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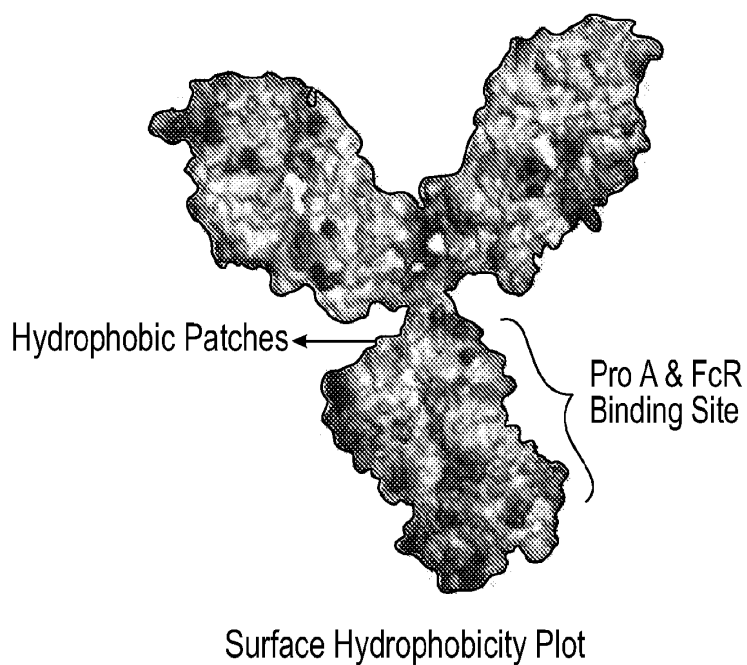
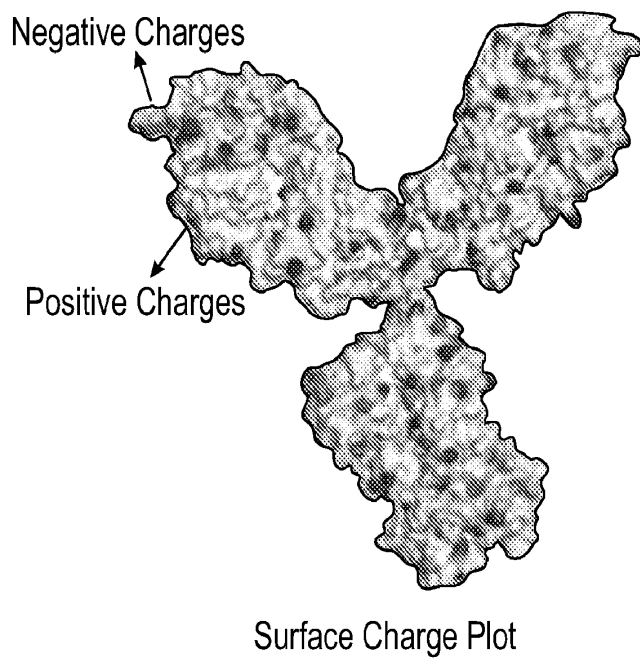


FIG. 1

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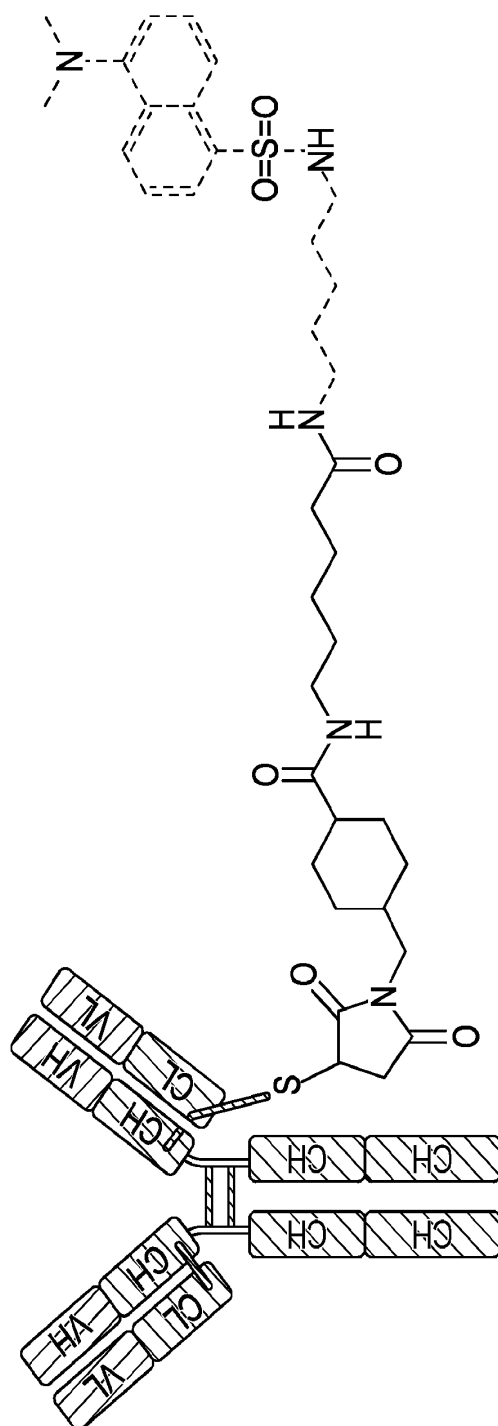
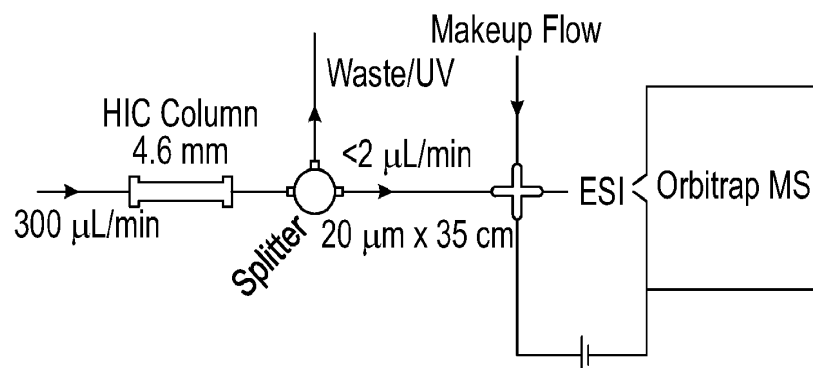


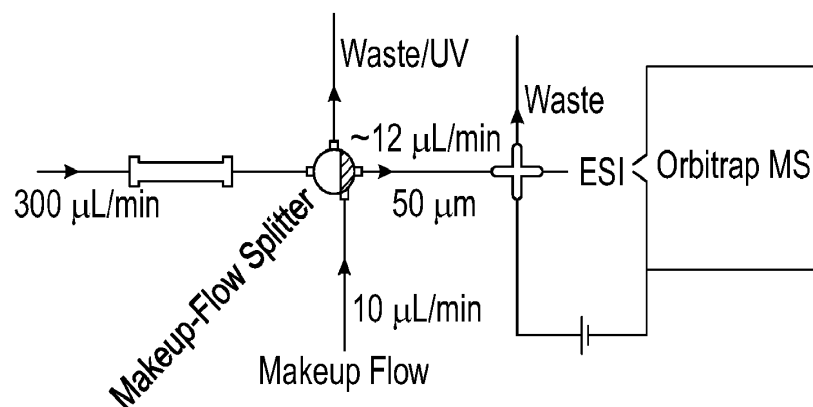
FIG. 2

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Flow Path Design A:



Flow Path Design B:



Flow Path Design C:

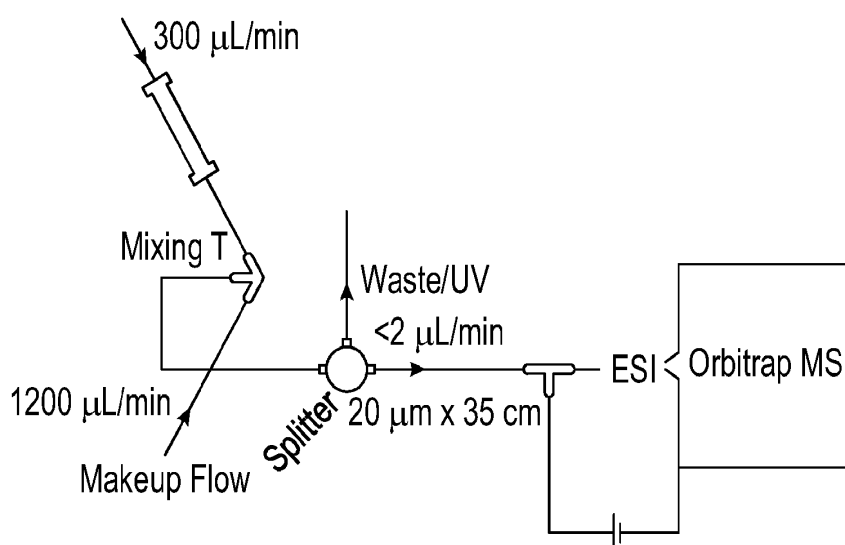
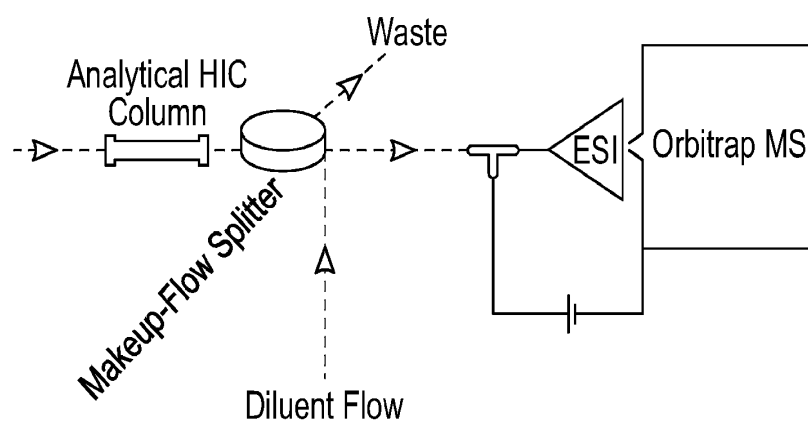
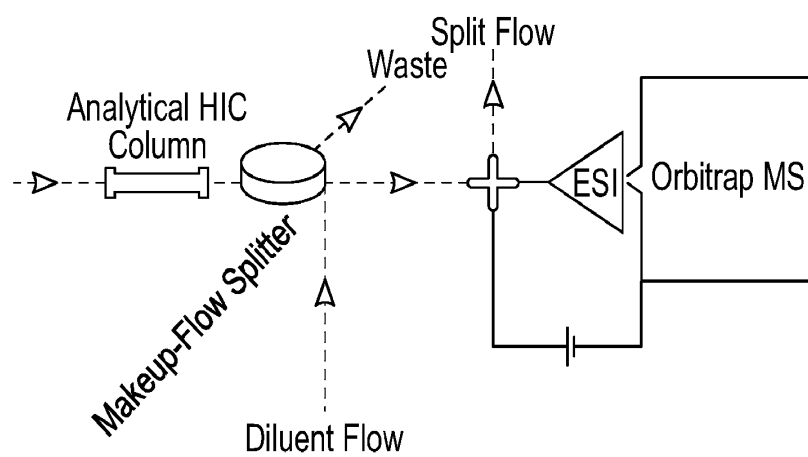


