

Experimental Spectrum Colour Code:

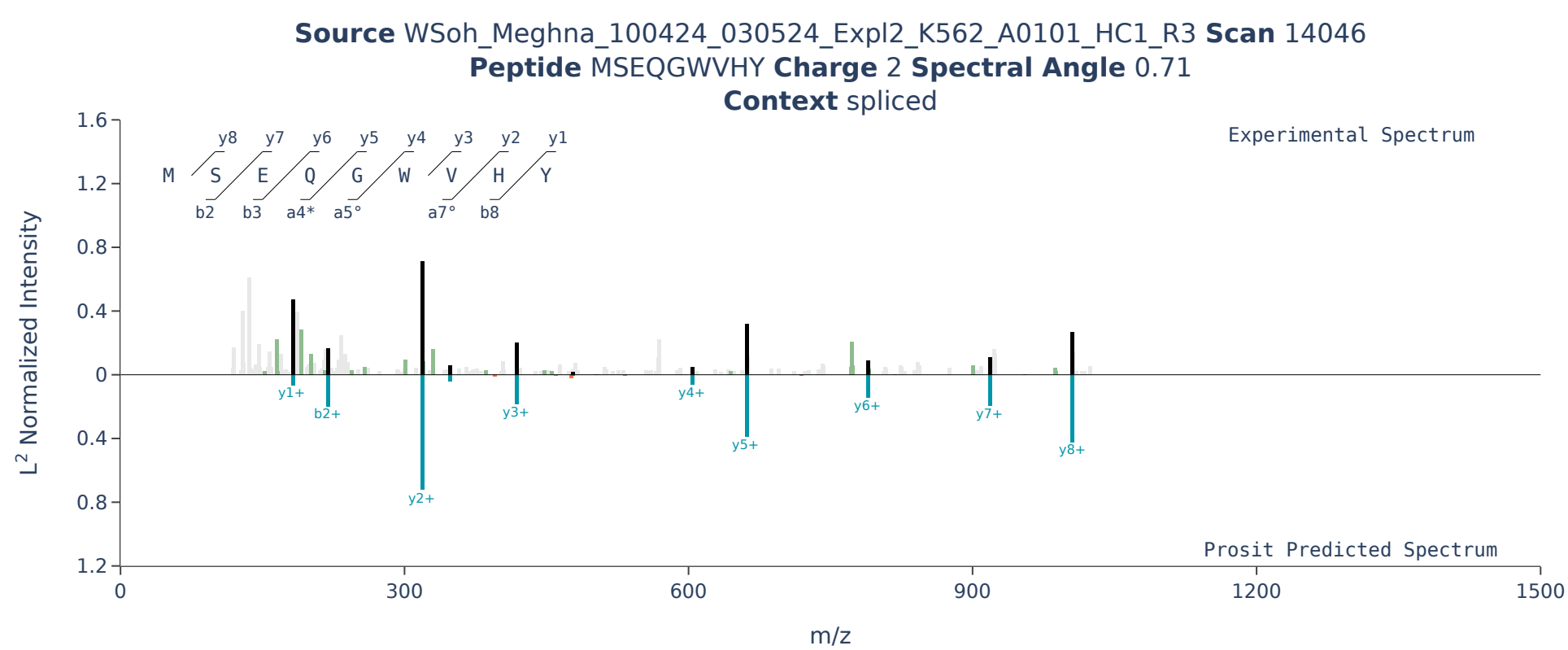
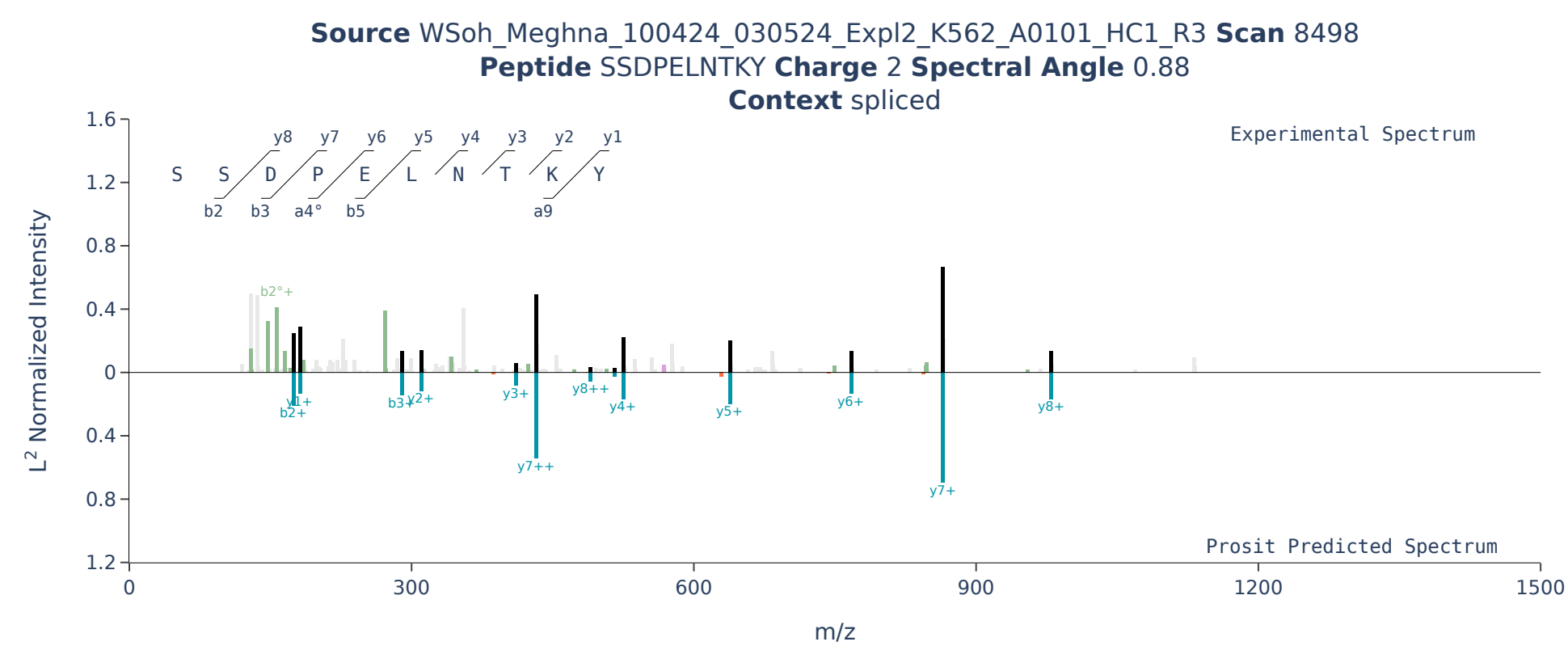
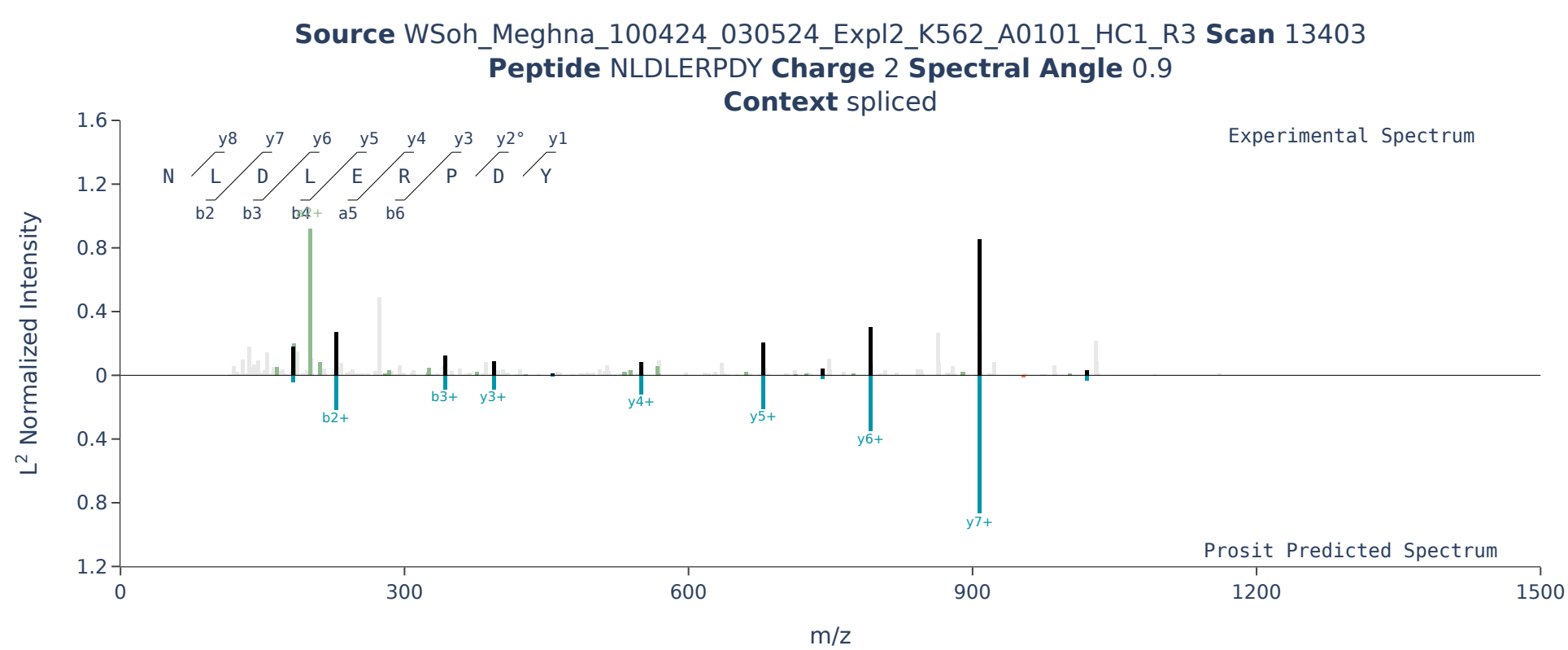
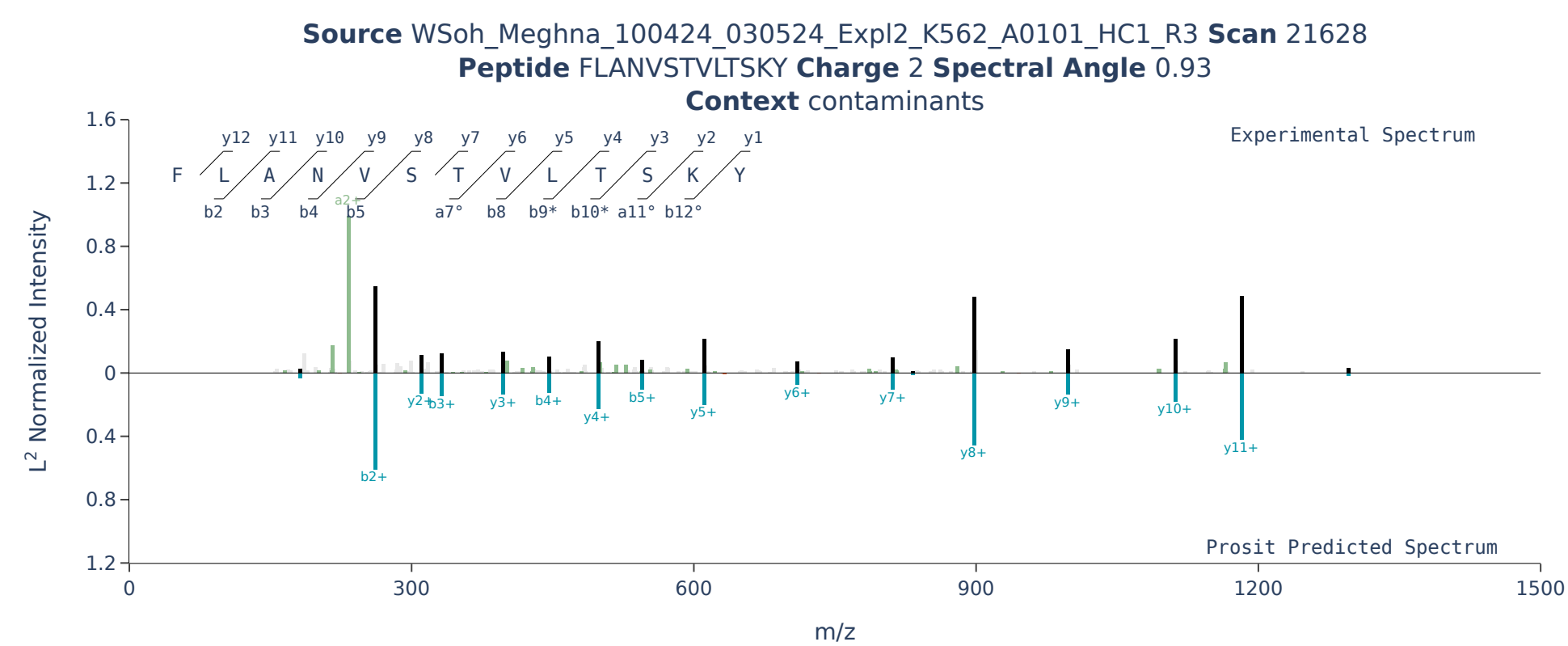
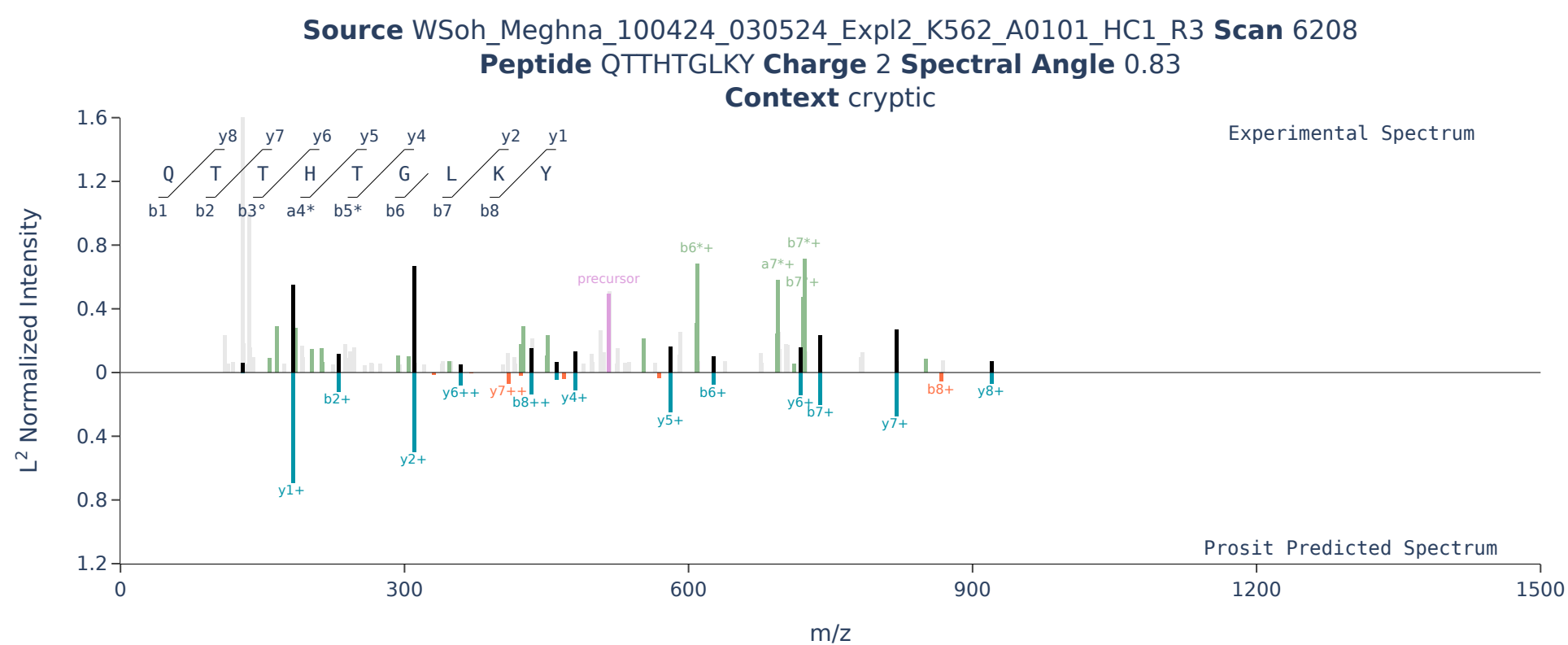
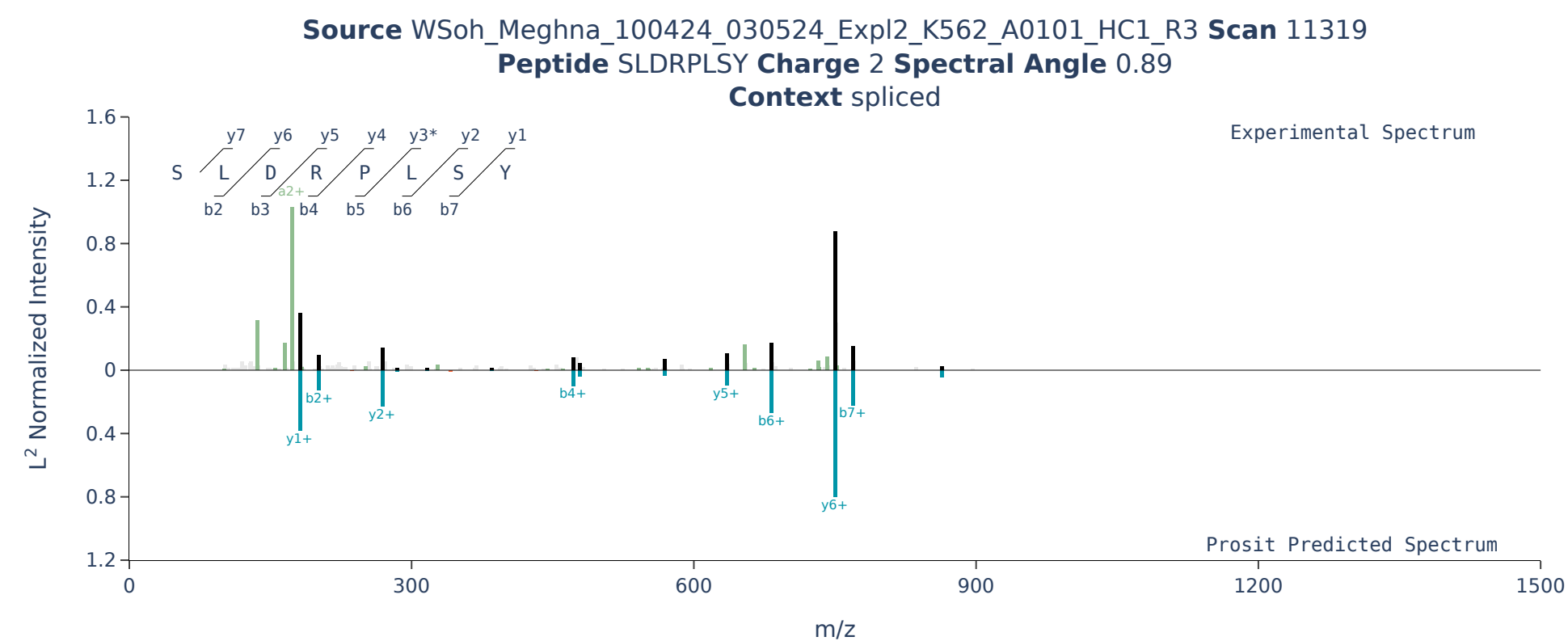
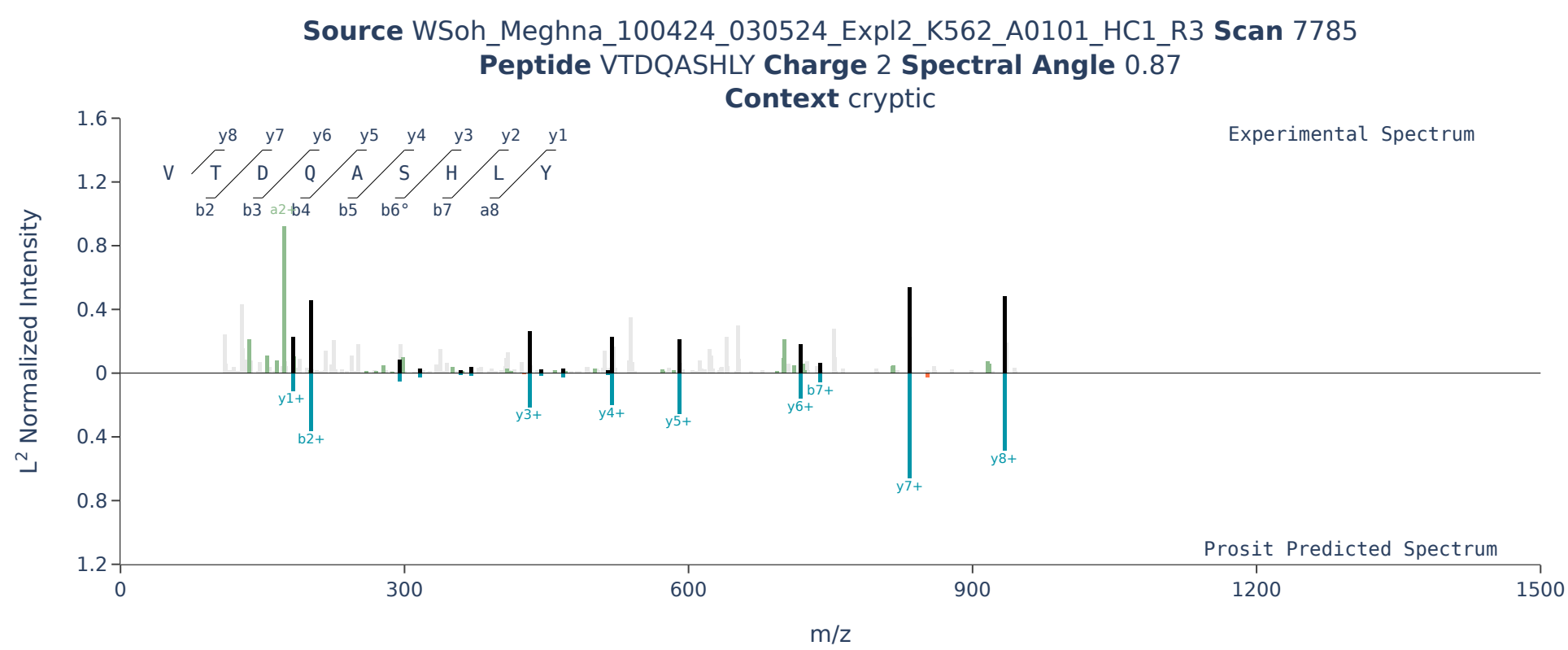
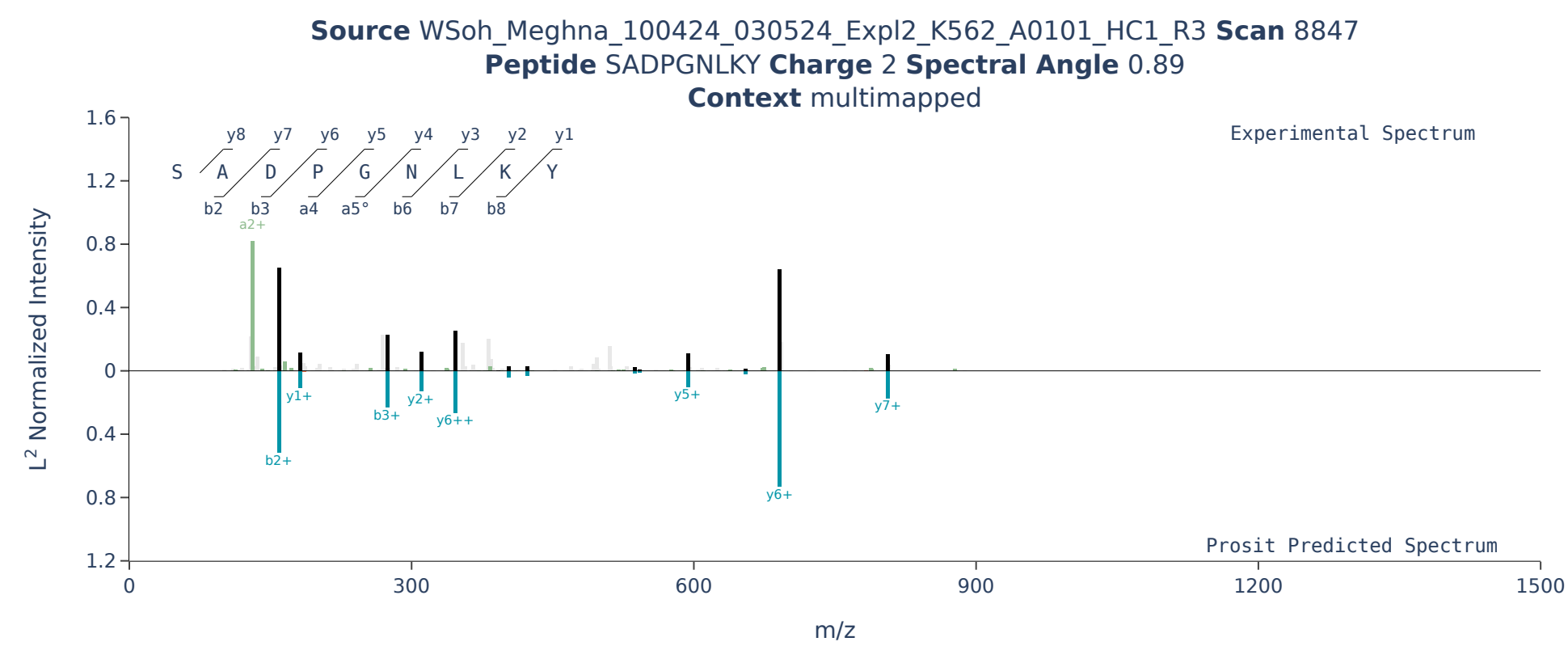
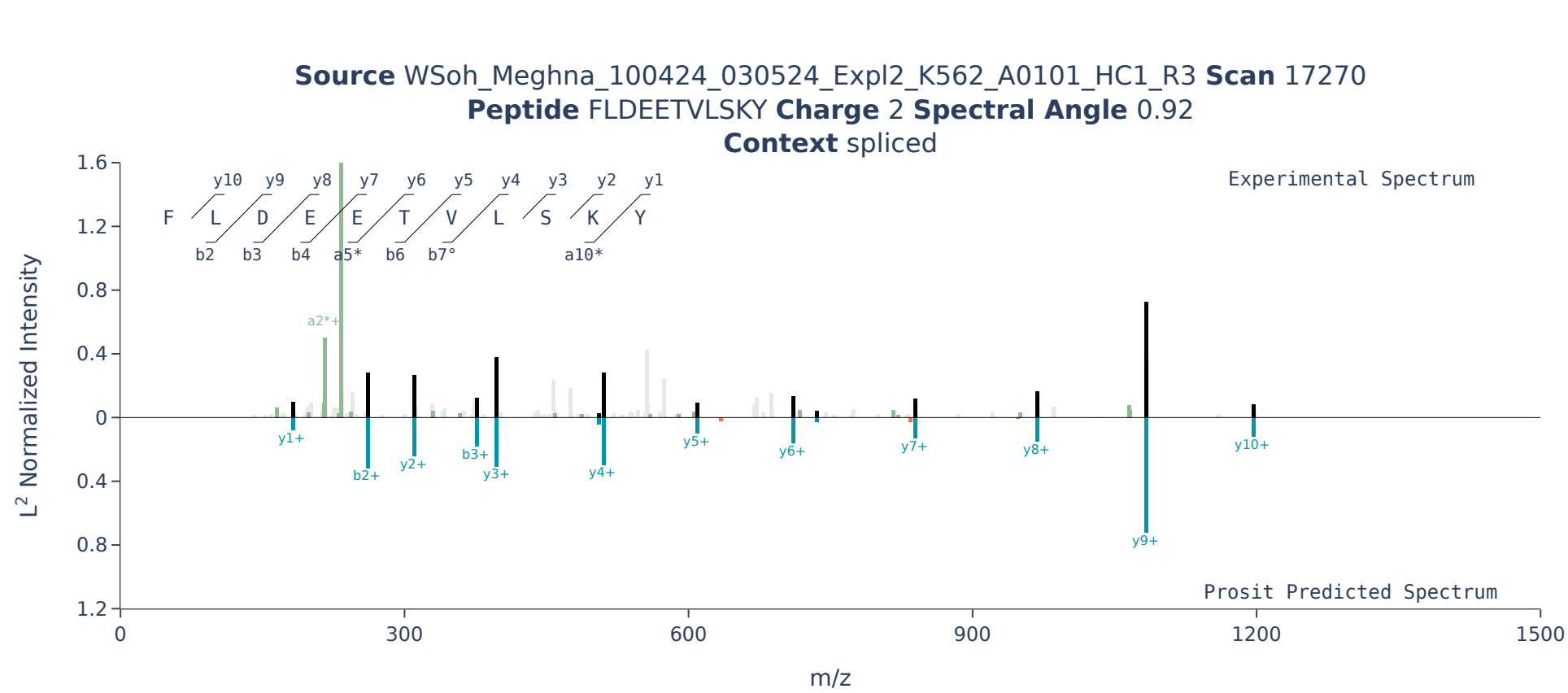
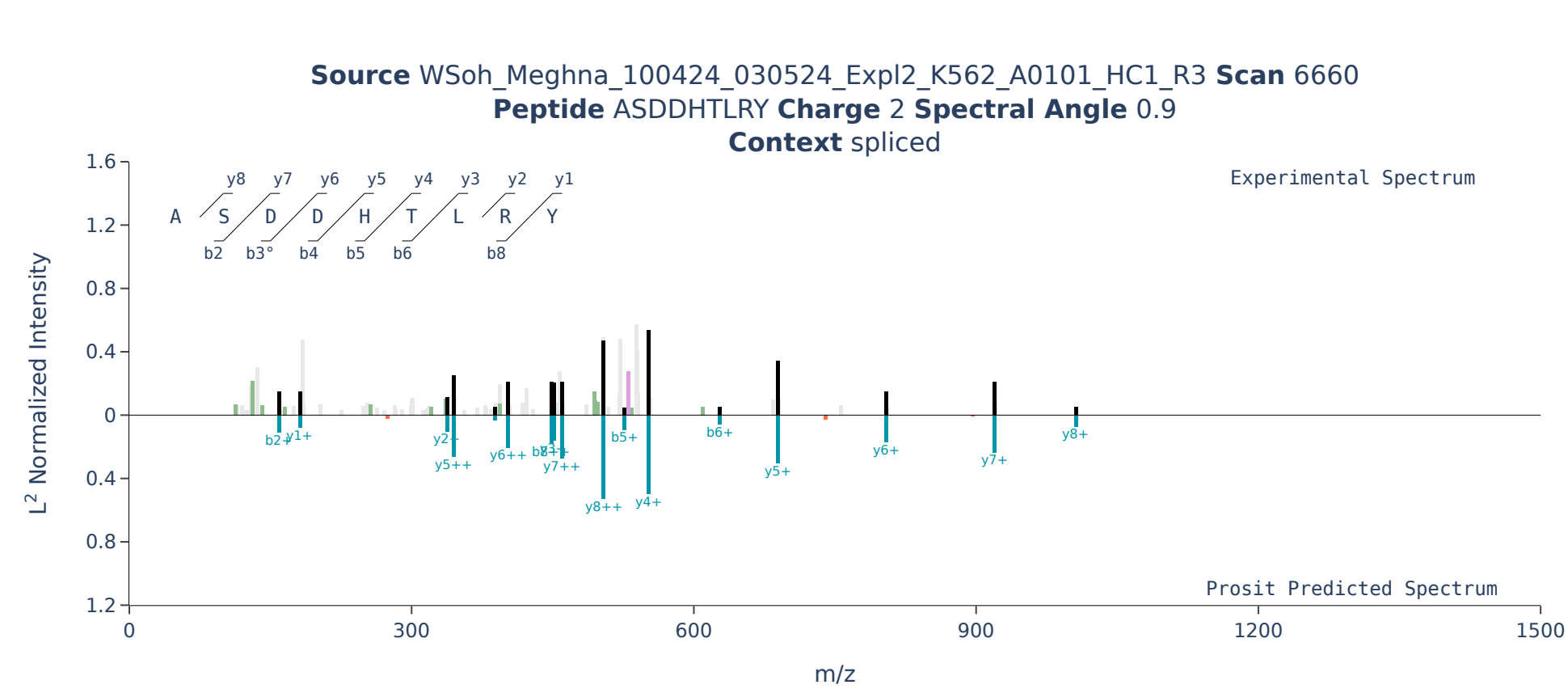
- Experimental peak matched to a Prosit predicted peak.
- Possible ion unknown to Prosit.
- Precursor matched peak.
- Experimental peak not matched to any potential ion.

