

Improving statistical certainty of glycosylation similarity between influenza A virus variants using data-independent acquisition mass spectrometry

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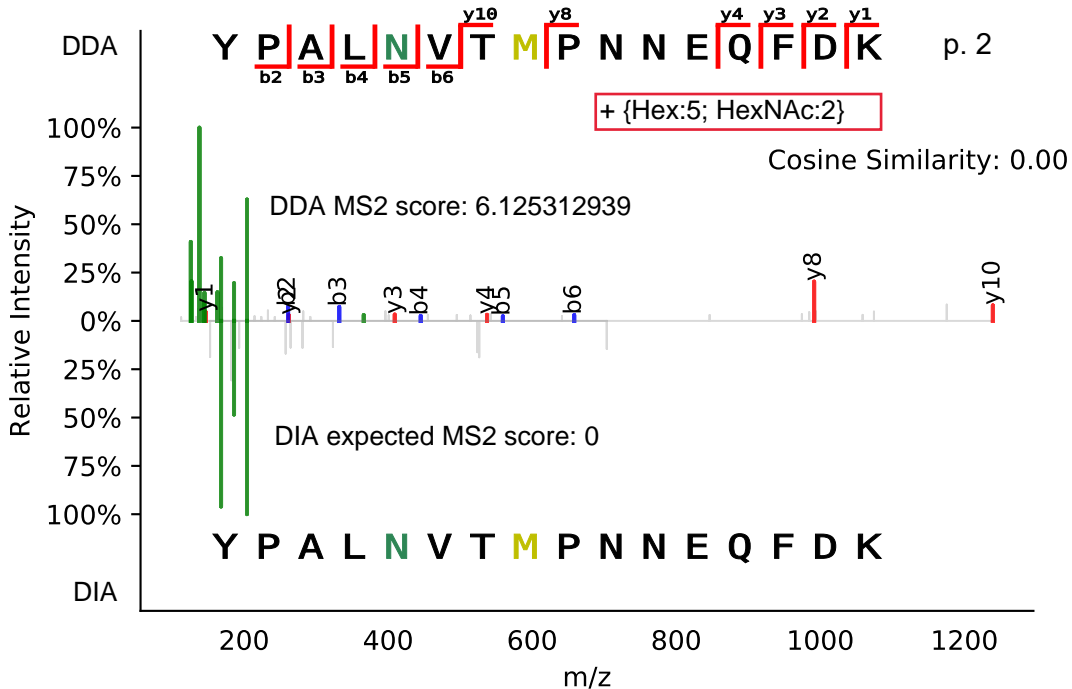
Supplementary File 3. Annotated tandem mass spectra for glycopeptides that were positively identified in the DDA data compared to spectra that failed to pass the scoring threshold in the DIA data.

