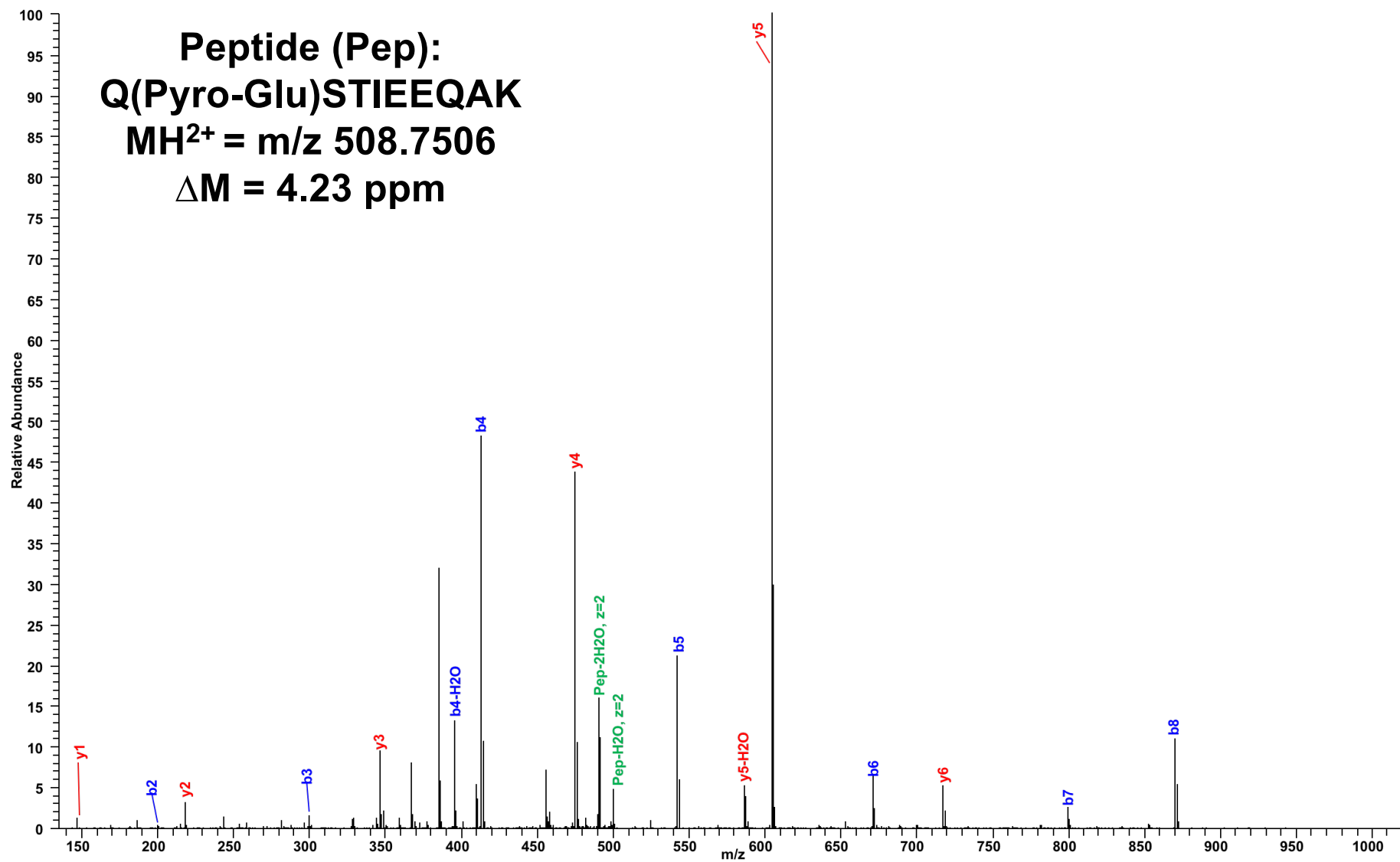


Peptide (Pep):
Q(Pyro-Glu)STIEEQAK
MH²⁺ = m/z 508.7506
 $\Delta M = 4.23$ ppm

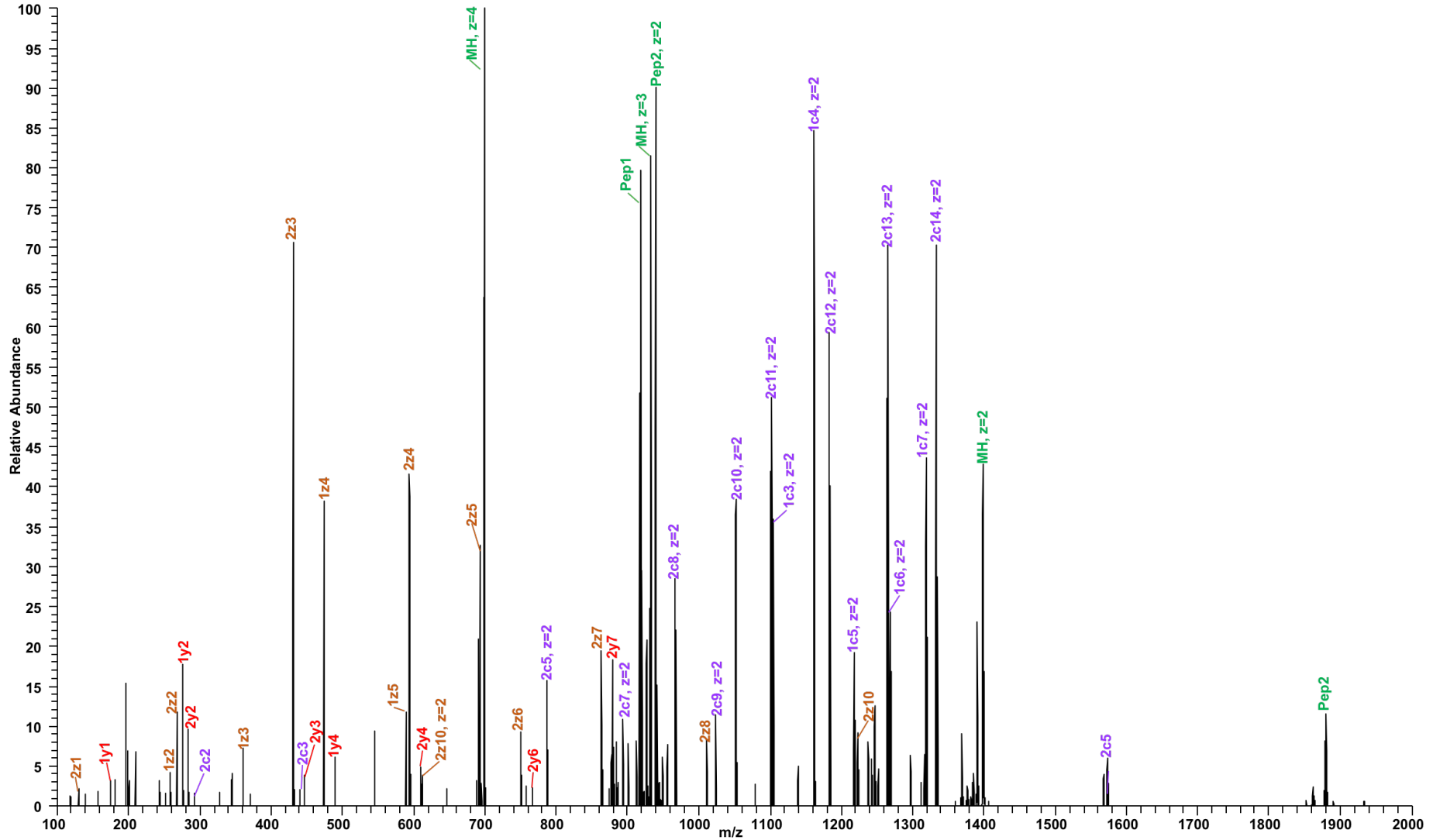


Pep1: Q(Pyro-Glu)C(Disulfide)VN(Deamidated)LTTR

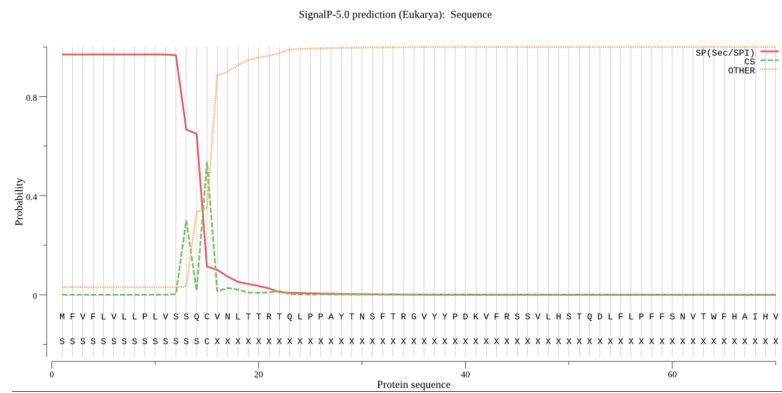
Pep2: FQFC(Disulfide)NDPFLGVYYHK

MH⁴⁺ = m/z 699.0799

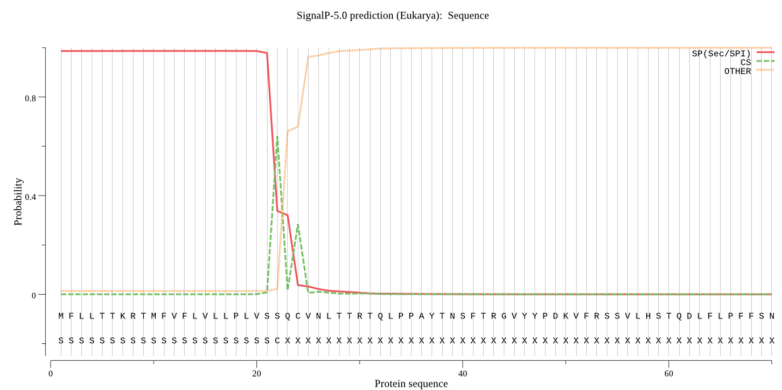
$\Delta M = 6.36$ ppm

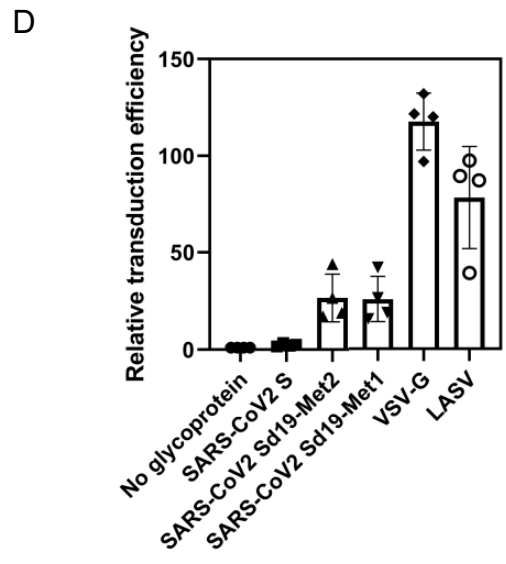
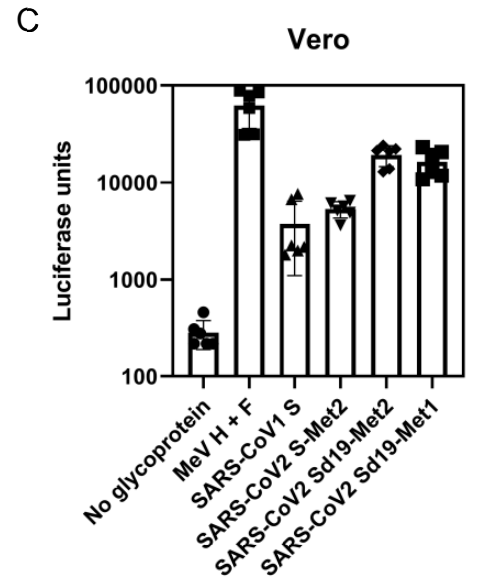
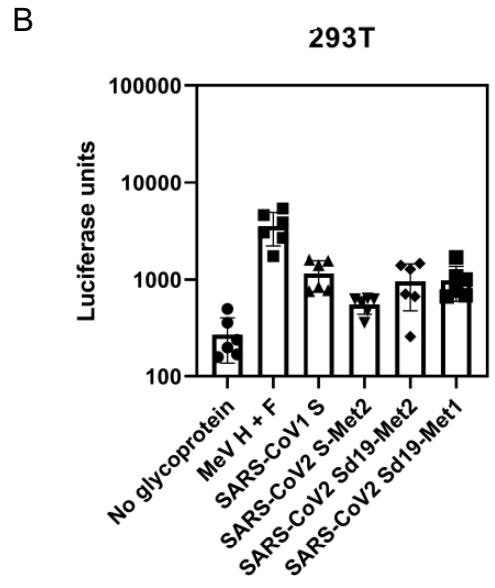
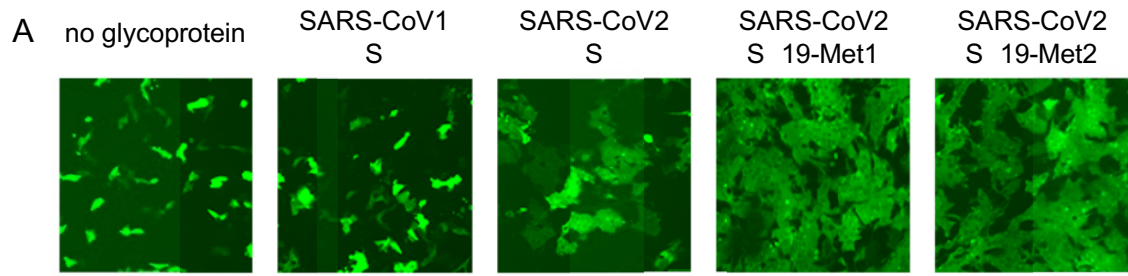