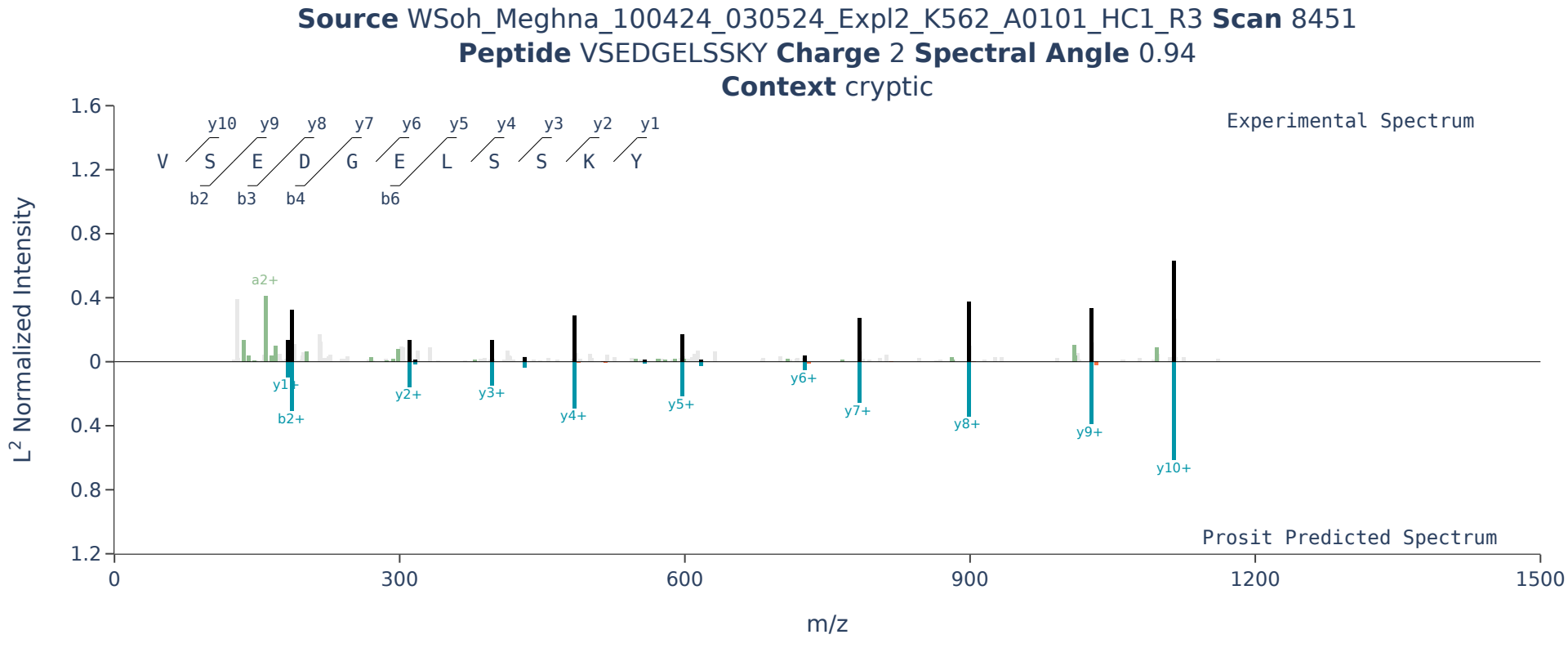
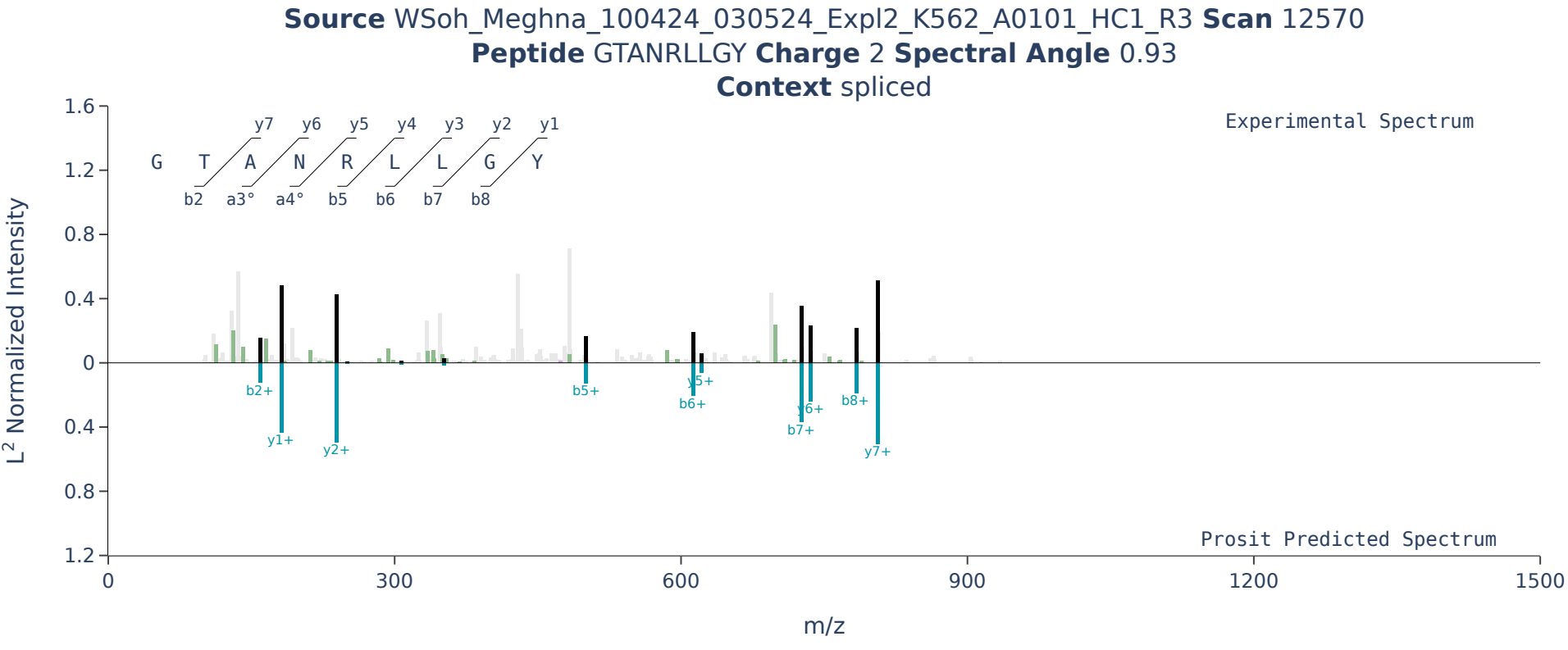
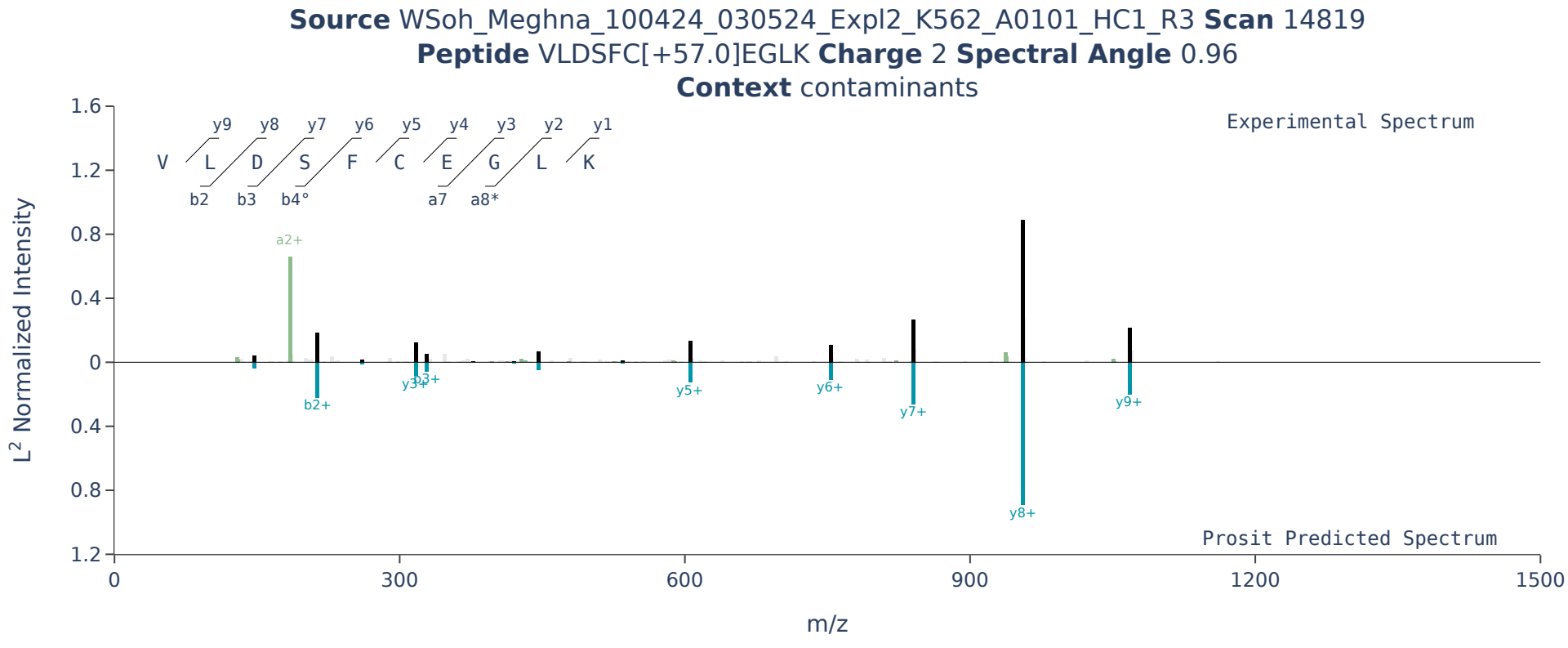
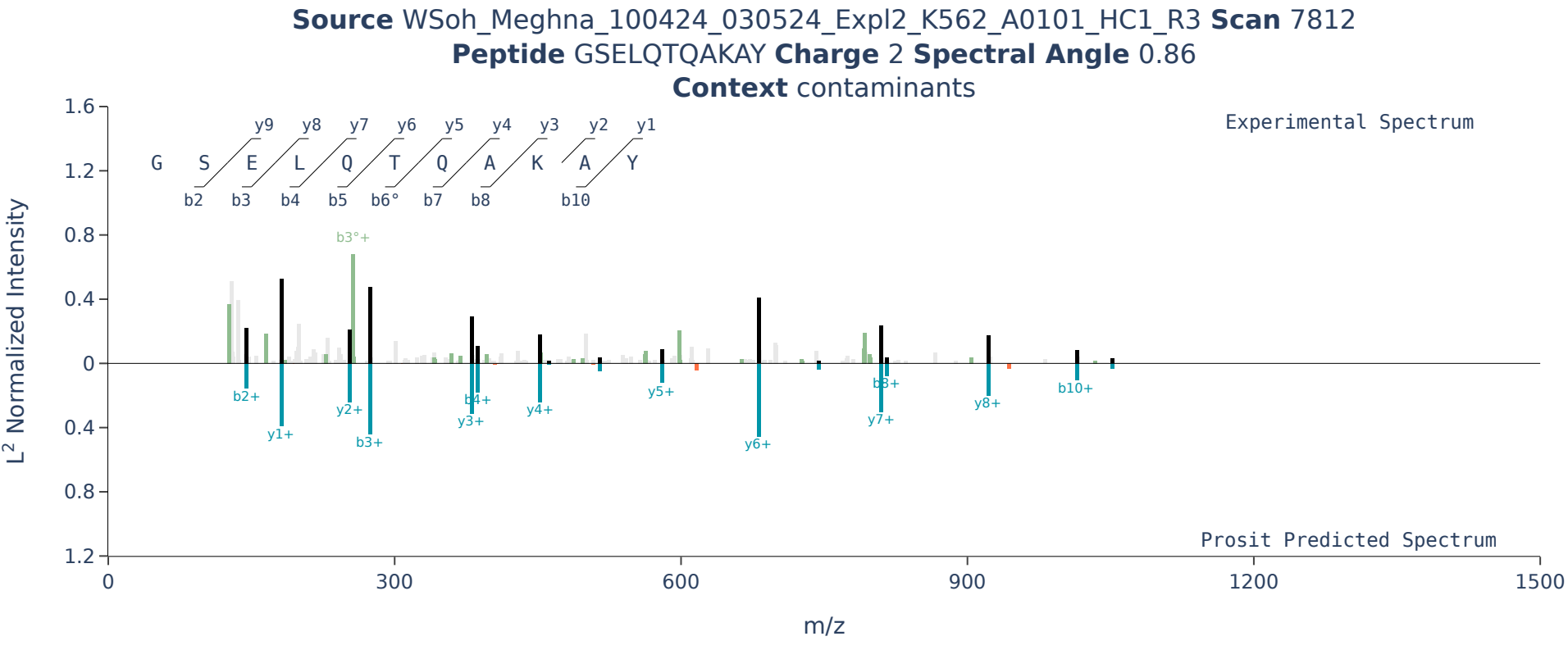
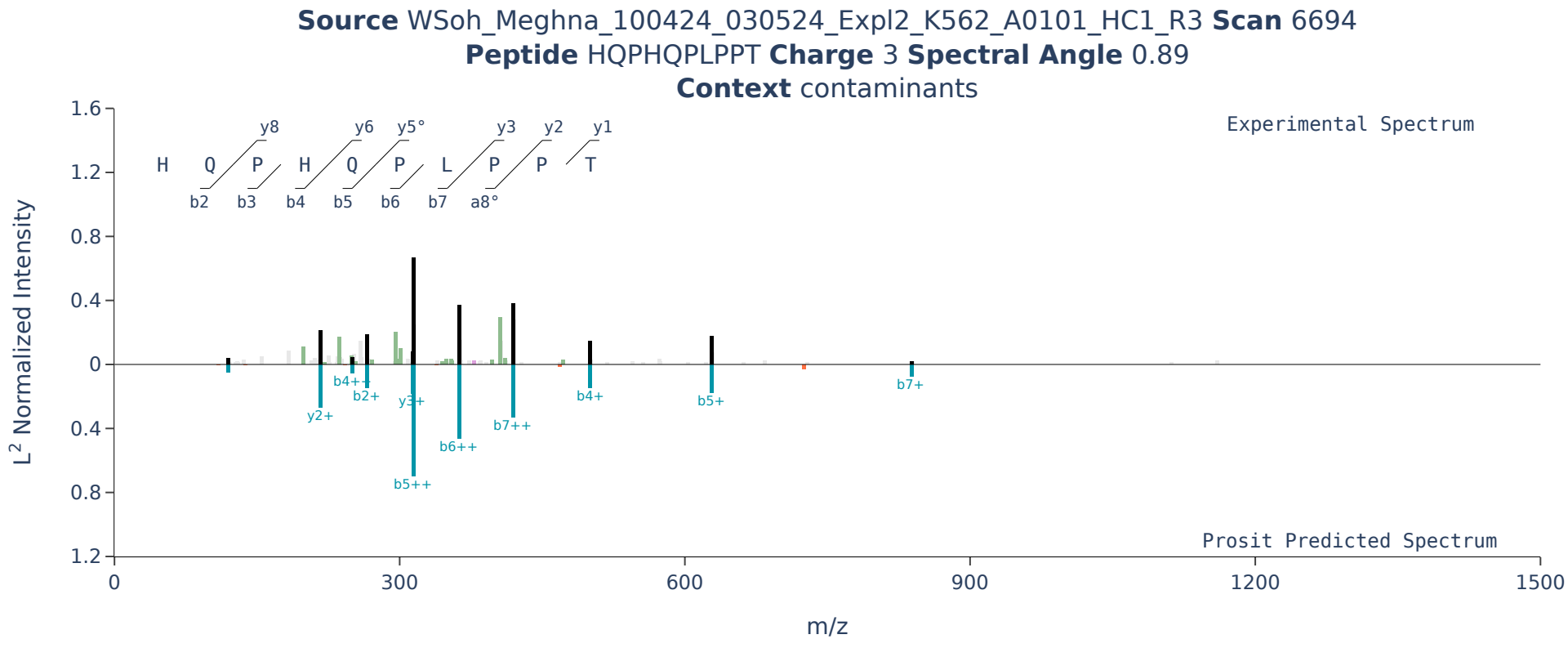
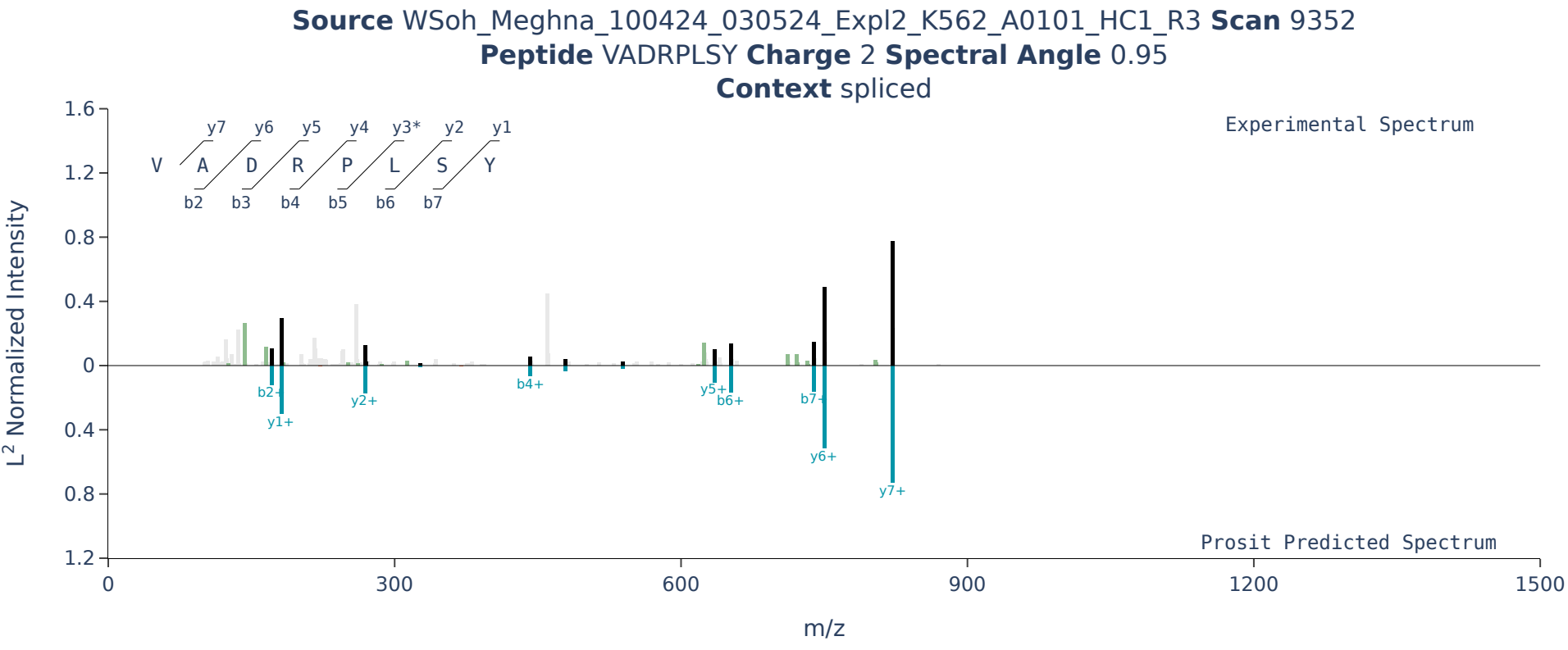
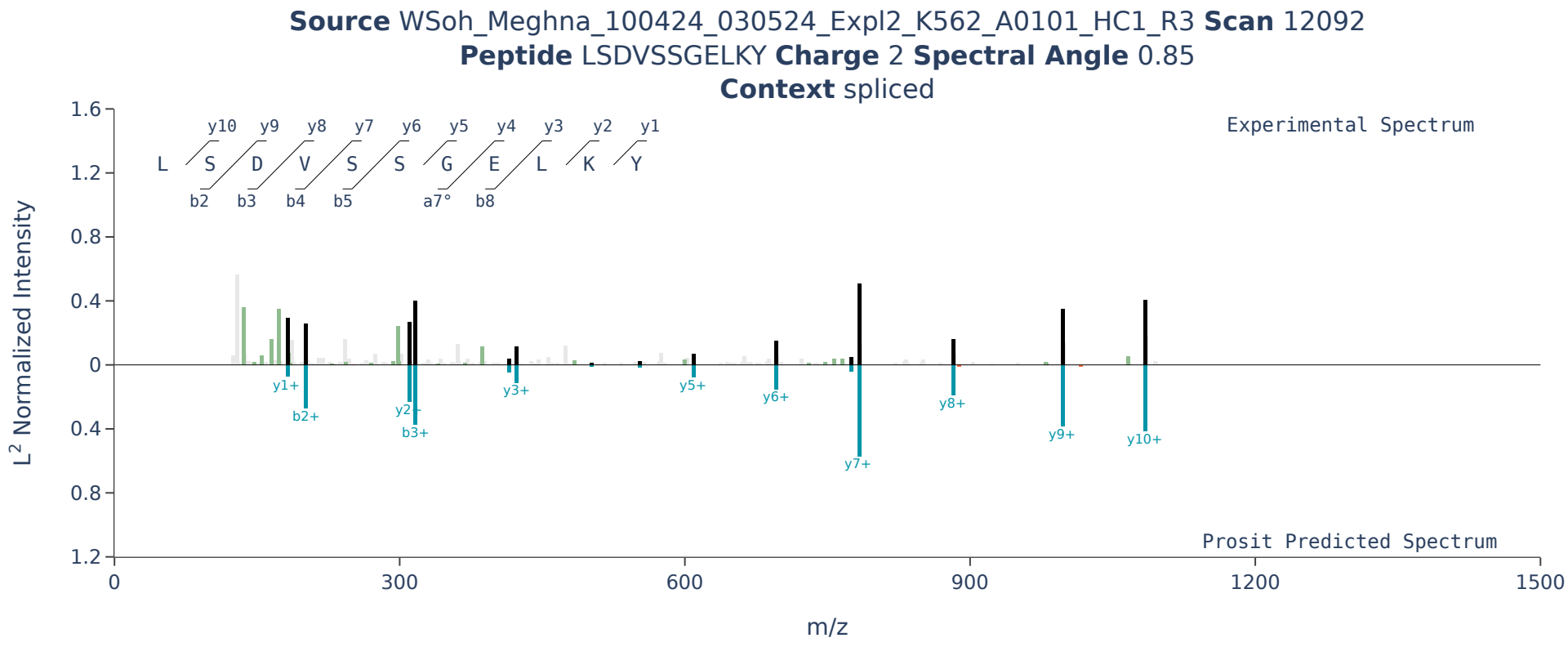
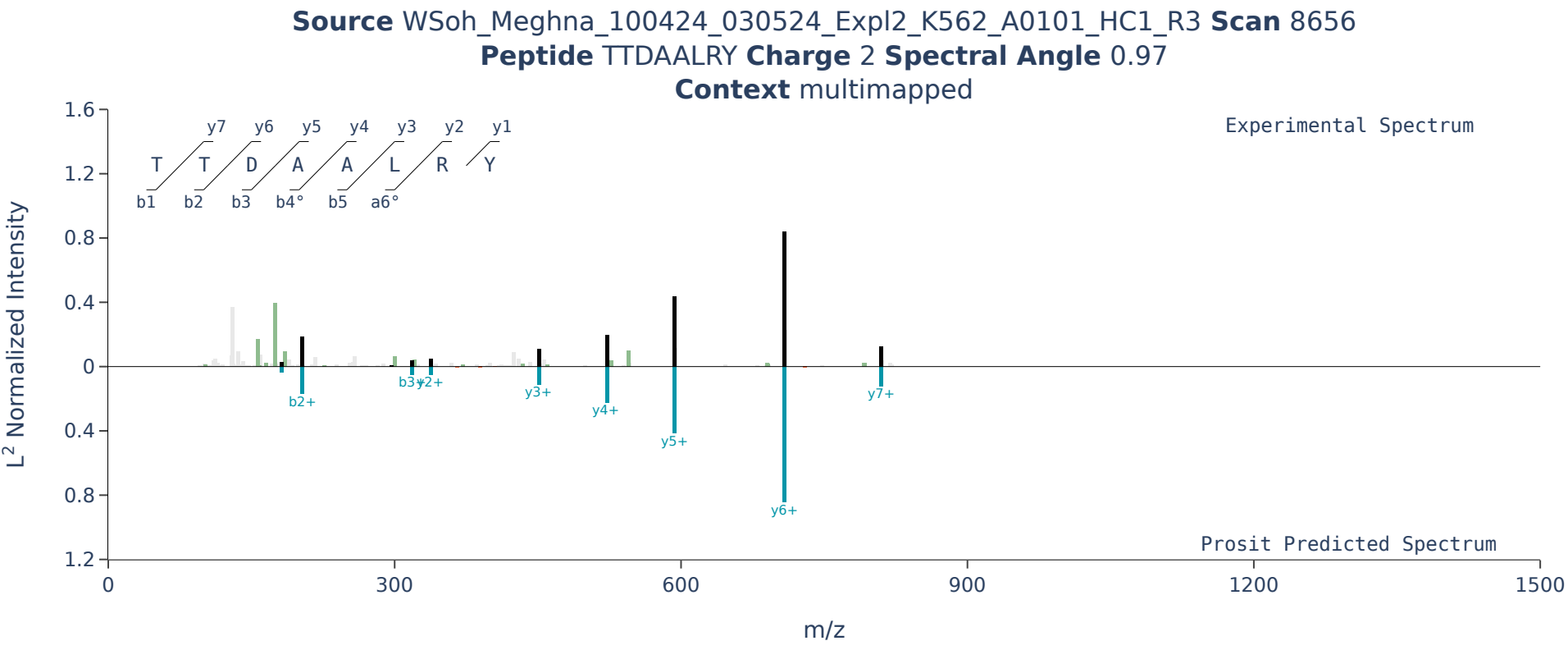
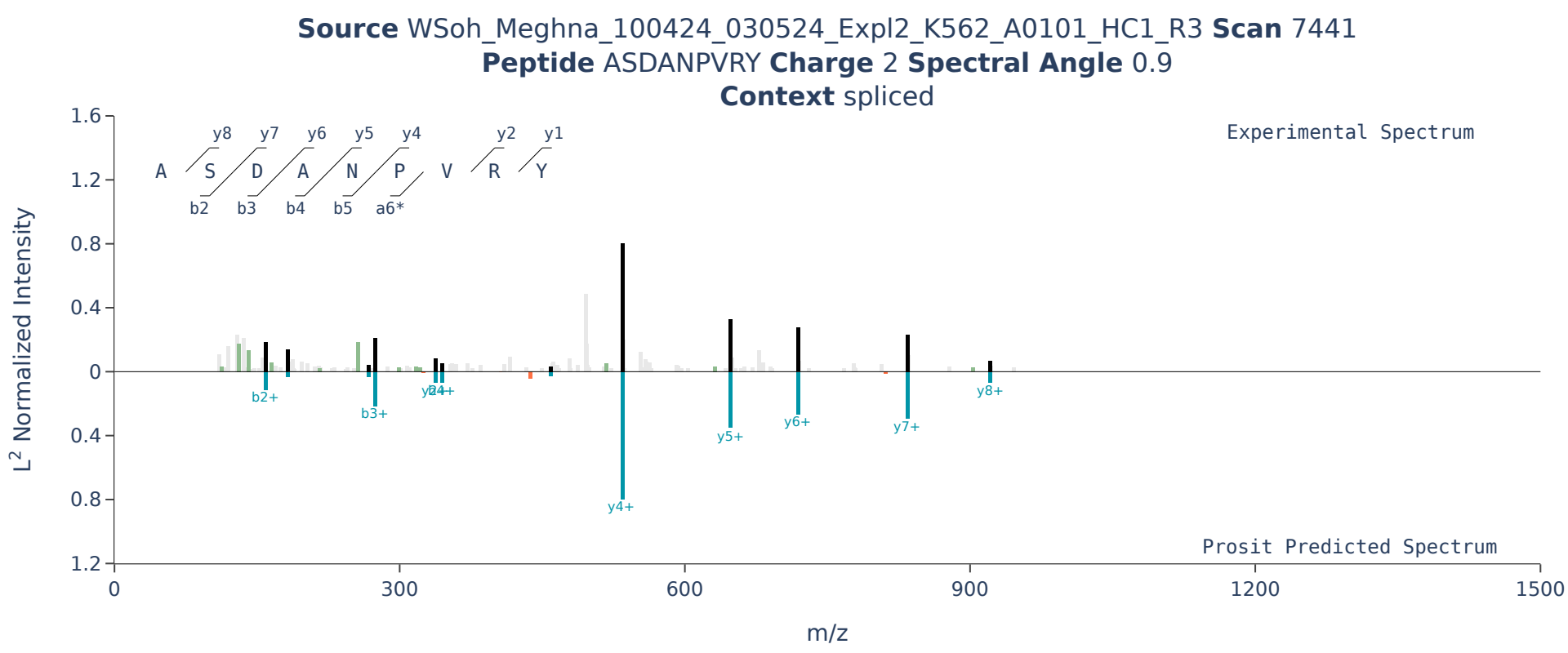
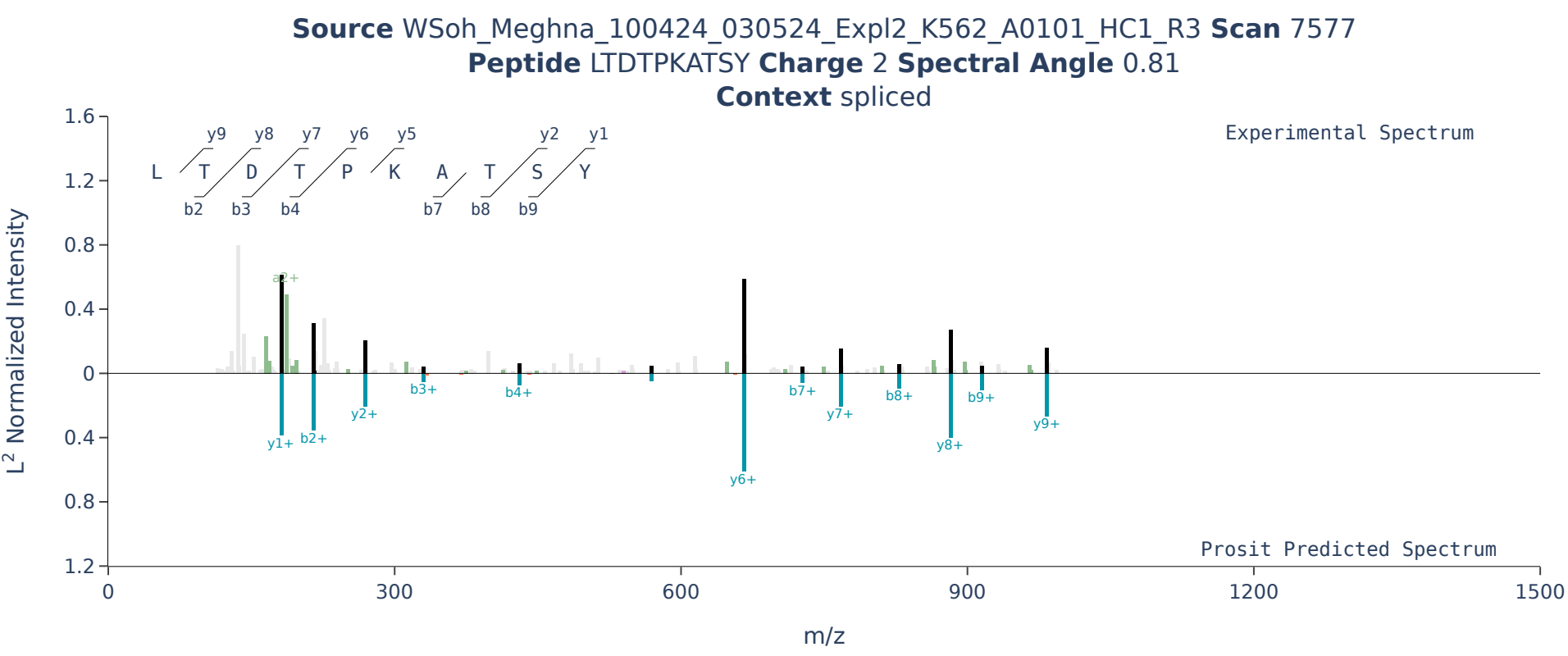
Prosit Spectrum Colour Code:

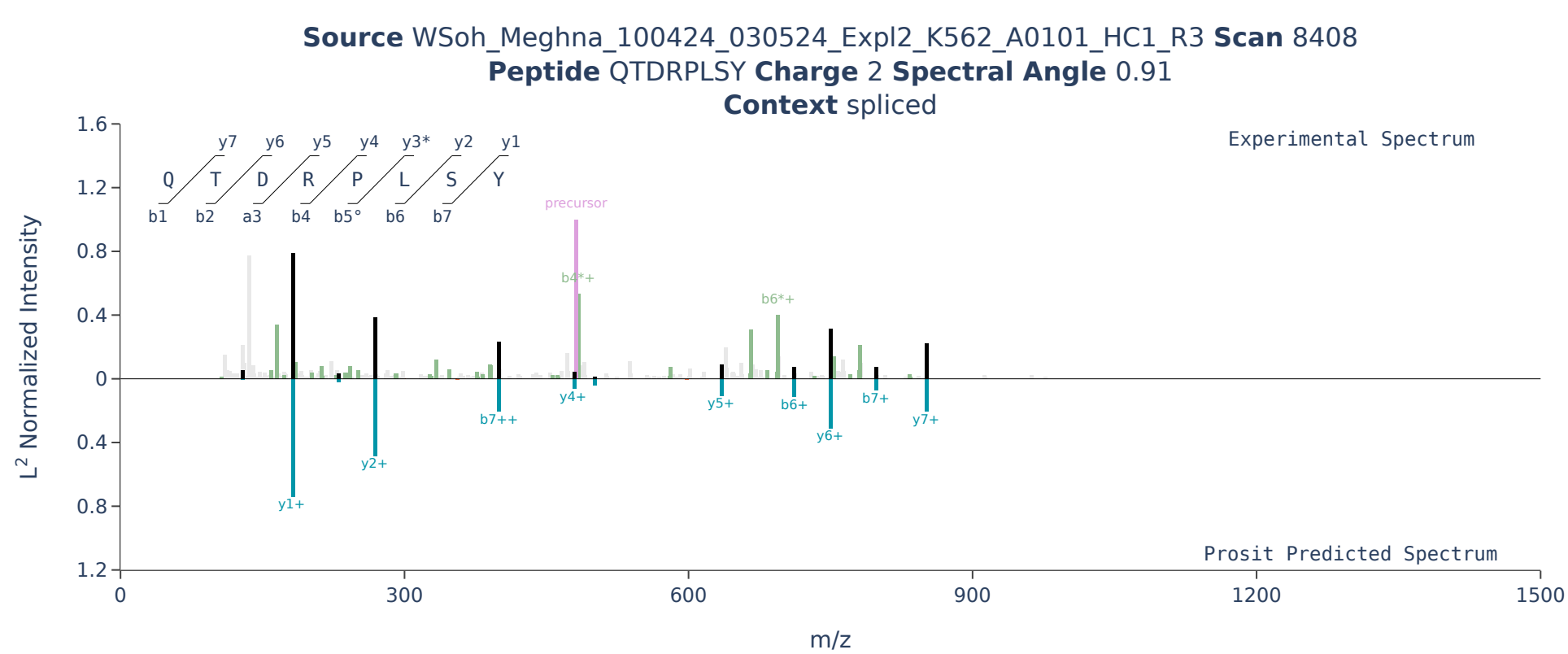
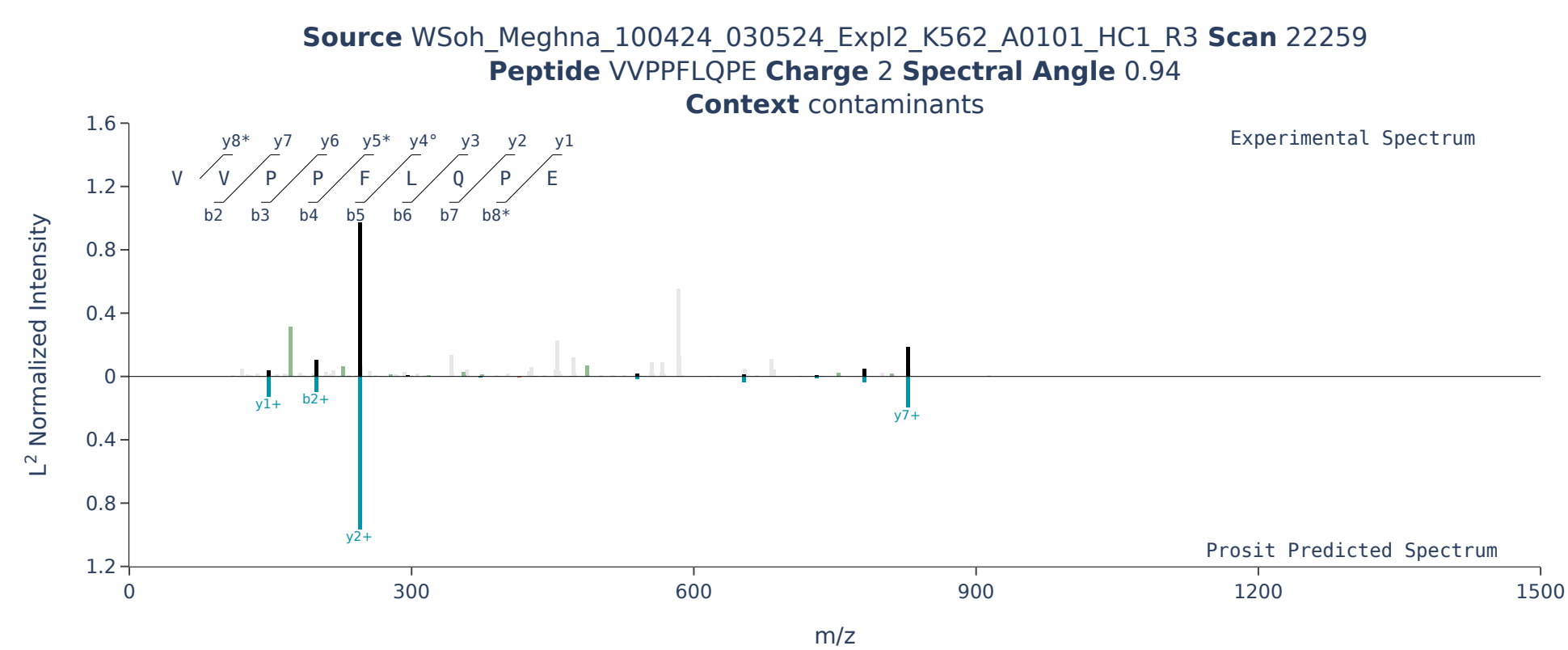
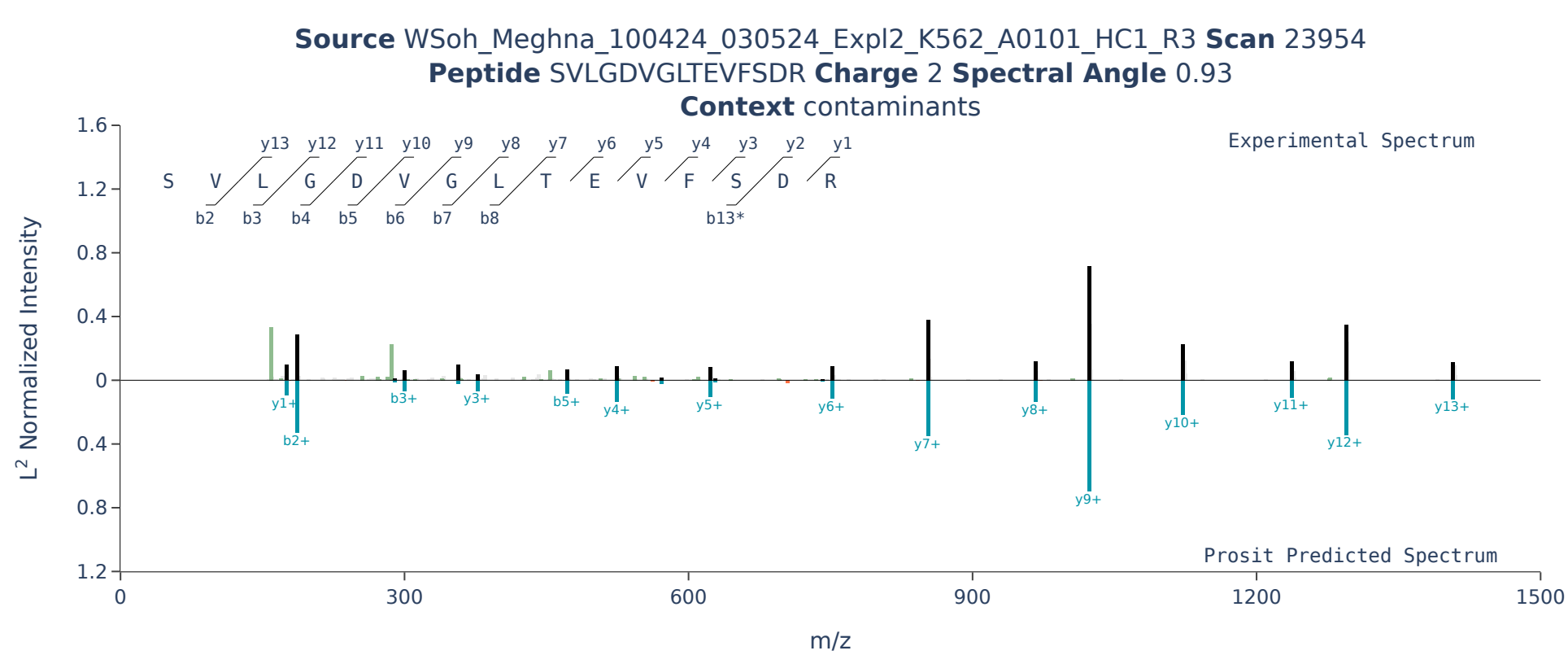
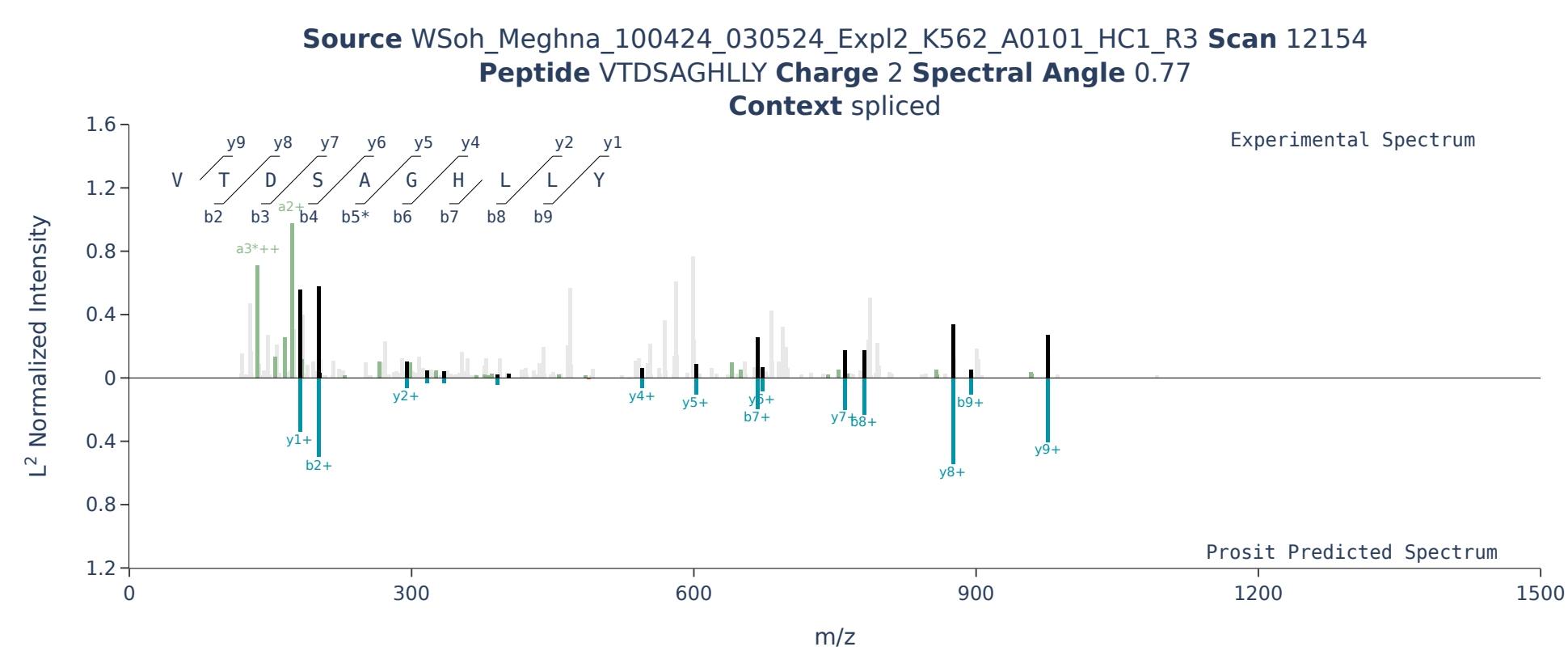
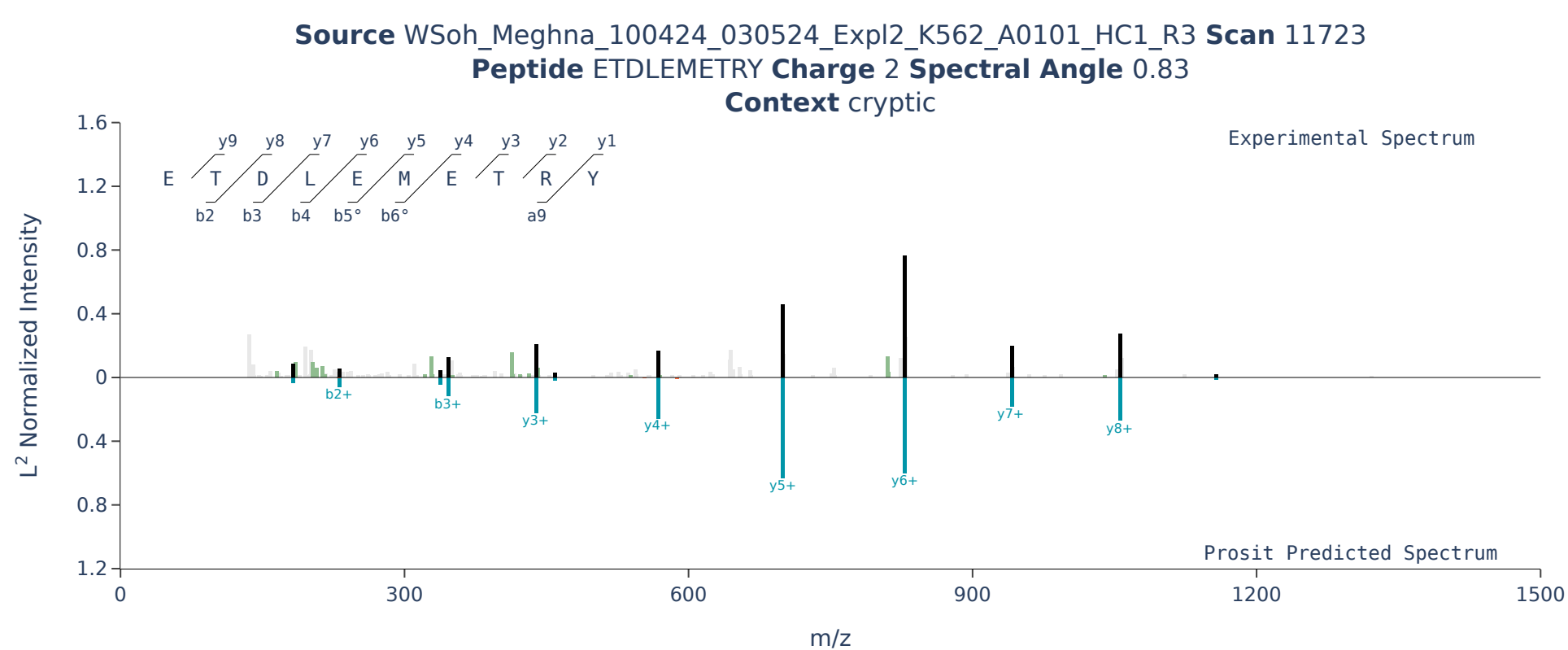
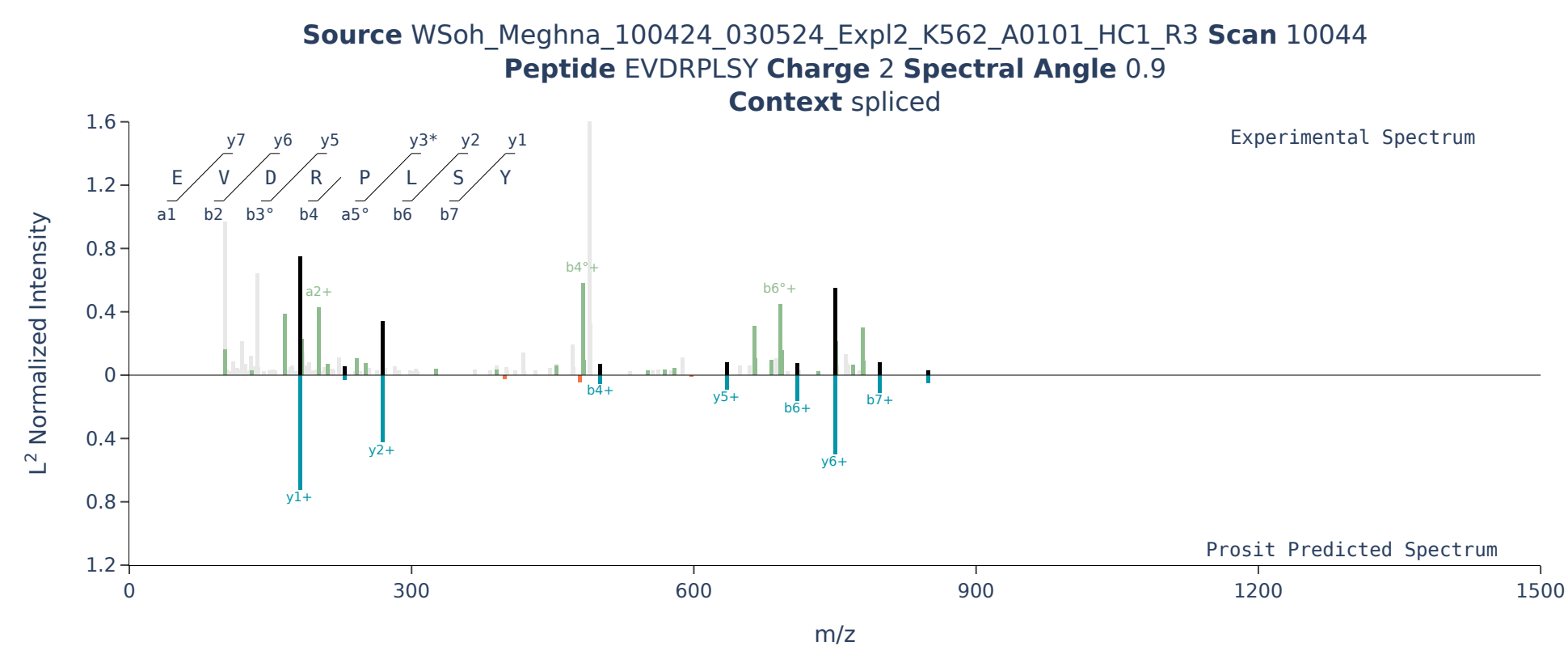