FIG. 3

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

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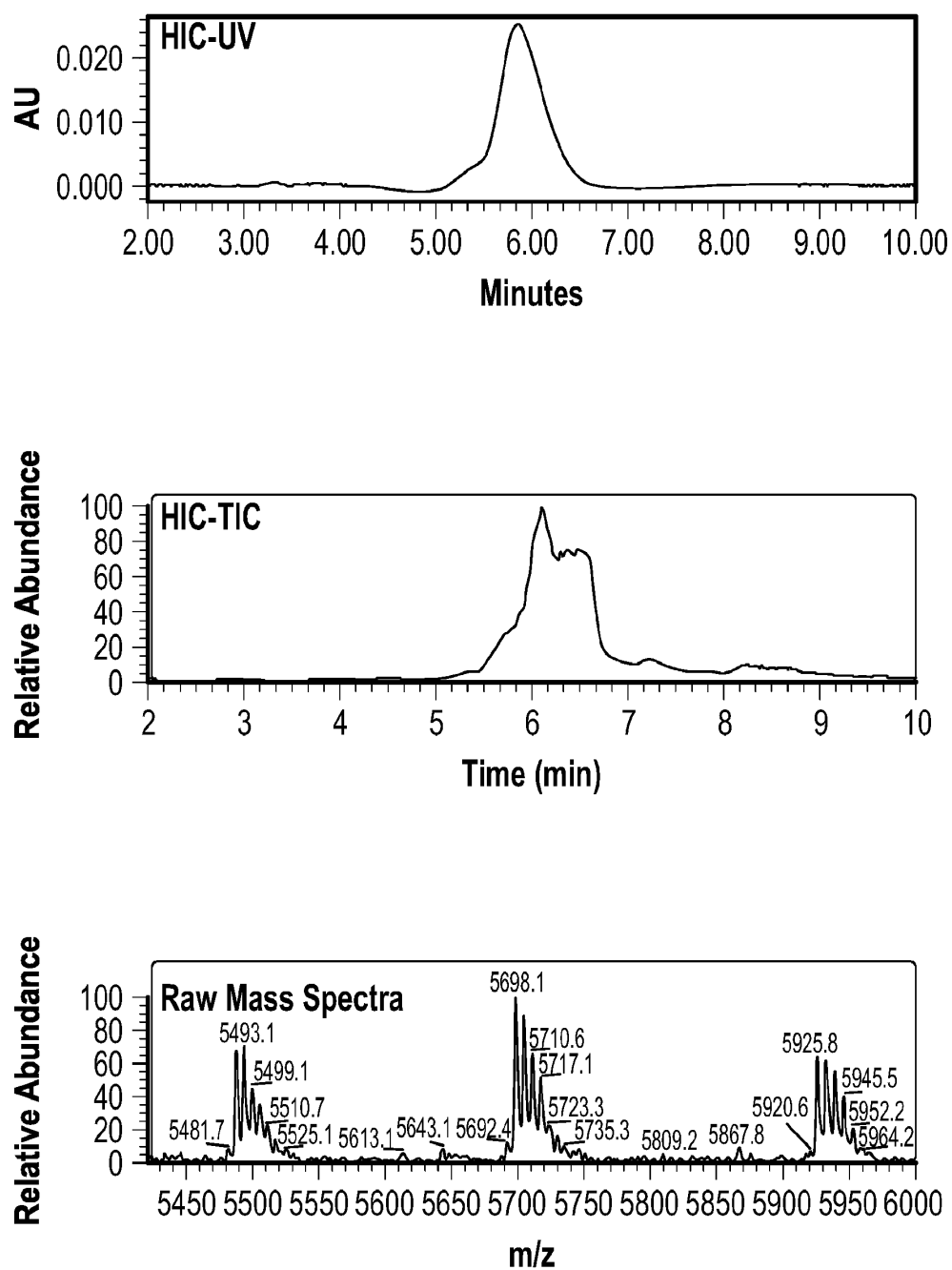


FIG. 5

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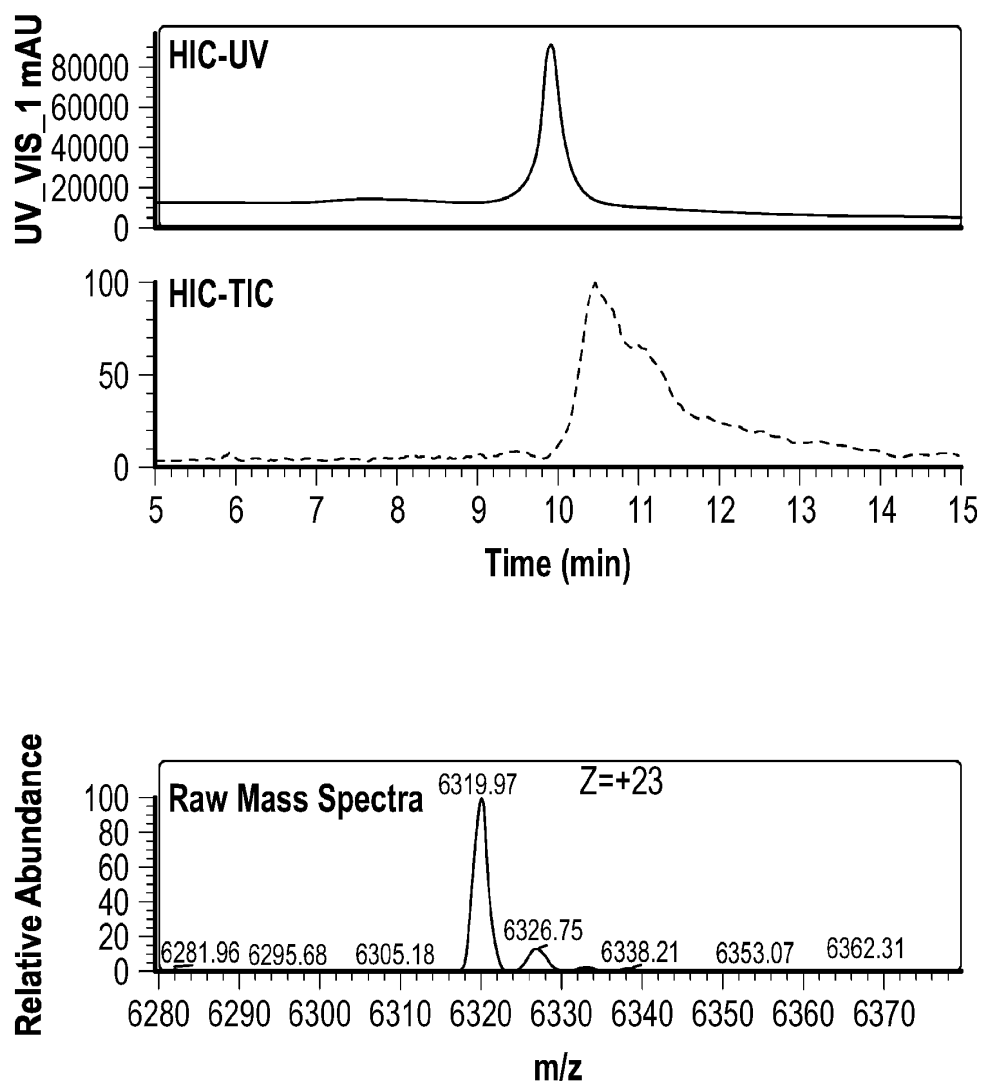


FIG. 6

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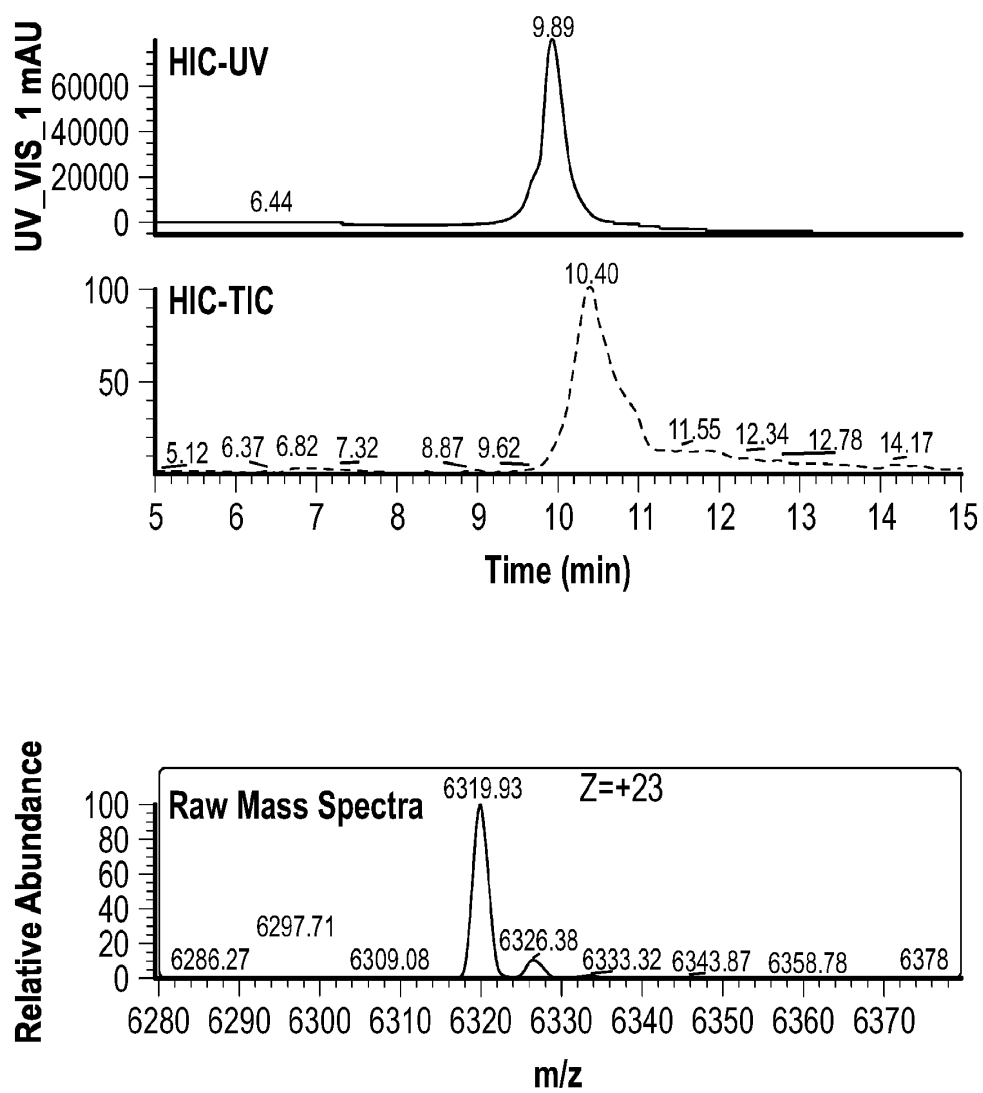