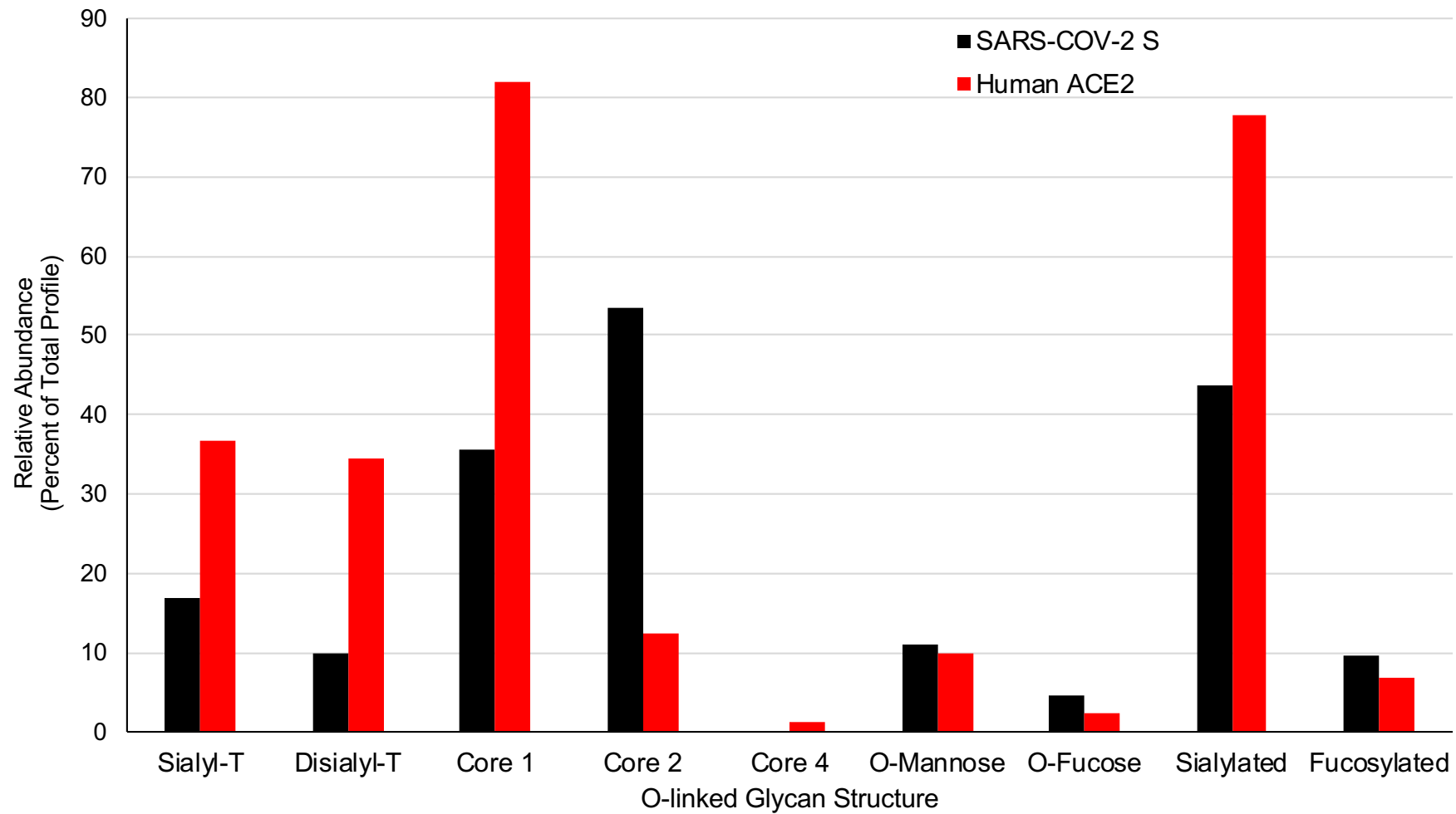
- **Utilized Start Met: MFVFLVLLPLVSSQCVNL...**
 - Signal P: SSQC-VN (.54)

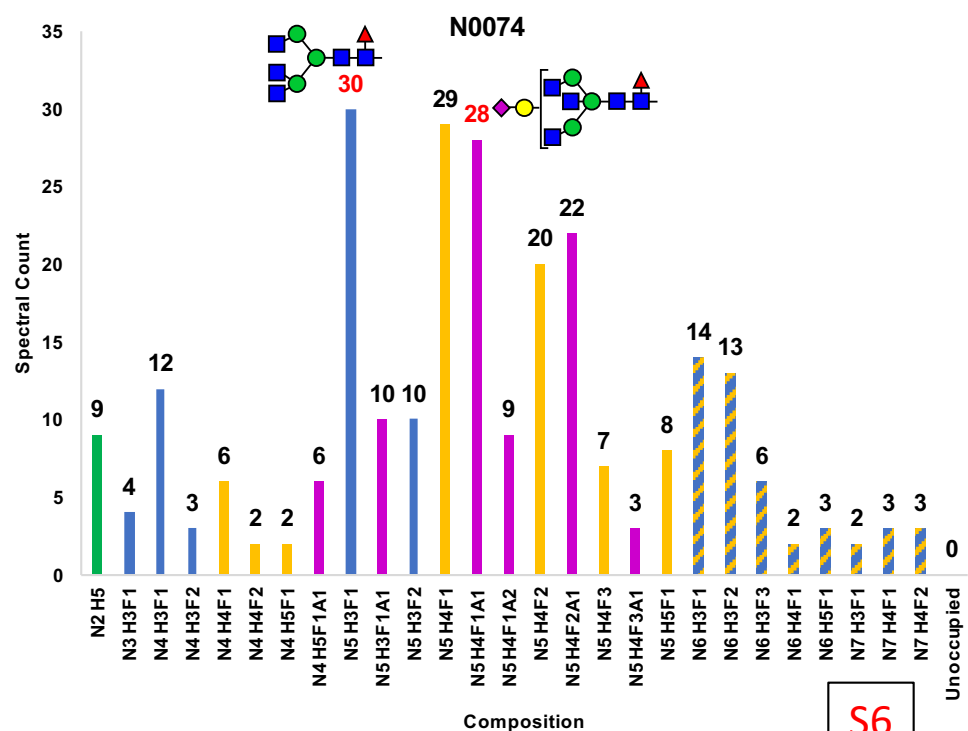
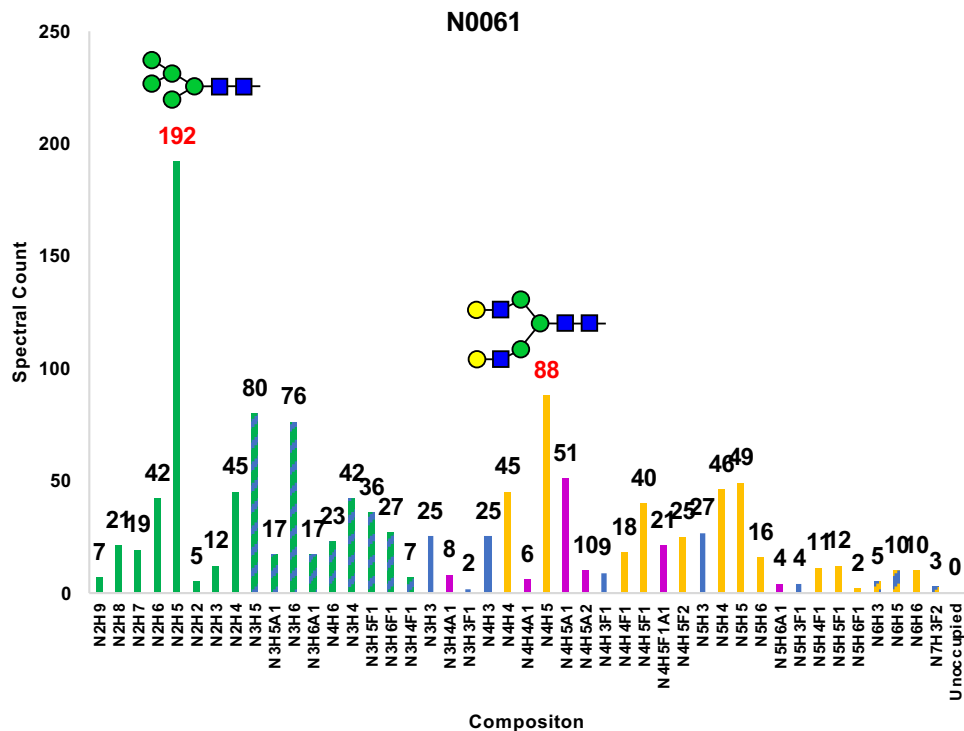
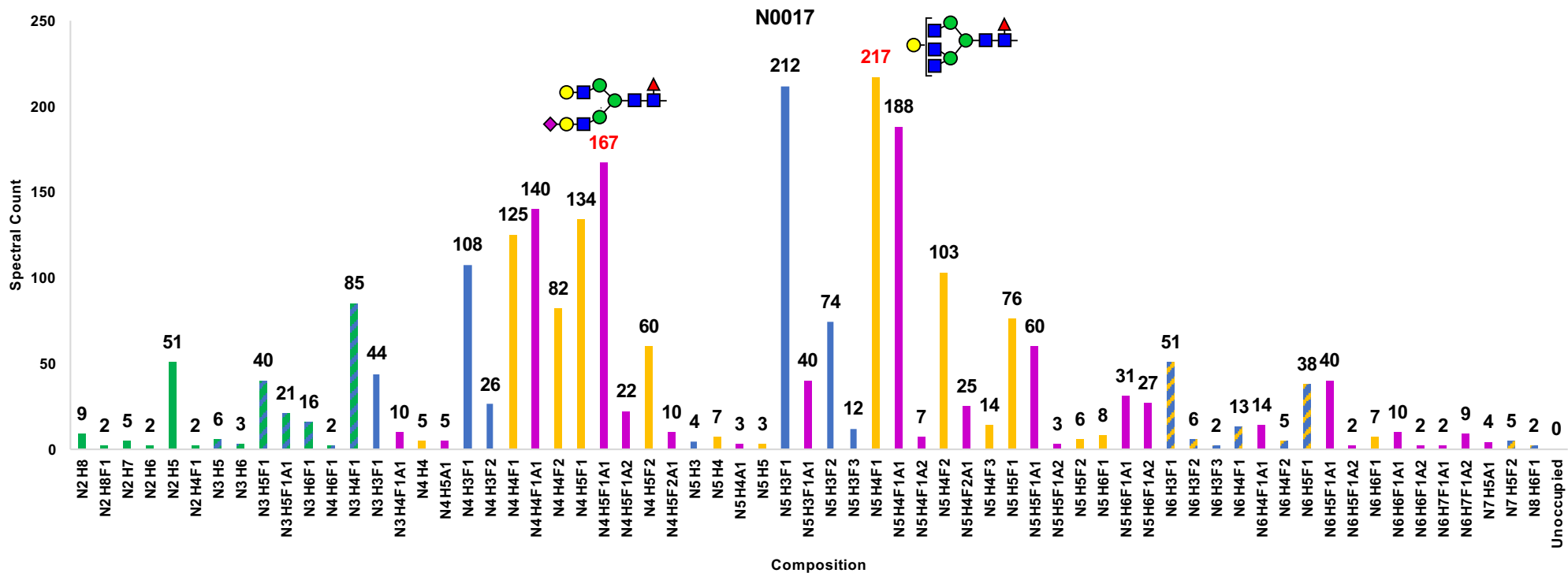


