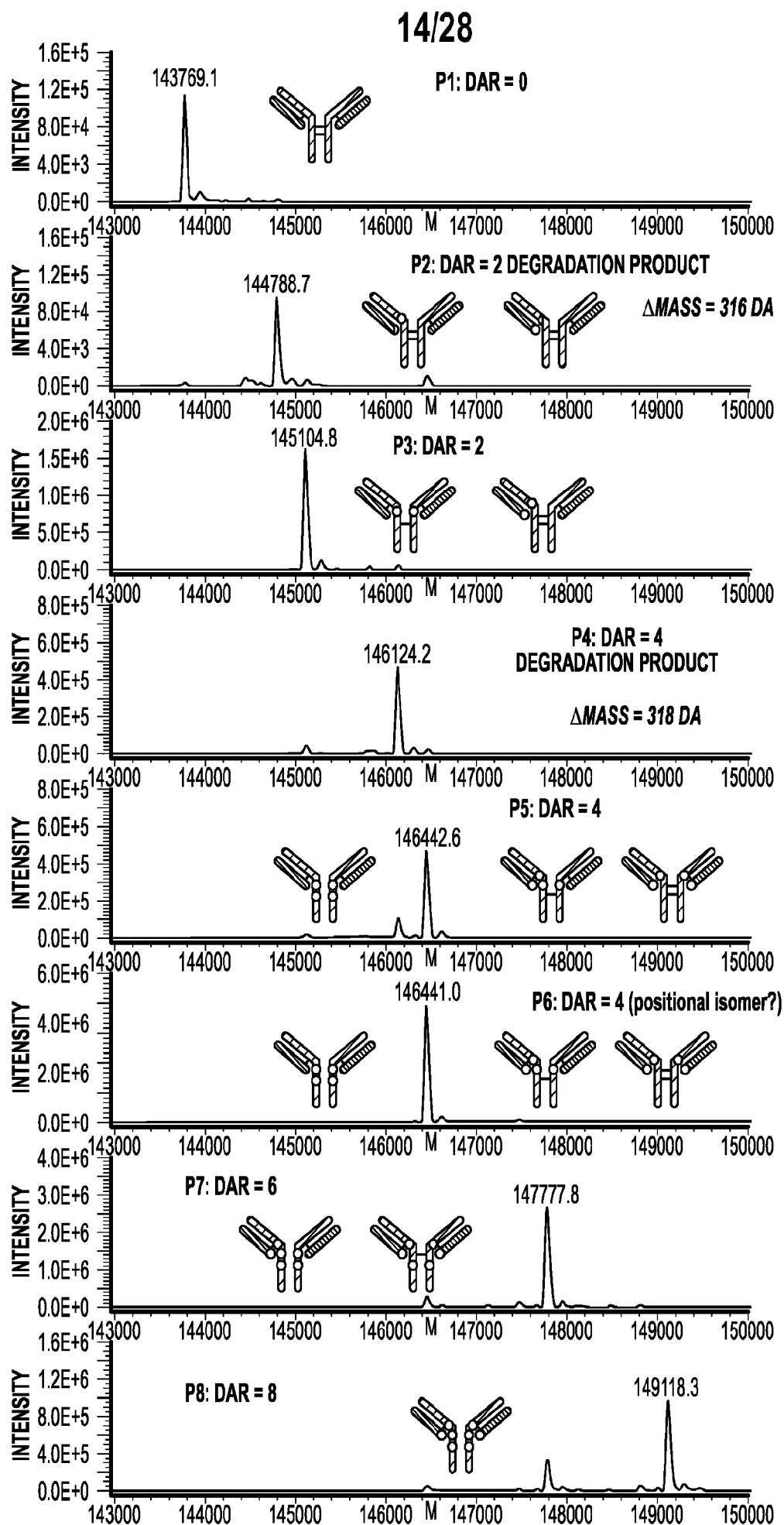


FIG. 14

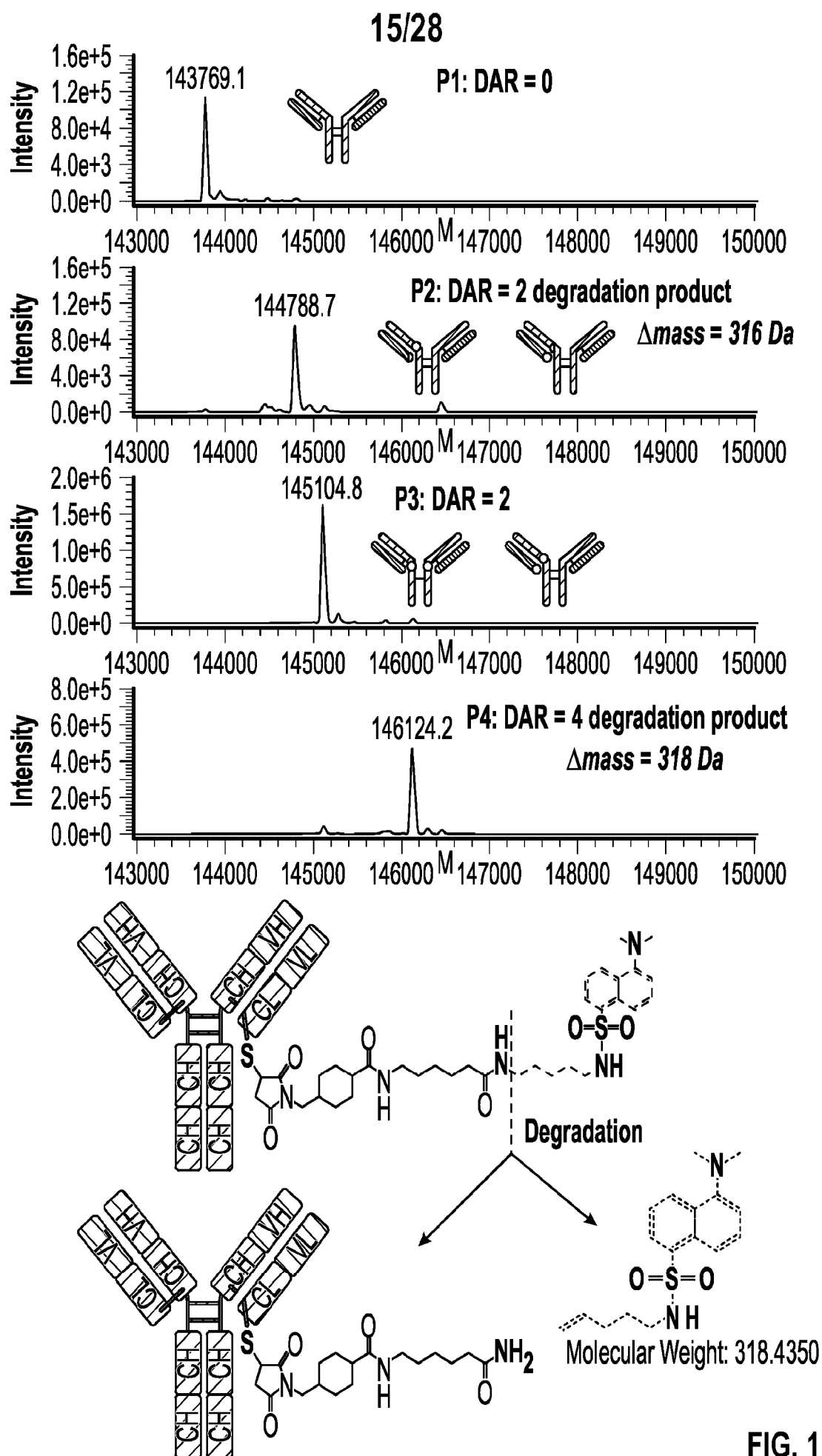


FIG. 15

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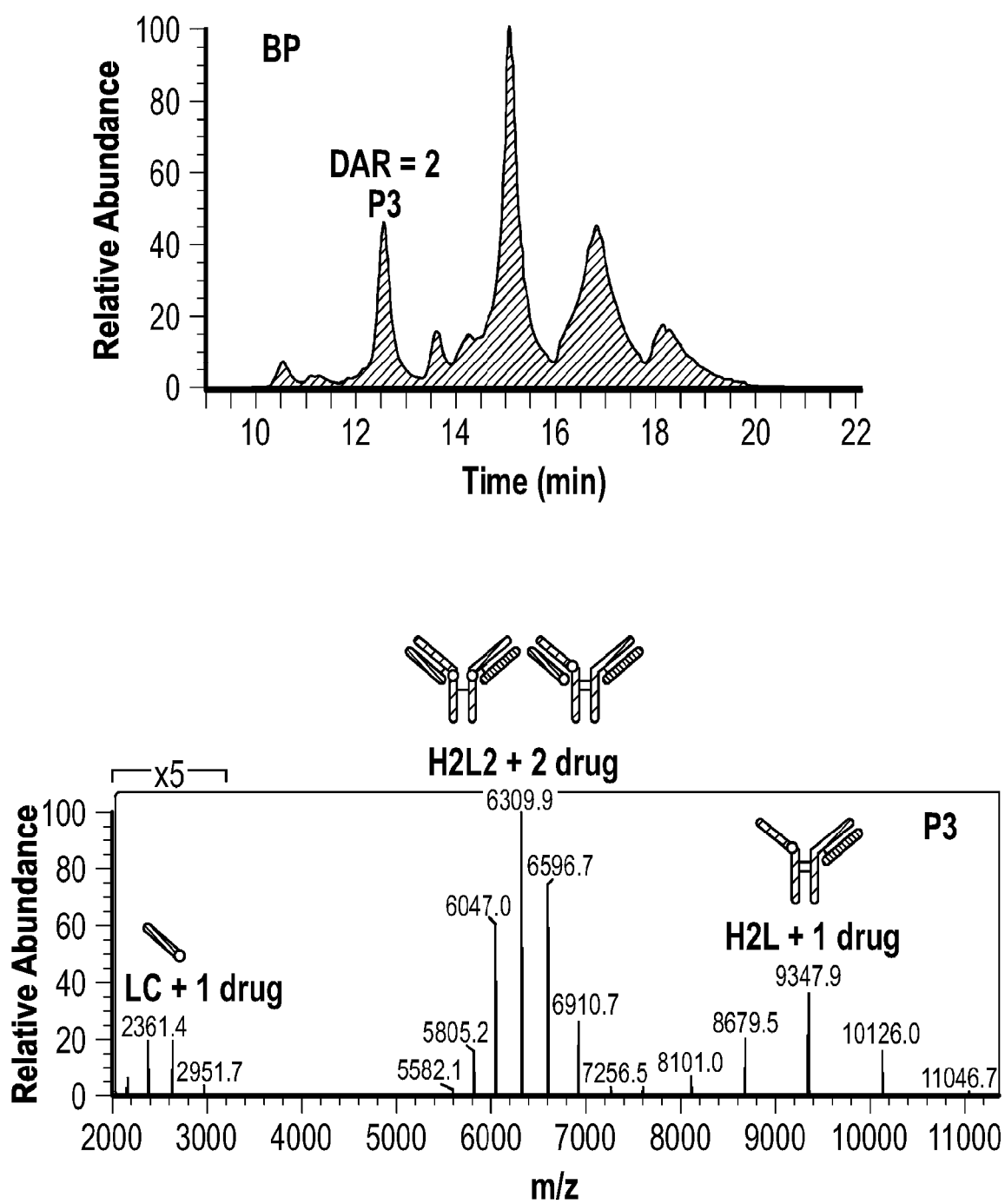