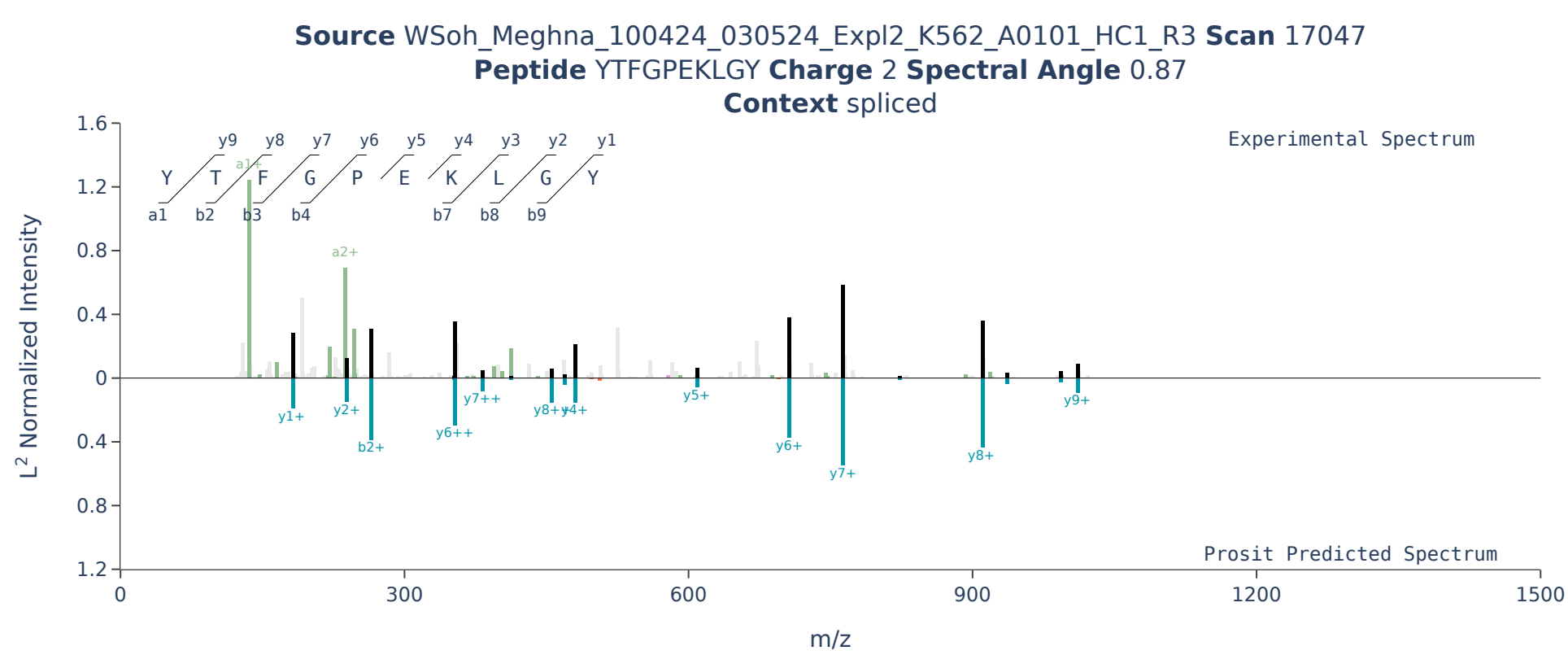
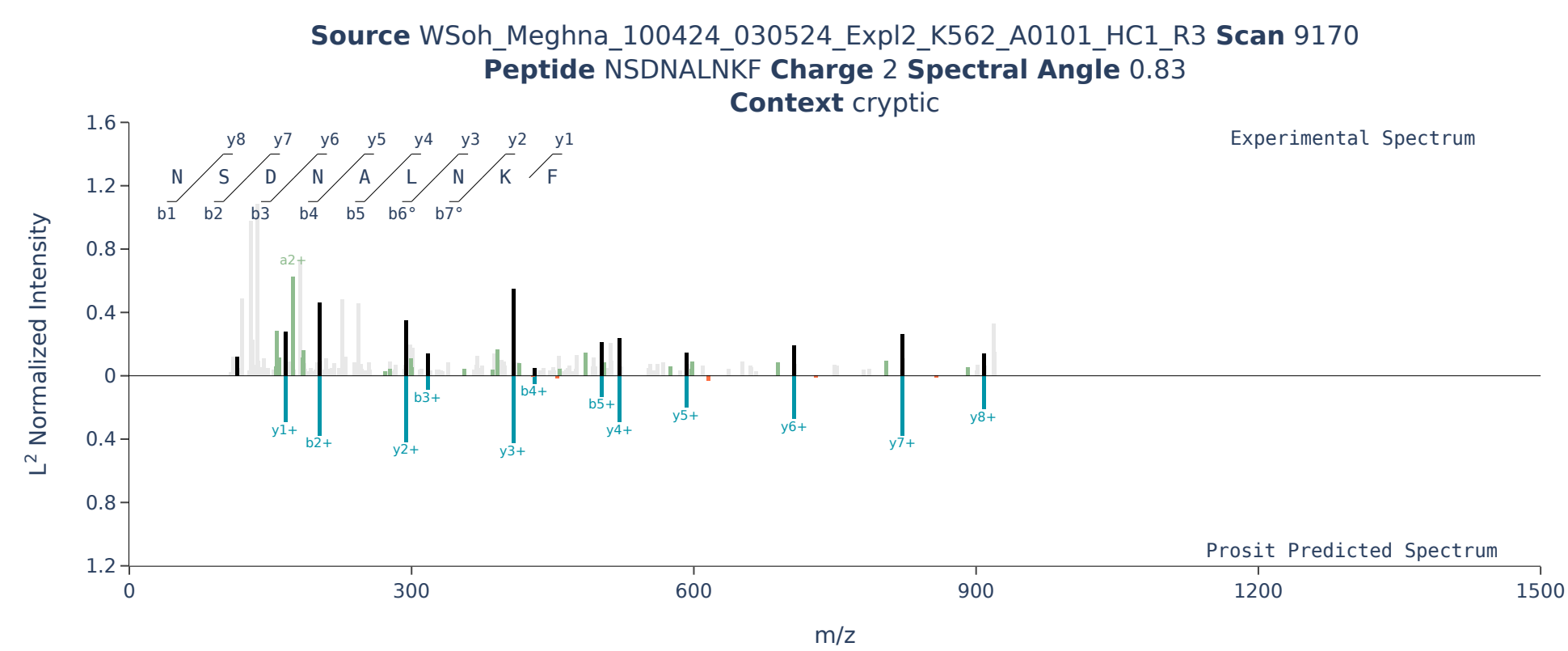
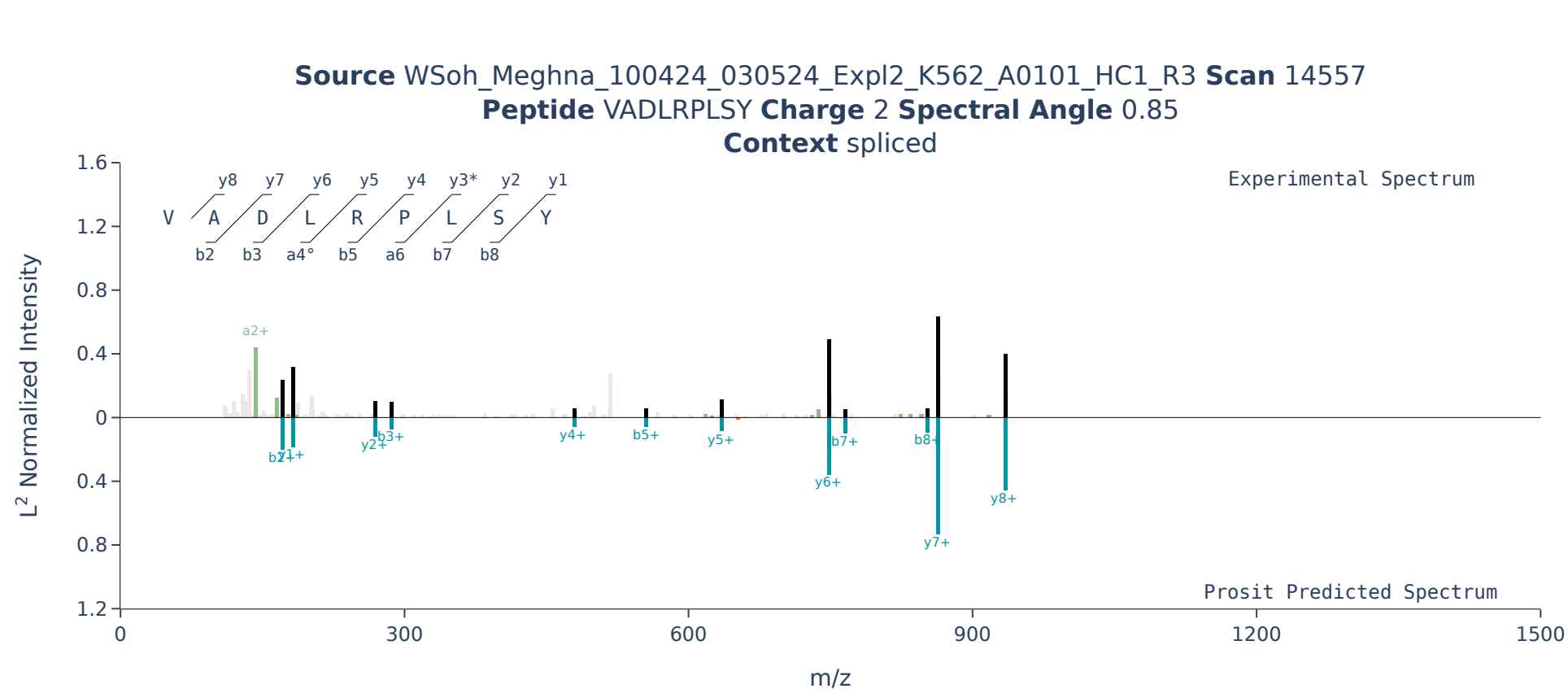
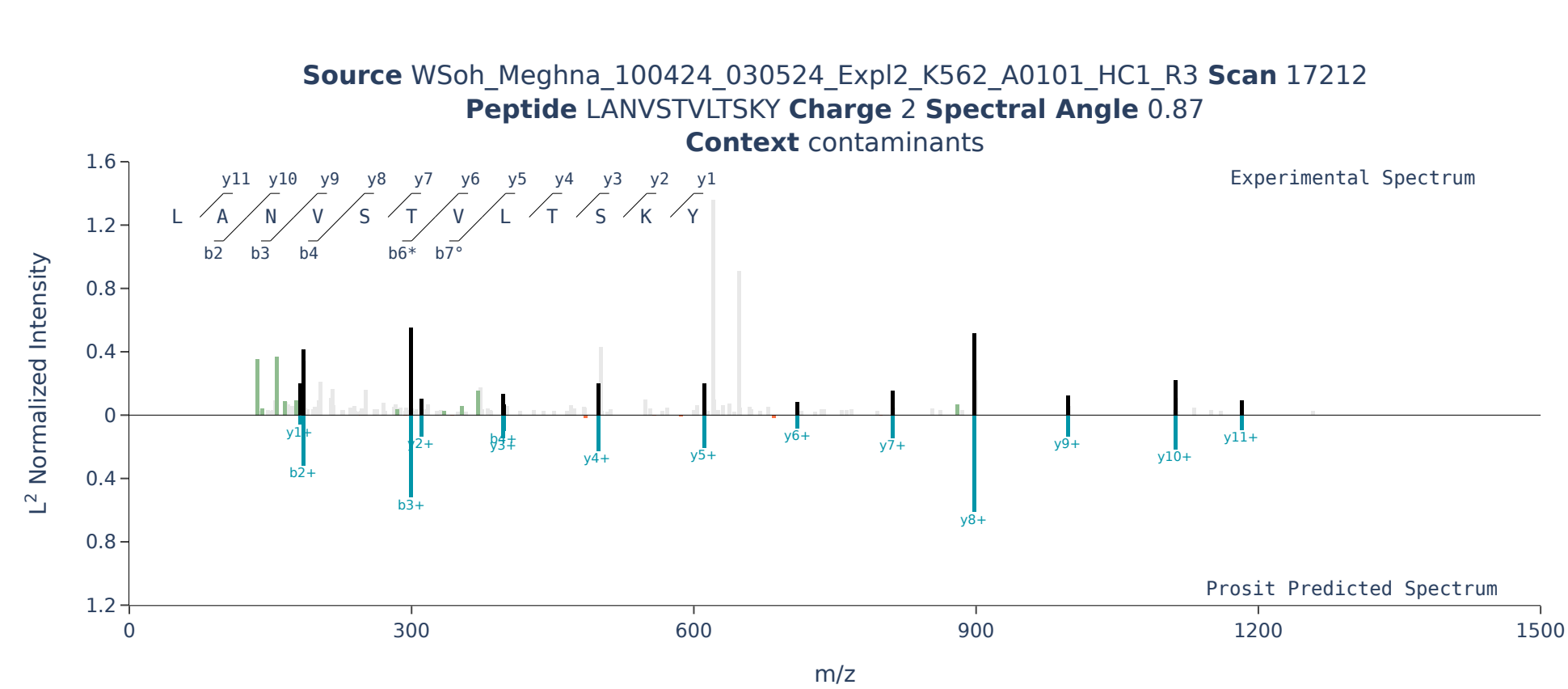
- Prosit predicted peak matched to experimental spectrum.
- Prosit predicted peak not matched to experimental spectrum.