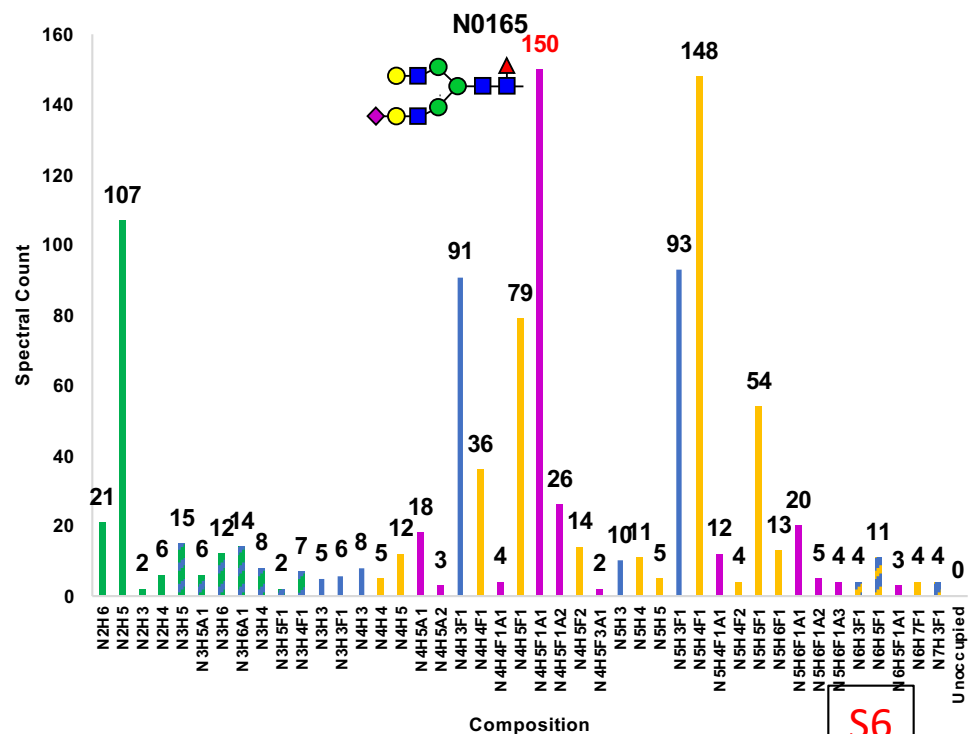
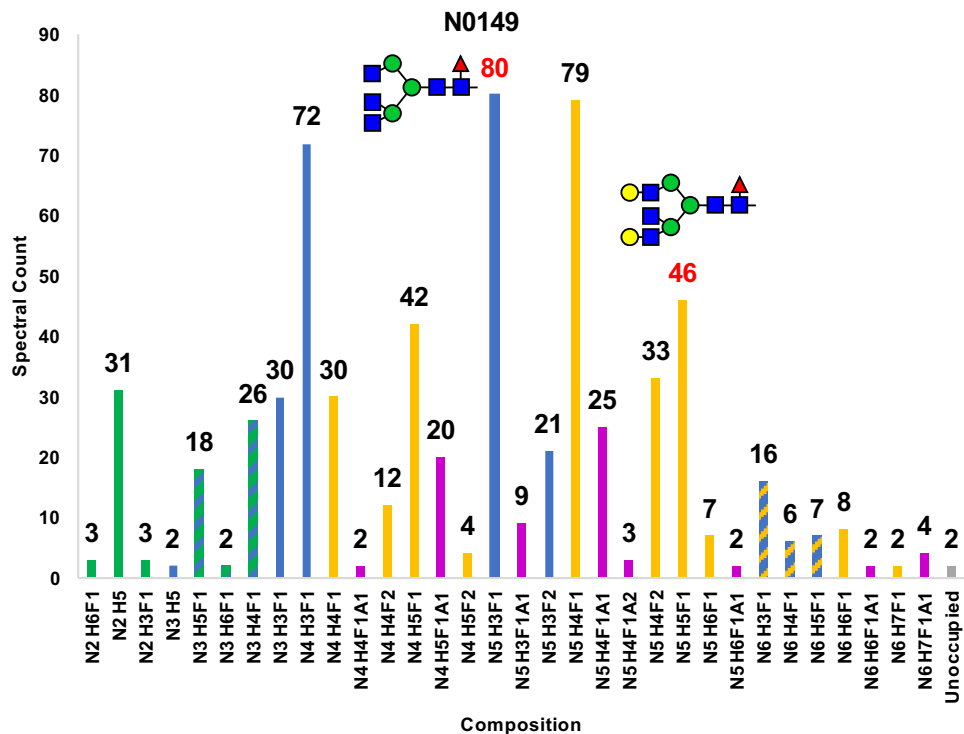
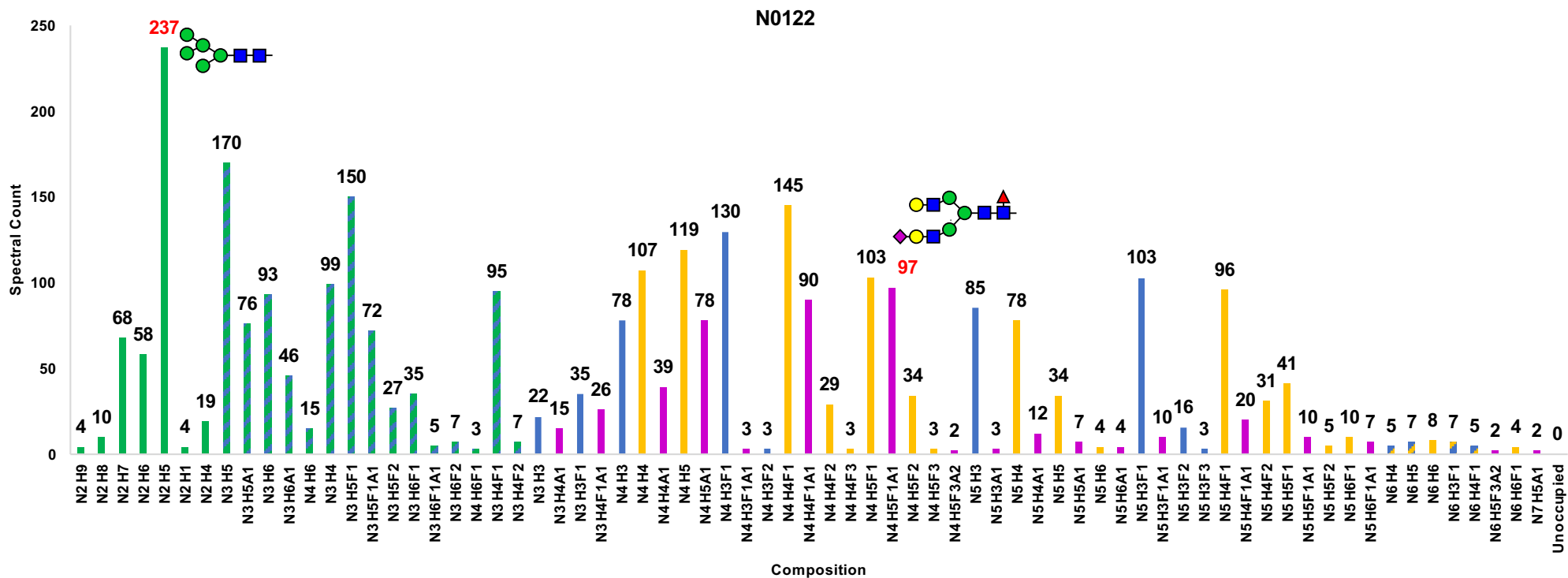
- **Upstream Met: MFLTTKRTMFVFLVLLPLVSSQCVNL...**
 - Signal P: SS-QCVN (.64)