FIG. 16

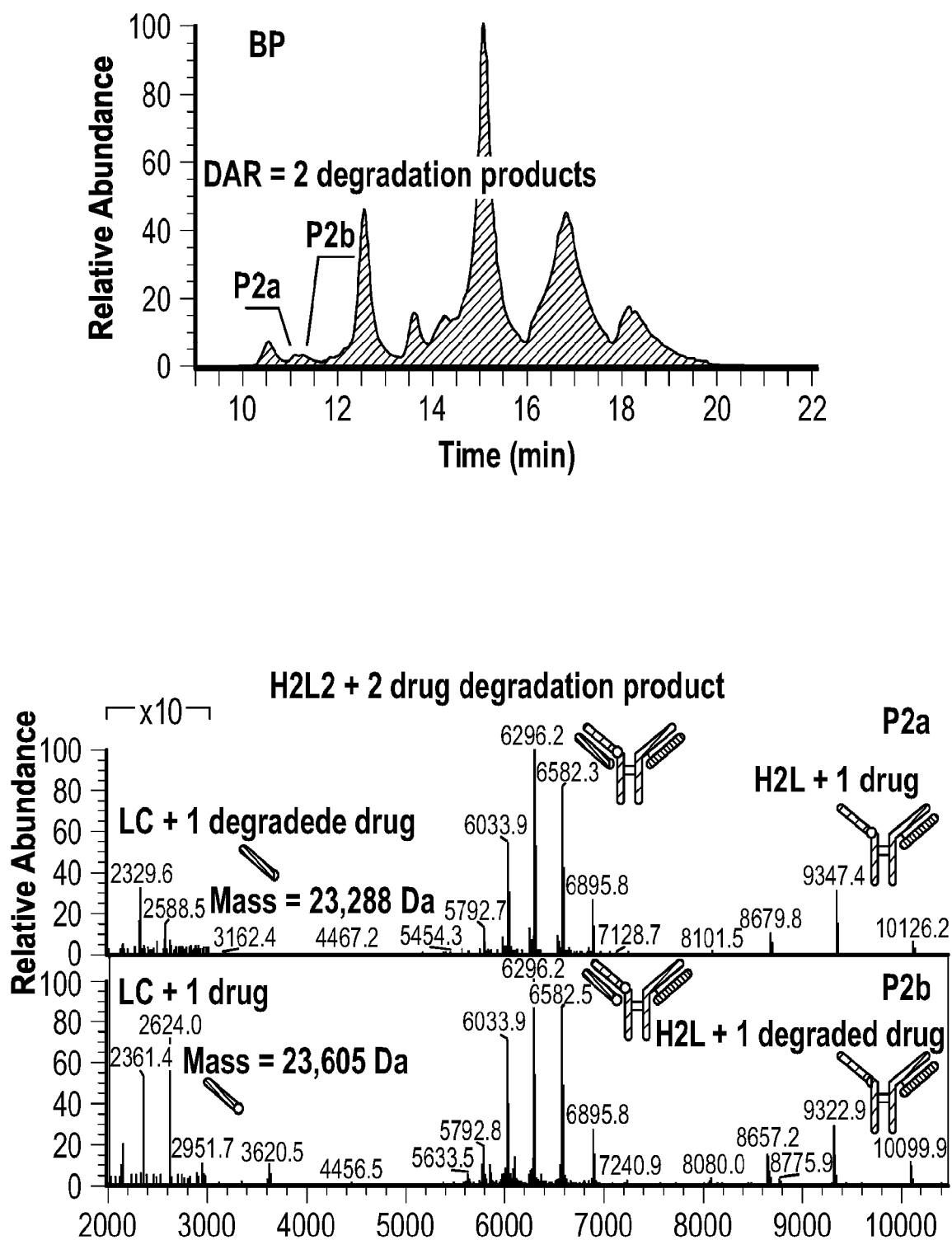


FIG. 17

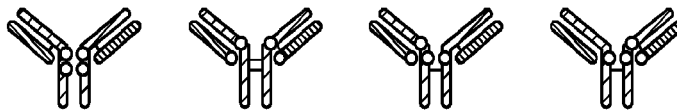
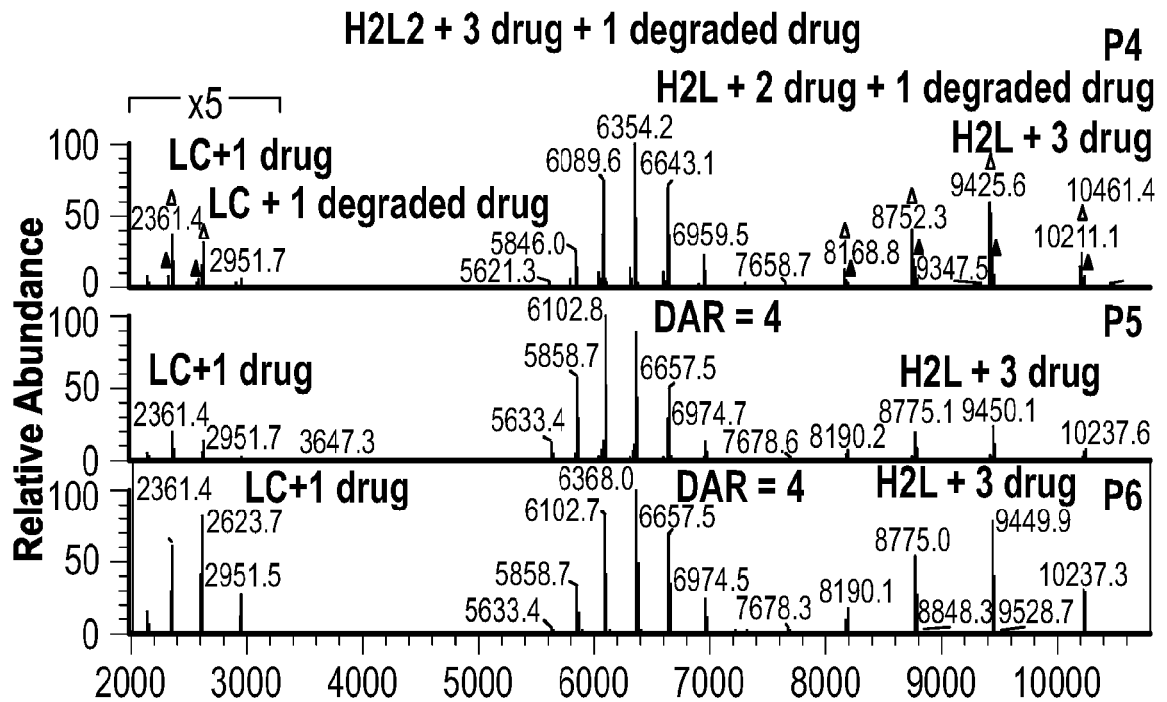
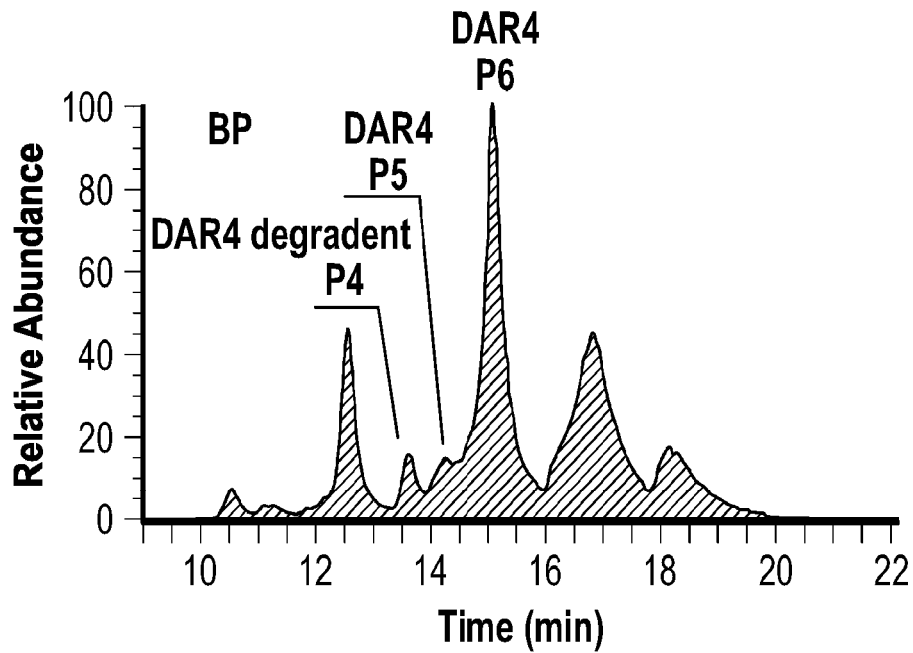