FIG. 7

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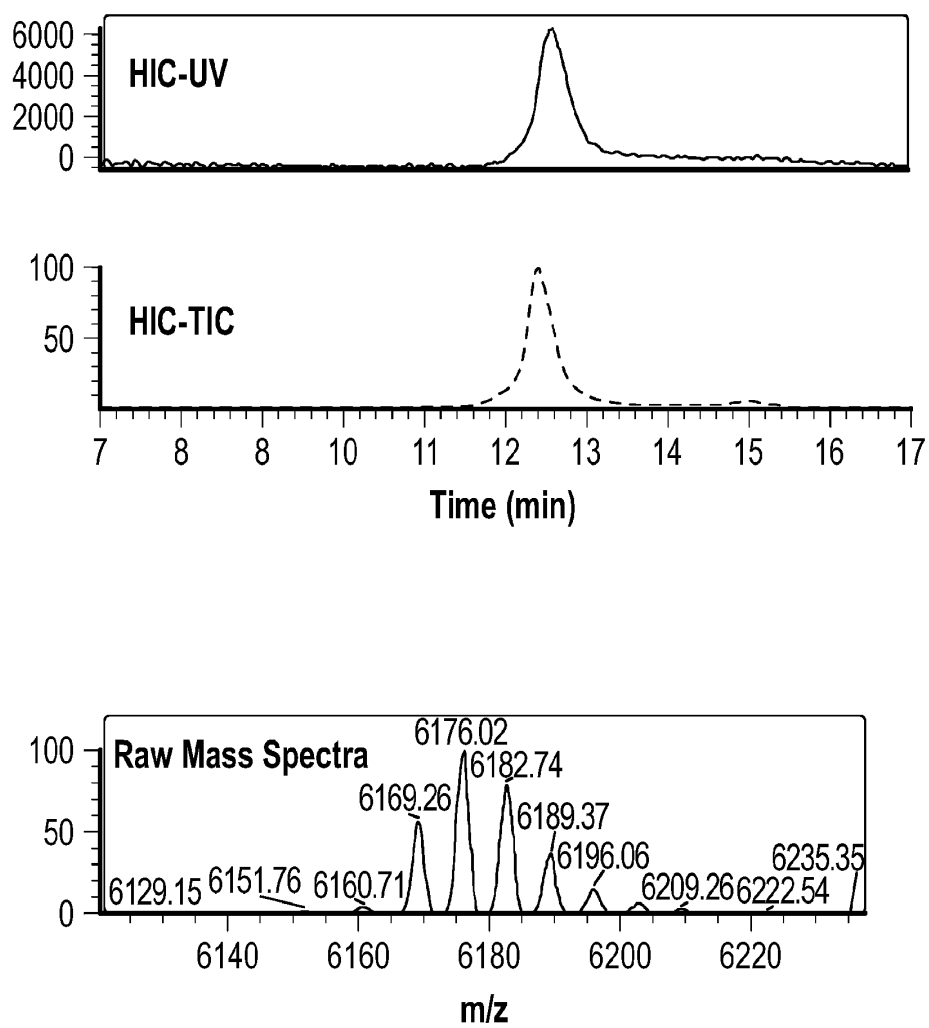
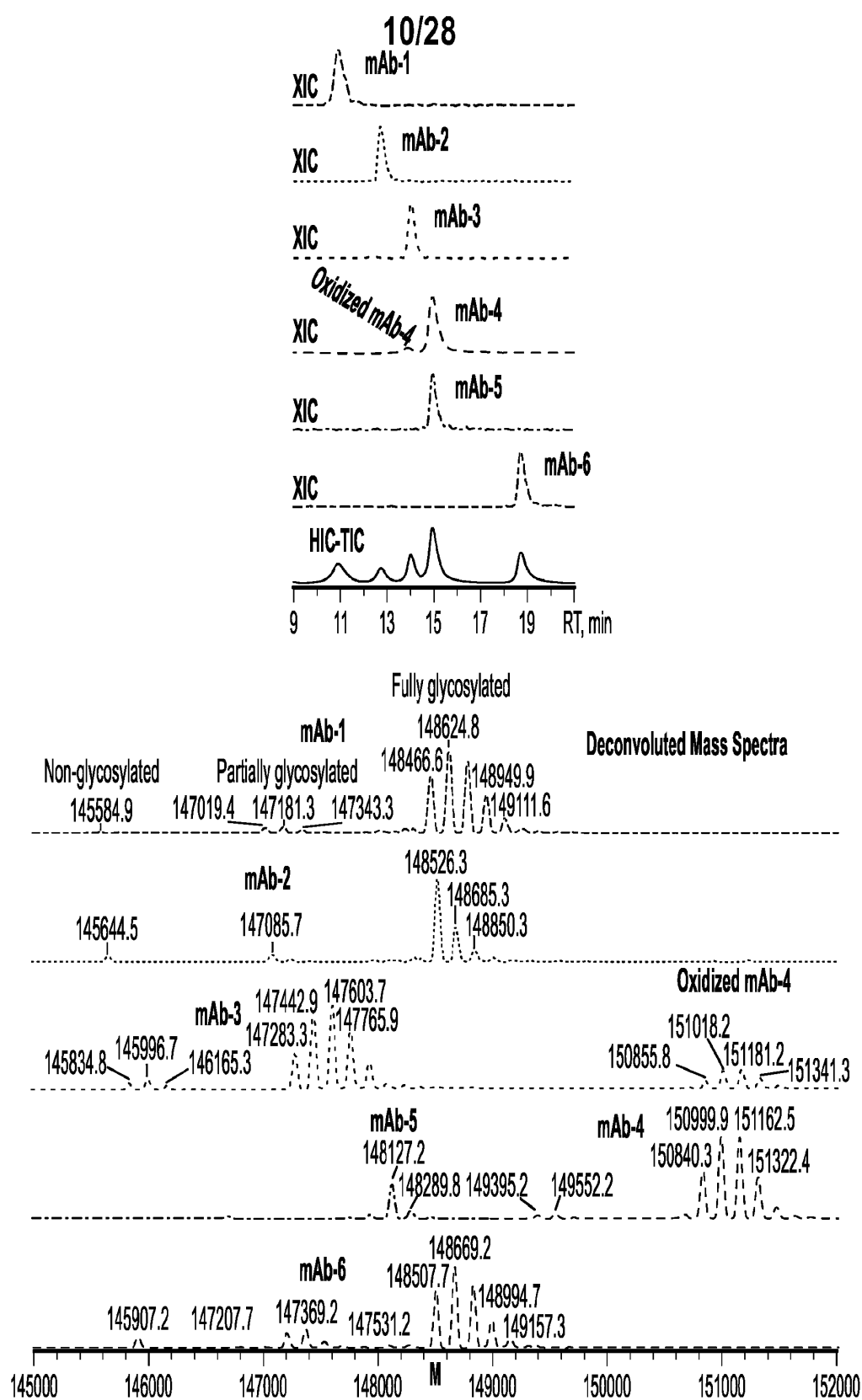
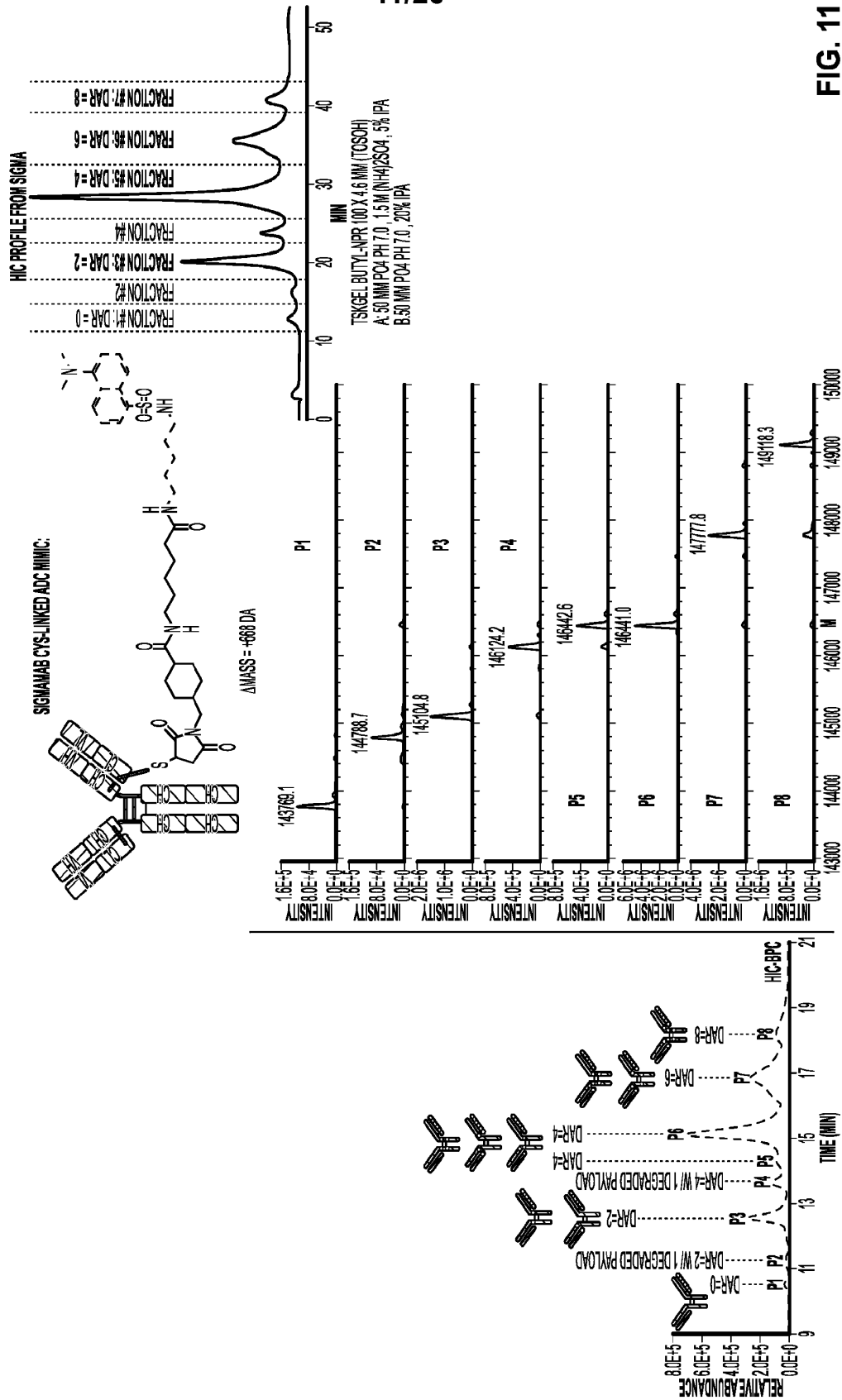