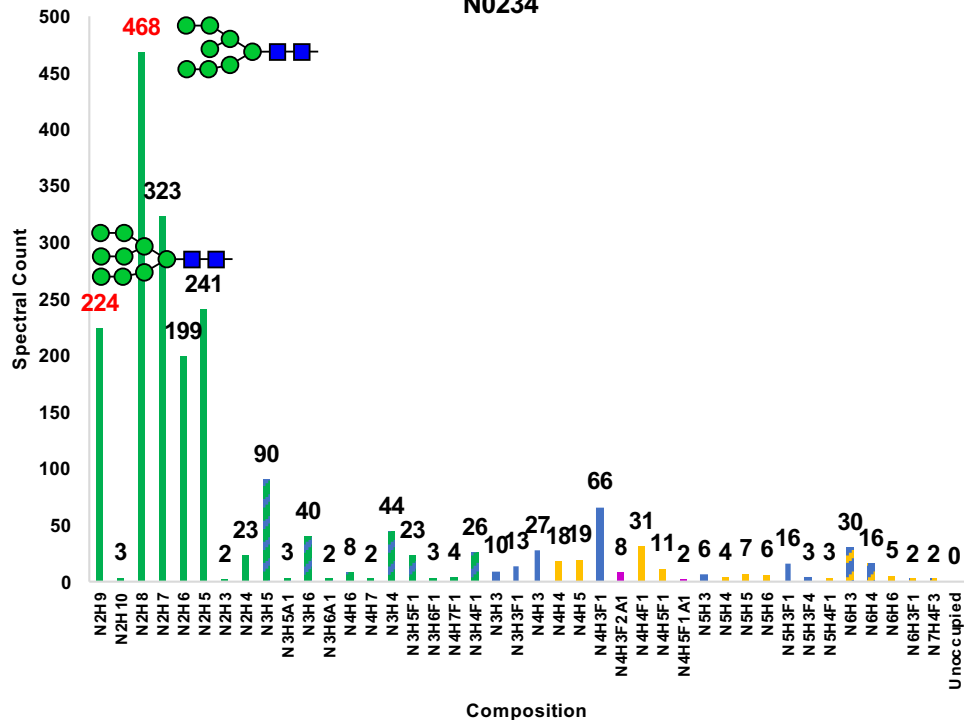




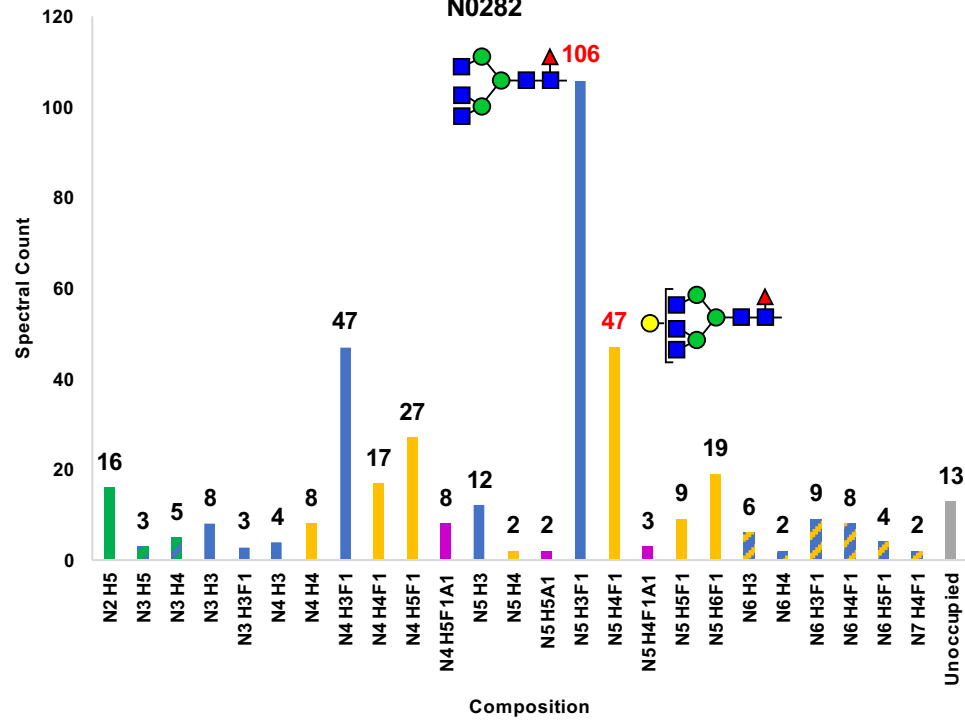




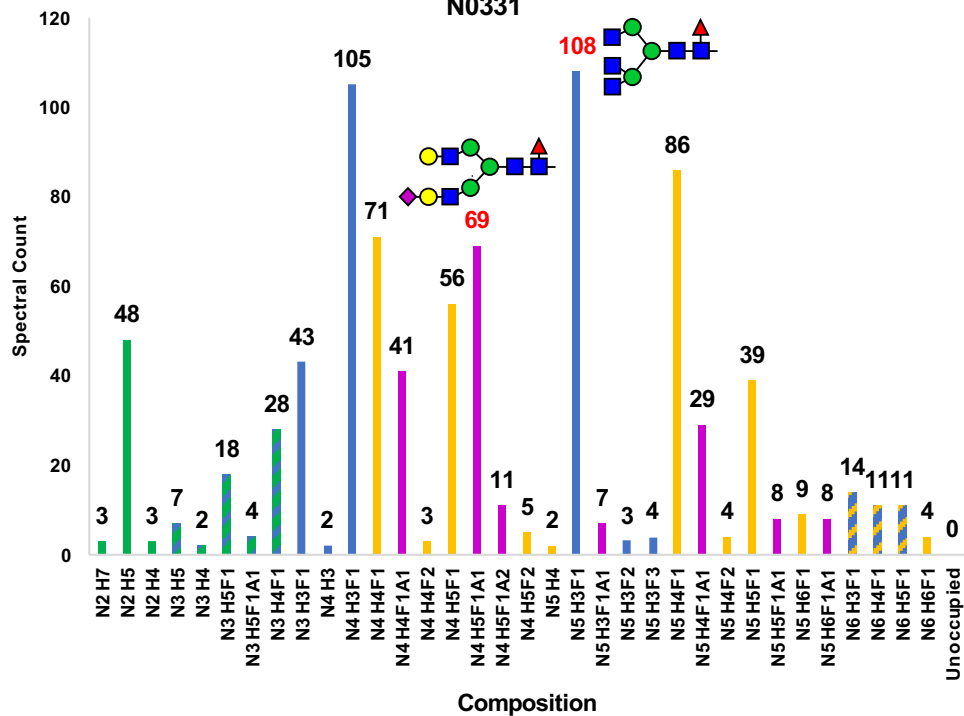
N0234



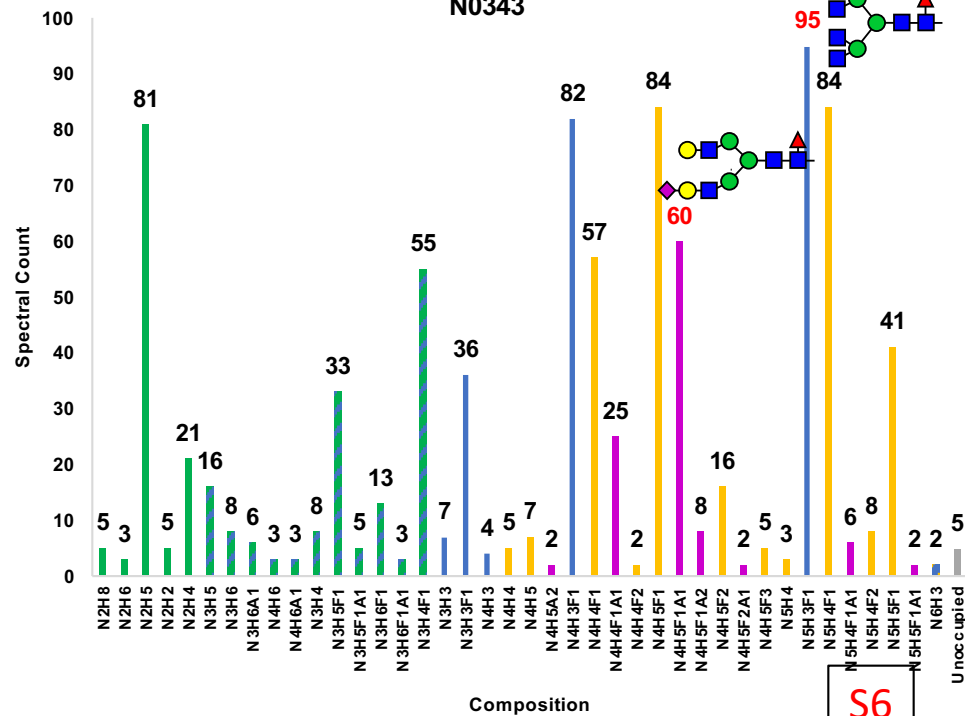
N0282



N0331

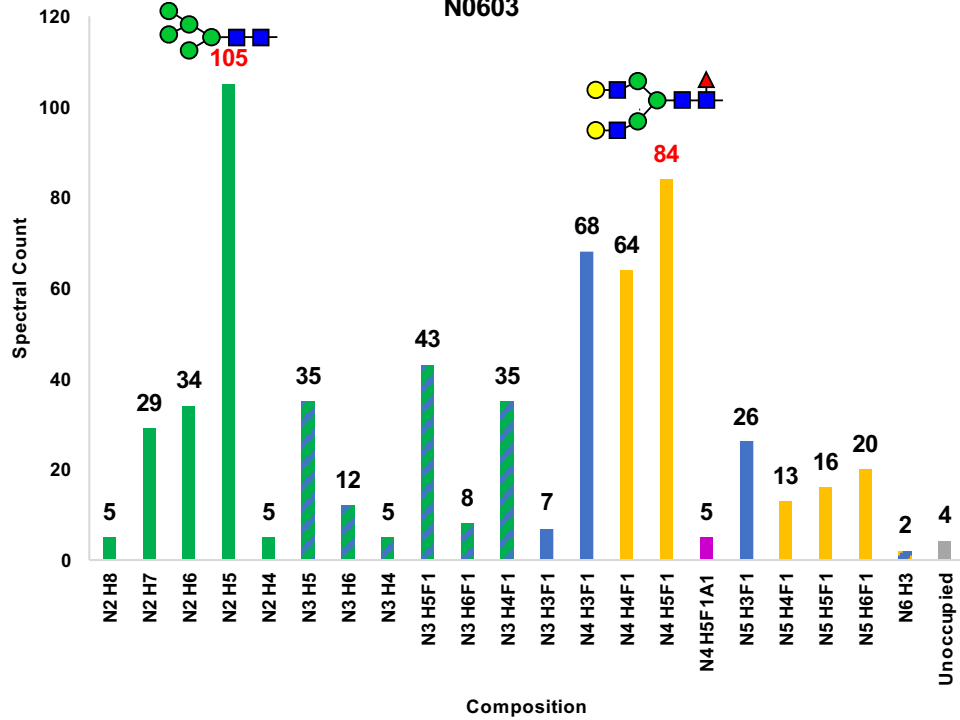


N0343

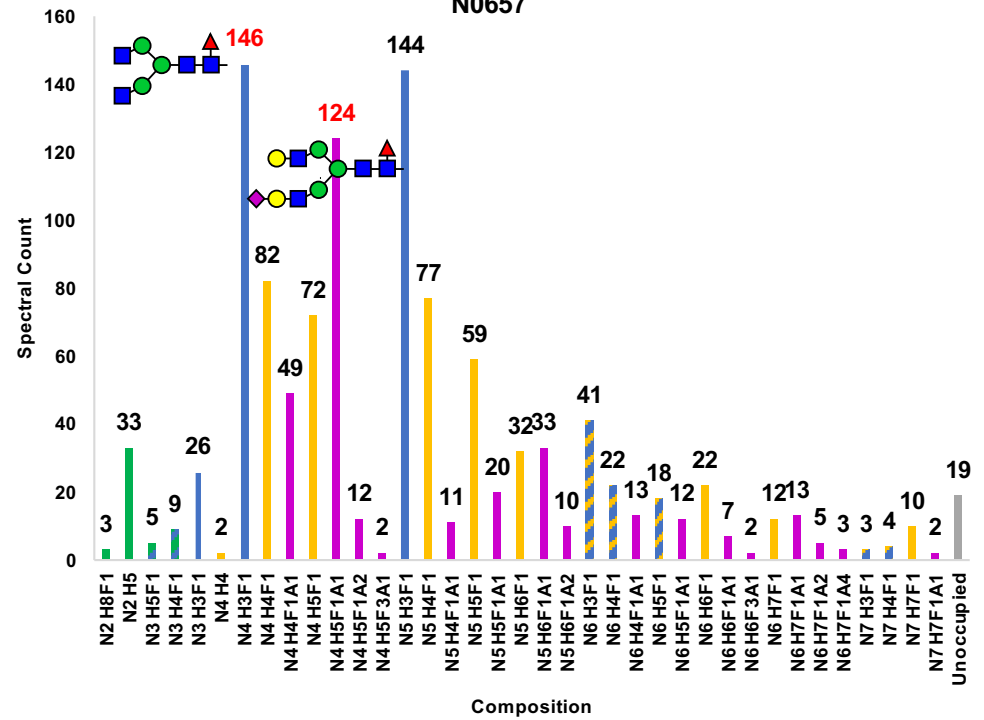


S6