FIG. 18

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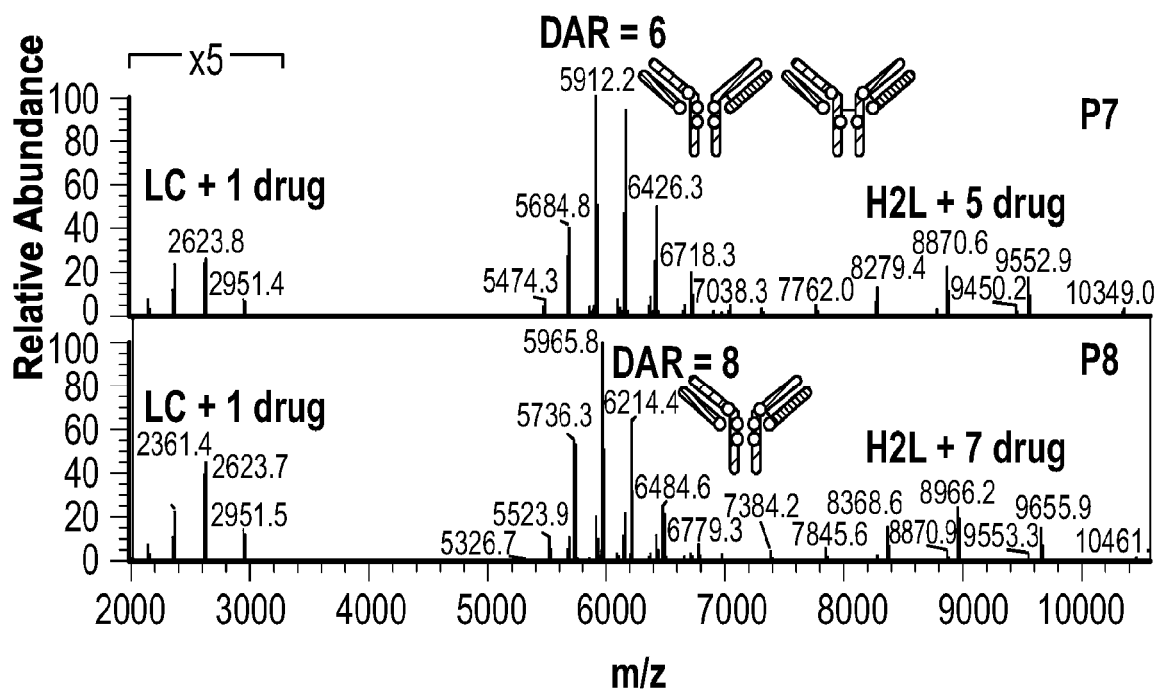
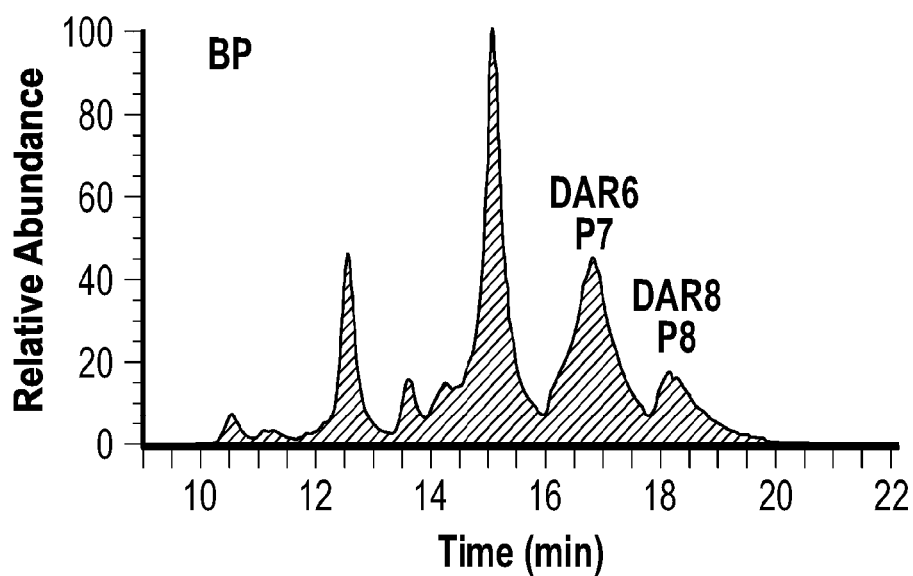