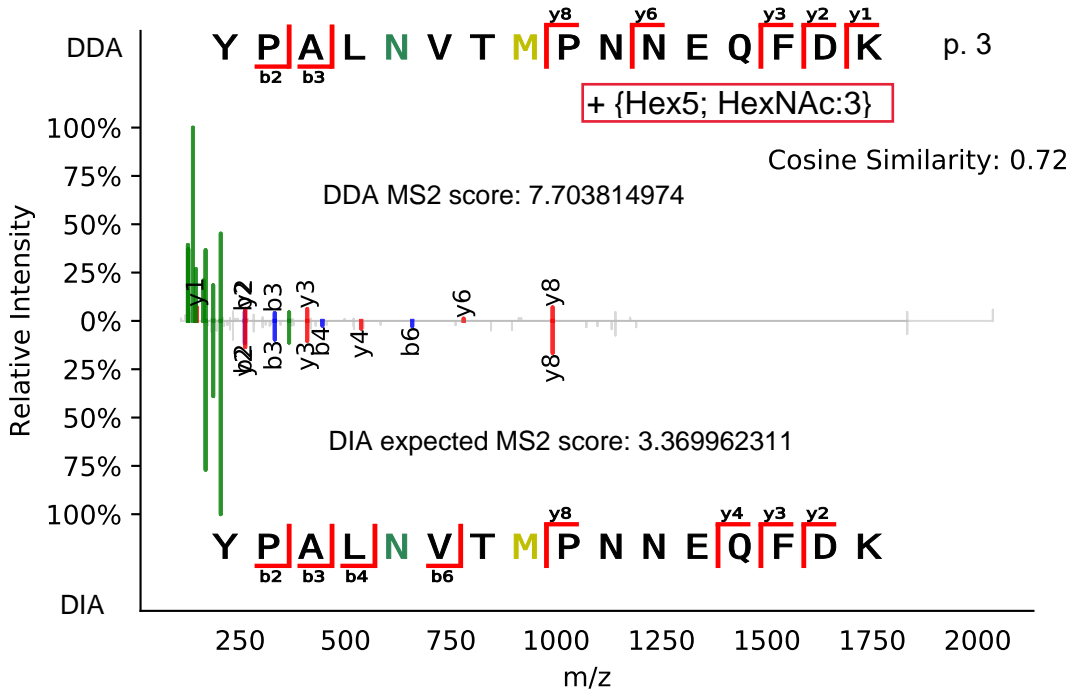
SWZ mutant cell pp. 2-3

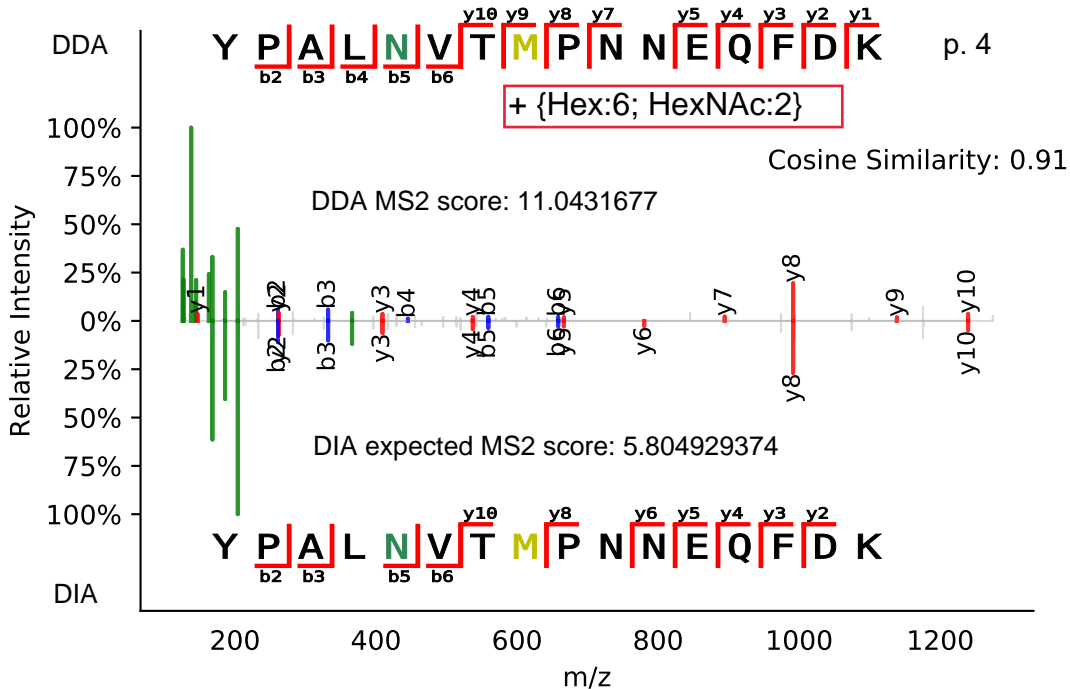
SWZ mutant egg pp. 4-7