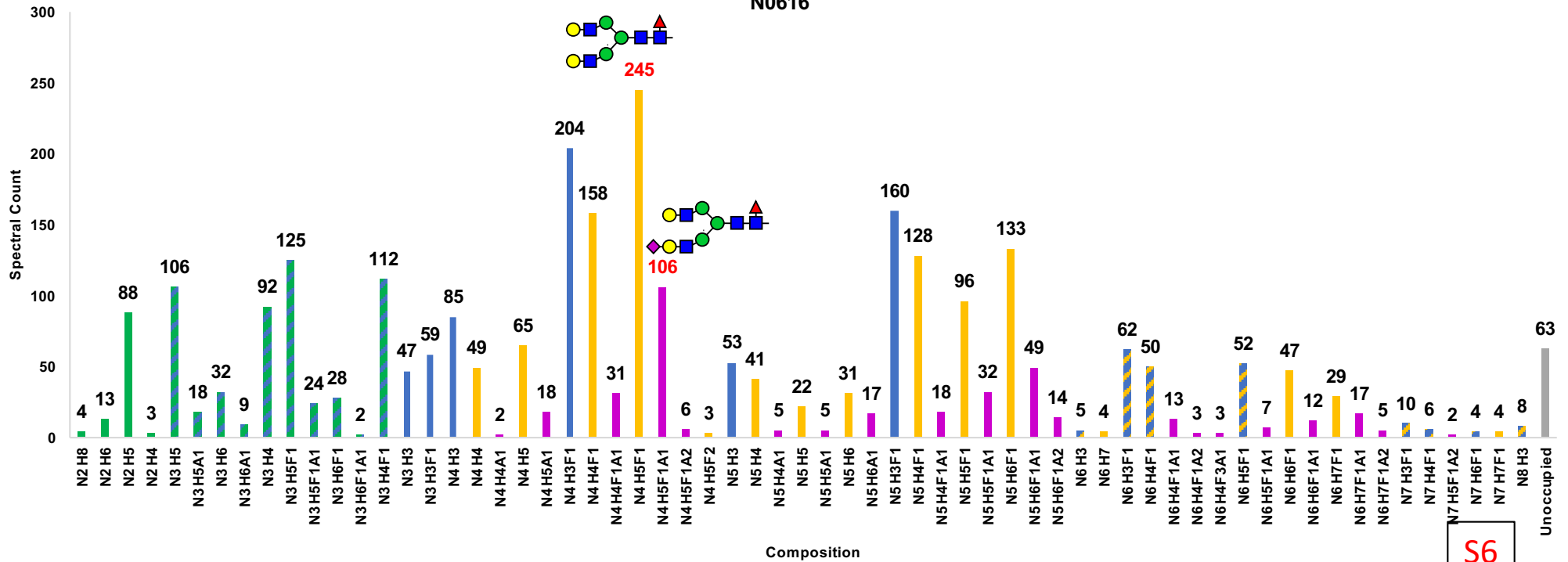
N0603



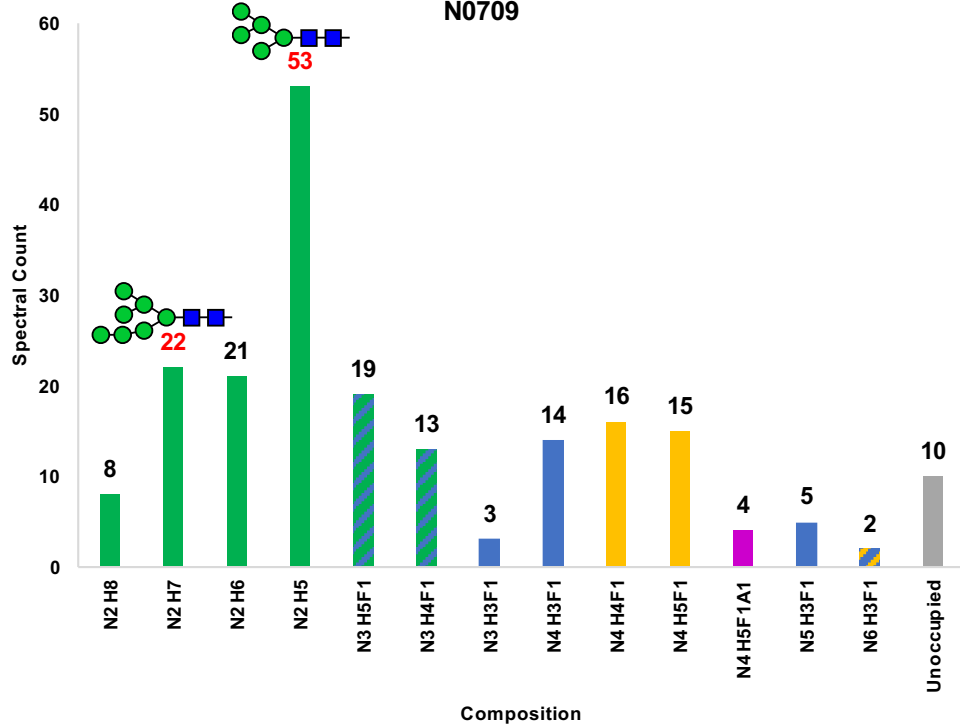
N0657



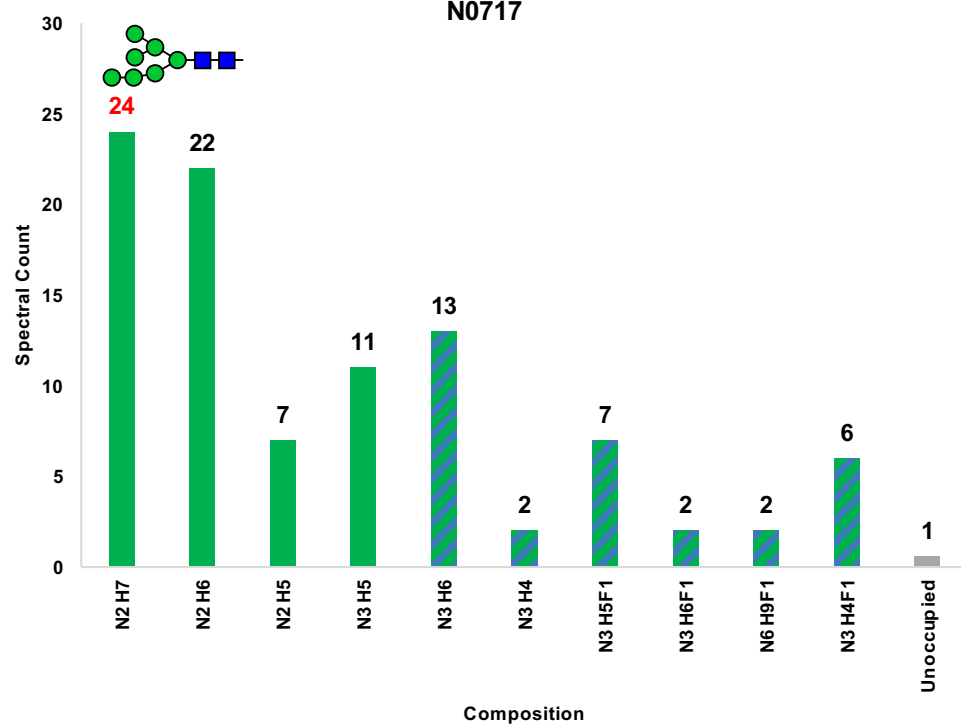
N0616



N0709



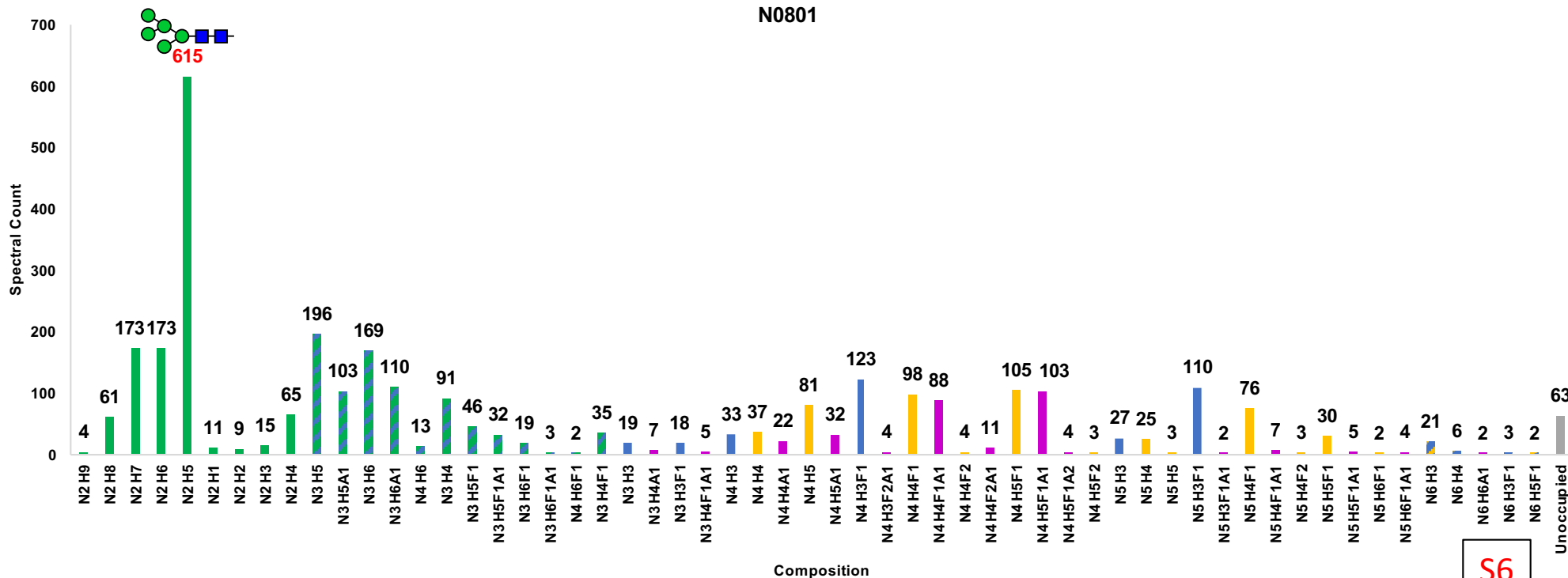
N0717



Composition

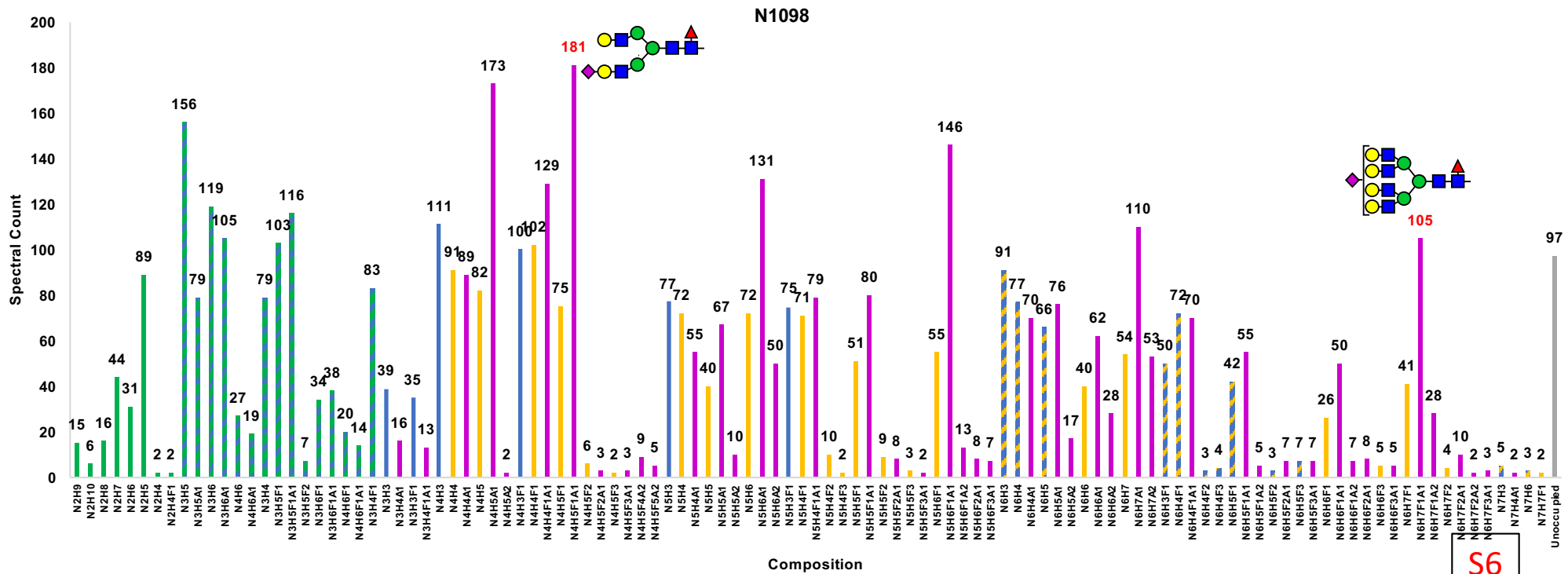
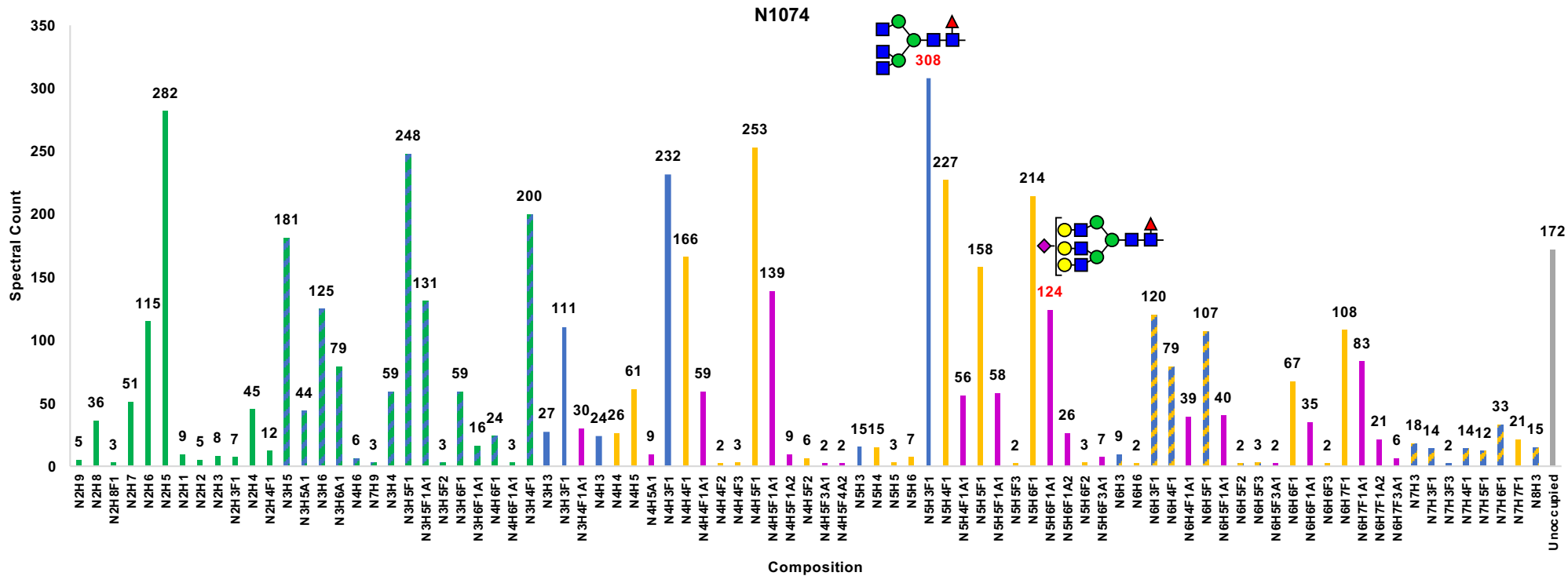
Composition