FIG. 8

**FIG. 10**

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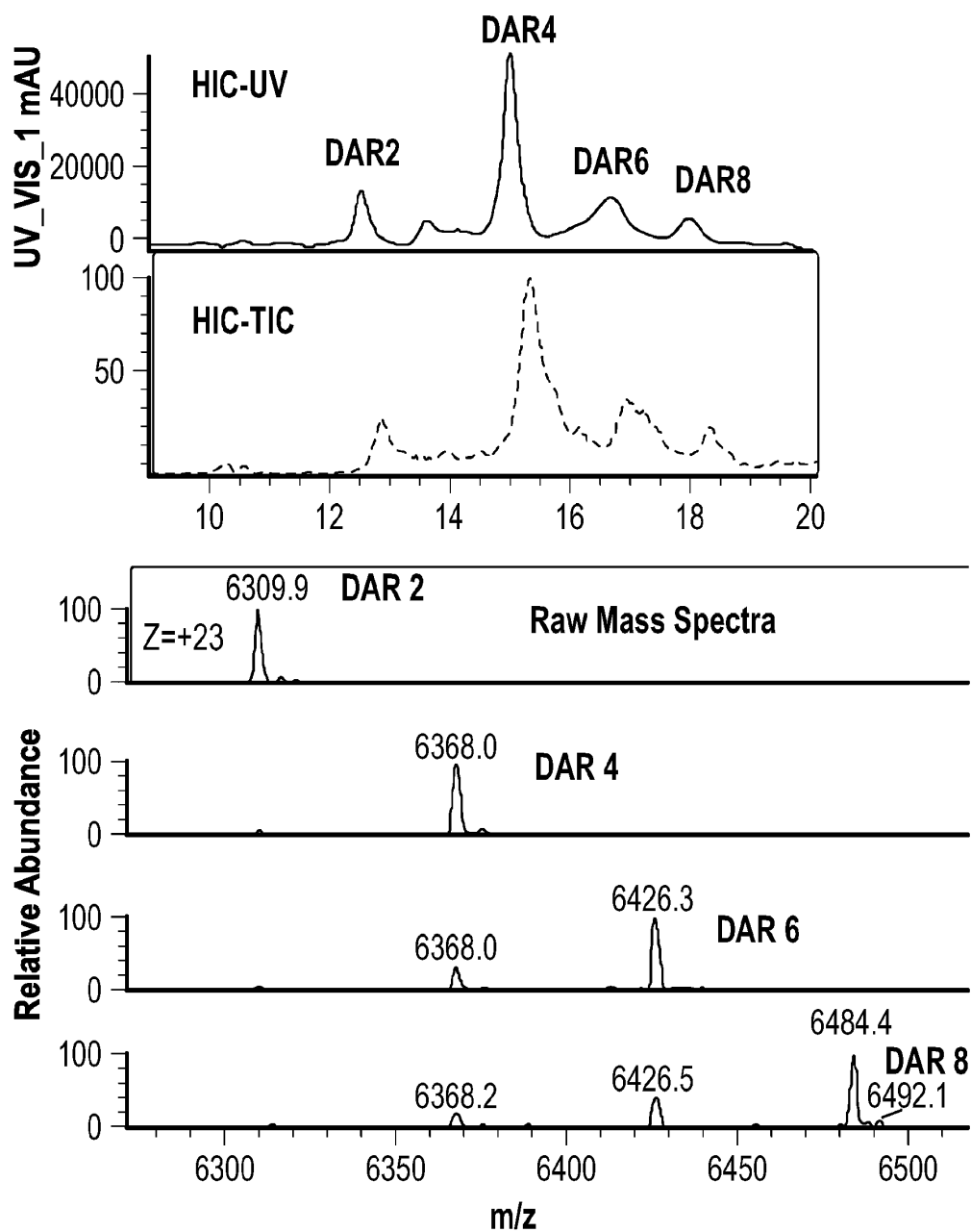
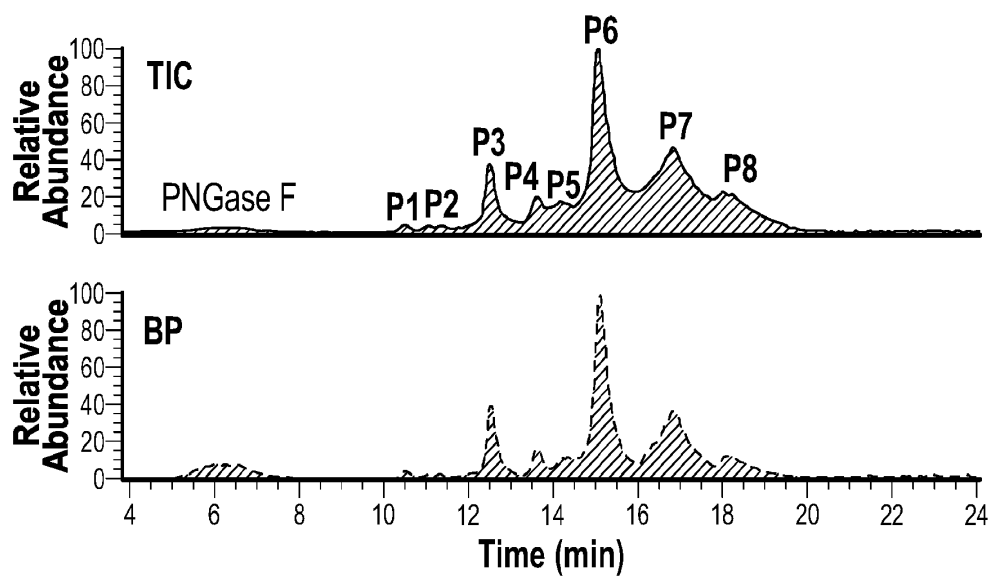