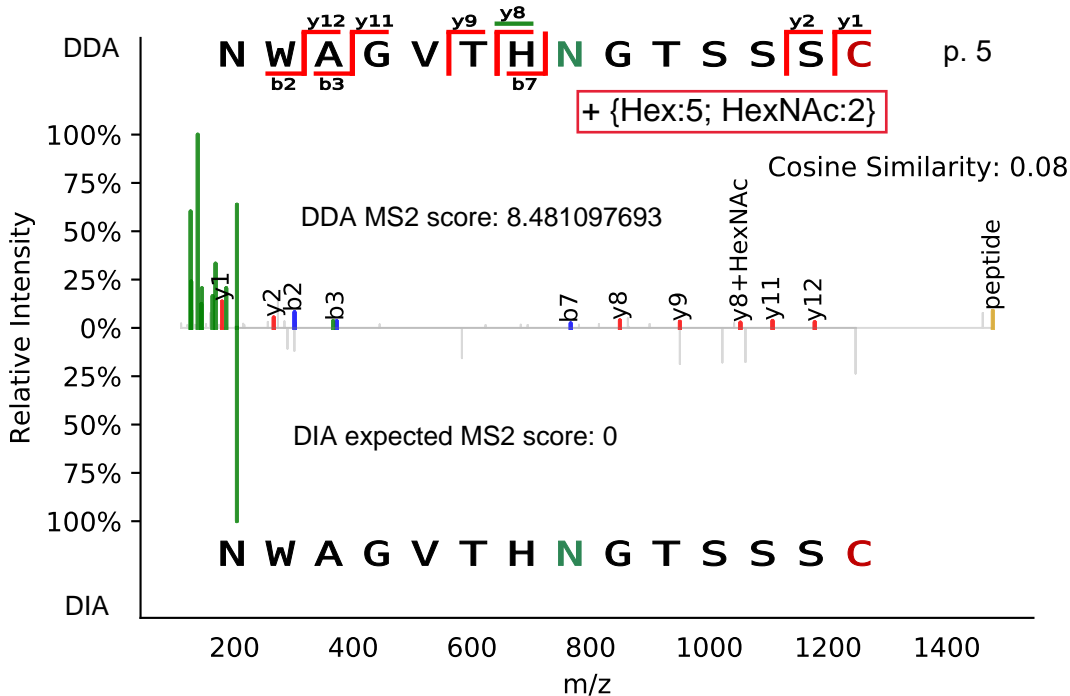
SWZ wild type cell pp. 8-11

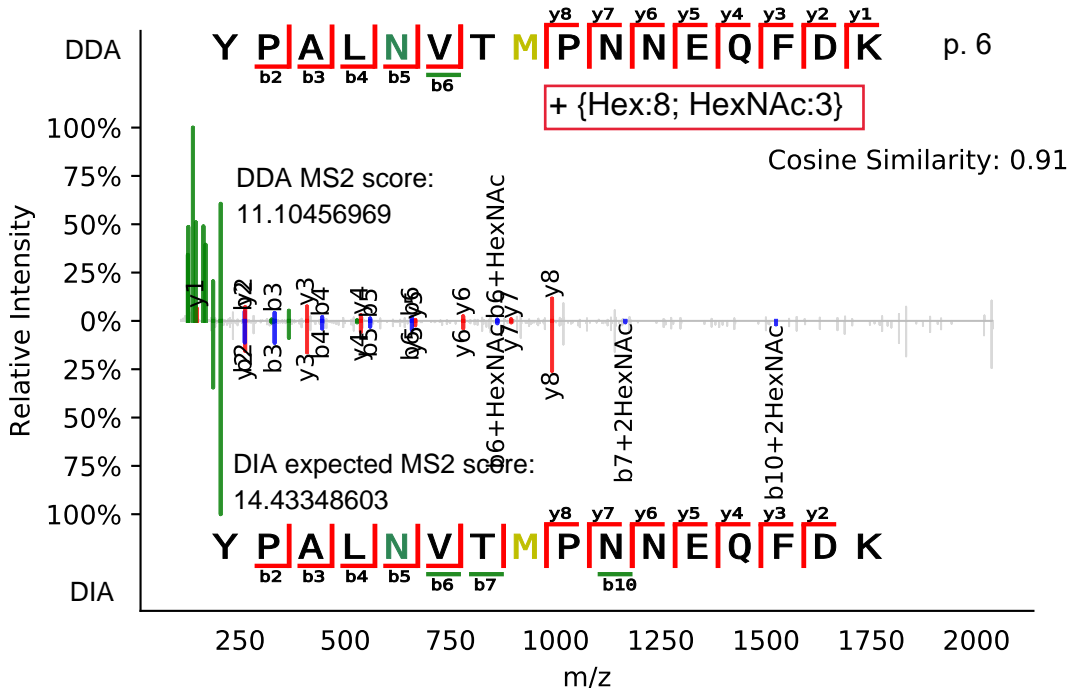
SWZ wild type egg pp. 12-21