Additional Notes:

- ° indicates an ion with loss of H₂O.
- * indicates an ion with loss of NH₃.







Context cryptic



Context cryptic



Context contaminants



Peptide QTEFEDLKSGT **Charge** 2 **Spectral Angle** 0.93
Context spliced



Peptide NSEEGSERDT **Charge** 2 **Spectral Angle** 0.5
Context unmapped



Peptide ALLSM[+10.0]ELGAVEDER **Charge** 10
Context unmapped



Peptide TEENGKETET **Charge** 2 **Spectral Angle** 0.7
Context spliced



Peptide DEDTMDGNERT **Charge** 2 **Spectral Angle** 0.78
Context unmapped

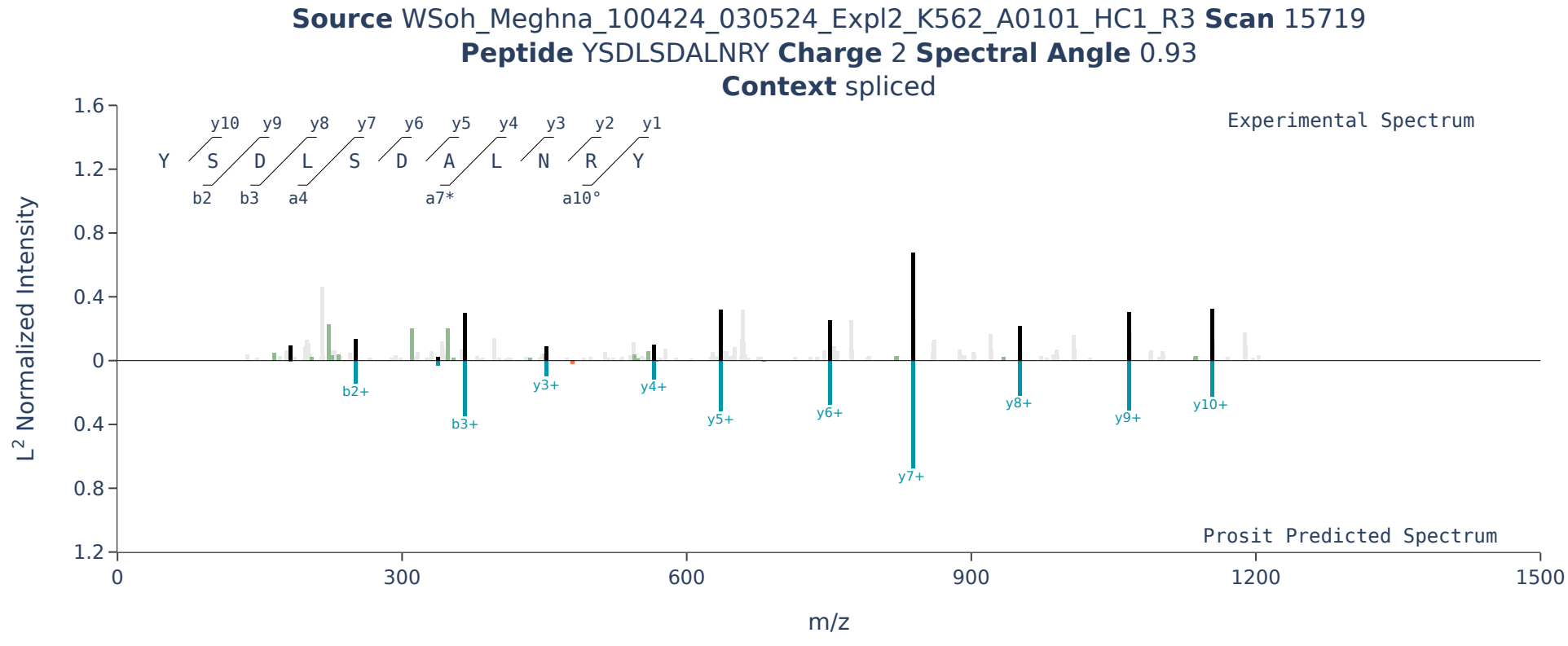
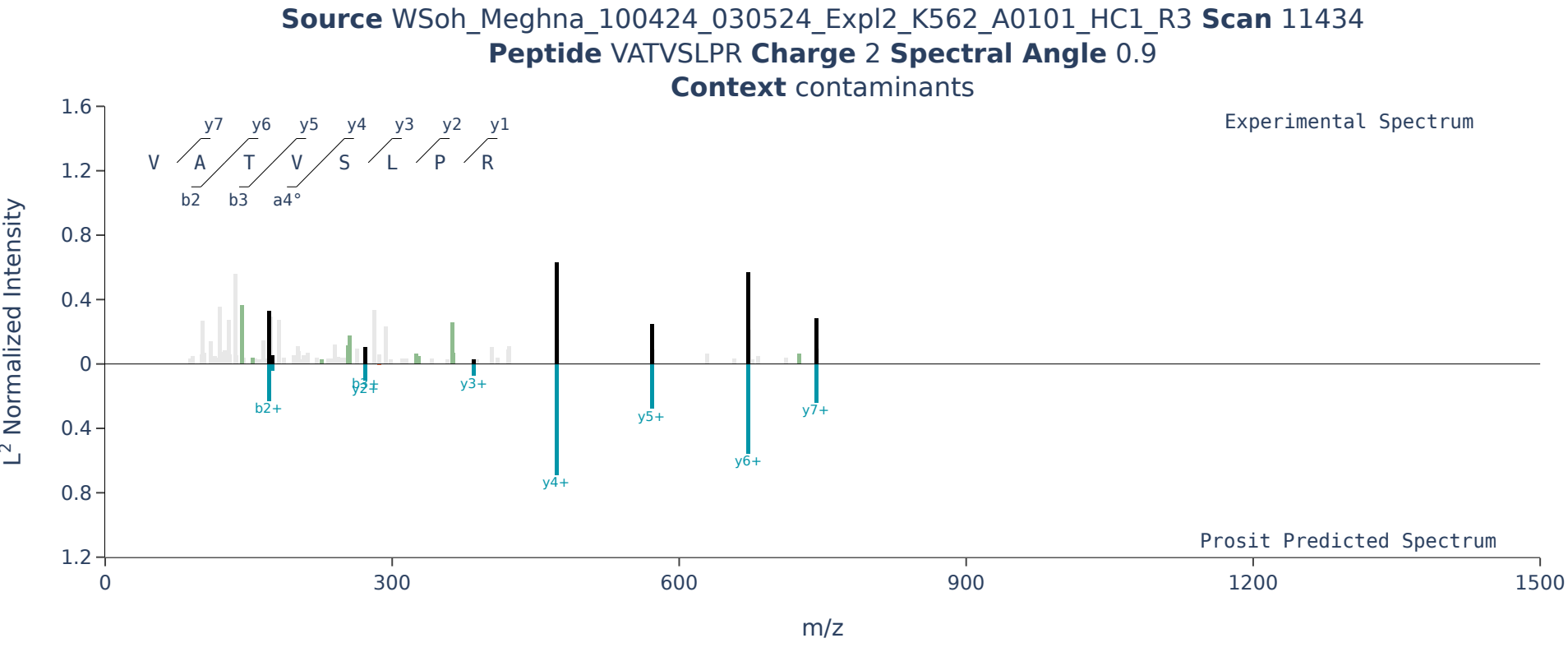
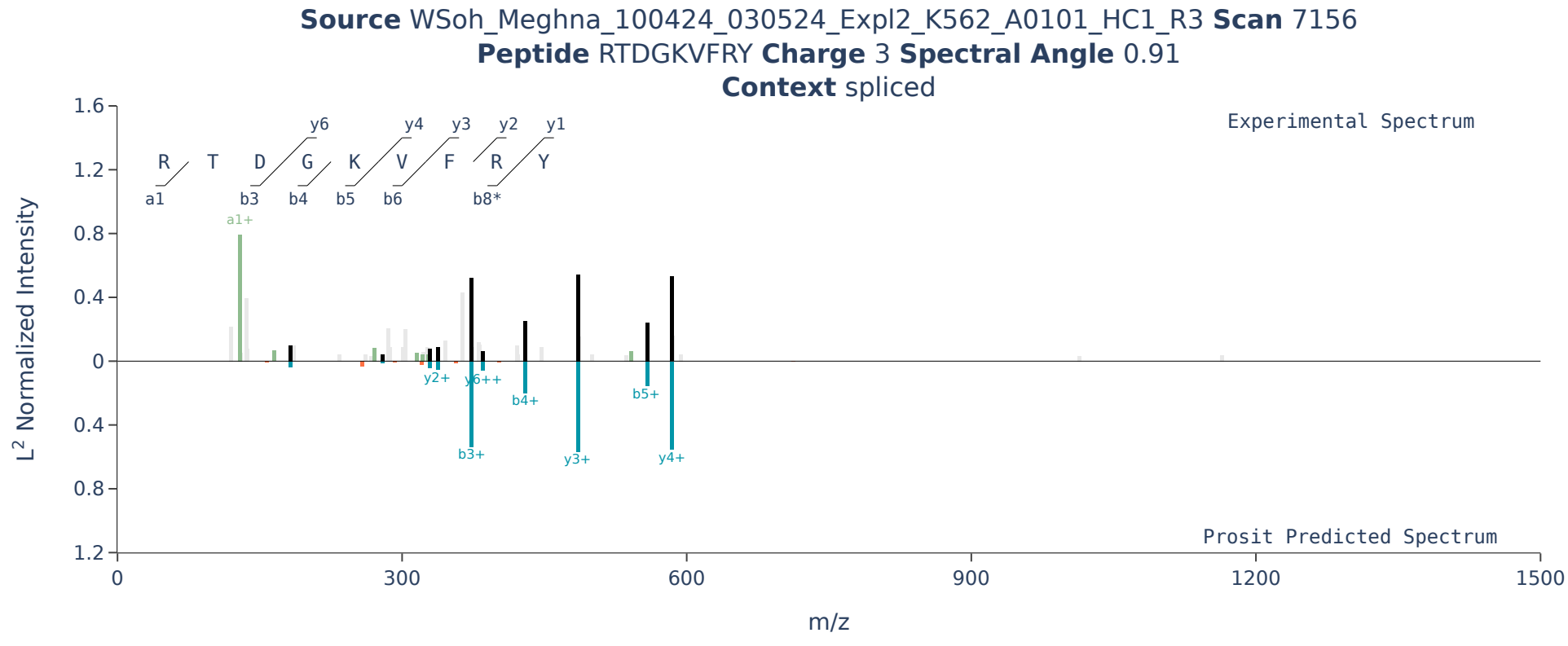
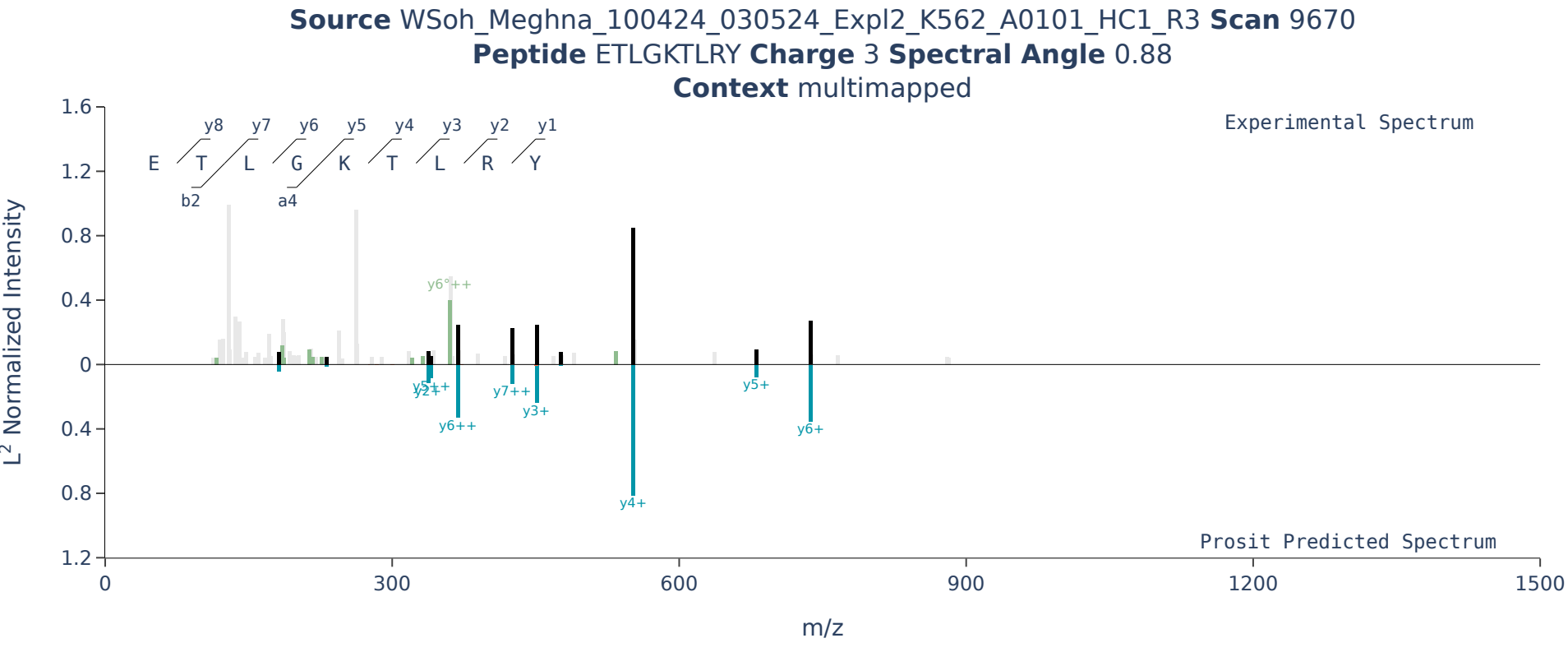
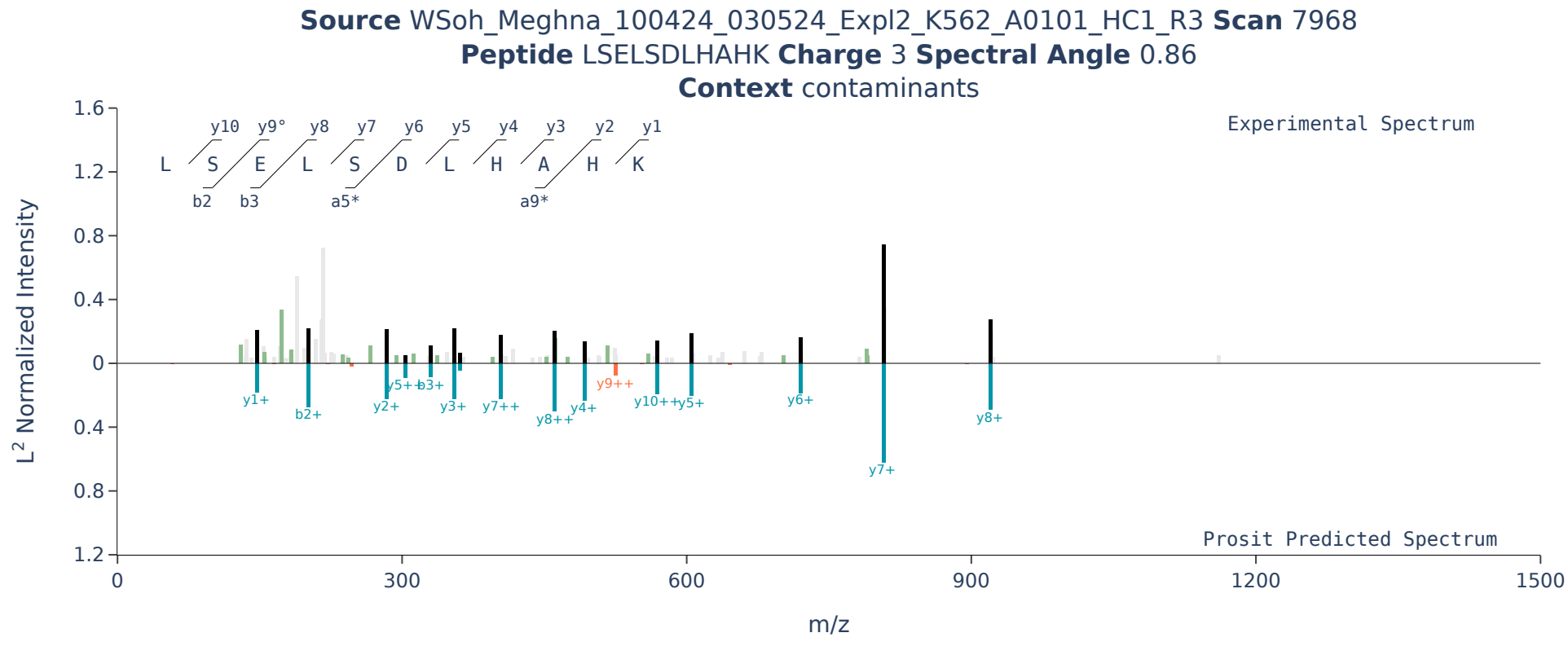
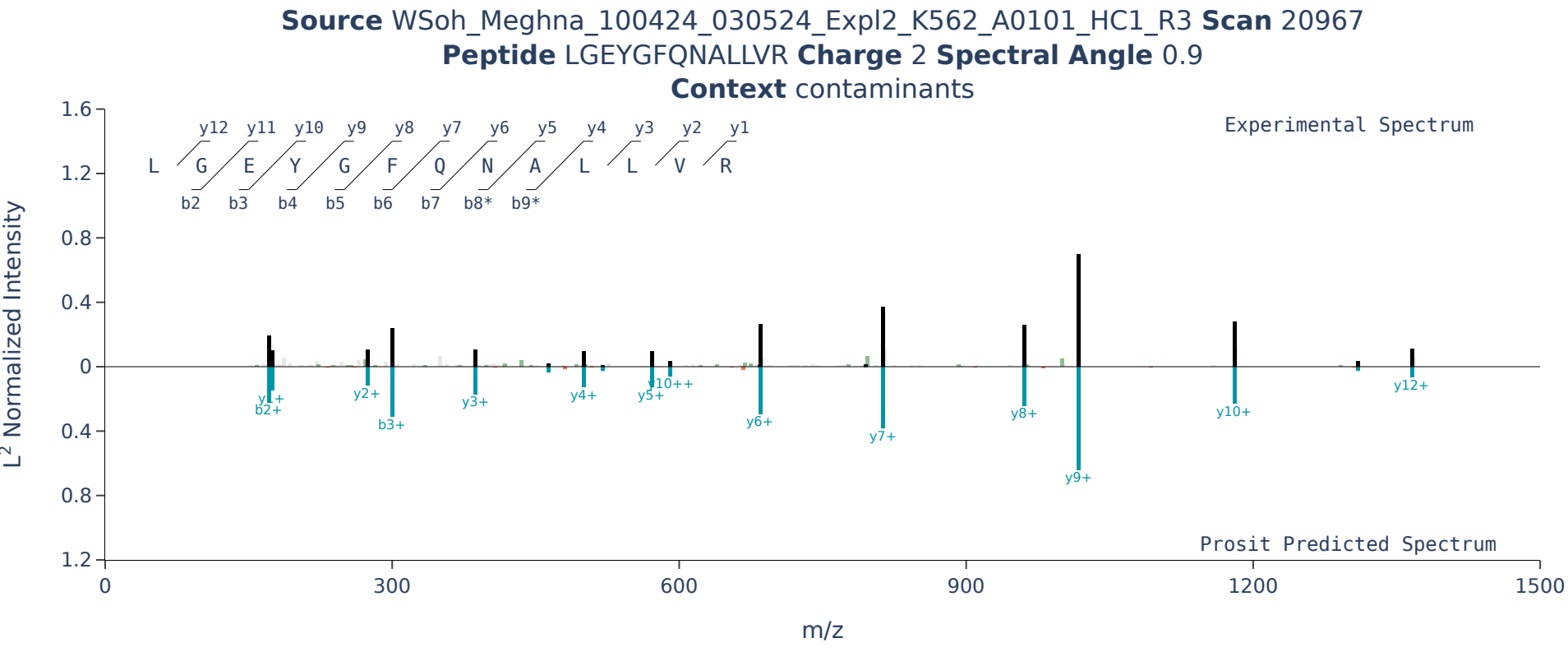
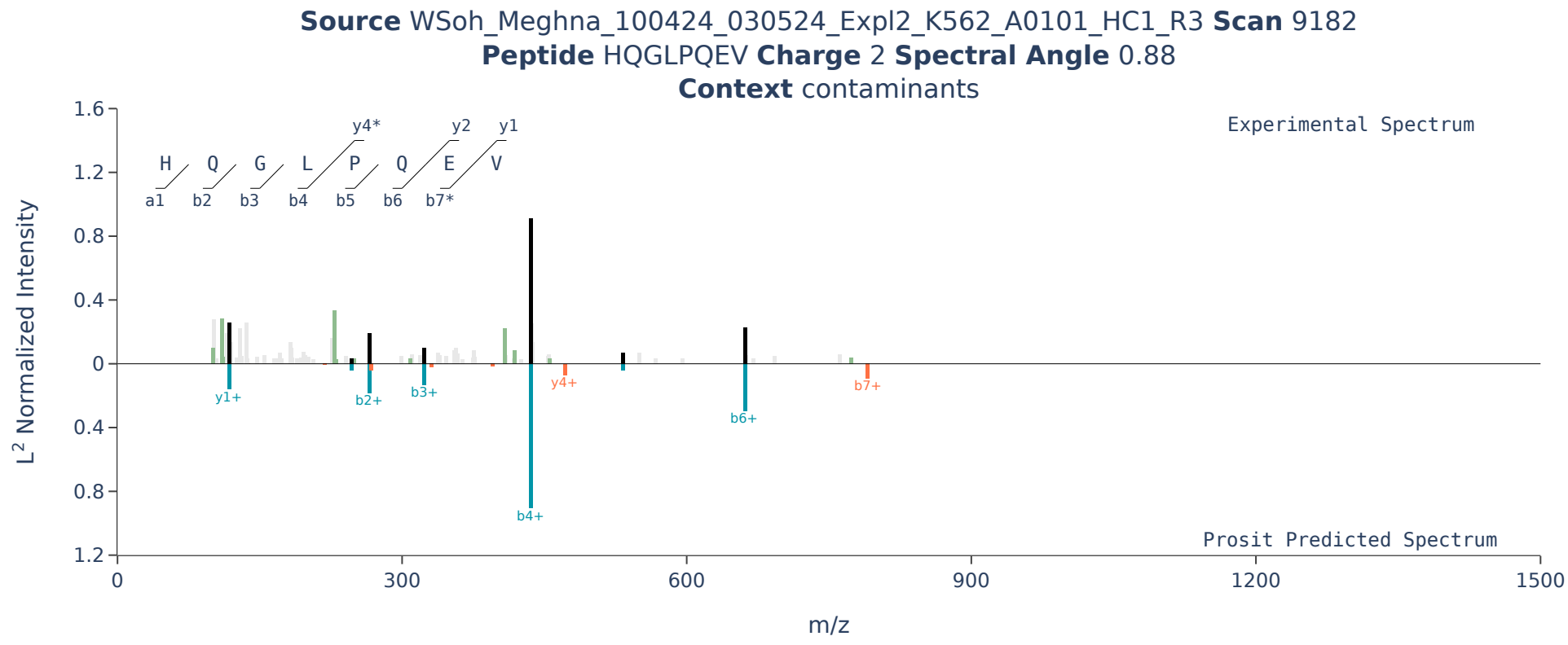
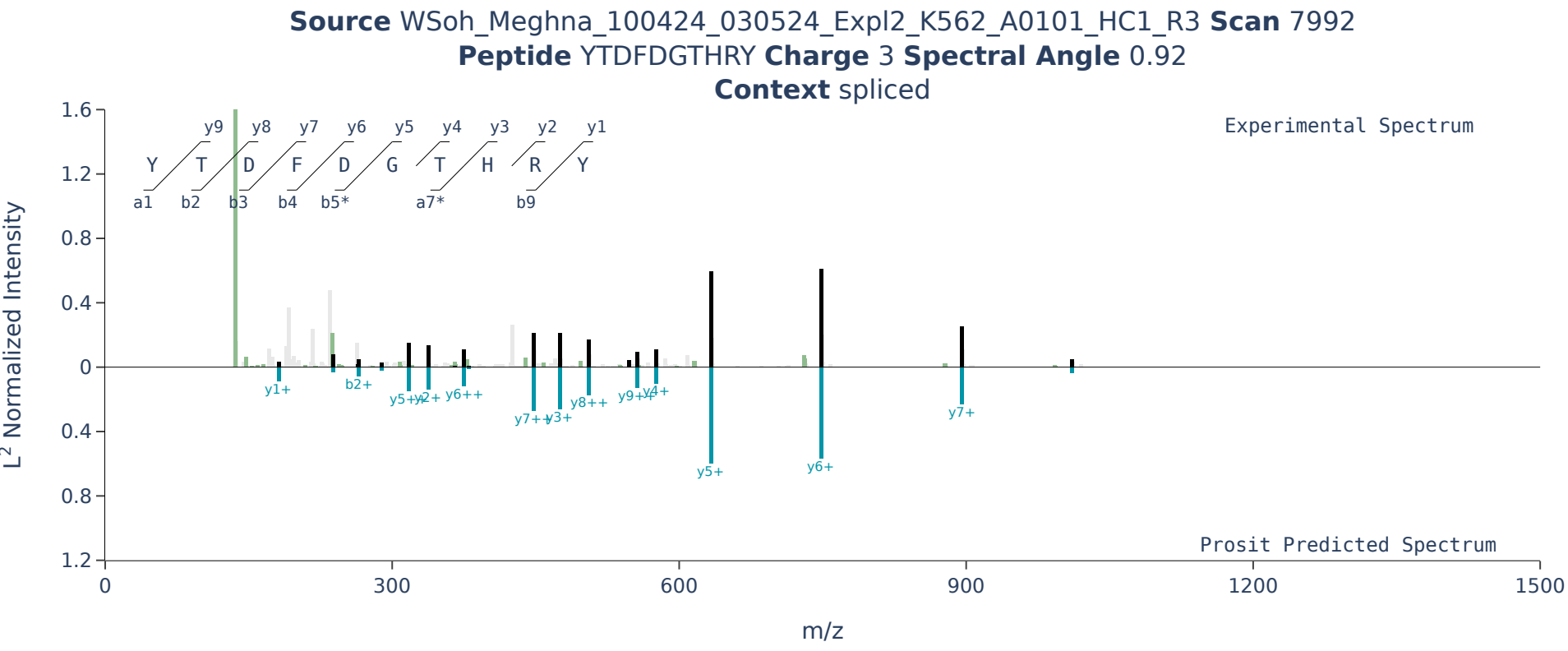
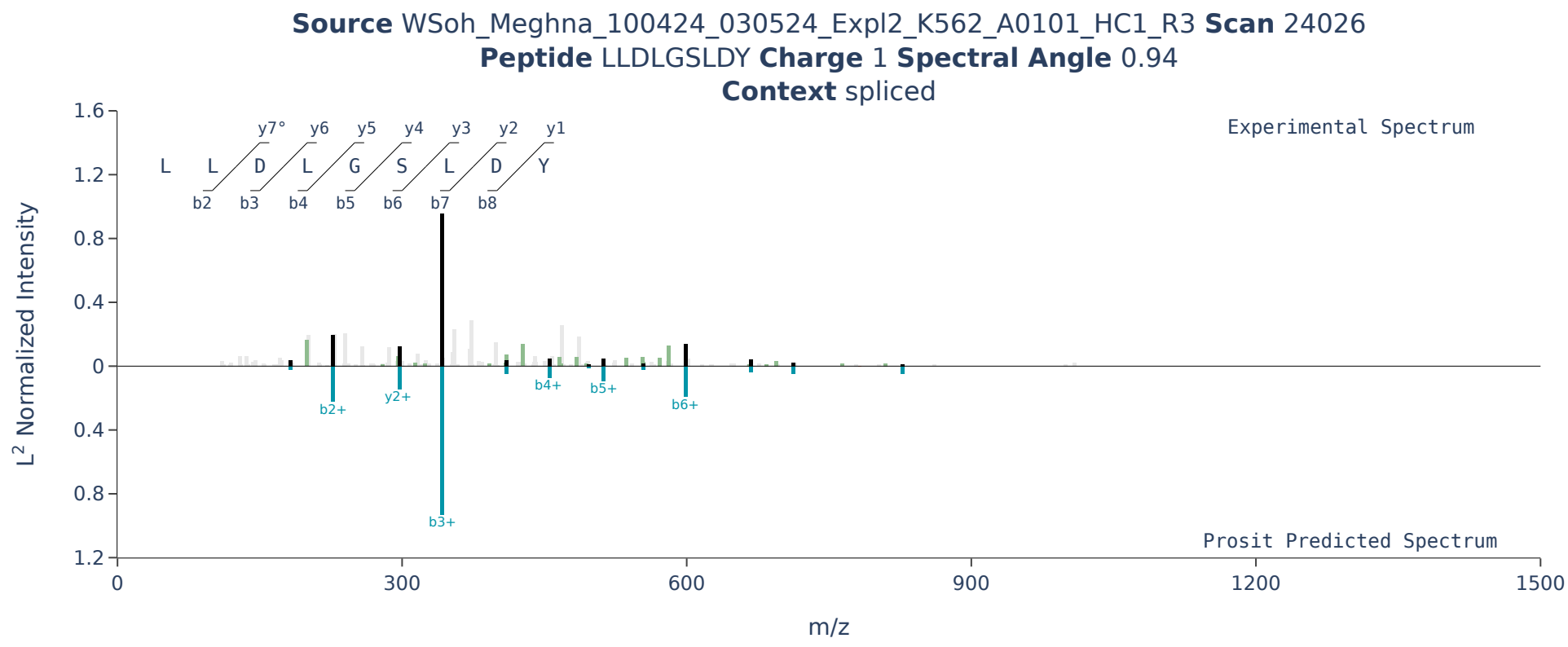
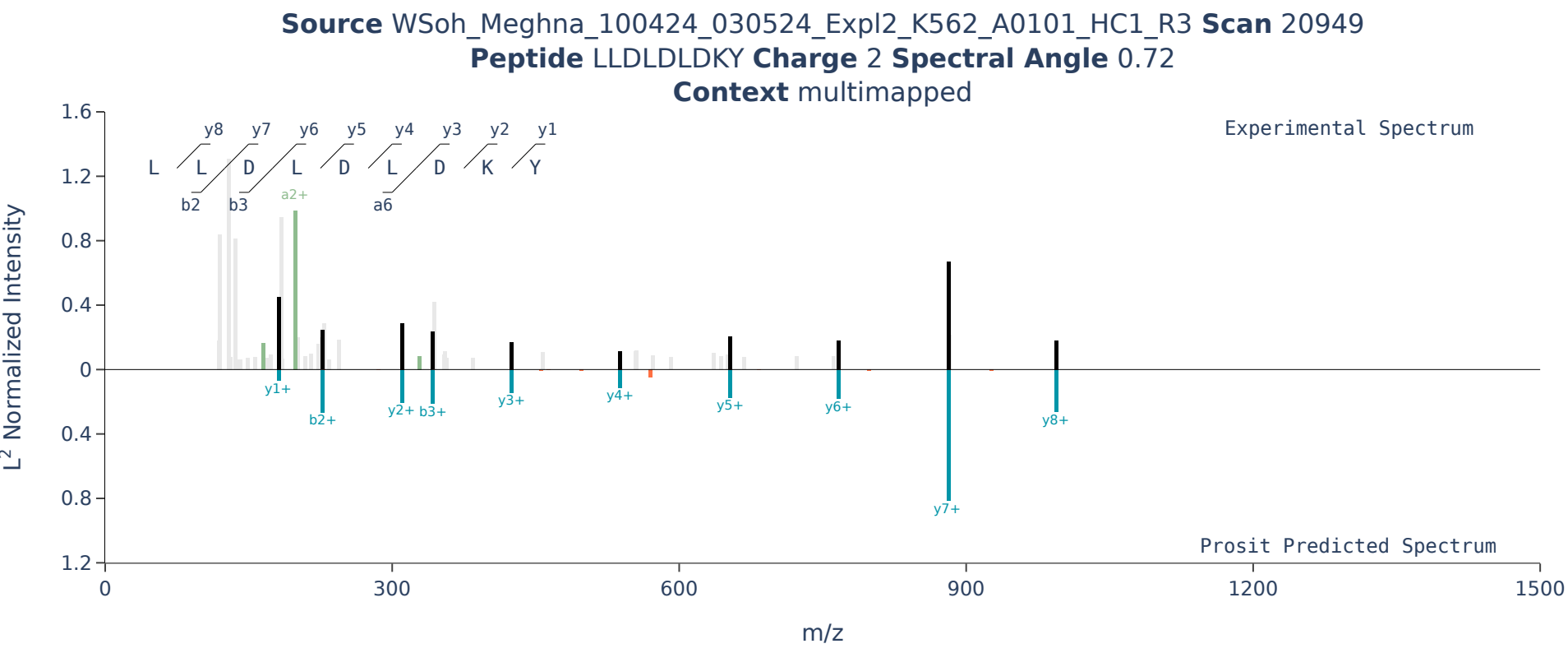