FIG. 12

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HIC profile from Sigma

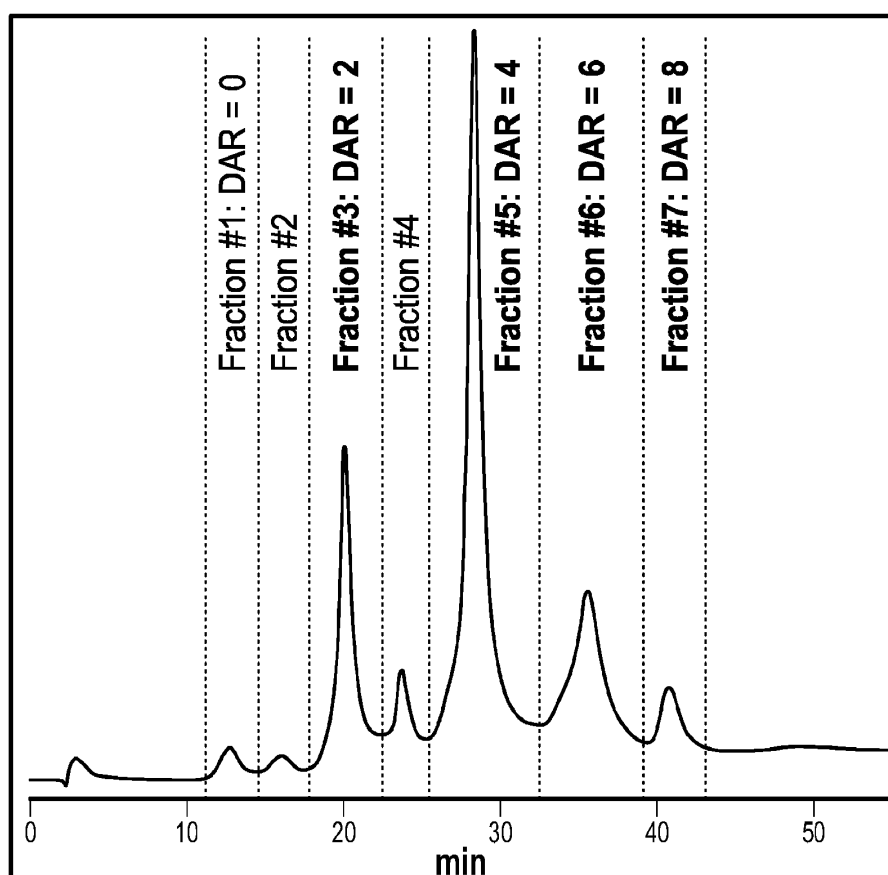


FIG. 13

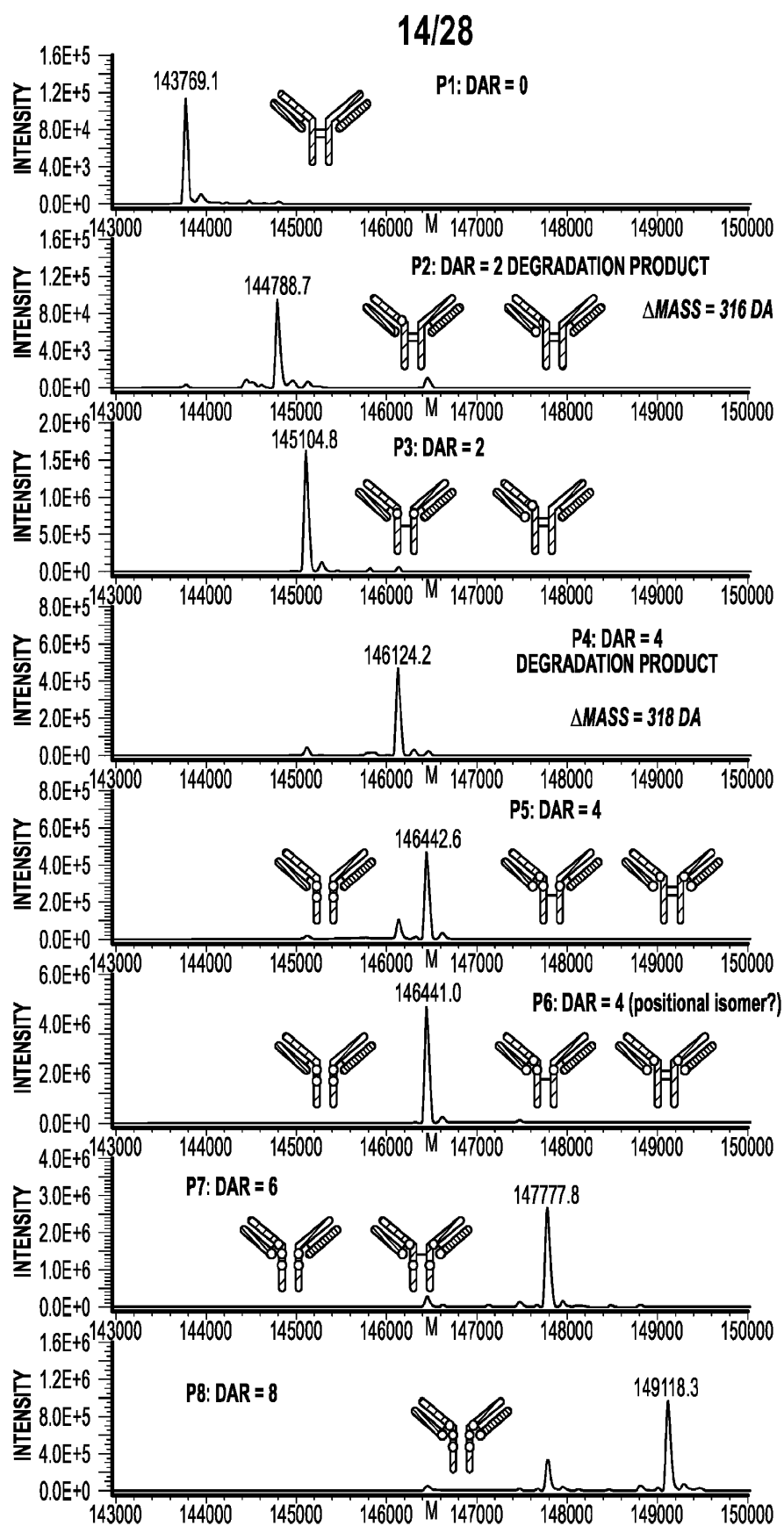


FIG. 14

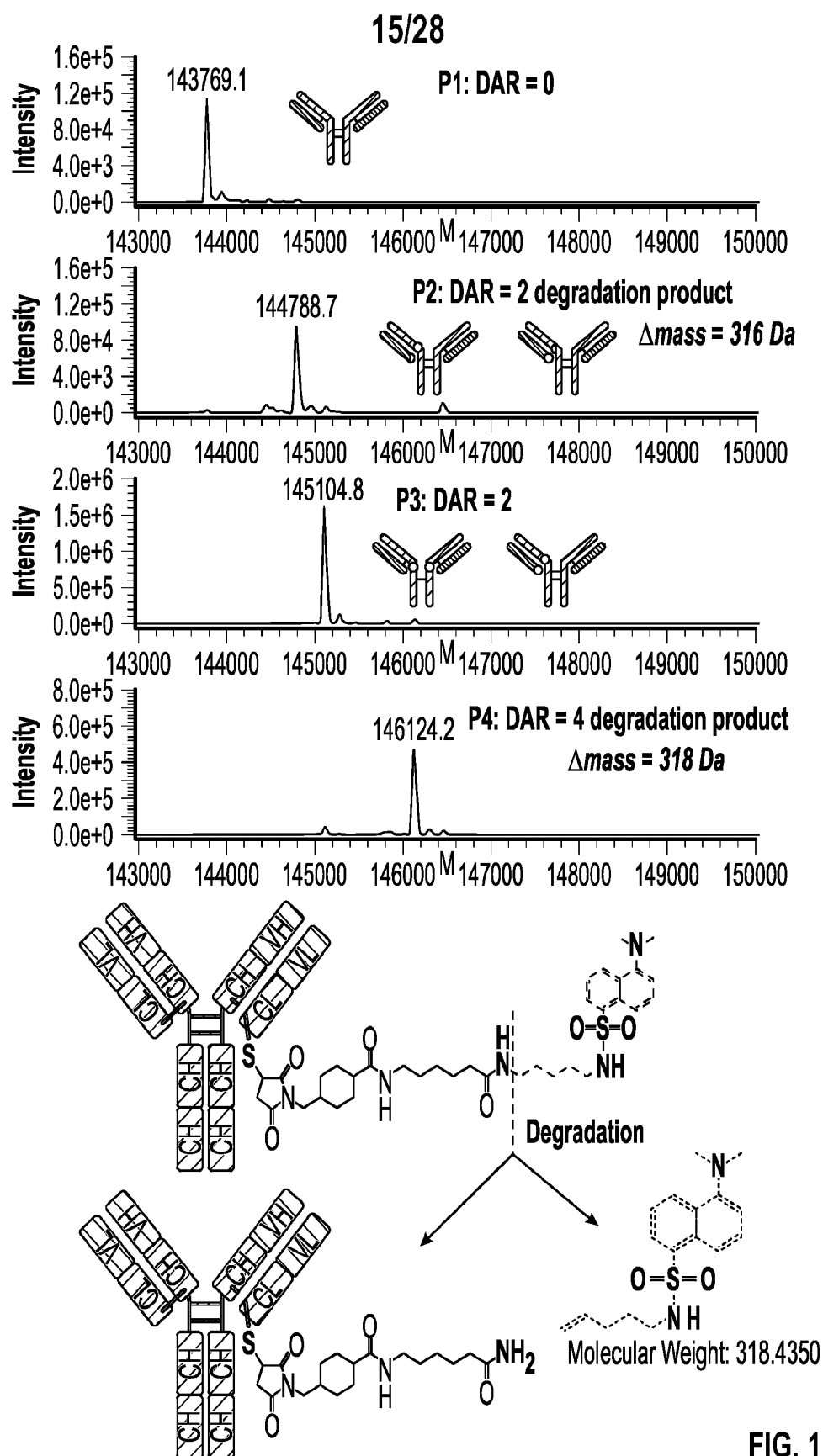


FIG. 15

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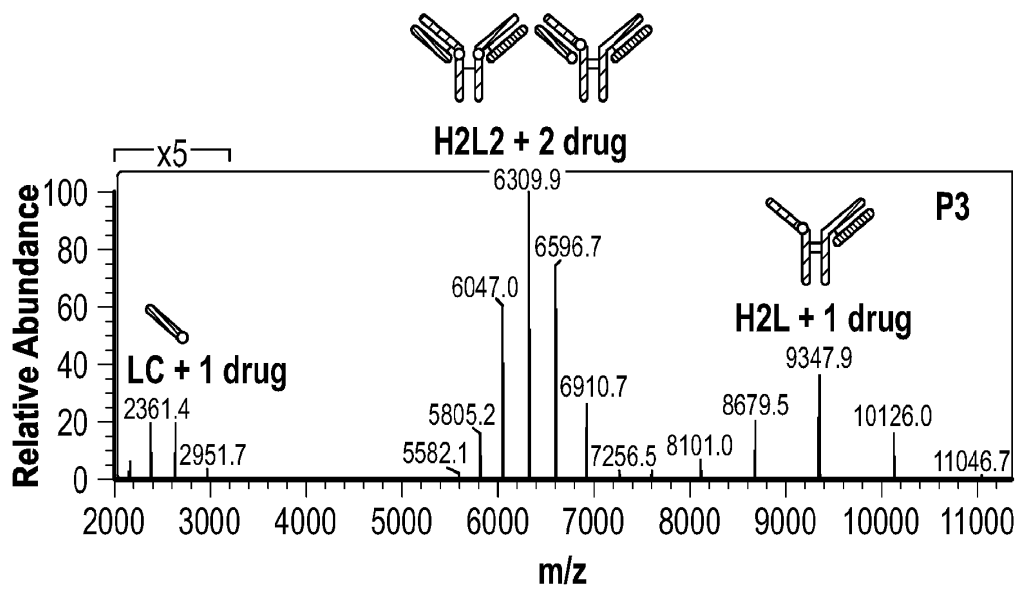
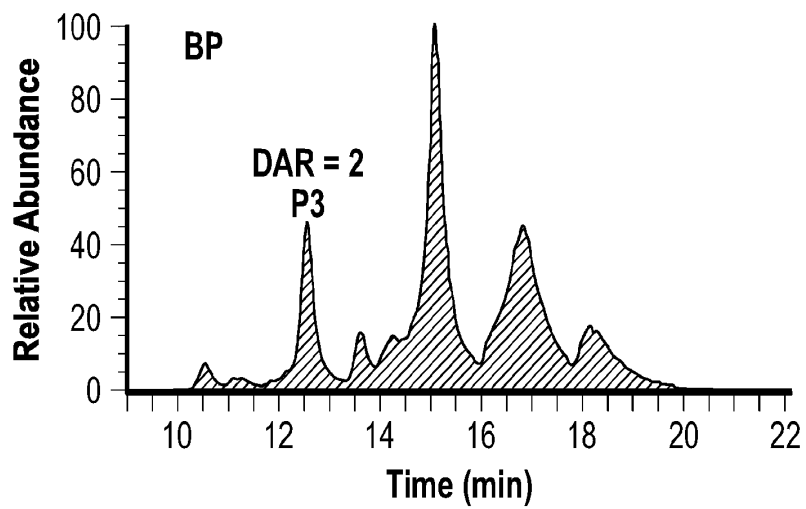


FIG. 16

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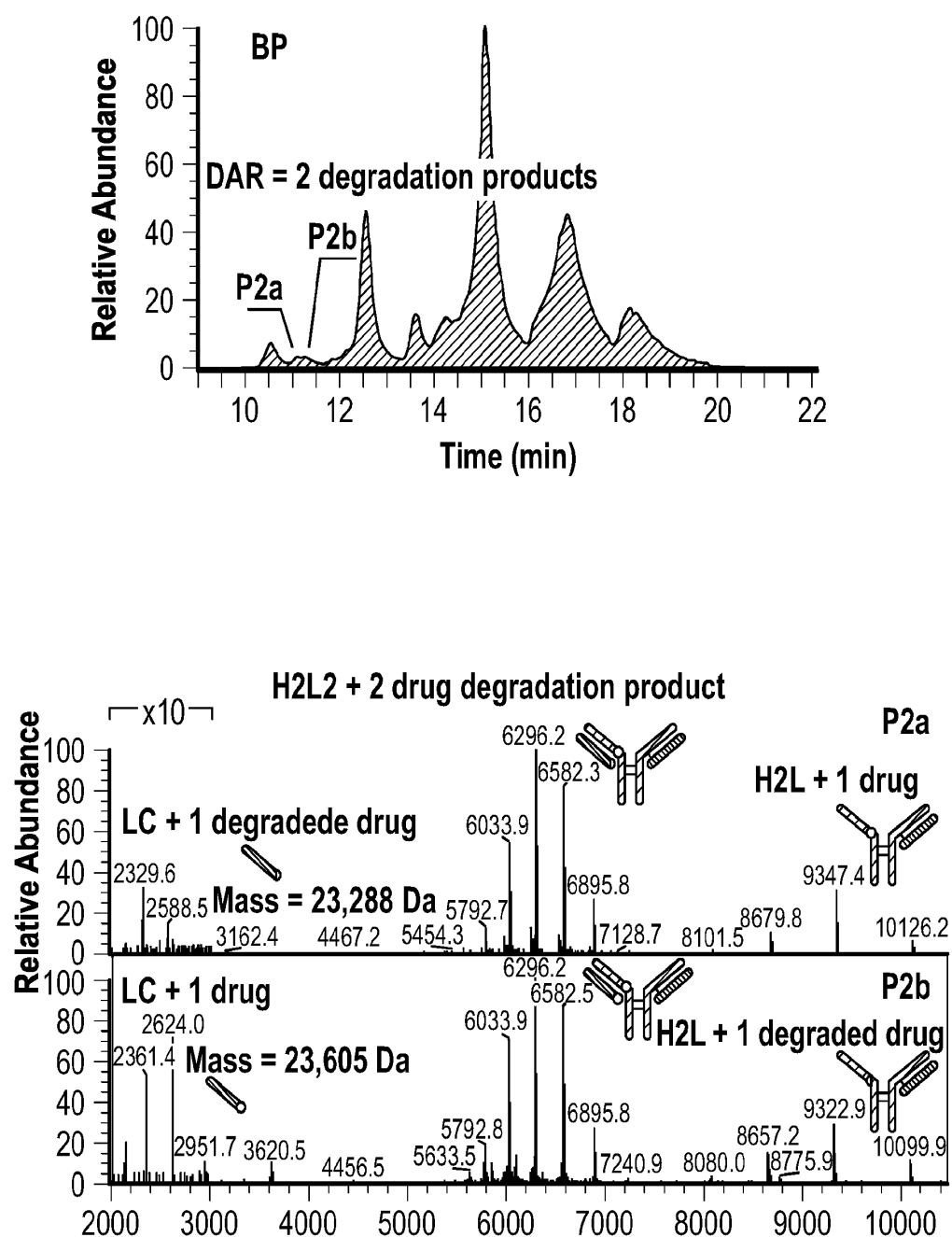