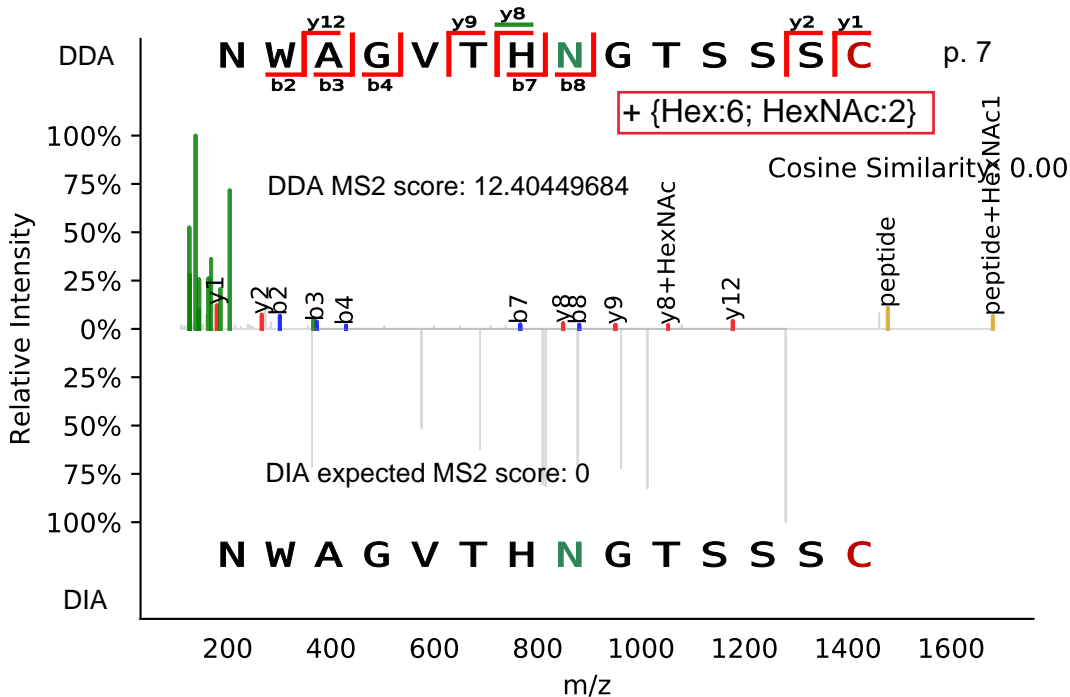


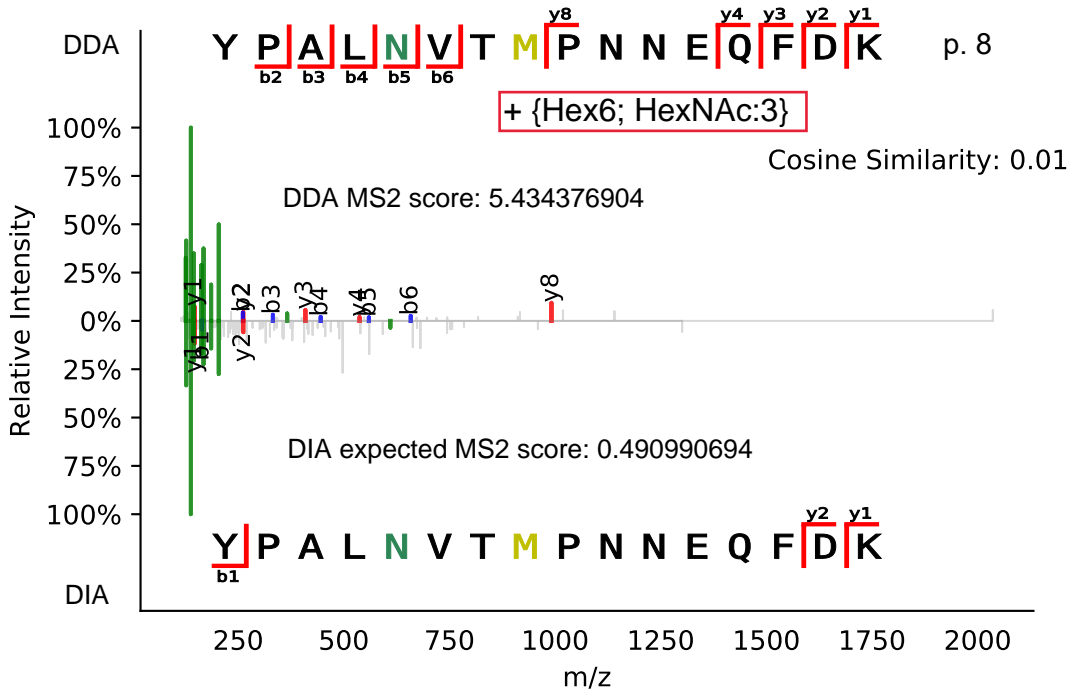


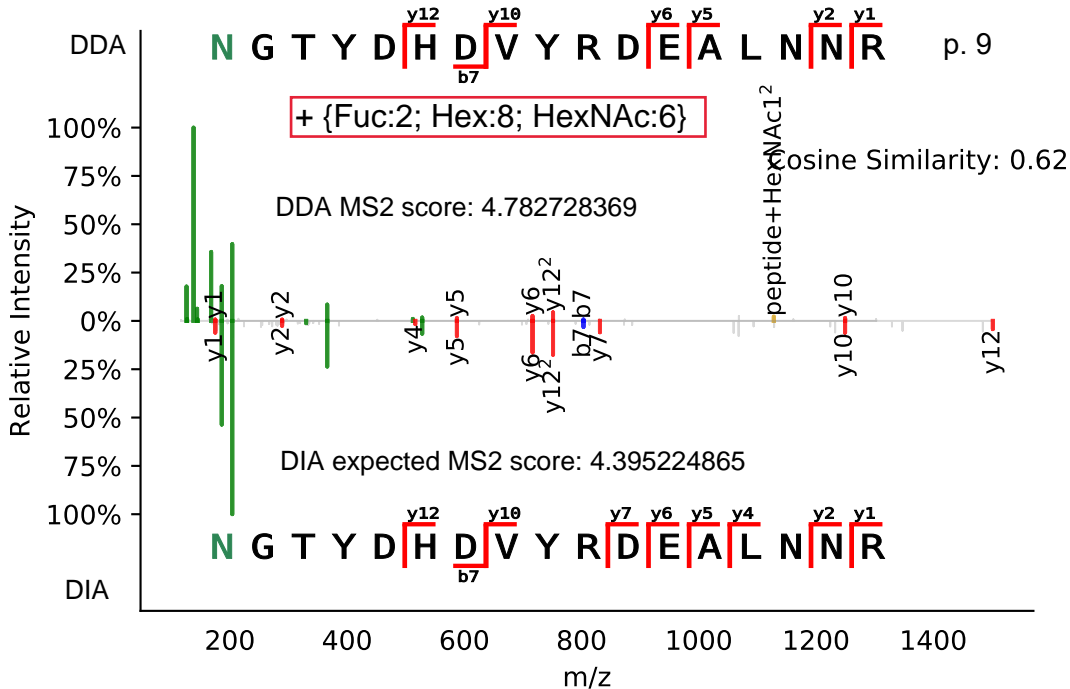