FIG. 19

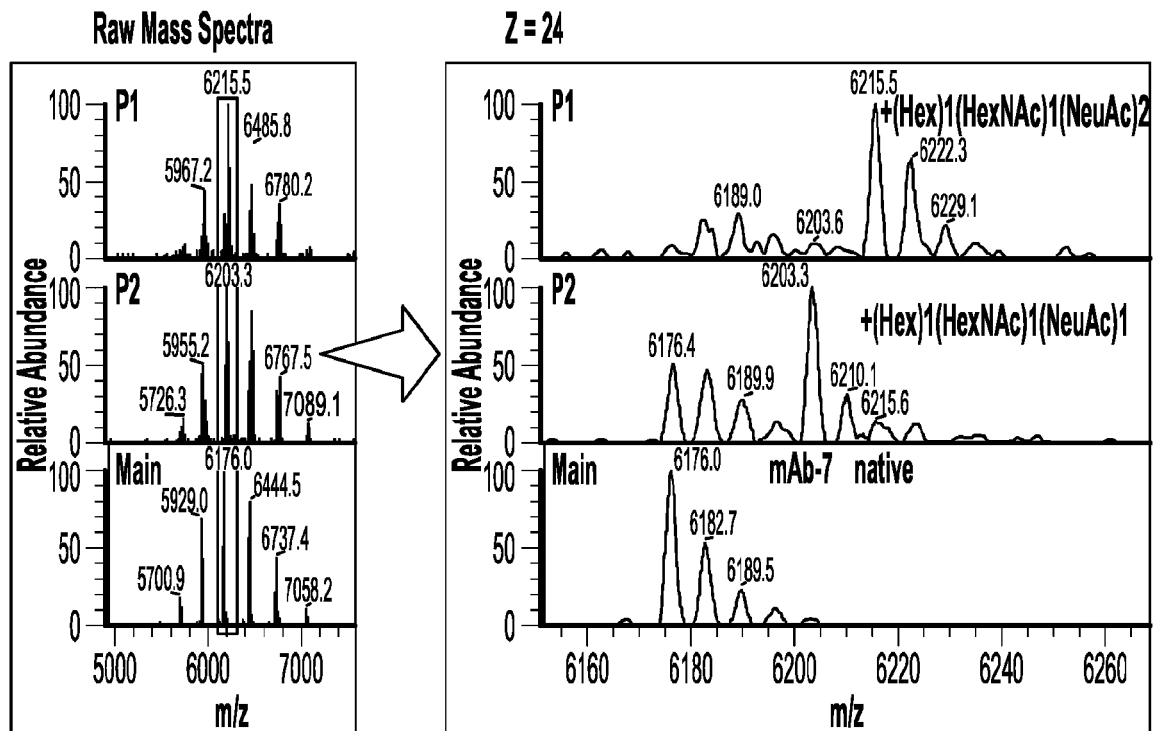
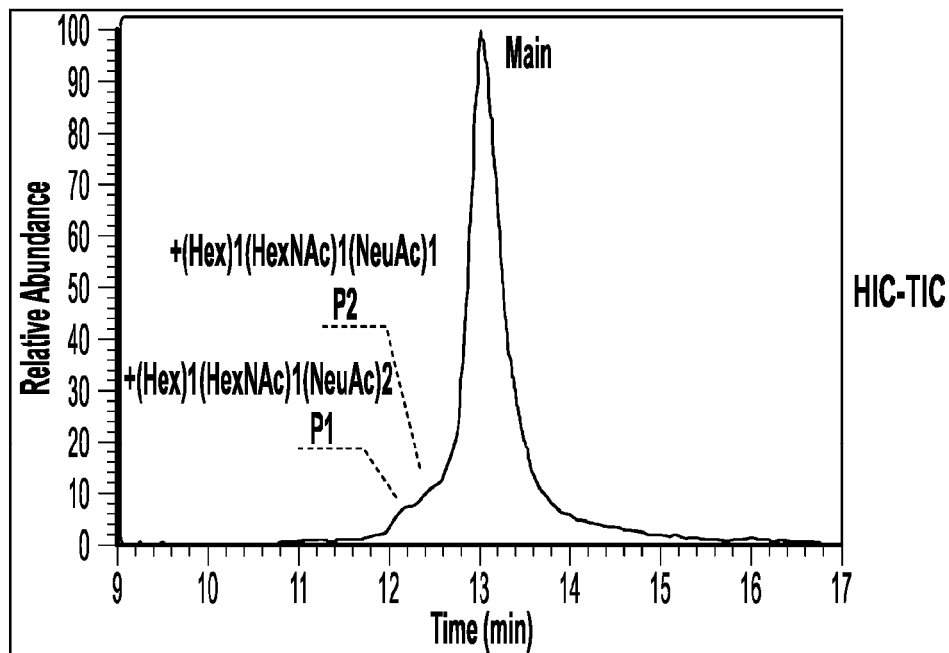