FIG. 17

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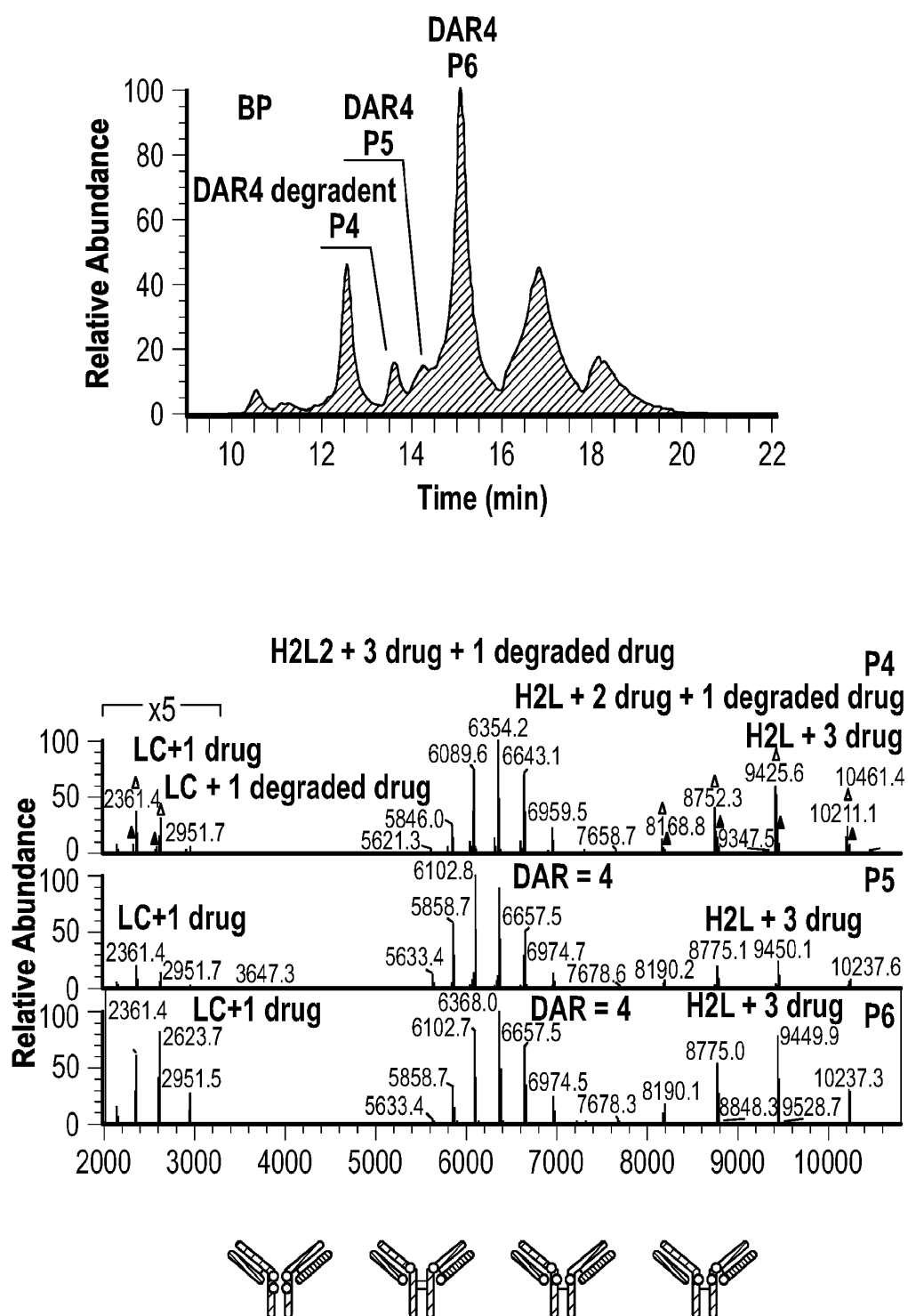


FIG. 18

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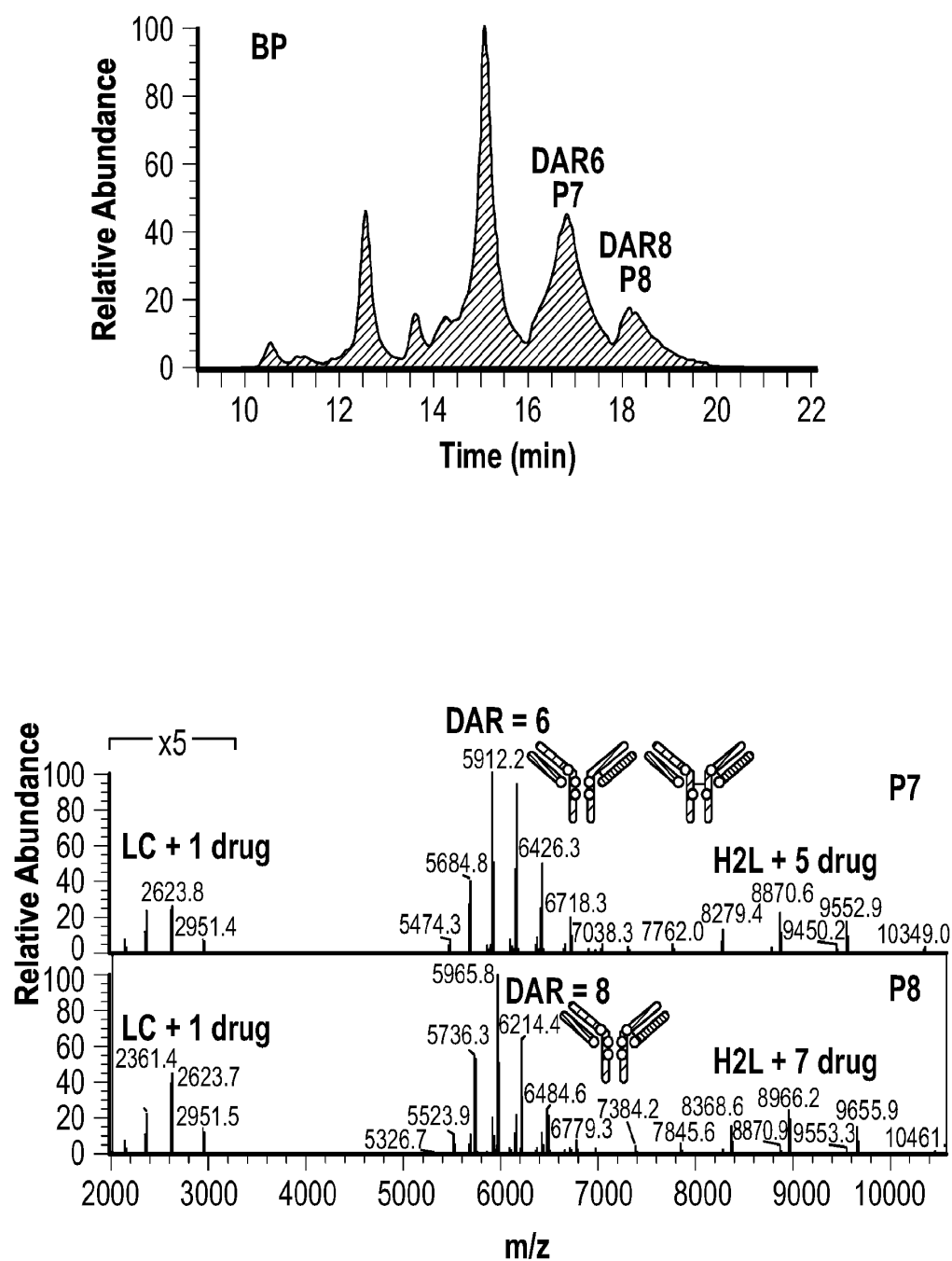


FIG. 19

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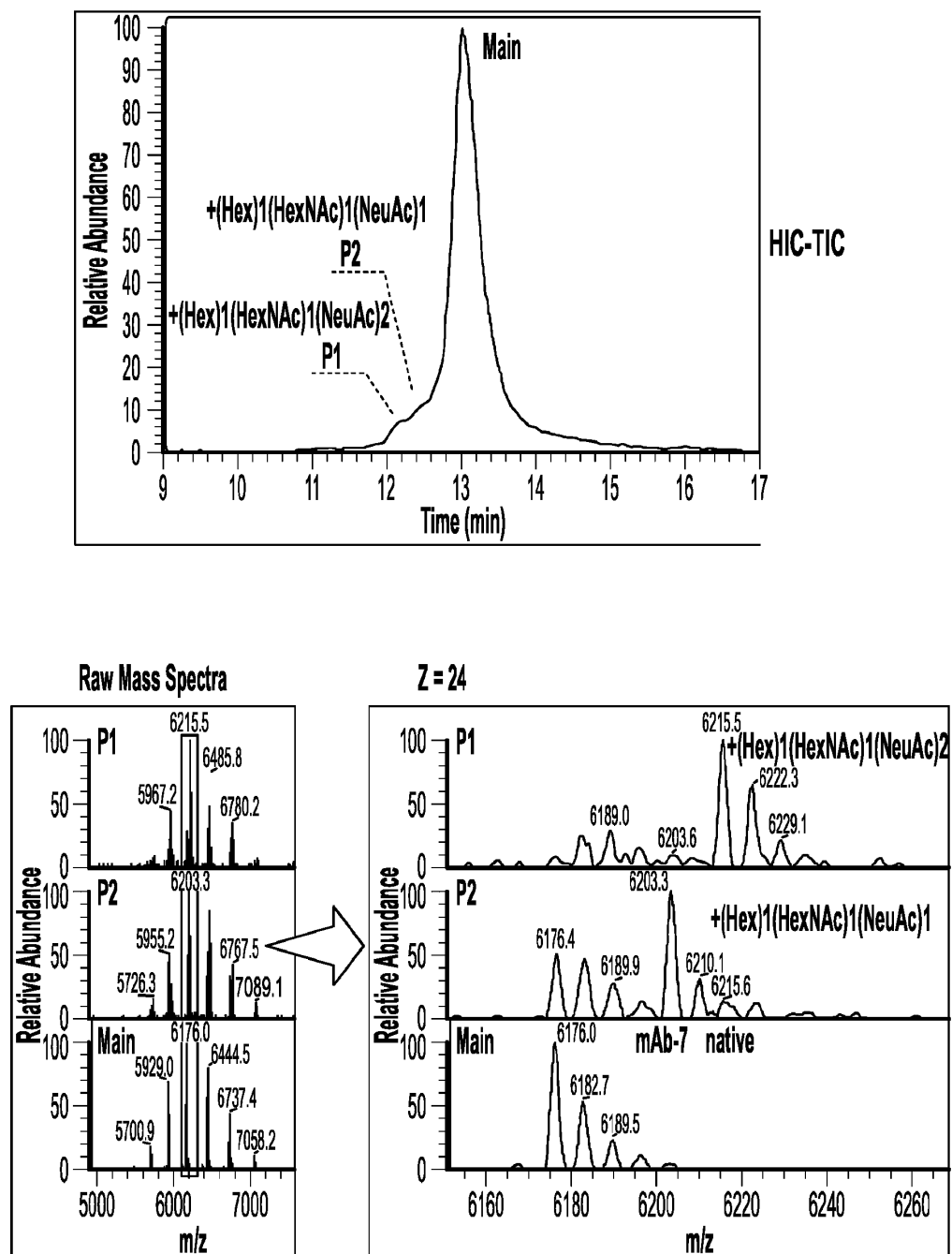