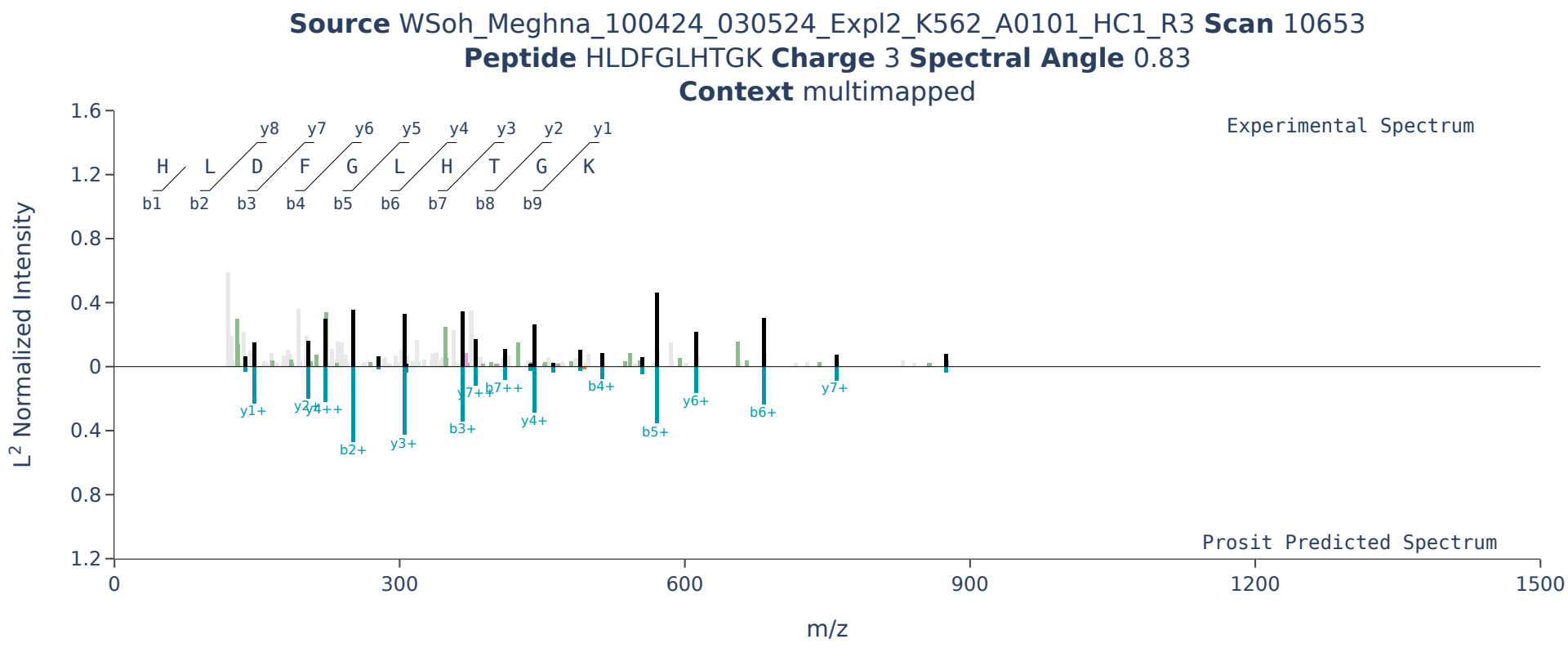
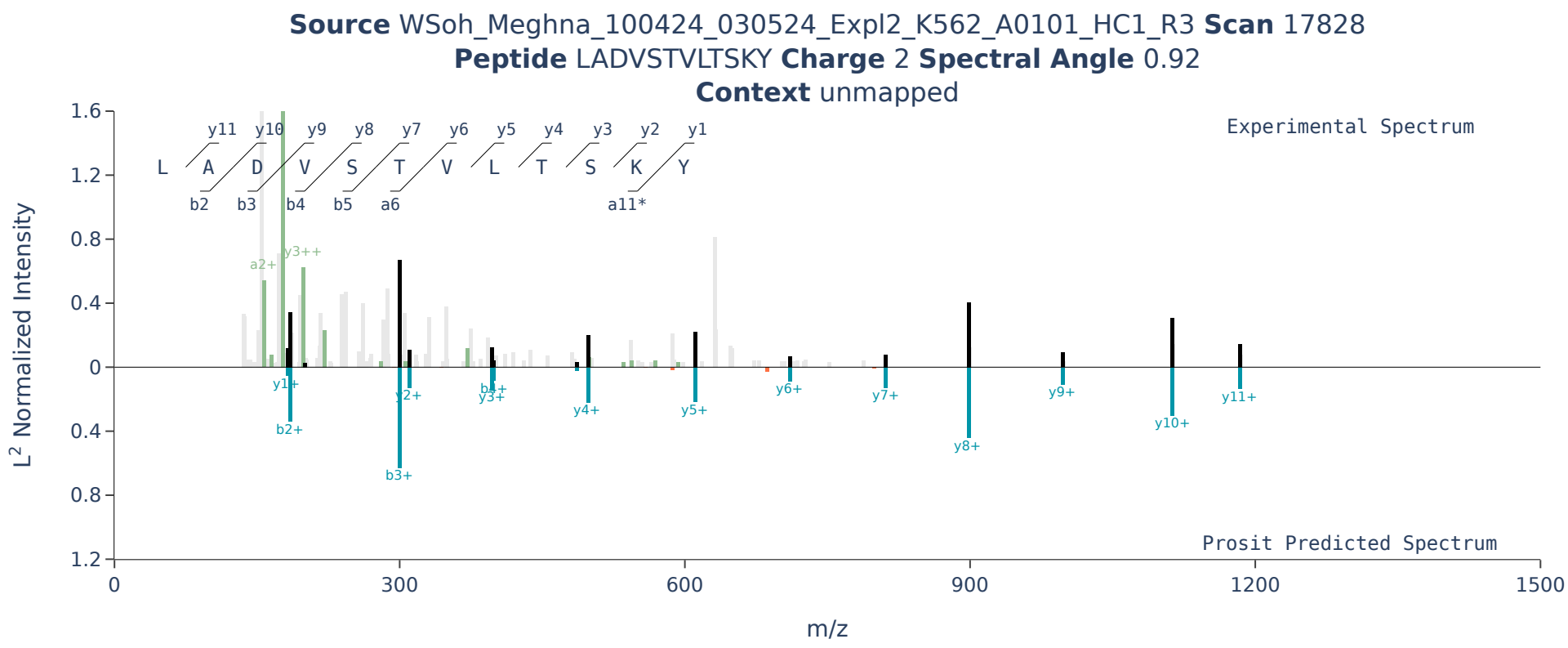
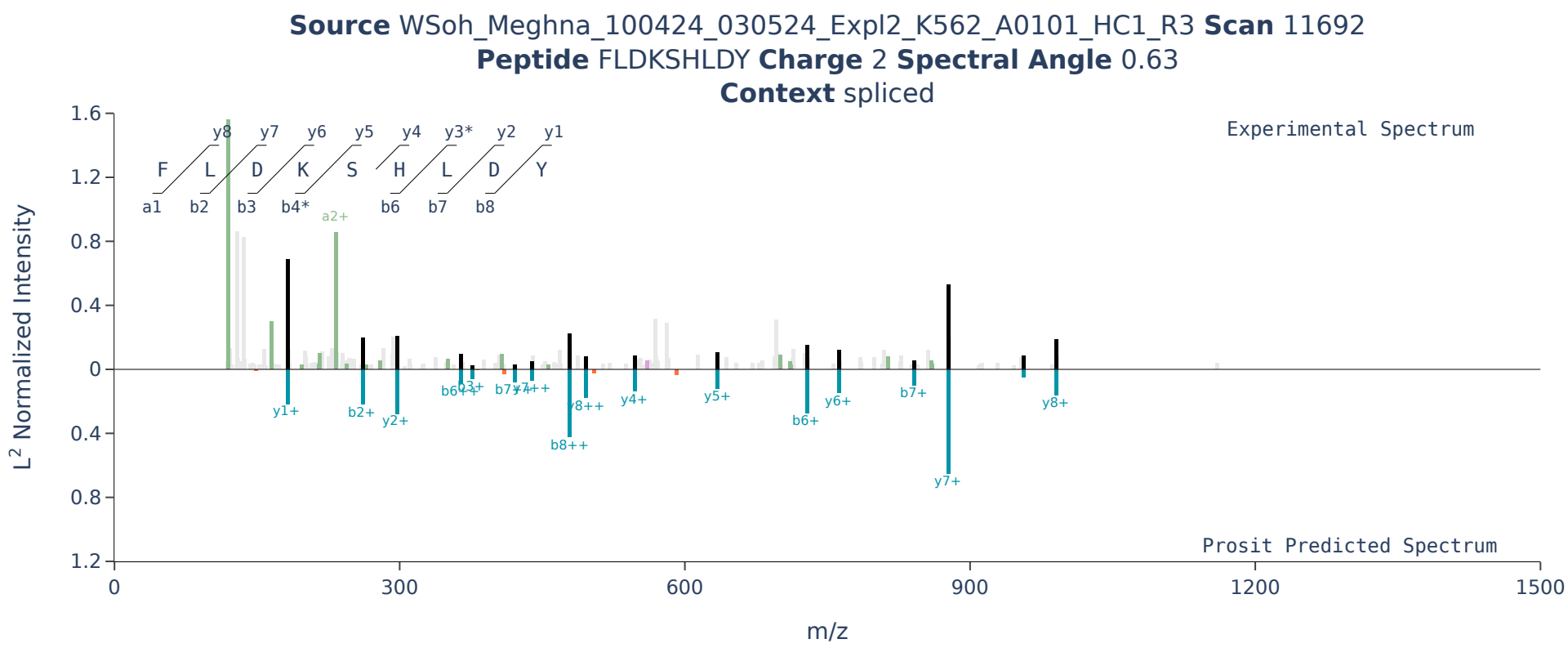
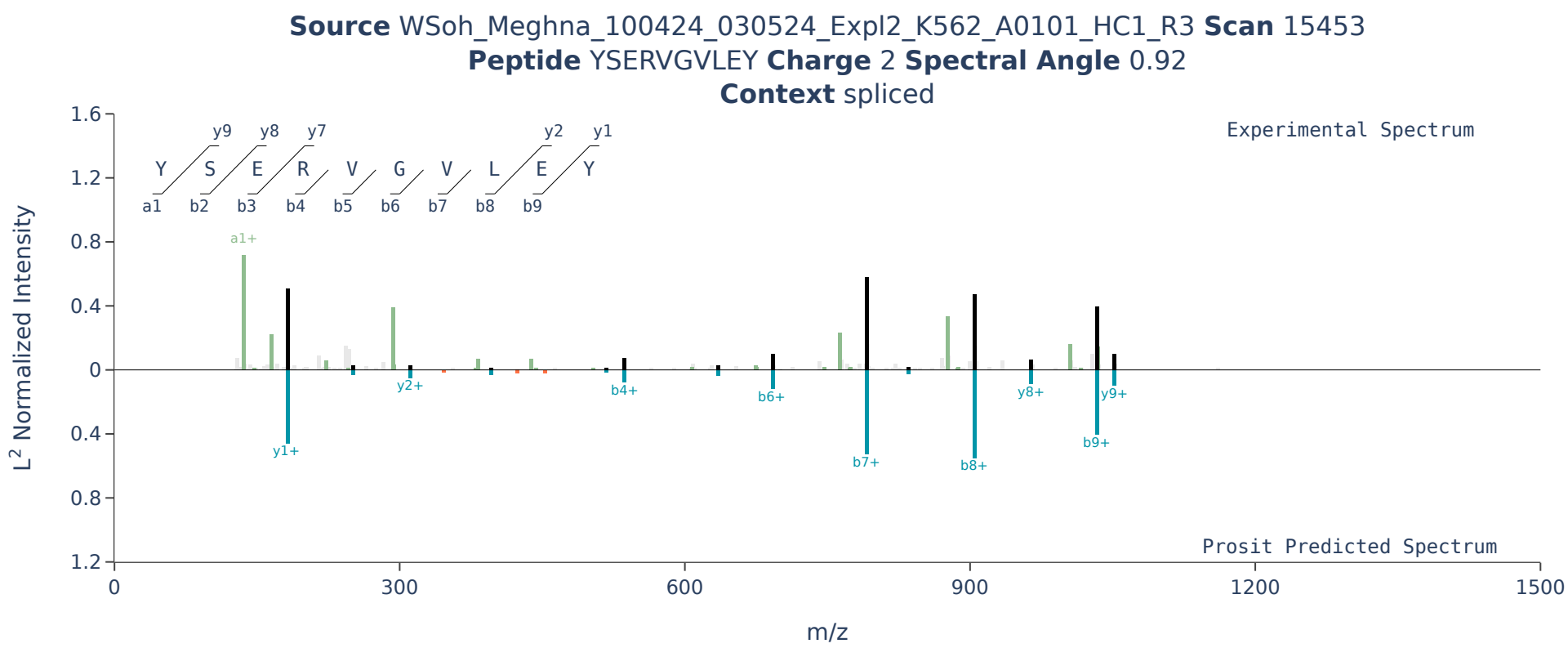
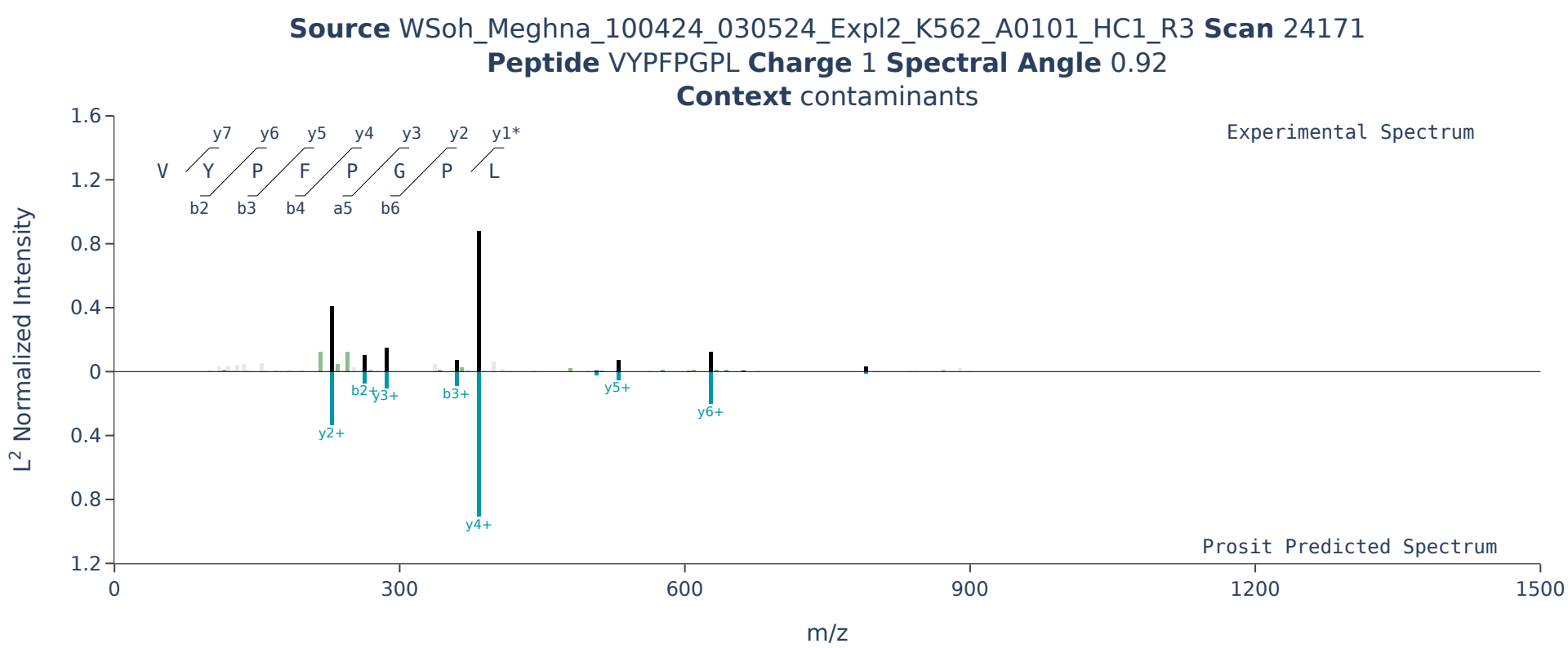
Context multimapped