FIG. 20

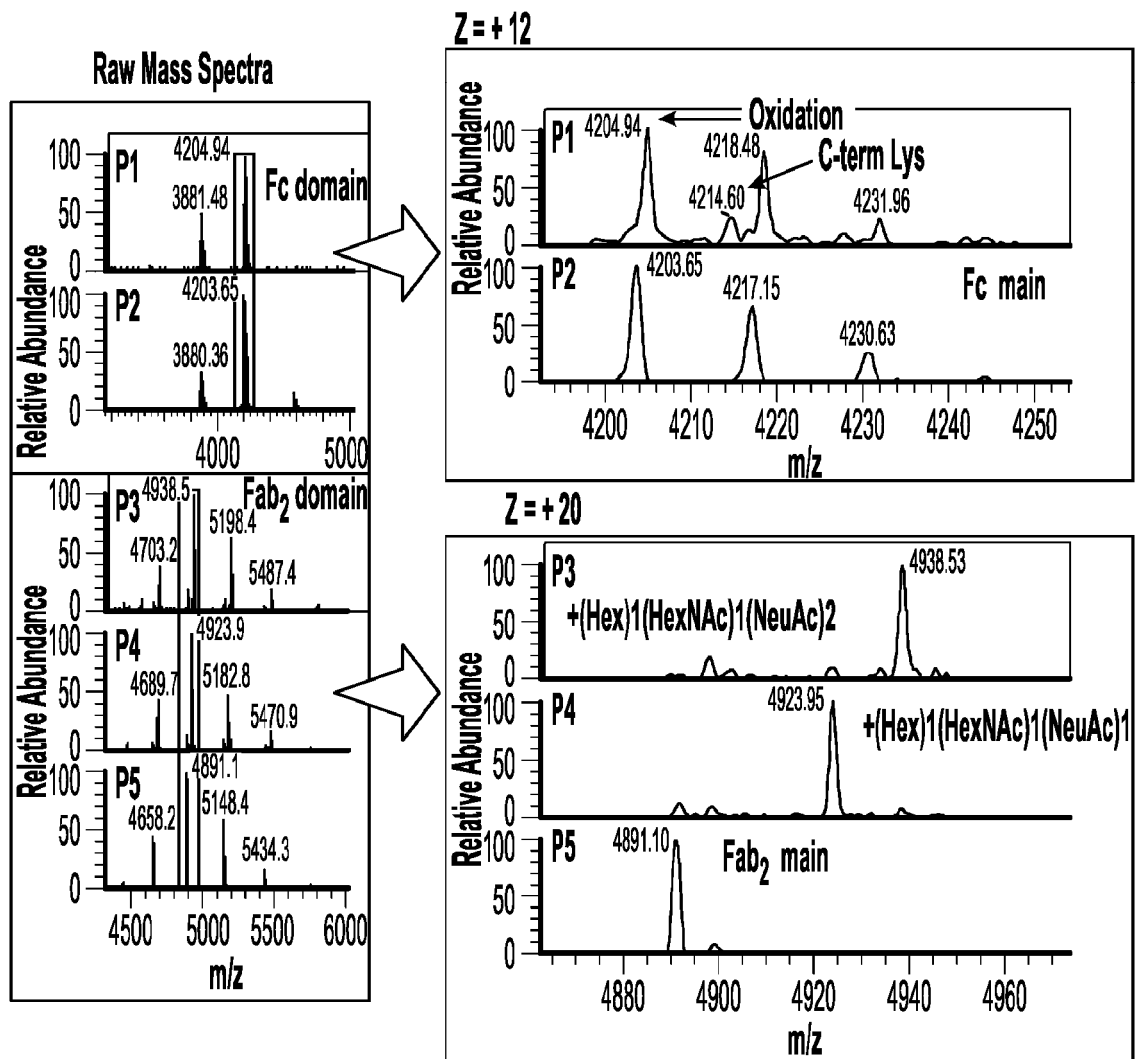
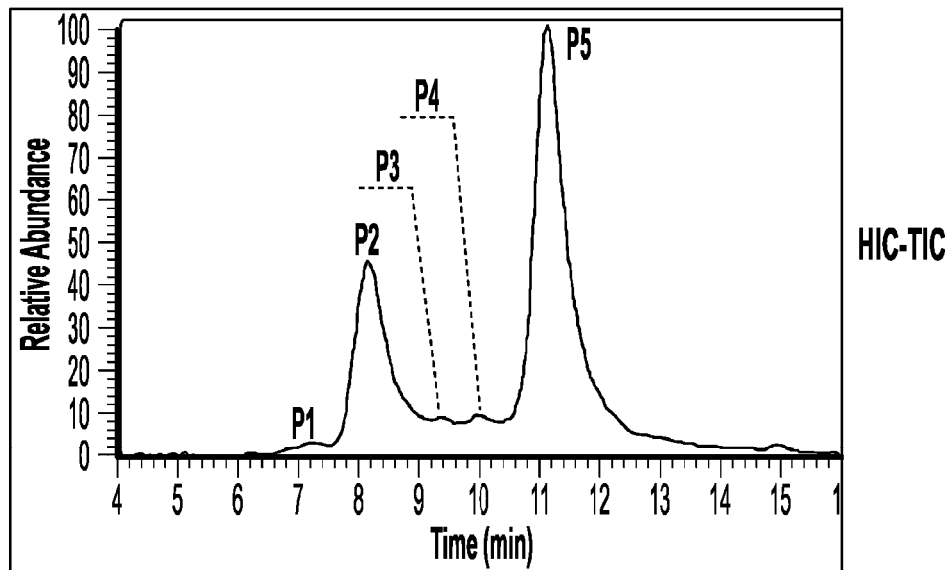


FIG. 21

Native SEC MS

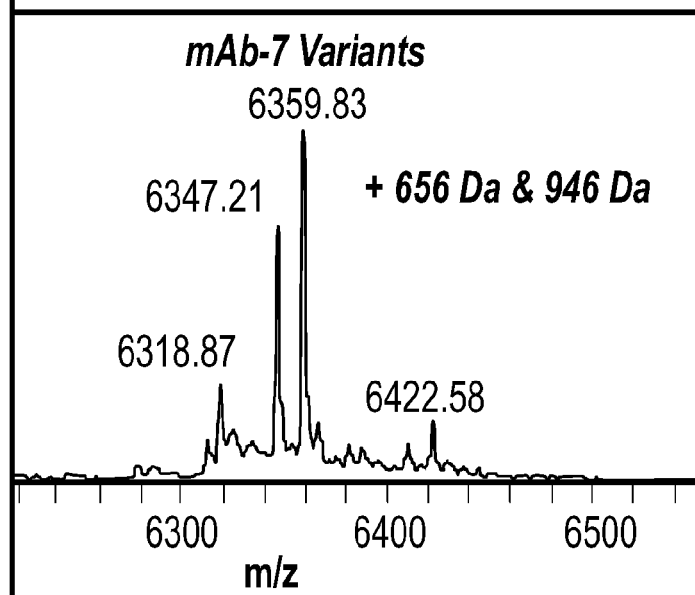
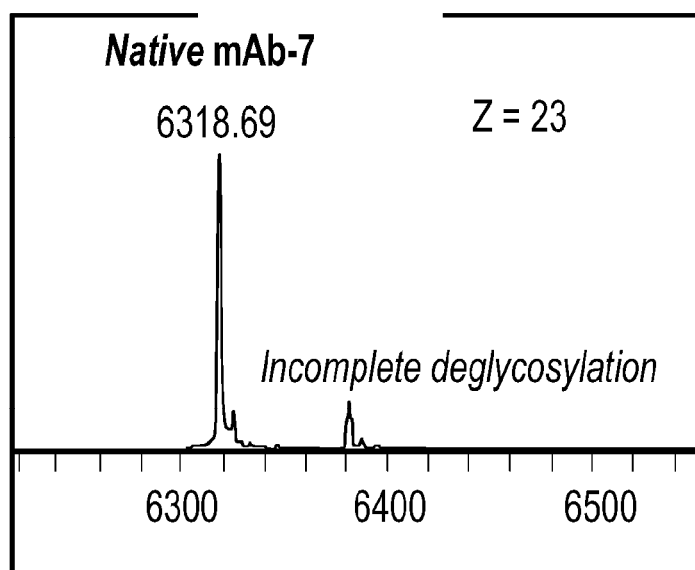
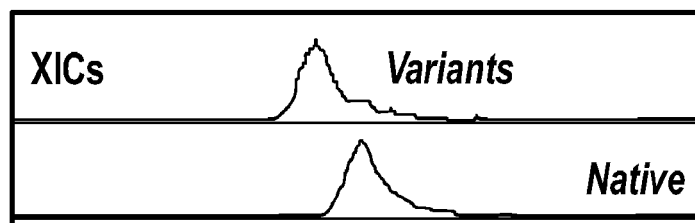