FIG. 20

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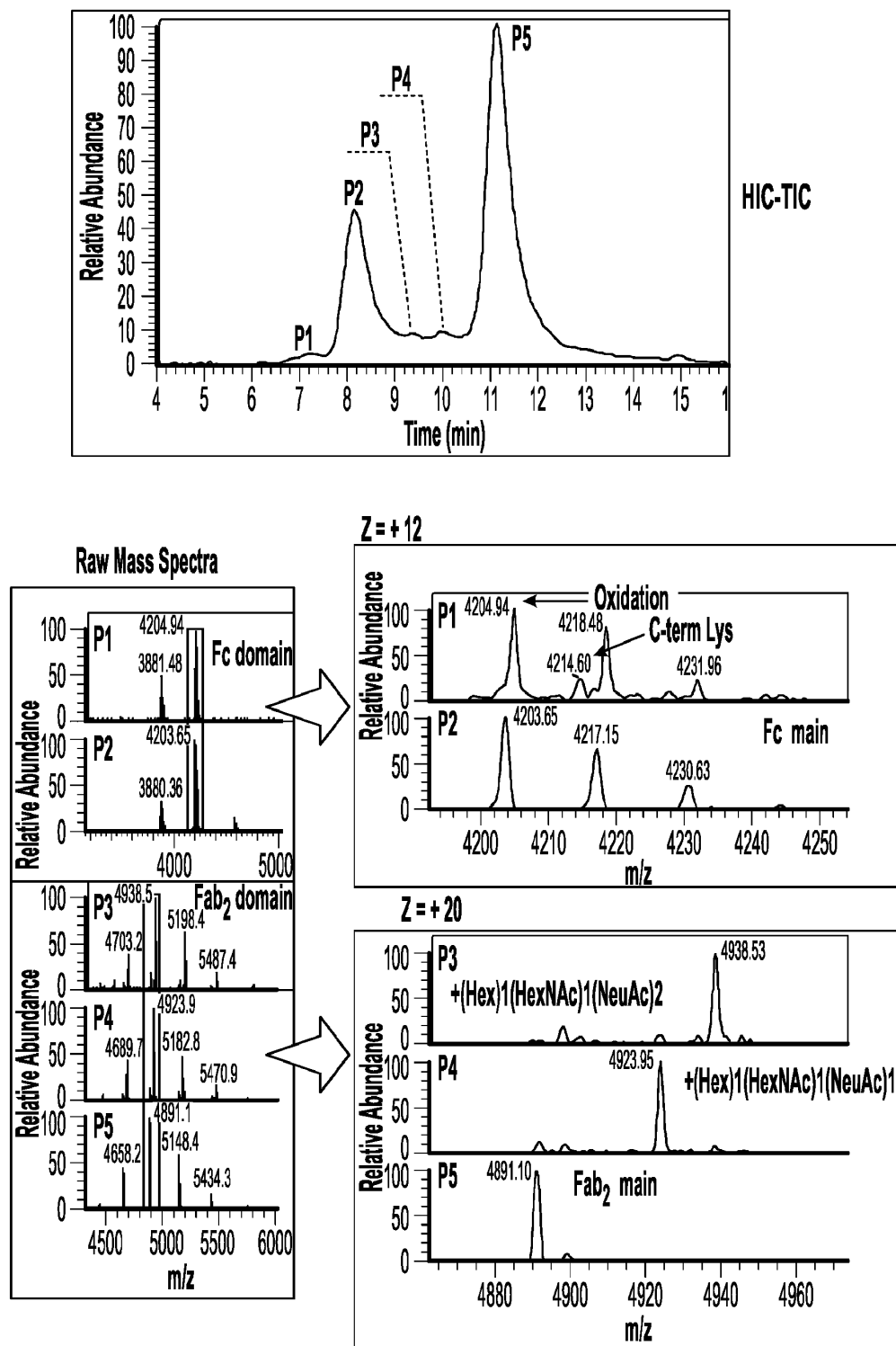


FIG. 21

SUBSTITUTE SHEET (RULE 26)

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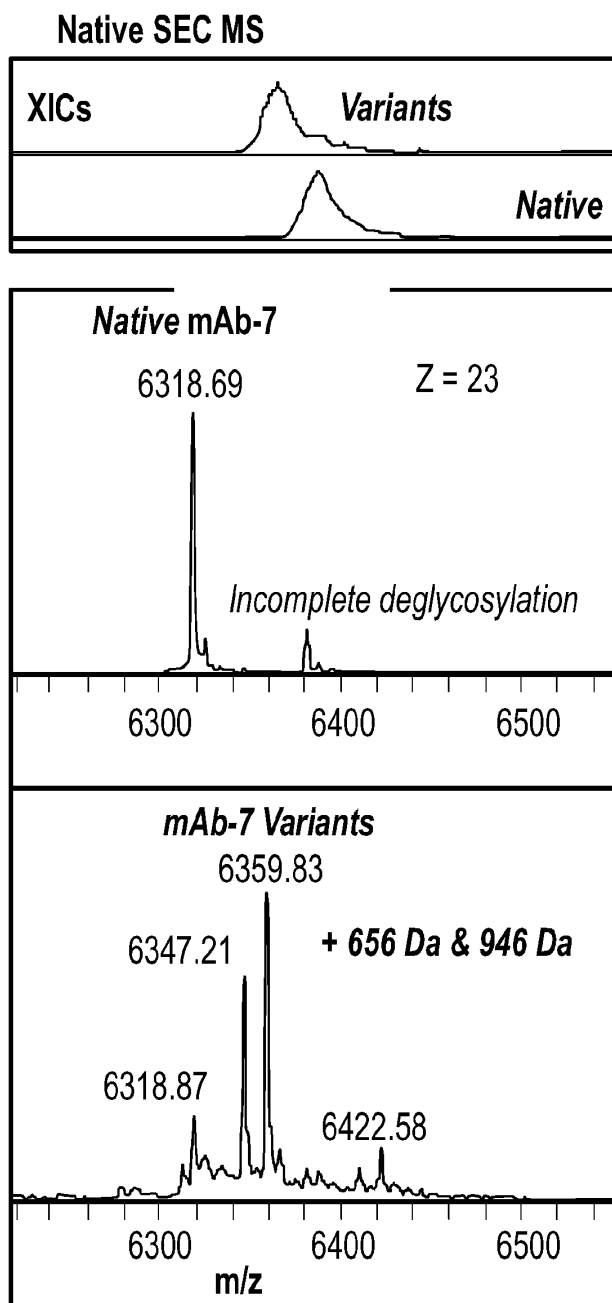
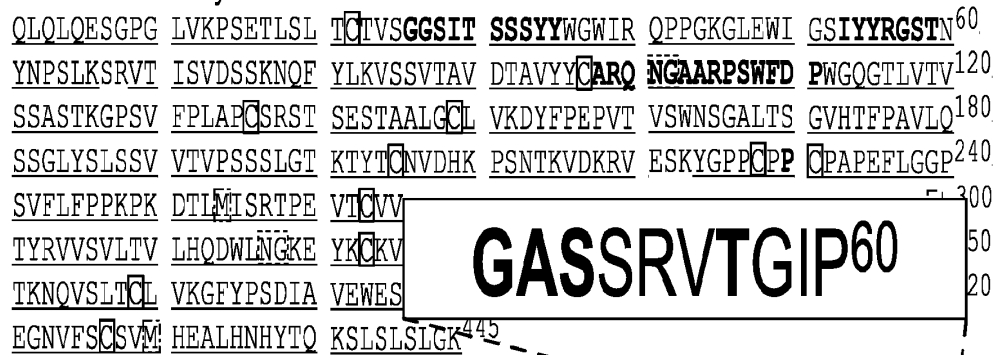


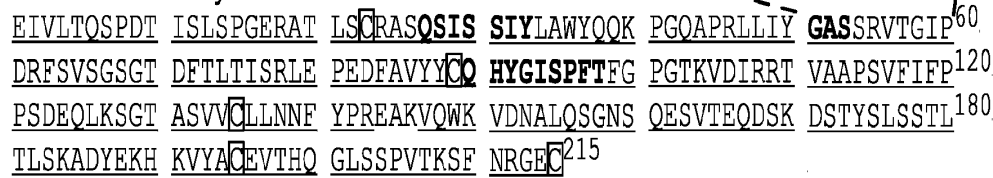
FIG. 22

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mAb-7 Heavy Chain



mAb-7 Heavy Chain



Reduced Peptide Mapping

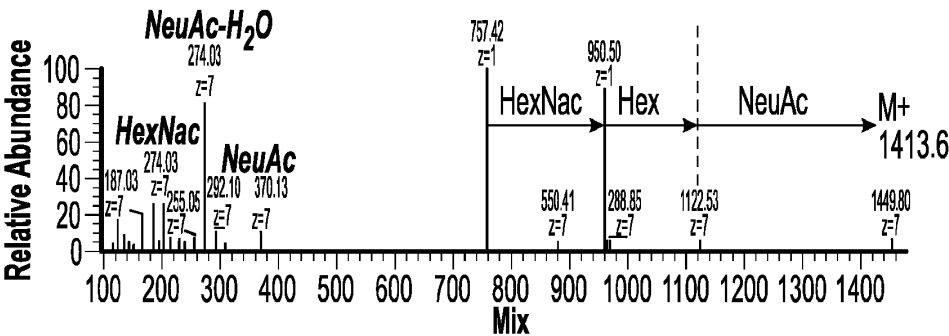
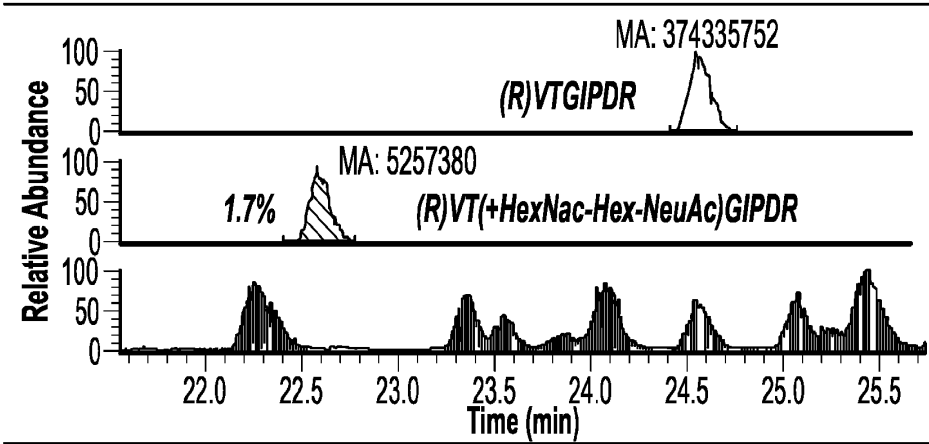