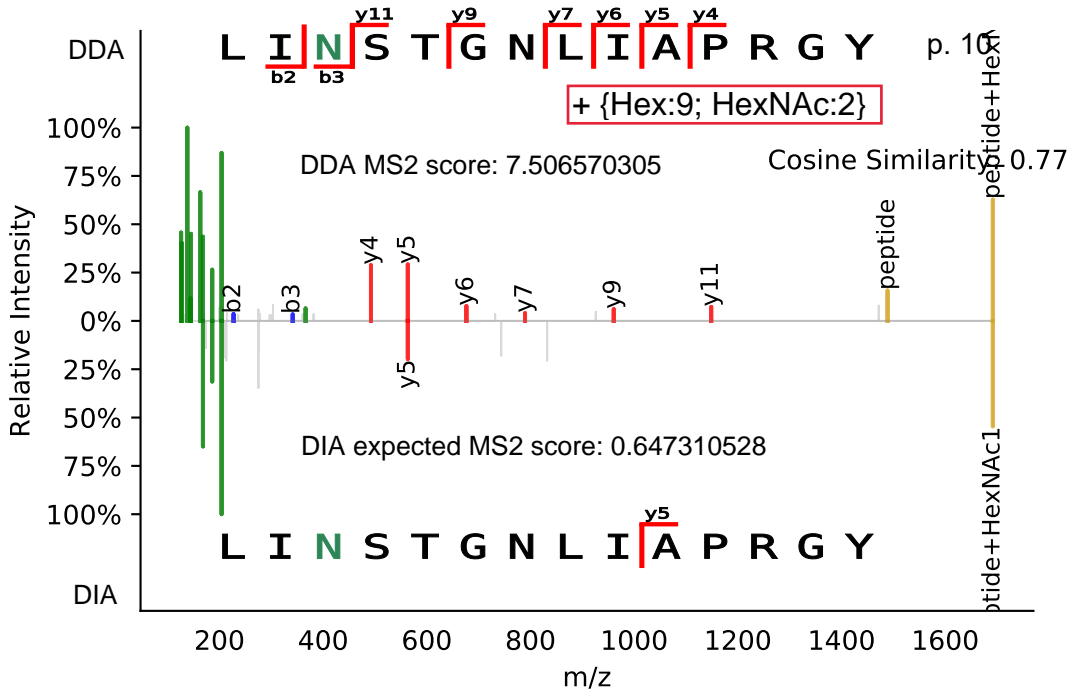




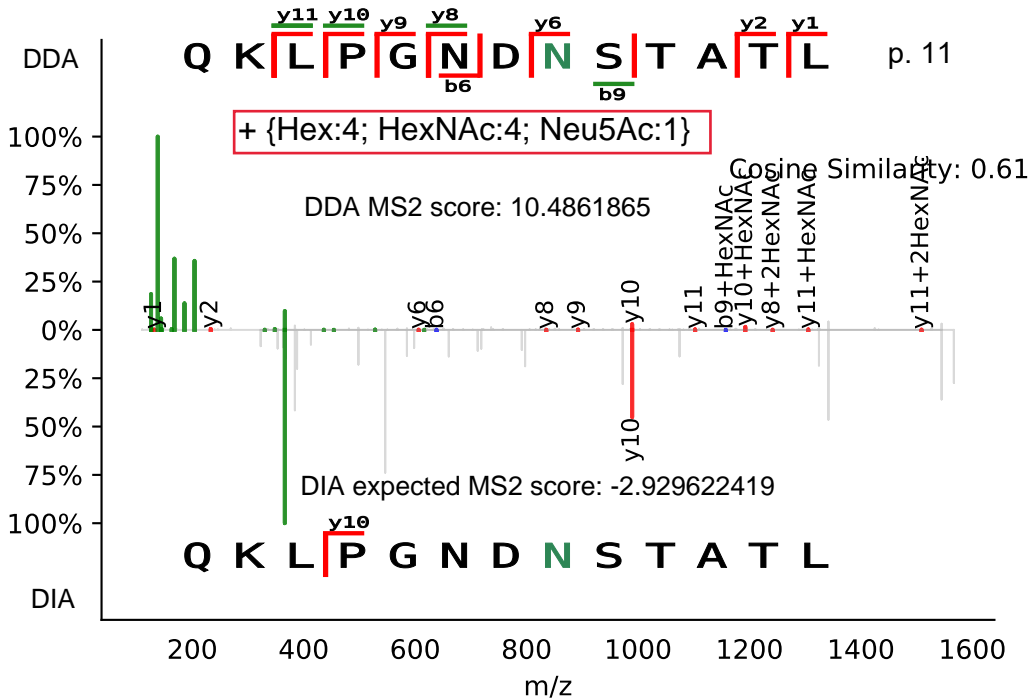


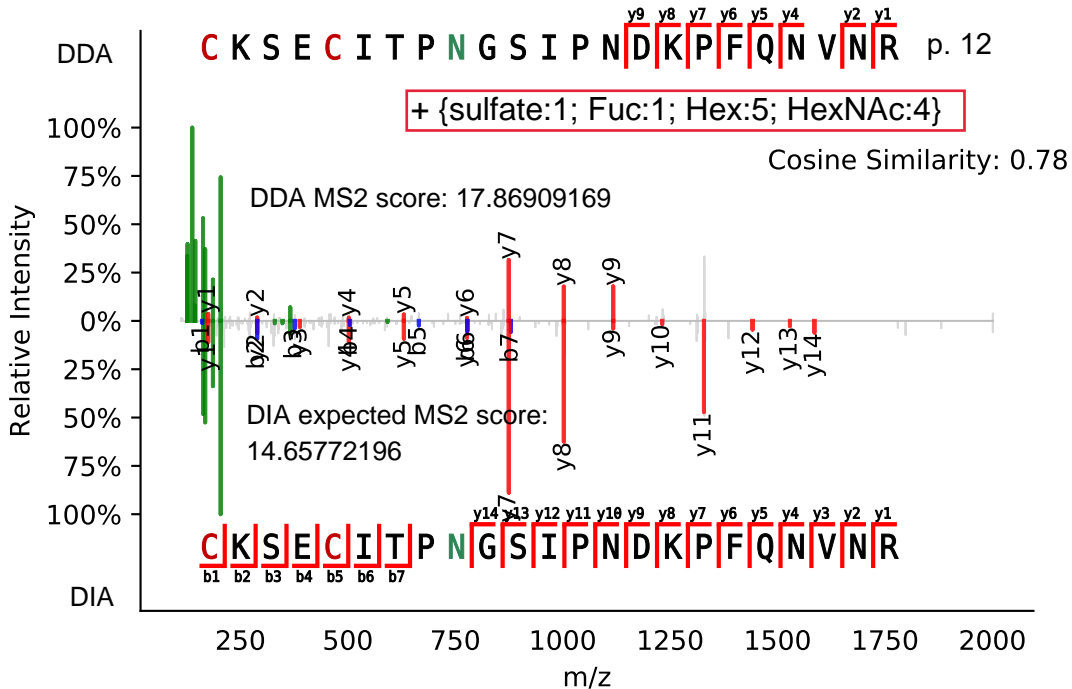