FIG. 22

mAb-7 Heavy Chain

QLOLOESGPG LVKPSETLSL TDTVSGGSIT SSSYYWGWIR OPPGKGLEWI GSIYYRGSTN⁶⁰
 YNPSLKSRVT ISVDSSKNQF YLKVSSVTAV DTAVYYCARQ NGAARPSWFD PWGQGTLLVTV¹²⁰
 SSASTKGPSV FPLAPCSRST SESTAALGQL VKDYFPEPVT VSWNSGALTS GVHTFPAVLO¹⁸⁰
 SSGLYSLSSV VTVPSSSLGT KTYTQNVDHK PSNTKVDKRV ESKYGPPQPP QPAPEFLGGP²⁴⁰
 SVFLFPPKPK DTFMISRTP VTDVV
 TYRVSVLTV LHQDWLNKE YKDKV
 TKNQVSLTQL VKGFYPSDIA VEWES
 EGNVFSQSVI HEALHNHYTO KSLSLSLGK⁴⁴⁵

mAb-7 Heavy Chain

EIVLTQSPDT ISLSPGERAT LSQ¹⁶⁰RASQ¹⁶⁰SIS SIYLAWYQOK PGOAPRLLIY GASSRVTGIP¹⁶⁰
DRFSVSGSGT DFTLTISRLE PEDFAVYYQ¹⁶⁰ HYGISPFTFG PGTKVDIRRT VAAPSVFIFP¹²⁰
PSDEQLKSGT ASVVDLLNMF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYLSSTL¹⁸⁰
TLSKADYEKH KVYAD²¹⁵EVTHO GLSSPVTKSF NRGE²¹⁵

Reduced Peptide Mapping

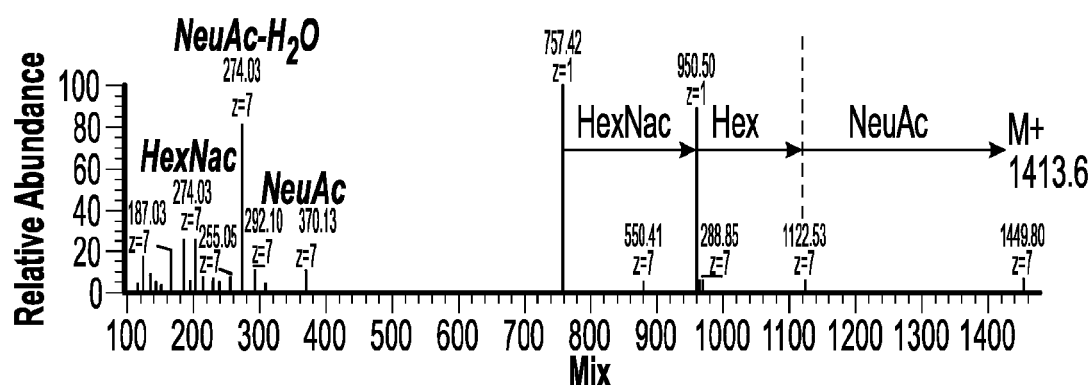
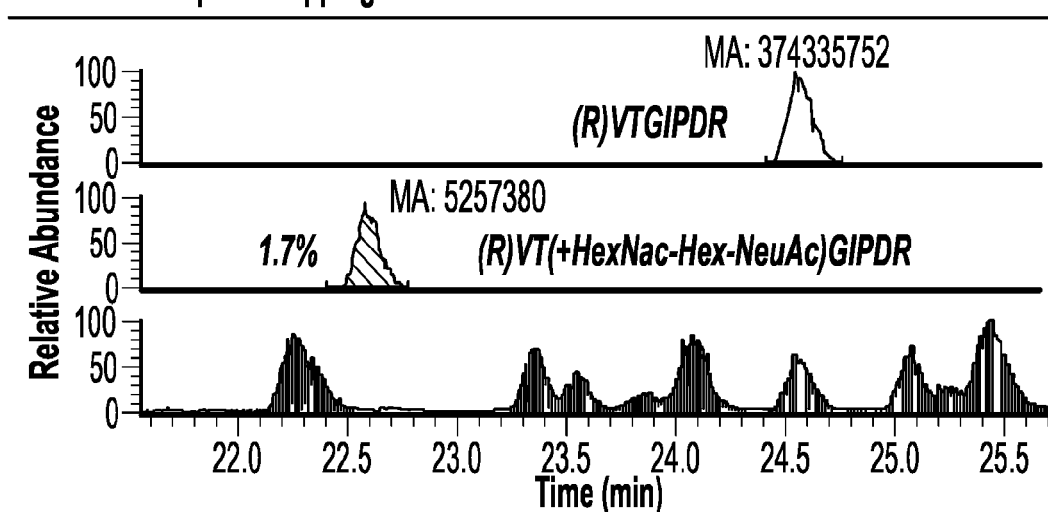
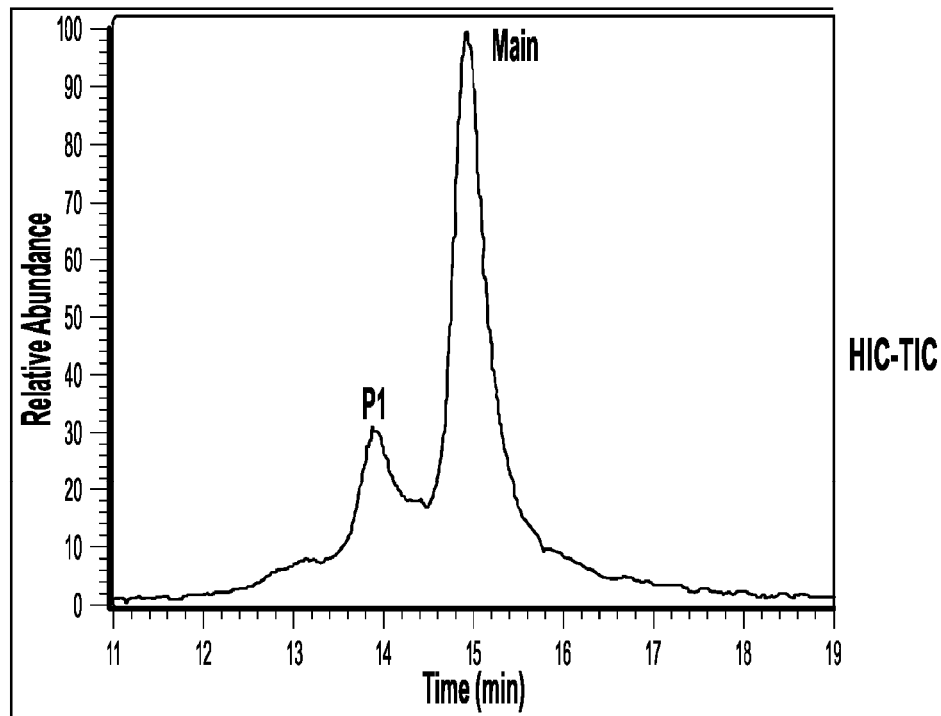