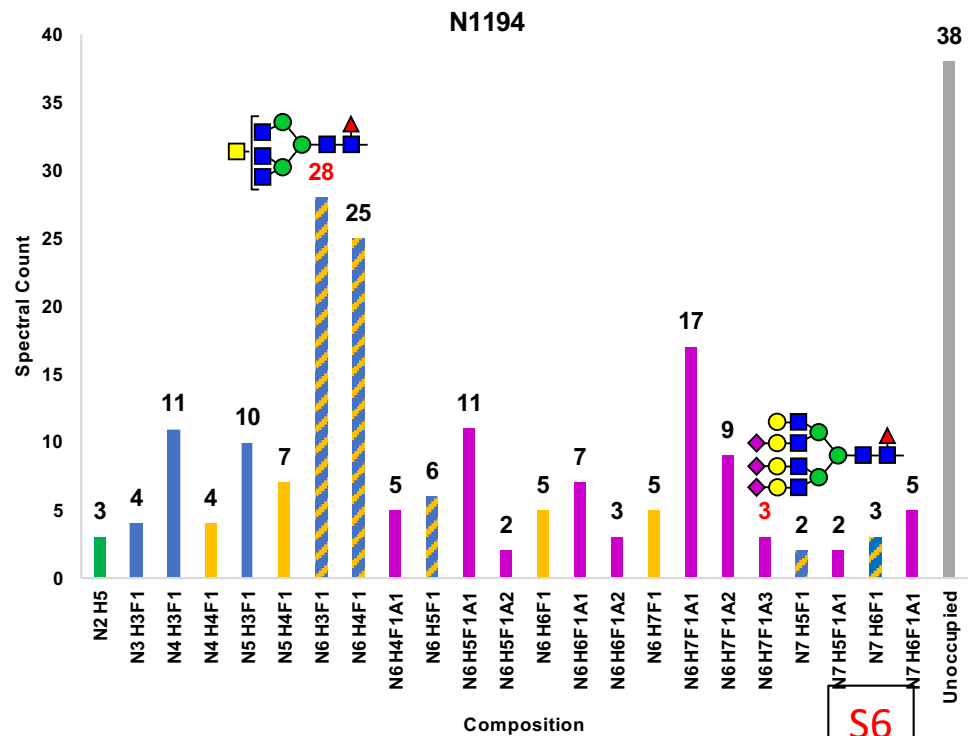
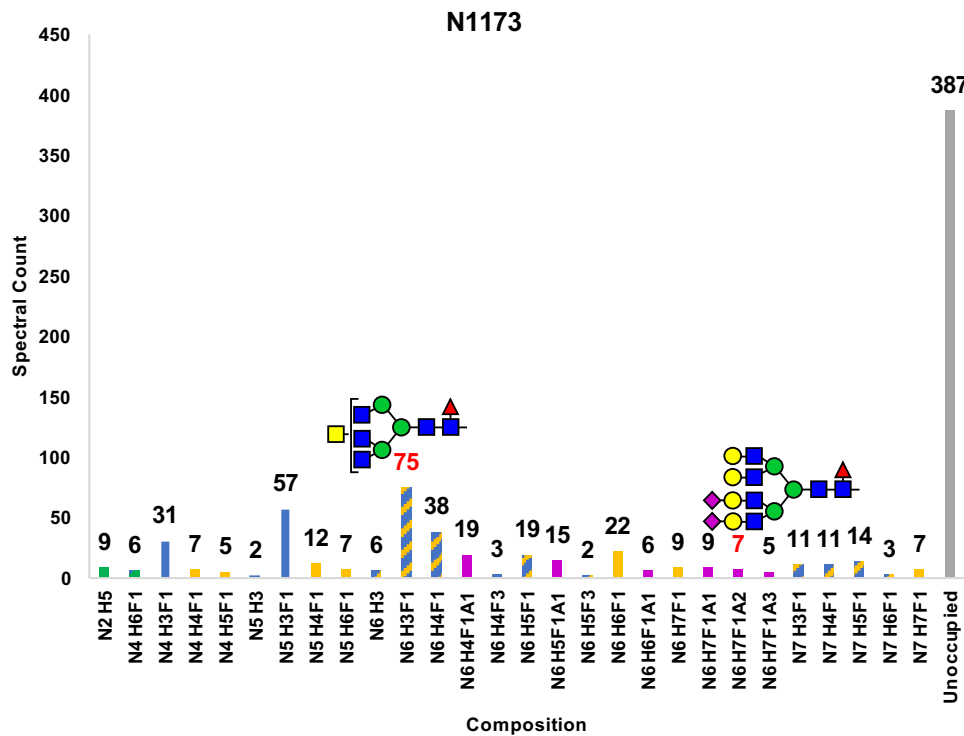
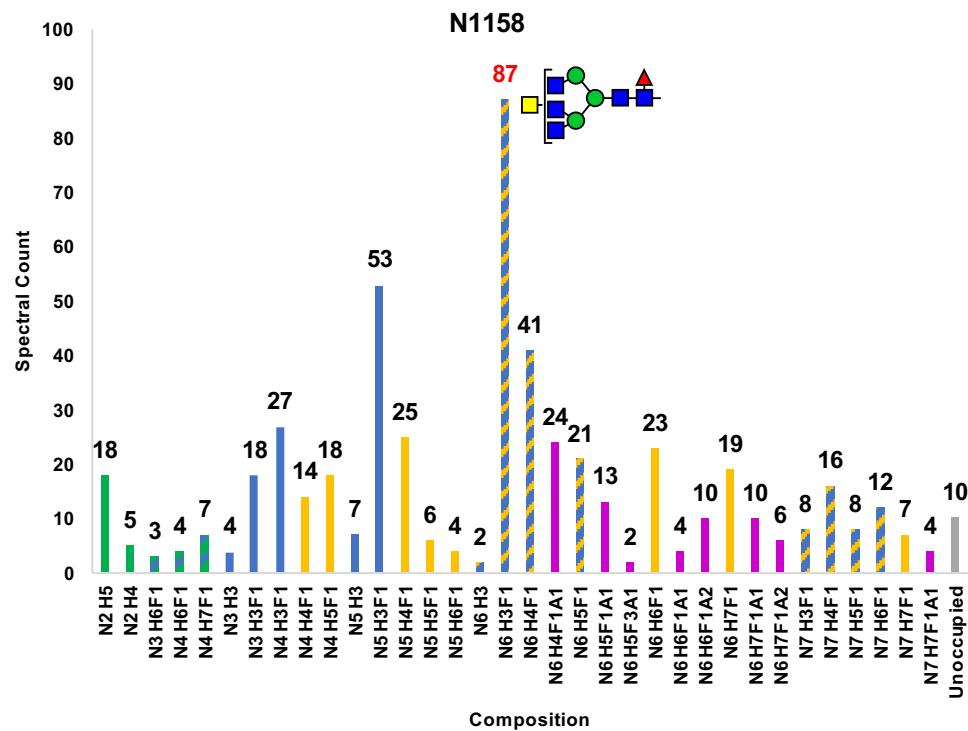
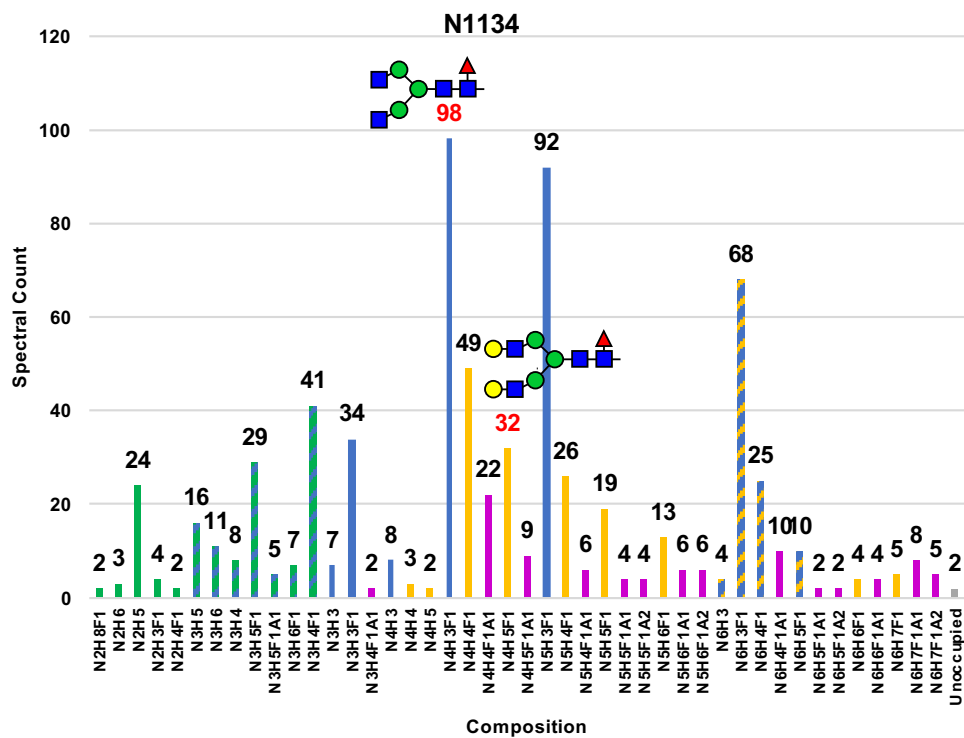
N0801



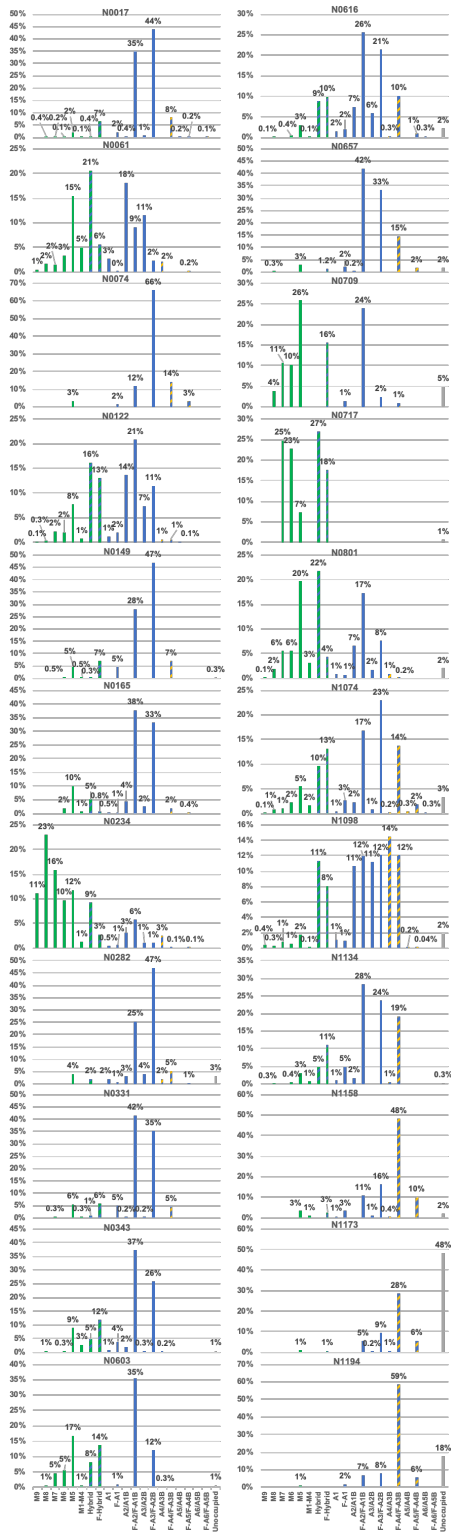
Composition

S6





S6



Legends






Pep+HexNAc1: precursor ions with reduced charge and/or neutral loss


HexNAc1: oxonium ions

b1: b- ions of peptide backbone (without additional glycans)

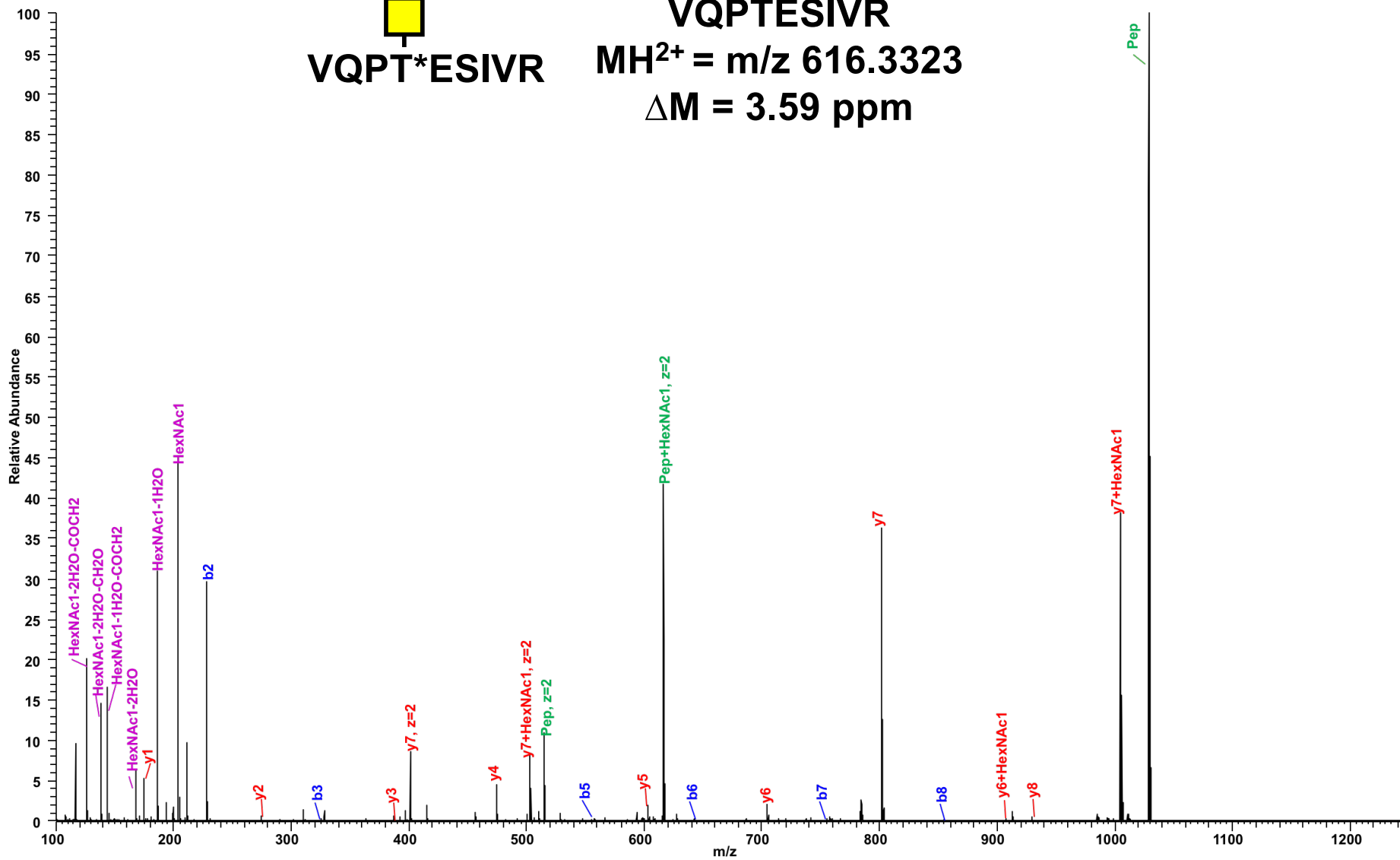
y1: y- ions of peptide backbone (without additional glycans)

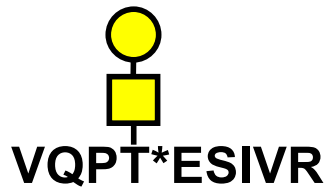
z: charge state

-  **Galactose (Gal)**
-  **Mannose (Man)**
-  ***N*-Acetylglucosamine (GlcNAc)**
-  **Fucose (Fuc)**
-  ***N*-Acetylneuraminic acid (Neu5Ac)**