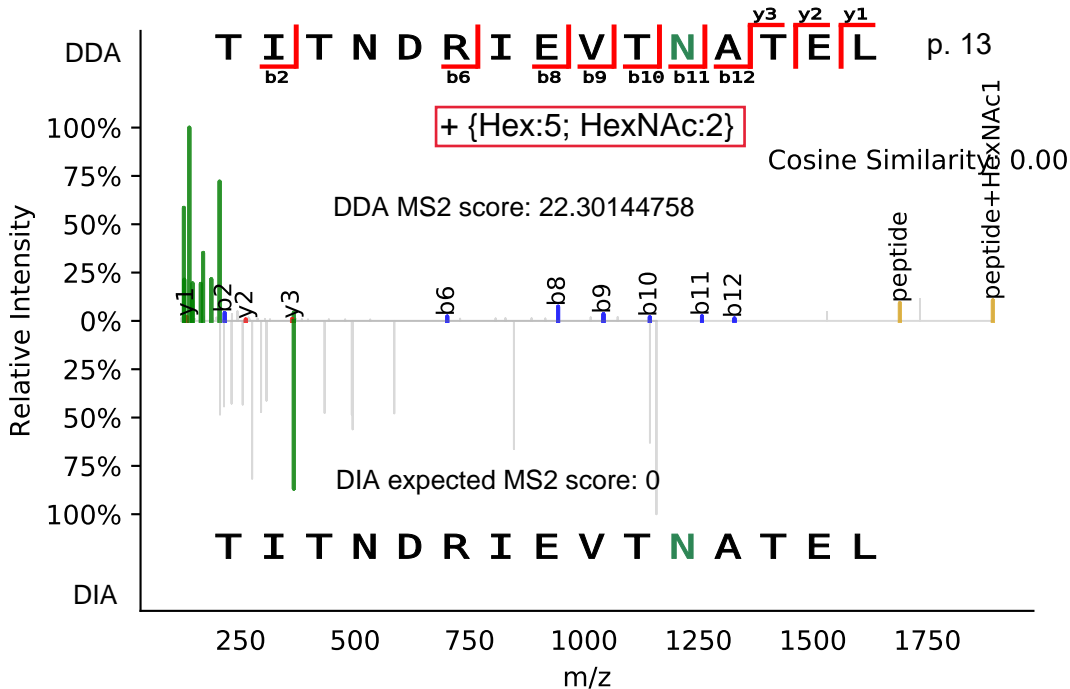


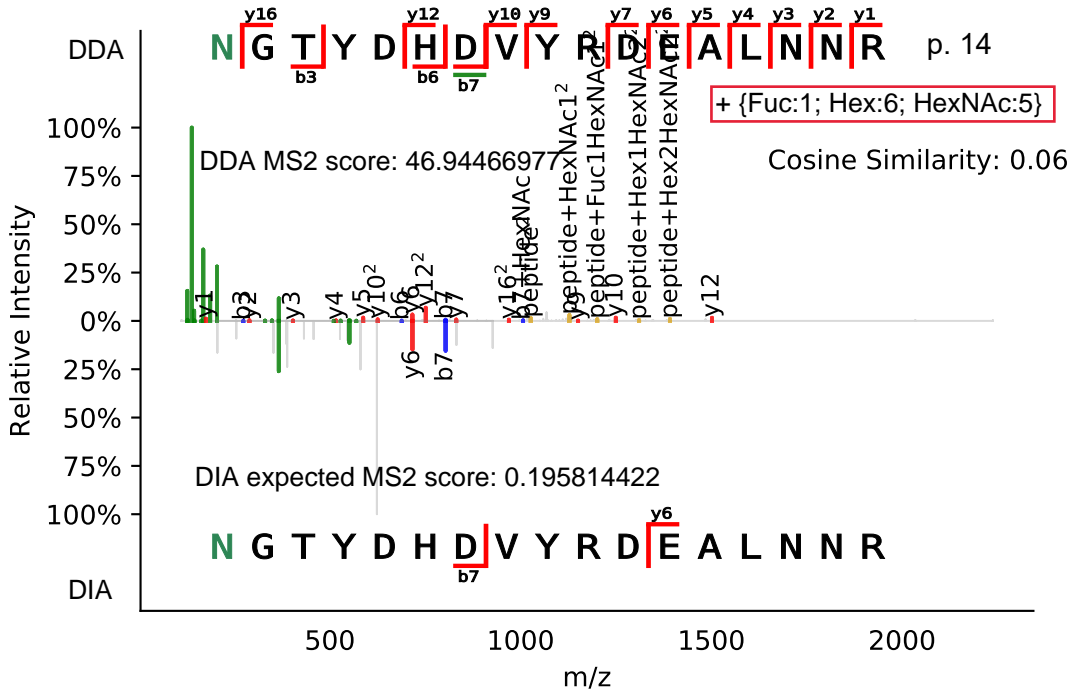


Relative Intensity