FIG. 23

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Raw Mass Spectra

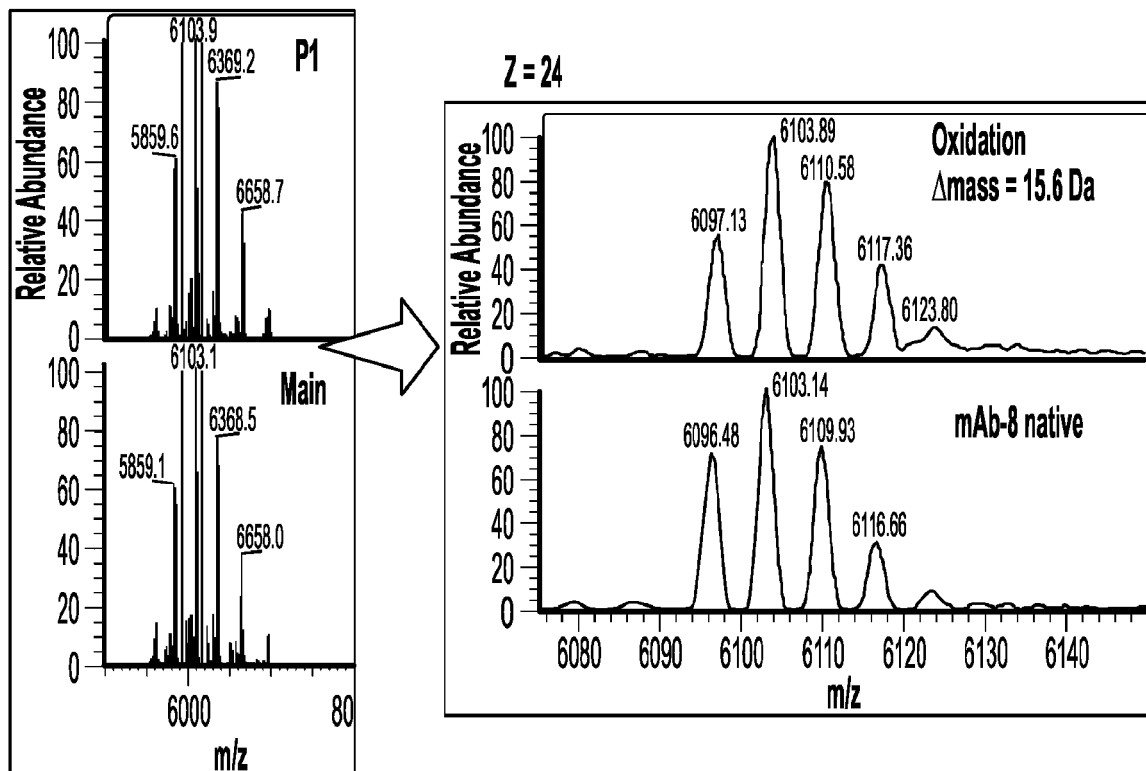


FIG. 24

mAb-8 Light Chain

DIQMTQSPSS LSASVGDRVT ITCRAS**Q**SIS **S**FLNWFQQKP GKAPKLLIYA **A**SSLSQSGVPS⁶⁰
 RFSGSGSGTD FTLTISSLQP EDFATYYC**Q****Q** **S**YSTLT**F**GQG TRLEIKRTVA APSVFIFPPS¹²⁰
 DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLT¹⁸⁰
 SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC²¹³

mAb-8 Heavy Chain

EVQLVESGGG LVQPGGSLRL SCAAS**G**FTSS **S**YAMNWRQA PGKGLEWVST **I**SGMGSTYY⁶⁰
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYC**A**KRG **Y**PHSFDIWGQ GTMVTVSSAS¹²⁰
 TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTWSN SGALTSGVHT FPAVLQSSGL¹⁸⁰
 YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS²⁴⁰
 VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST³⁰⁰
 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRDEL³⁶⁰
 KNQVSLTCLV KGFYPSTIAV EWESNGQPEN NYKTTTPVLD SDGSFFLYSK LTVDKSRWQQ⁴²⁰
 GNVFSCSVMH EALHNHYTQK SLSLSPGK⁴⁴⁸

**Reference Standard Characterization PTM table**

PTMs with Site Location	Lot A	Lot B
HC C-Terminal Peptide with Lys ⁴⁴⁸	1.4	1.5
Non-Glycosylation at HC Asn ²⁹⁸	10.0	12.8
Deamidation at HC Asn ³¹⁶	<1.0	<1.0
Deamidation at HC Asn ³⁸⁵	1.2	1.0
Oxidation at HC Met⁵⁴	13.6	10.5
Oxidation at HC Met ¹¹³	2.2	1.7
Oxidation at HC Met ²⁵³	4.3	3.1
N-terminal pyroglutamate formation at HC Glu ¹	2.1	1.8
Isomerization at HC Asp ²⁸¹	2.2	2.2
Isomerization at HC Asp ⁴⁰²	2.1	2.1

FIG. 25

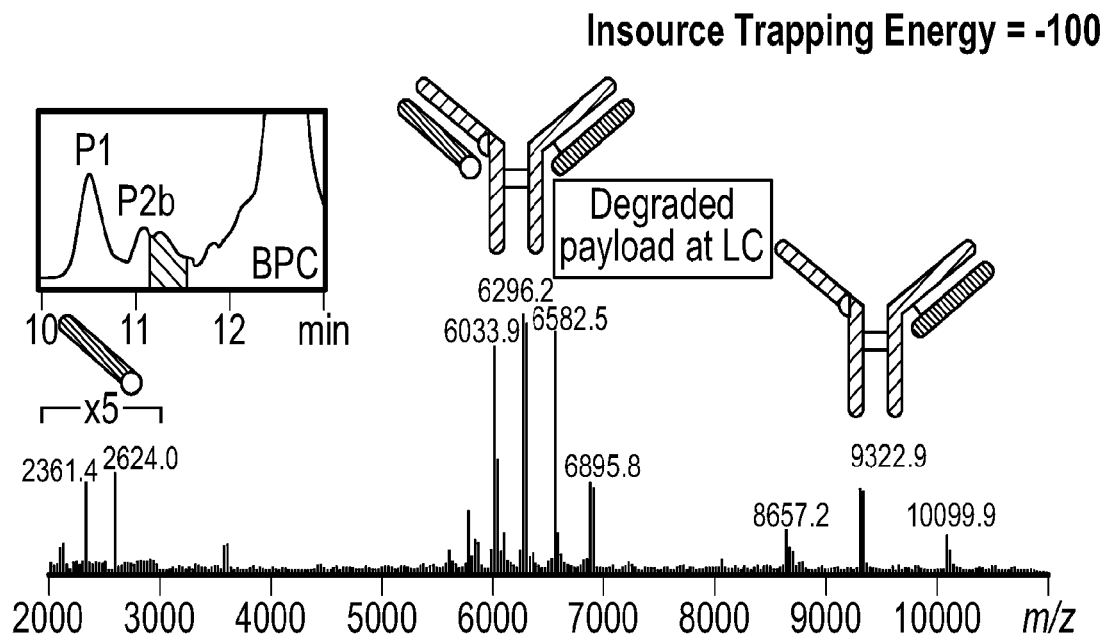
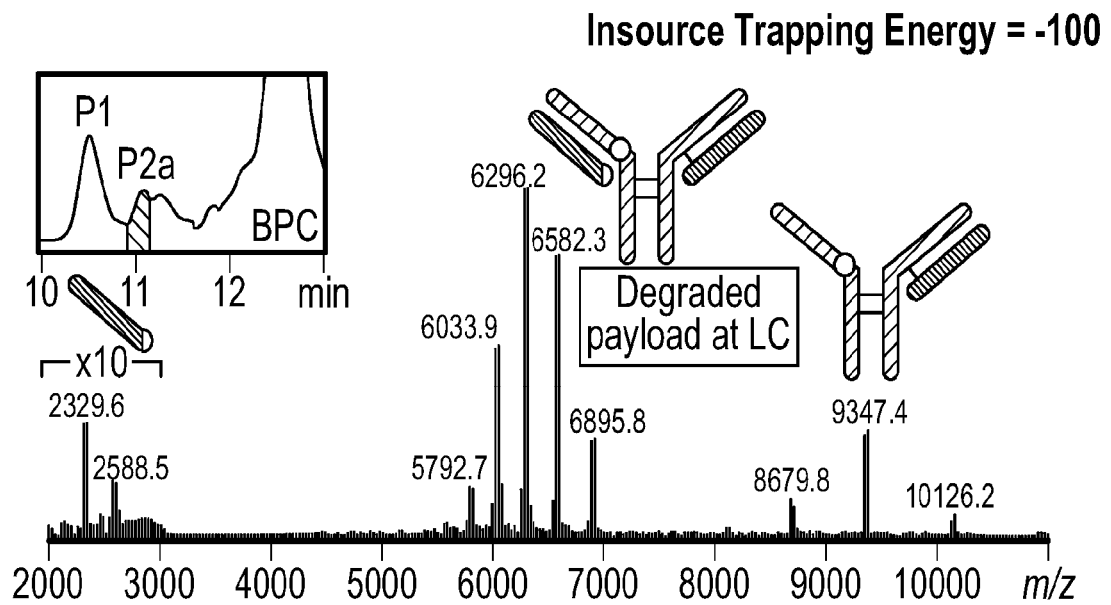