FIG. 23

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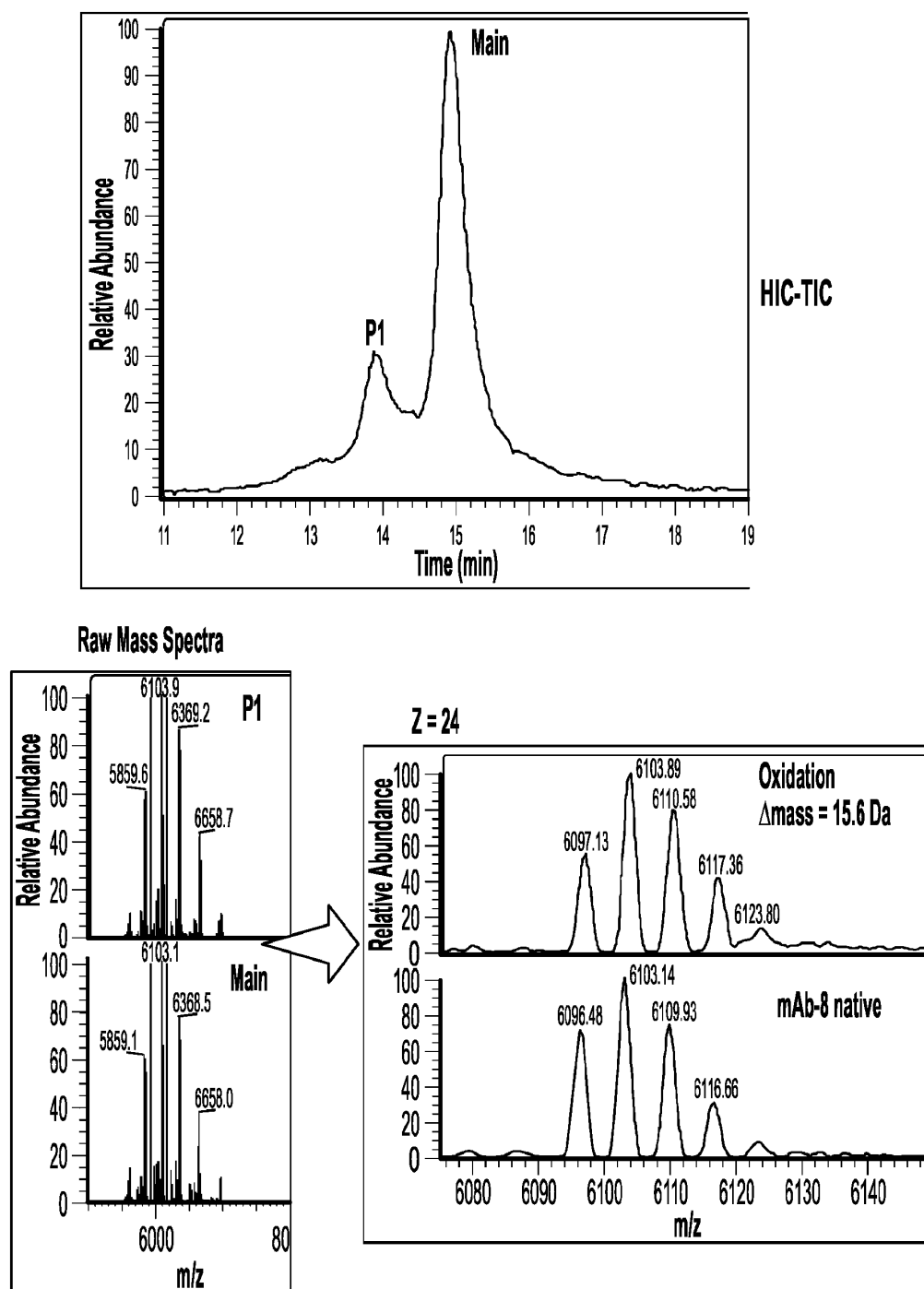


FIG. 24

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mAb-8 Light Chain

DIQMTQSPSS LSASVGDRVT ITCRAS**Q**SIS **S**FLNWIYQQKPK GKAPKLLIYA **A**SSLQSGVPS⁶⁰
 RFSGSGSGTD FTLTISSLQP EDFATYYC**Q****Q** **S**YSTLT**F**GGG TRLEIKRTVA APSVFIFPPS¹²⁰
 DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLT¹⁸⁰
 SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC²¹³

mAb-8 Heavy Chain

EVQLVESGGG LVQPGGSLRL SCAAS**G****F****T****S**S **S**YAMNWRQA PGKGLEWVST **I****S****G****M****G****G****S****T**YY⁶⁰
 ADSVKGRFTI SRDNSKNTLY LQMSLRAED TAVYYC**A****K****R****G** **Y****P****H****S****F****D****I****W****G****Q** GTMTVSSAS¹²⁰
 TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL¹⁸⁰
 YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS²⁴⁰
 VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST³⁰⁰
 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRDEL³⁶⁰
 KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD SDGSFFLYSK LTVDKSRWQ⁴²⁰
 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

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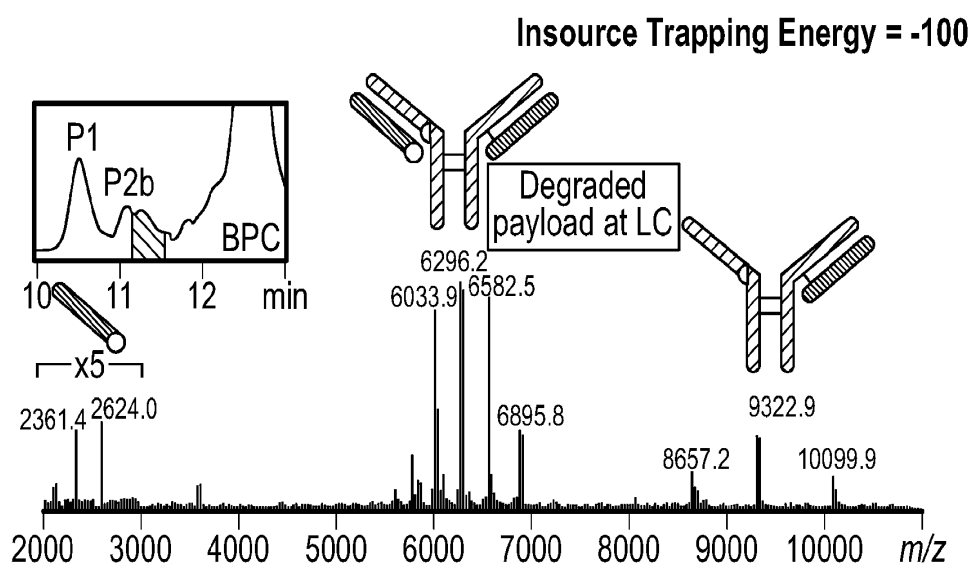
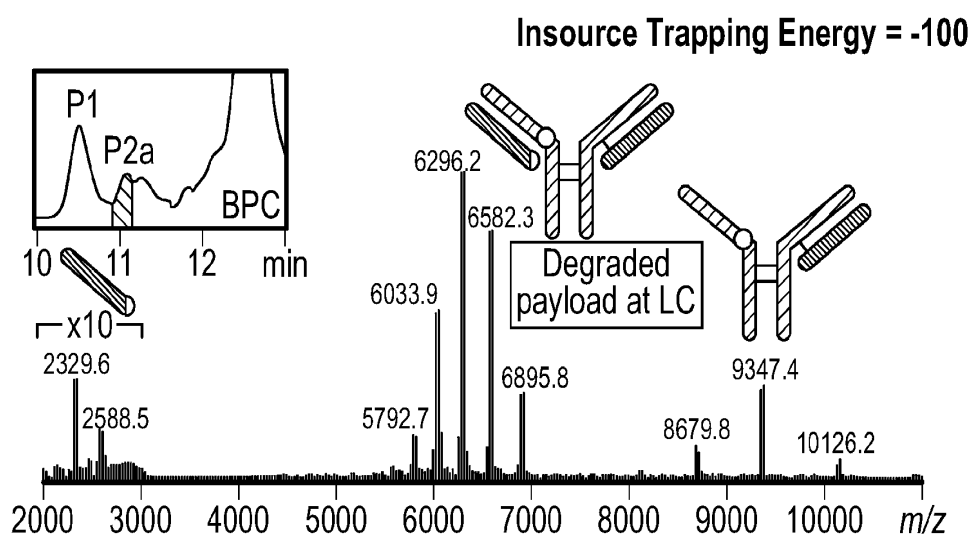


FIG. 26

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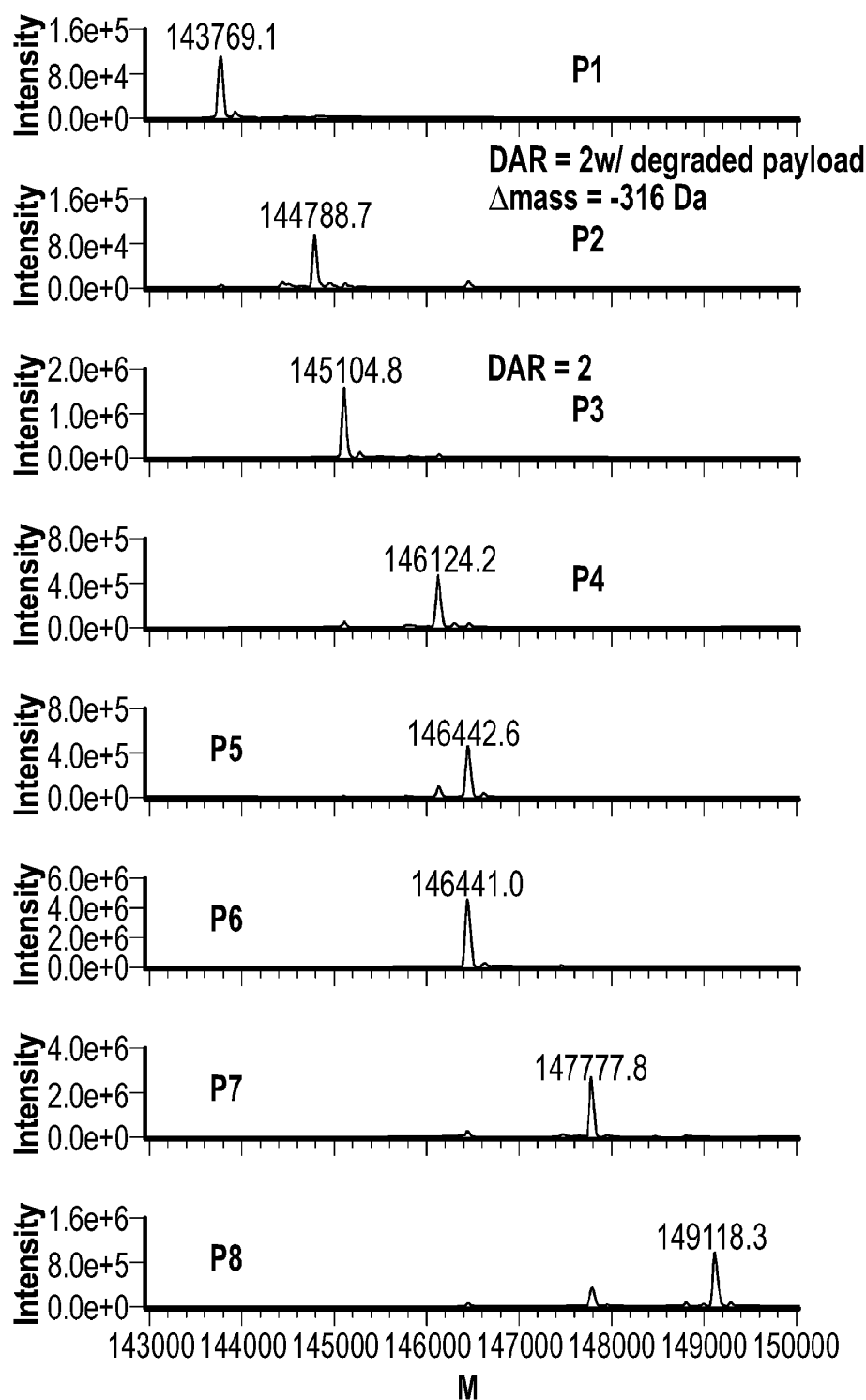


FIG. 27