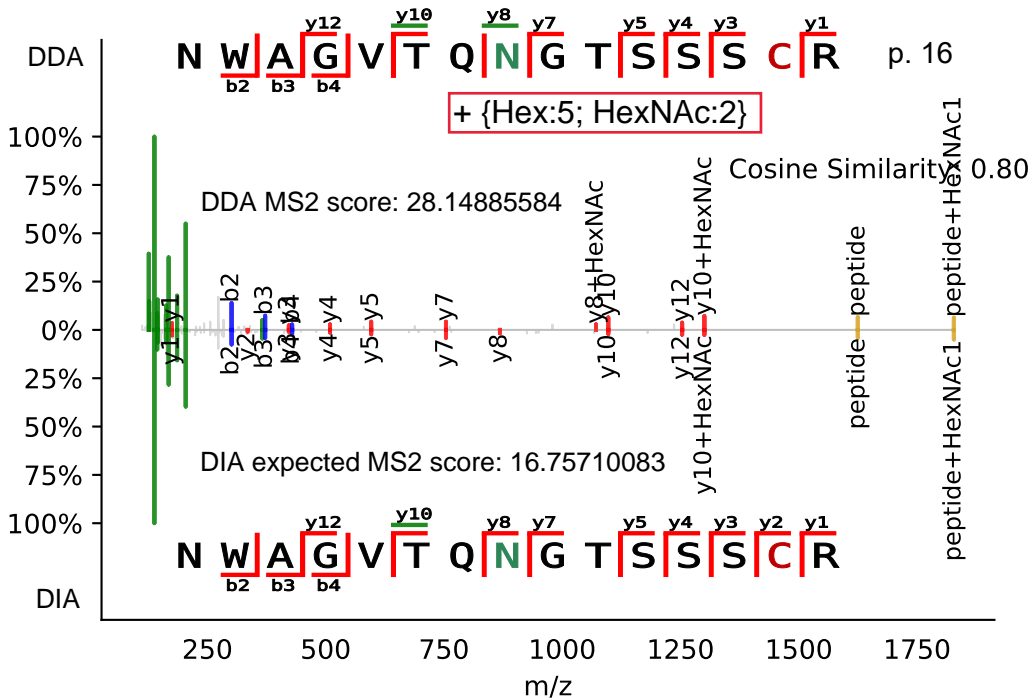


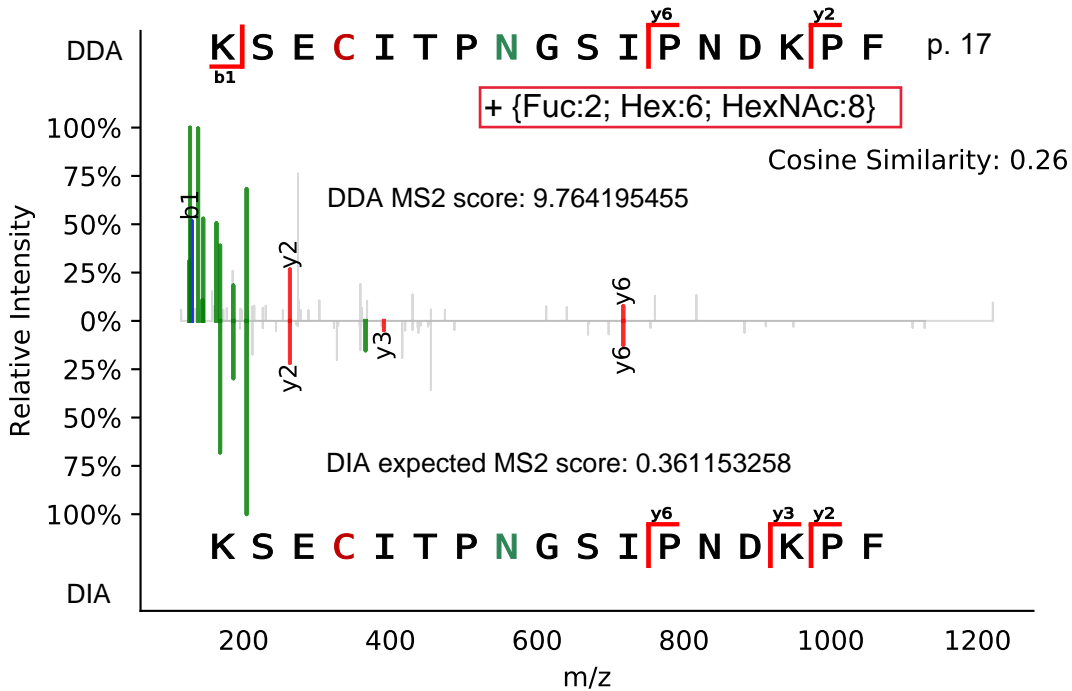


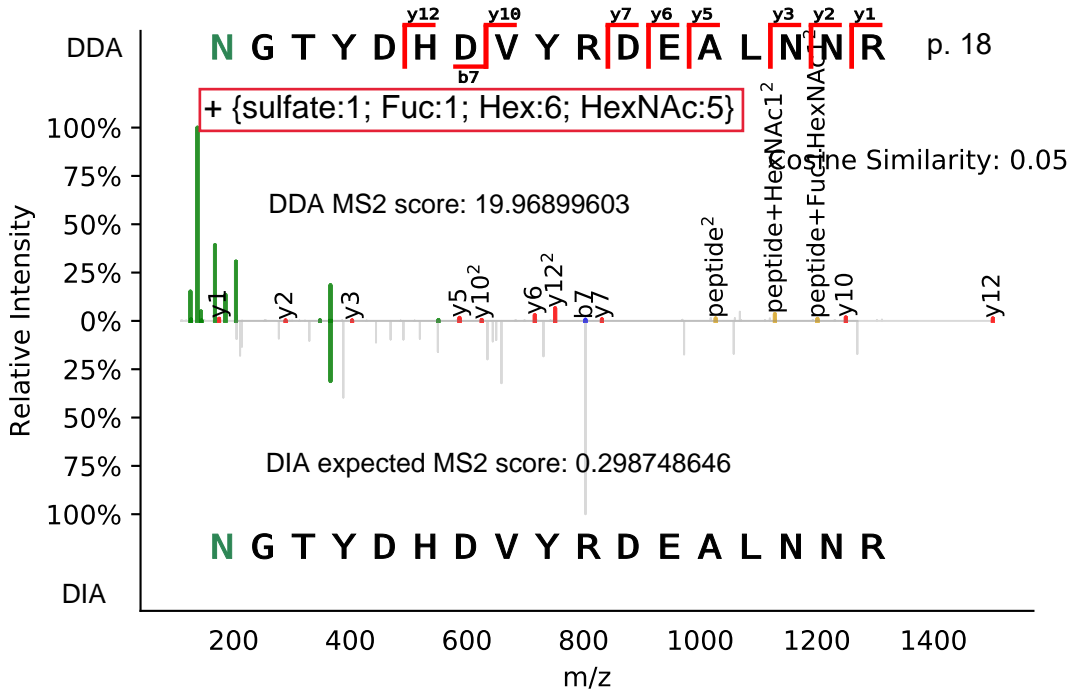