FIG. 26

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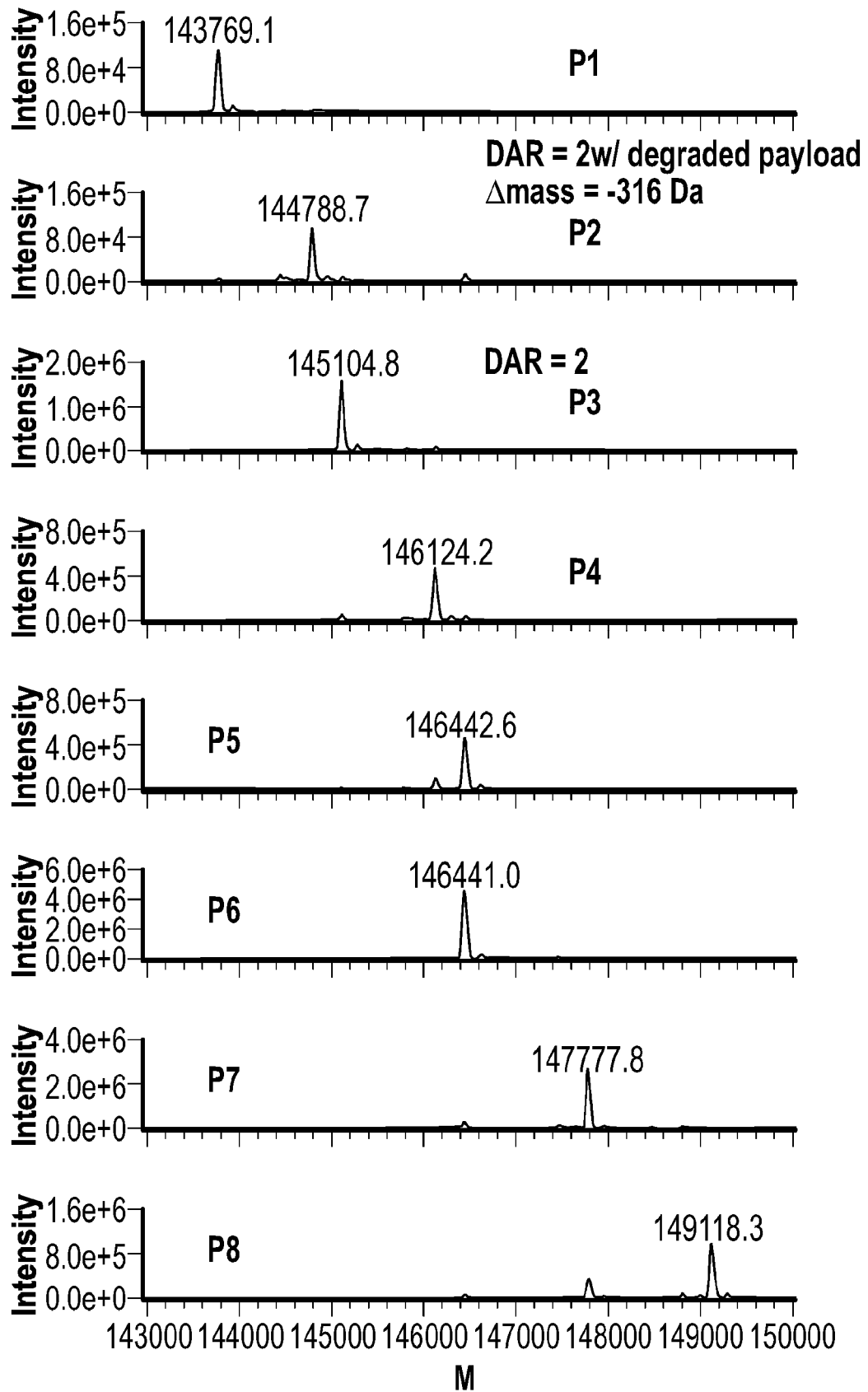


FIG. 27

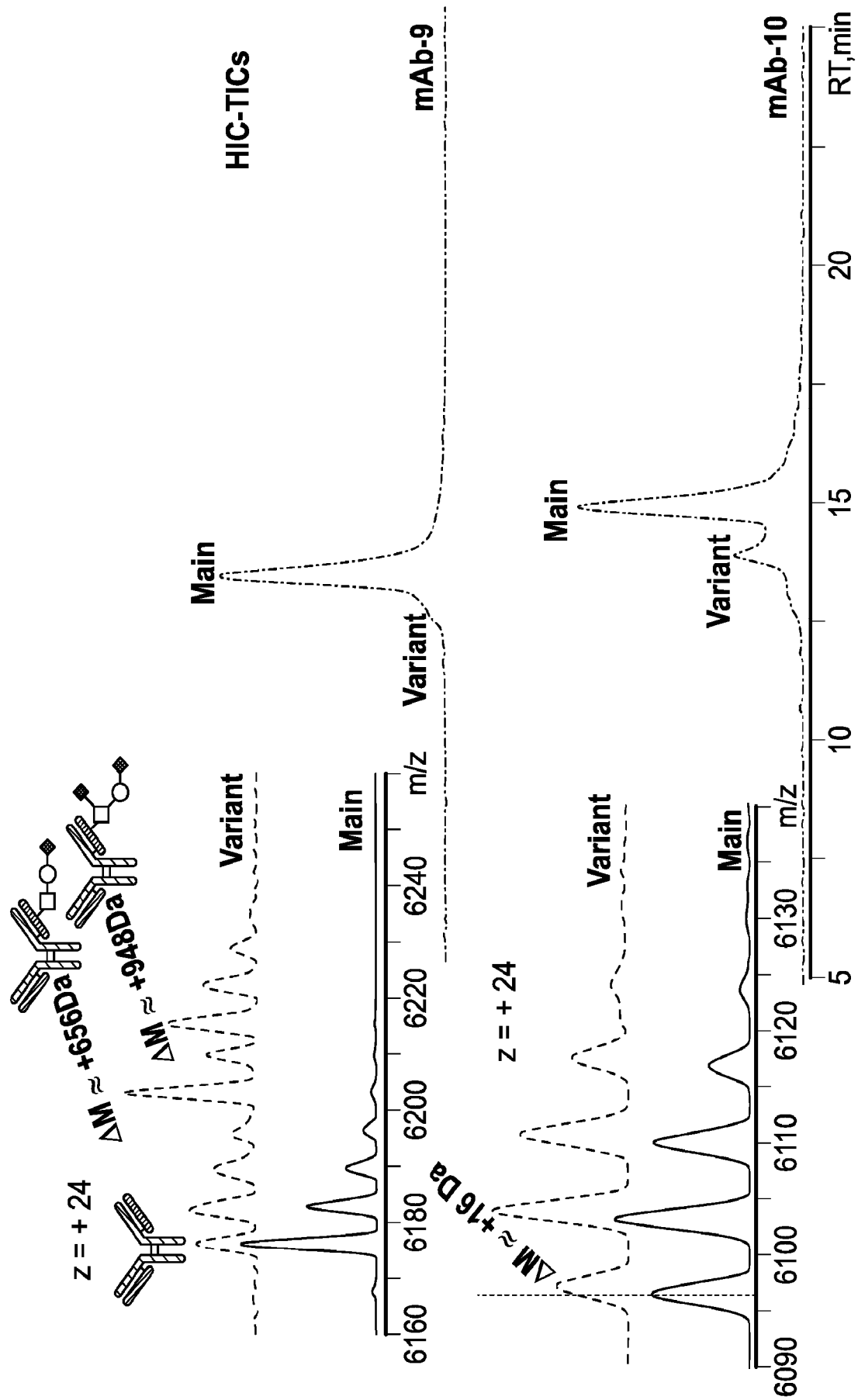


FIG. 28