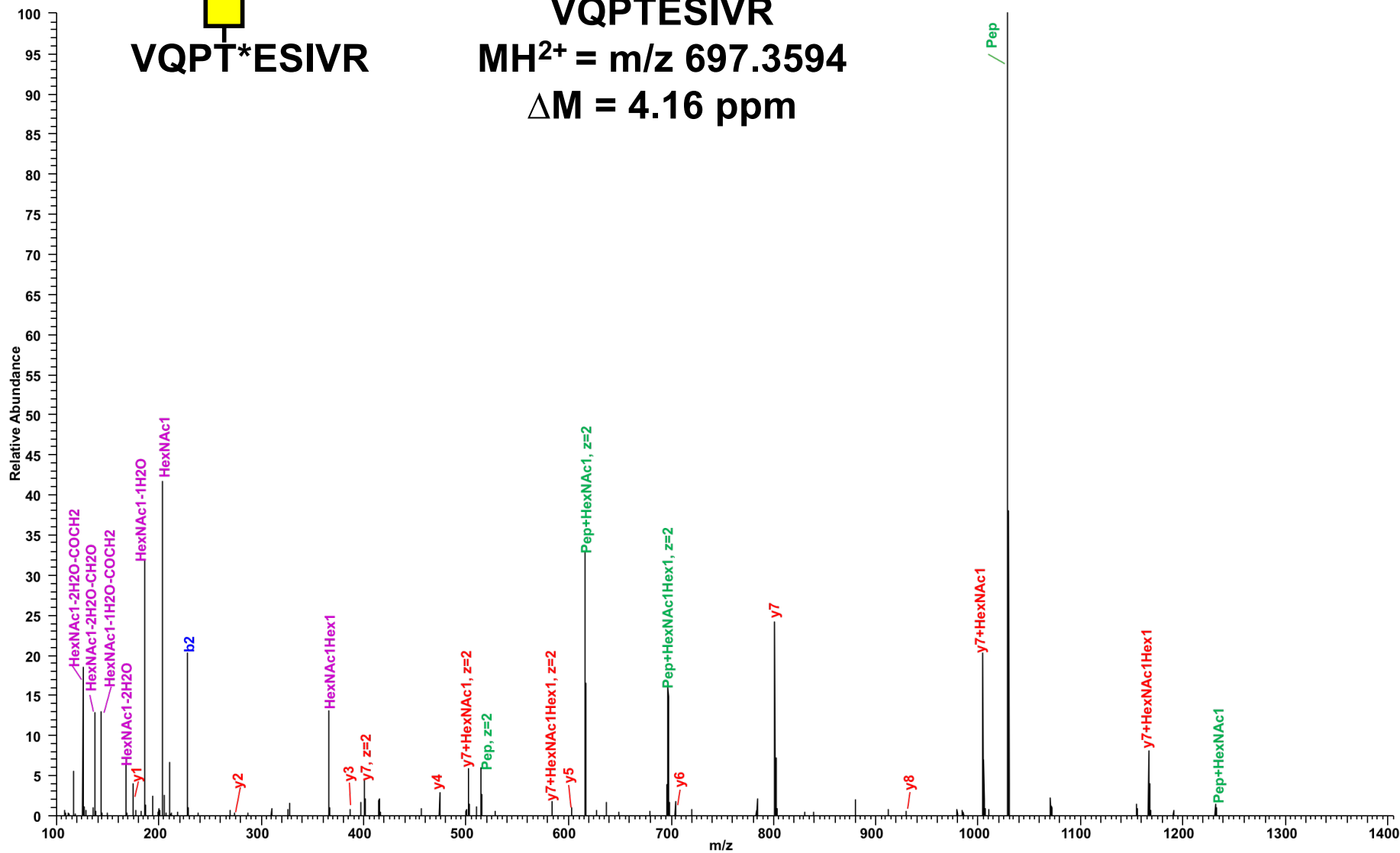

VQPT*ESIVR

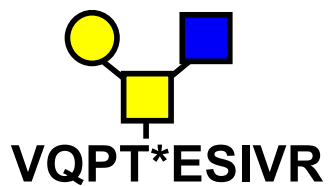
Peptide (Pep):
VQPTESIVR
 $MH^{2+} = m/z\ 616.3323$
 $\Delta M = 3.59\ \text{ppm}$



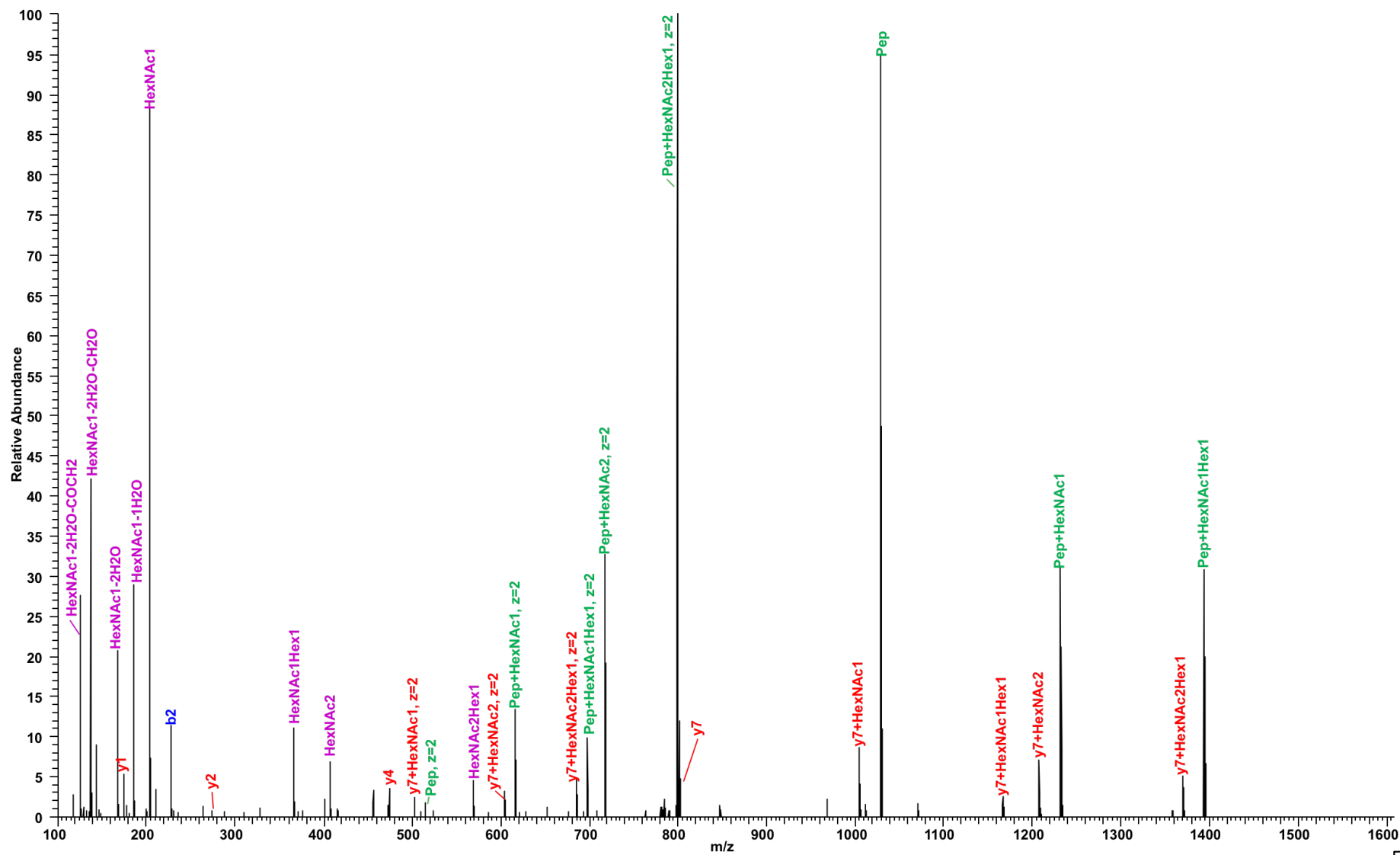


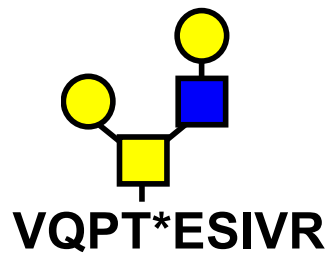
Peptide (Pep):
VQPTESIVR
 $MH^{2+} = m/z 697.3594$
 $\Delta M = 4.16 \text{ ppm}$