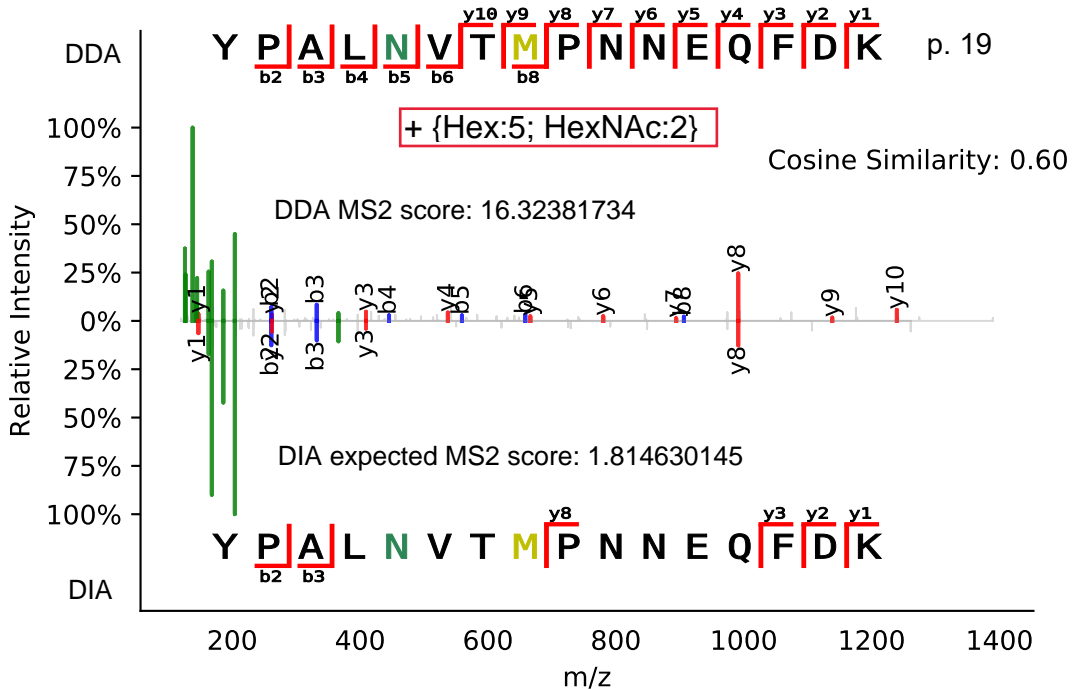


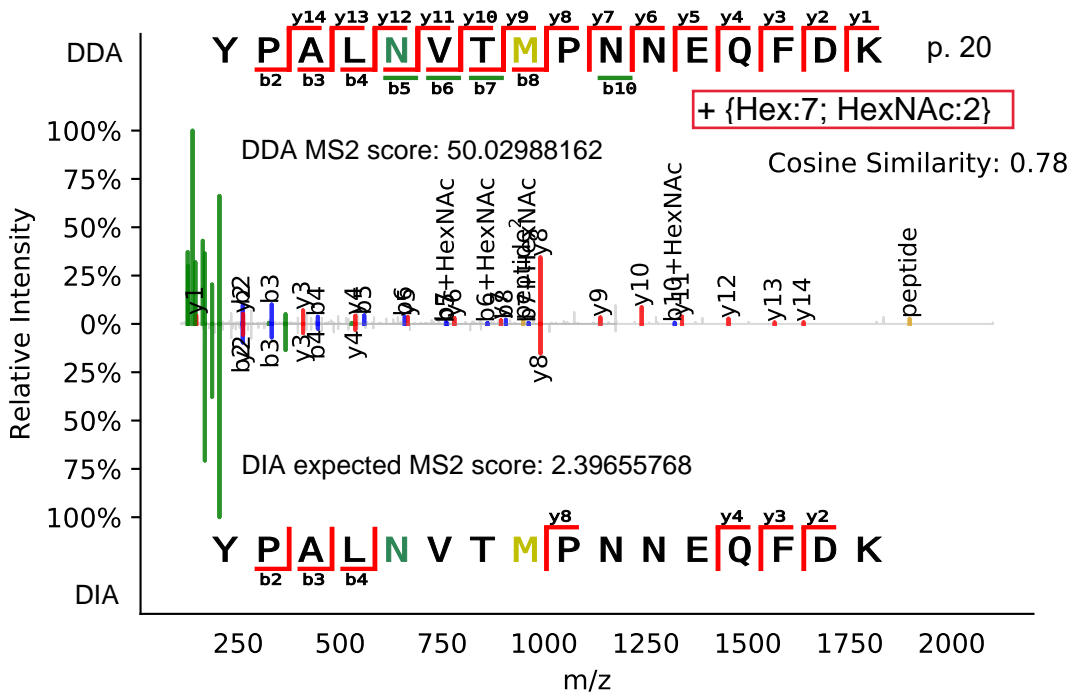
Relative Intensity











Relative Intensity