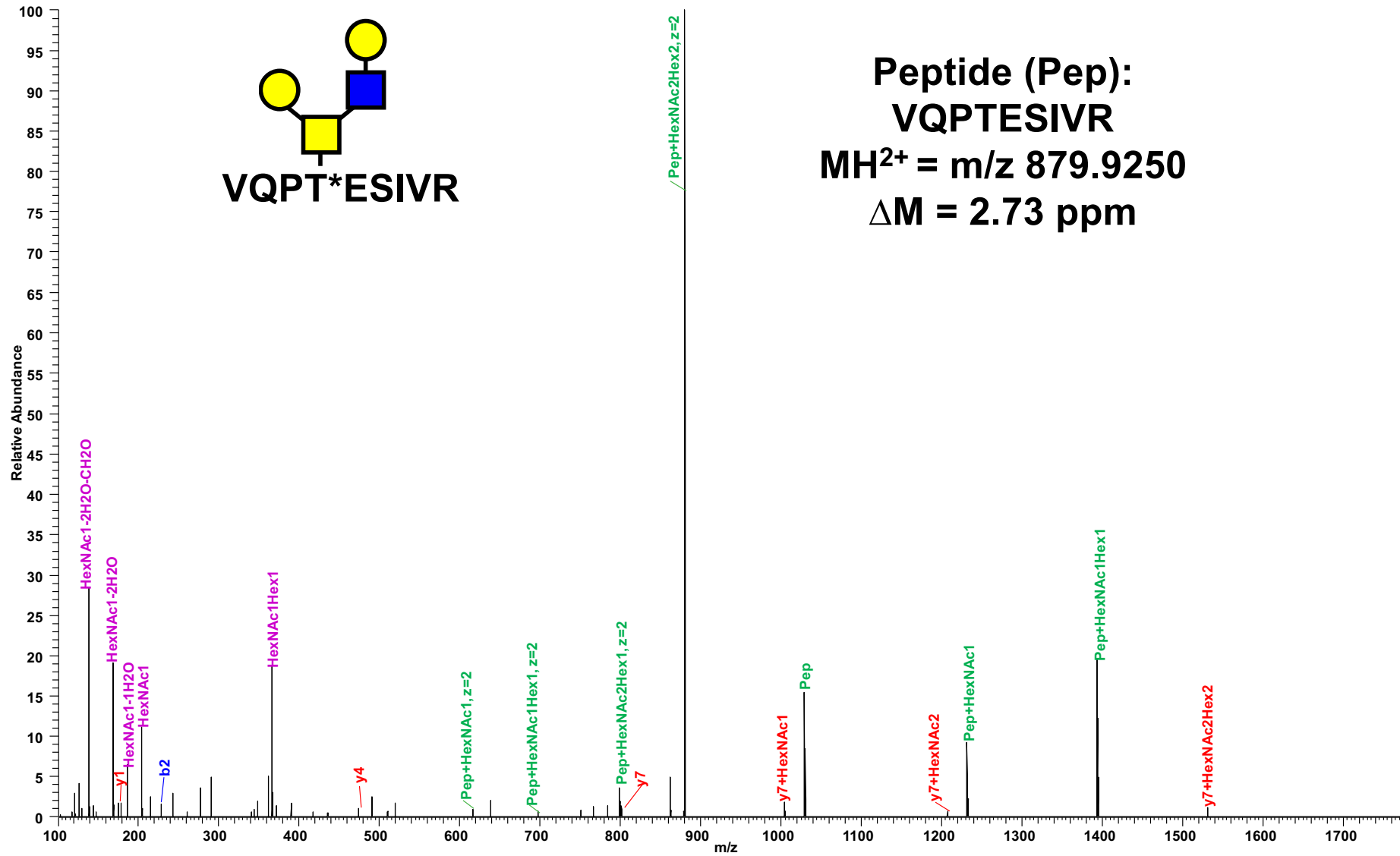


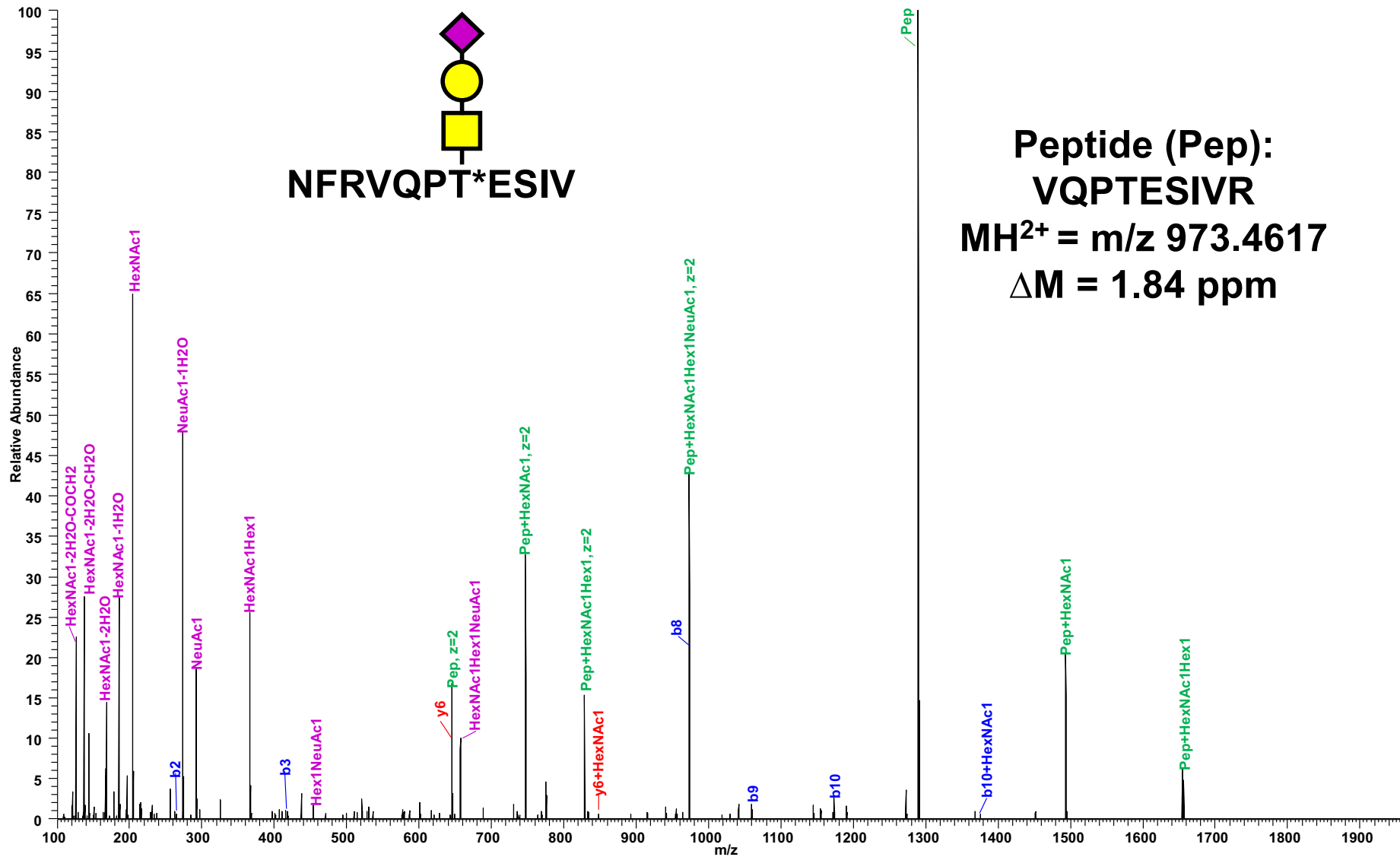
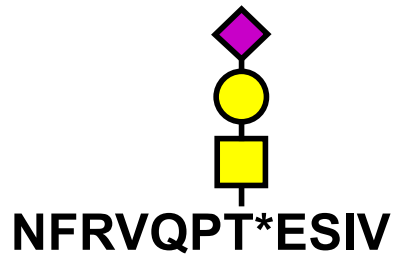
Peptide (Pep):
 VQPTESIVR
 $MH^{2+} = m/z\ 798.8979$
 $\Delta M = 2.15\ \text{ppm}$



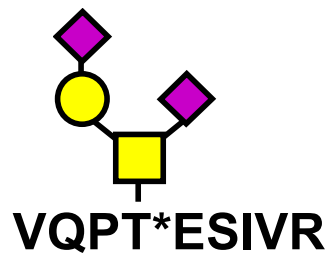


Peptide (Pep):
VQPTESIVR
 $MH^{2+} = m/z\ 879.9250$
 $\Delta M = 2.73\ \text{ppm}$

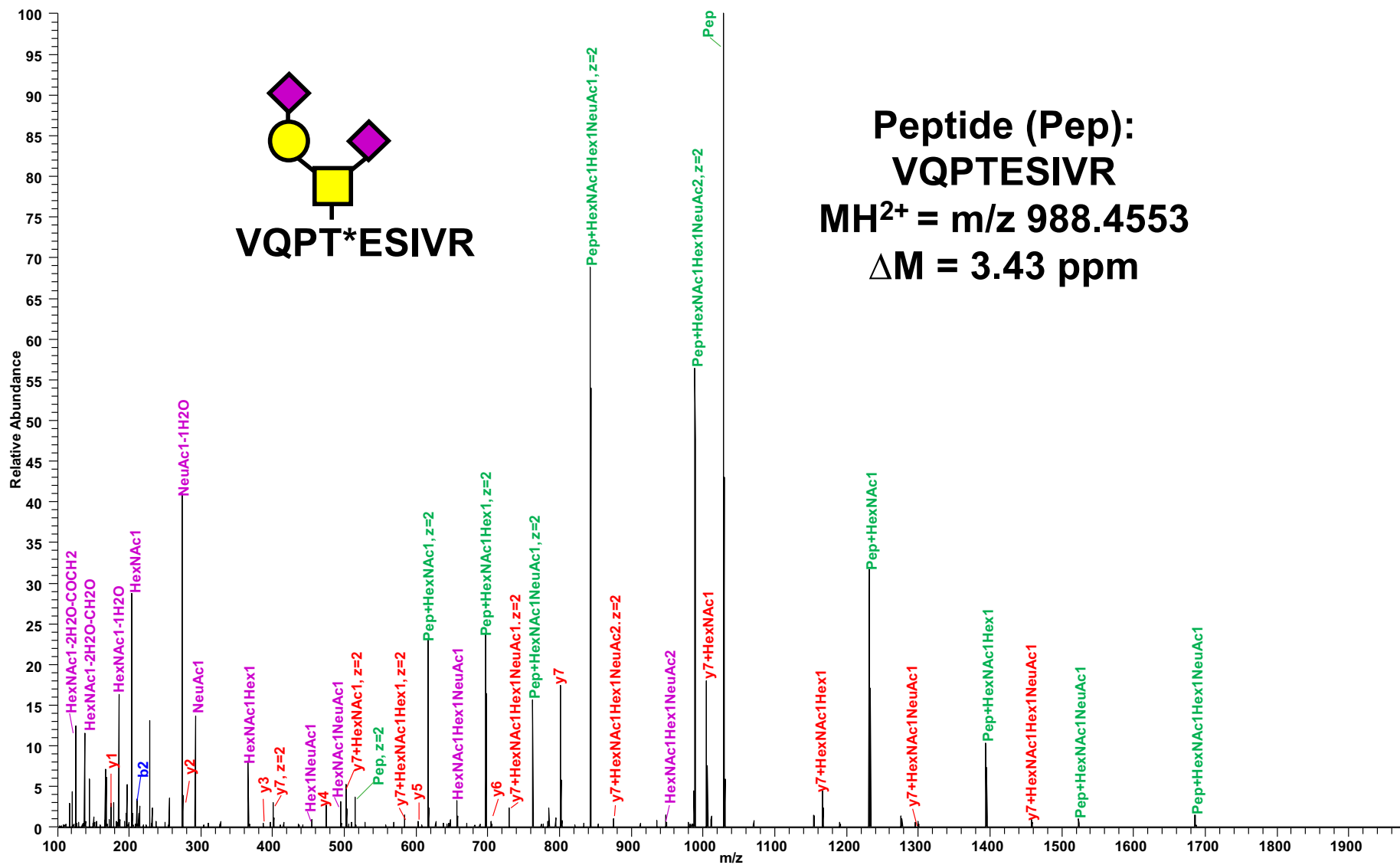




Peptide (Pep):
VQPTESIVR
MH²⁺ = m/z 973.4617
ΔM = 1.84 ppm



Peptide (Pep):
VQPTESIVR
 $MH^{2+} = m/z\ 988.4553$
 $\Delta M = 3.43\ \text{ppm}$




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AAP13441.1 ... LTSGSDLRCTTFDDVQA--PNYTQHTSSMRGVVYPD ... FLPFYSNVTGFHTI-----NHT--FGNPVI ...
AGZ48831.1 ... LVSSYTIEKCLDFDDRT--PPANTQFLSSHRGVVYPD ... FLPFDSNVTRFITFGLN-----FDNPII ...
AVP78031.1 ... LVNS----QCVNLTGRTPLNPNYTN--SSQRGVVYPD ... FLPFYSNVSWYYSLTTNNA-ATKRTDNPIL ...
AVP78042.1 ... LVNS----QC-DLTGRTPLNPNYTN--SSQRGVVYPD ... FLPFYSNVSWYYSLTTNNA-ATKRTDNPIL ...
QIA48641.1 ... LVSS----QCVNLTTRTGIPPGYTN--SSTRGVVYPD ... FLPFFSNVTWFNTI--TYQGGSKKFDNPVL ...
QIA48614.1 ... LVSS----QCVNLTTRTGIPPGYTN--SSTRGVVYPD ... FLPFFSNVTWFNTI--NYQGGSKKFDNPVL ...
QIQ54048.1 ... LVSS----QCVNLTTRTGIPPGYTN--SSTRGVVYPD ... FLPFFSNVTWFNTIHLNYQGGSKKFDNPVL ...
QIA48623.1 ... LVSS----QCVNLTTRTGIPPGYTN--SSTRGVVYPD ... FLPFFSNVTWFNTI--NYQGGSKKFDNPVL ...
QIA48632.1 ... LVSS----QCVNLTTRTGIPPGYTN--SSTRGVVYPD ... FLPFFSNVTWFNTI--NYQGGSKKFDNPVL ...
YP_009724390.1 ... LVSS----QCVNLTTRTQLPPAYTN--SFTRGVVYPD ... FLPFFSNVTWFHAIHVSGTNGTKRFDNPVL ...
QHR63300.2 ... LVSS----QCVNLTTRTQLPPAYTN--SSTRGVVYPD ... FLPFFSNVTWFHAIHVSGTNGIKRFDNPVL ...
*... * : * * : * ***** **** ** : : : ** :

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AAP13441.1 ... FGSTMNNKSQSVIIINNSTNVIRAC ... PFFAVSKPMGTQTHM---IFDNAFNCTFEYIS ...
AGZ48831.1 ... FGSTMNNKSQSVIIMNSTNLVIRAC ... PFF--VLKSNNTQ-IPSY-IFNNAFNCTFEYVS ...
AVP78031.1 ... FGTTLDNTSQSLLIVNNATNVIKVC ... PYLSGYYH-NKTWSIREFAVSSYANCTFEYVS ...
AVP78042.1 ... FGTTLDNTSQSLLIVNNATNVIKVC ... PYLSGYYH-NKTWSIREFAVSFYANCTFEYVS ...
QIA48641.1 ... FGTTLDARTQSLLIVNNATNVIKVC ... PFLGVYYHNNKTWENEFRVSSANNCTFEYIS ...
QIA48614.1 ... FGTTLDARTQSLLIVNNATNVIKVC ... PFLGVYYHNNKTWENEFRVSSANNCTFEYIS ...
QIQ54048.1 ... FGTTLDARTQSLLIVNNATNVIKVC ... PFLGVYYHNNKTWENEFRVSSANNCTFEYIS ...
QIA48623.1 ... FGTTLDARTQSLLIVNNATNVIKVC ... PFLGVYYHNNKTWENEFRVSSANNCTFEYIS ...
QIA48632.1 ... FGTTLDARTQSLLIVNNATNVIKVC ... PFLGVYYHNNKTWENEFRVSSANNCTFEYIS ...
YP_009724390.1 ... FGTTLDSKTQSLLIVNNATNVIKVC ... PFLGVYYHKNNKSWMESEFRVSSANNCTFEYVS ...
QHR63300.2 ... FGTTLDSKTQSLLIVNNATNVIKVC ... PFLGVYYHKNNKSWMESEFRVSSANNCTFEYVS ...
**:* : **:*:*:*:*:*:*:* * : : : **:*:*:*:*

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AAP13441.1 ... FSLDVSEKSGNFKHLREFVF ... LPLGINITNFRAIL ...
AGZ48831.1 ... FNLDLGEKPGNFKDLREFVF ... LPLGINITNFRTLL ...
AVP78031.1 ... FMLNISGNGGLFNTLREFVF ... LPVSINITKFRTLL ...
AVP78042.1 ... FMLNISGNGGLFNTLREFVF ... LPVSINITKFRTLL ...
QIA48641.1 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
QIA48614.1 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
QIQ54048.1 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
QIA48623.1 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
QIA48632.1 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
YP_009724390.1 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
QHR63300.2 ... FLMDLEGKQGNFKNLREFVF ... LPIGINITRFQTL ...
* : : : * * : ***** **:*:*:*:*:*

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SARS-CoV-2 S related sequences alignments.

SARS-CoV-1 as well as bat and pangolin coronavirus sequences reported to be closely related to SARS-CoV-2 were selected and downloaded from NCBI. The S protein sequences from all of these genomes were aligned and analyzed in the regions containing sites of N-glycosylation.