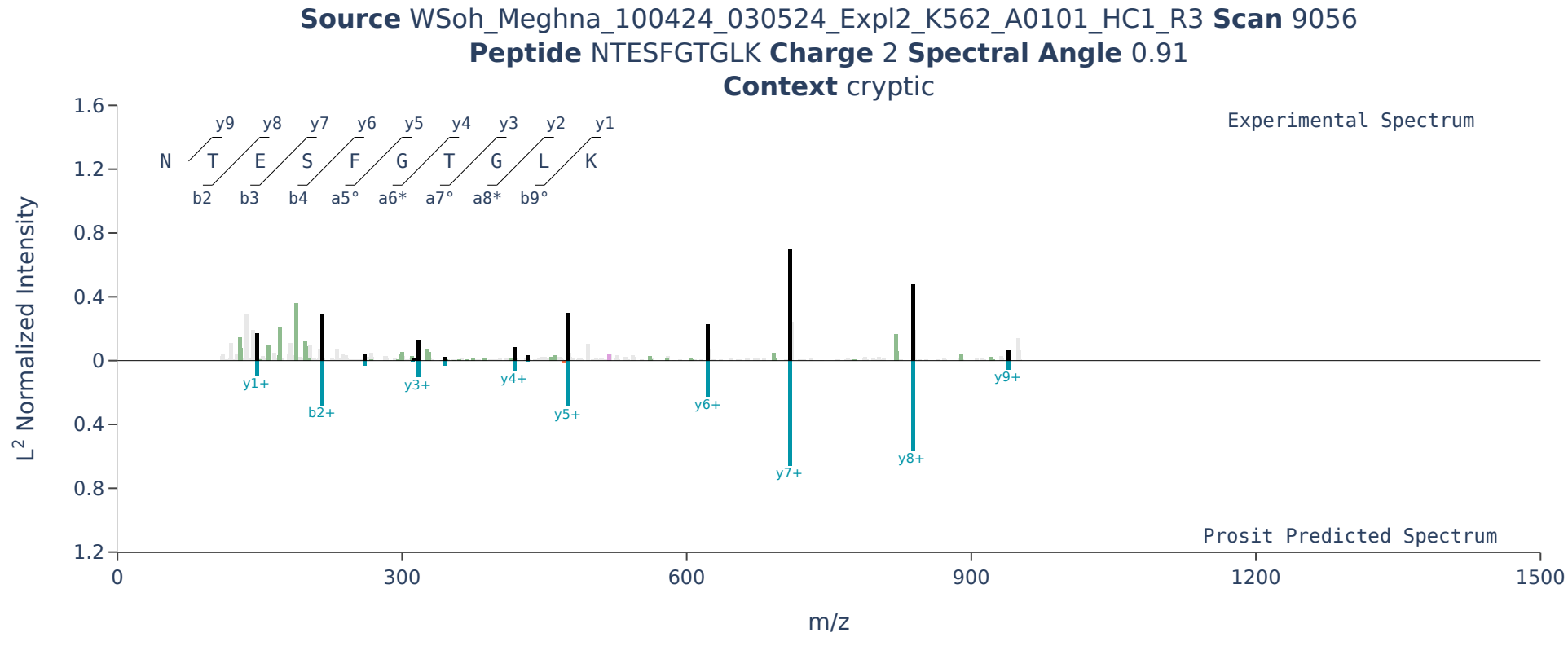
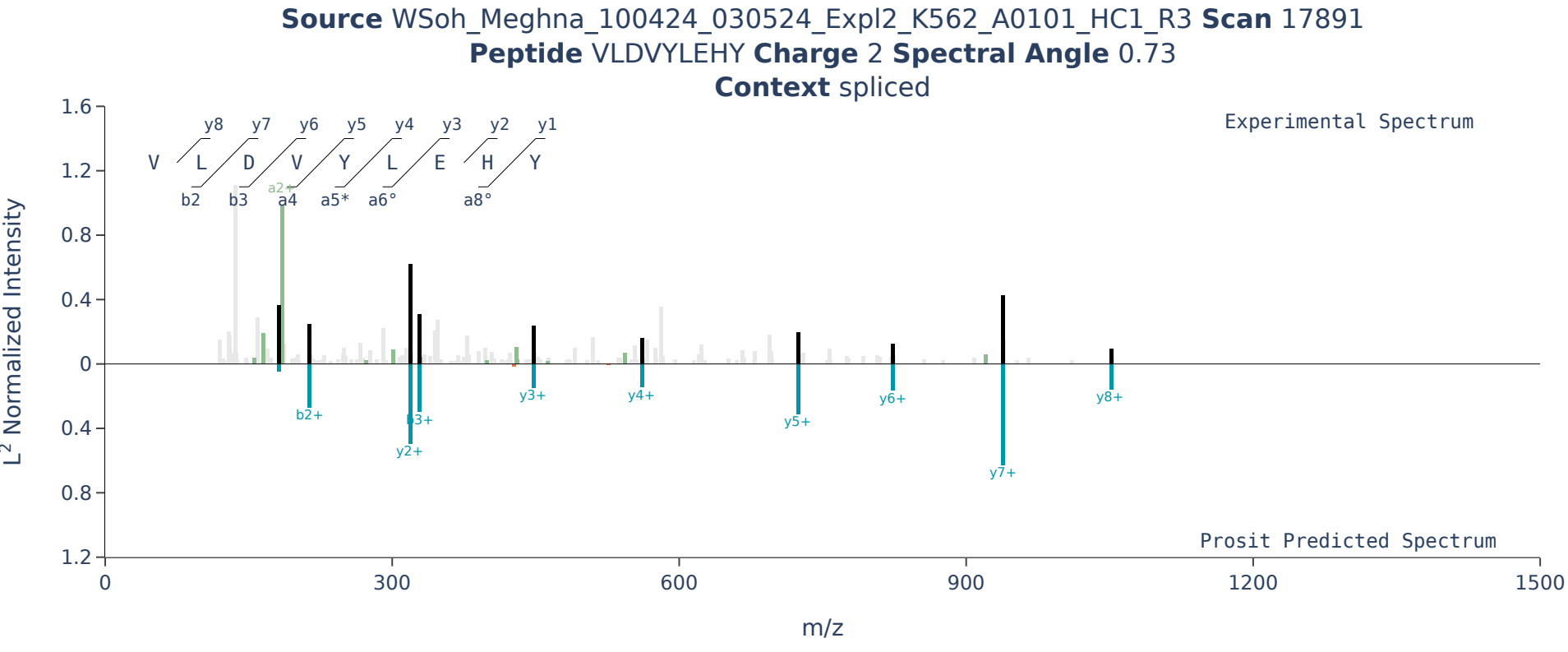
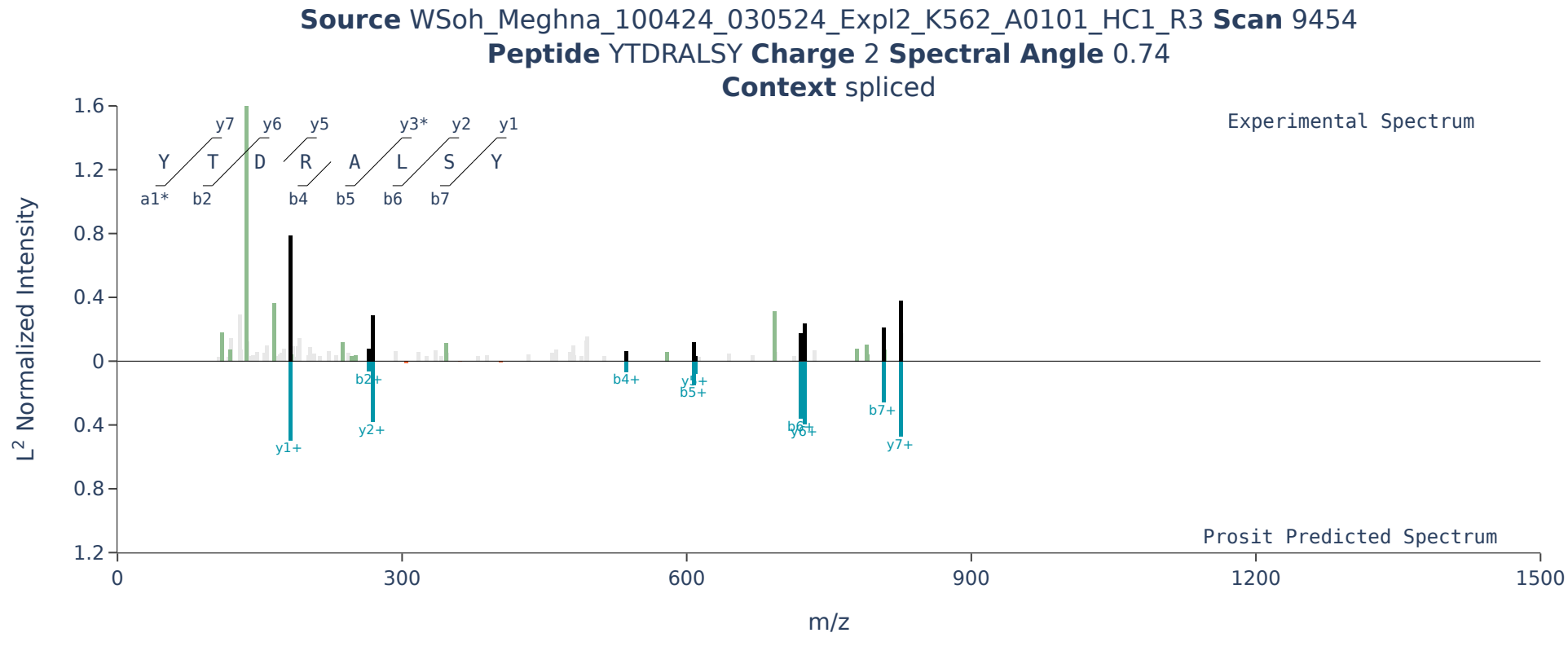
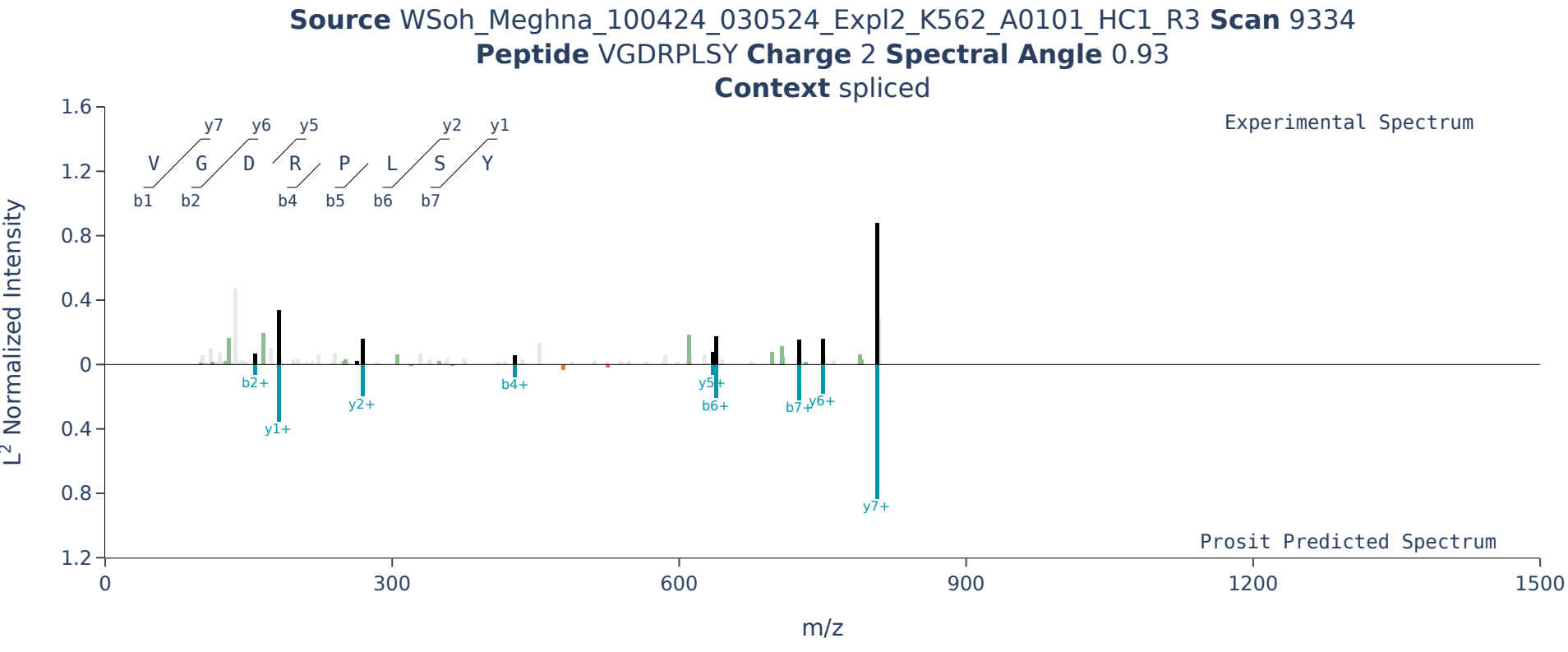
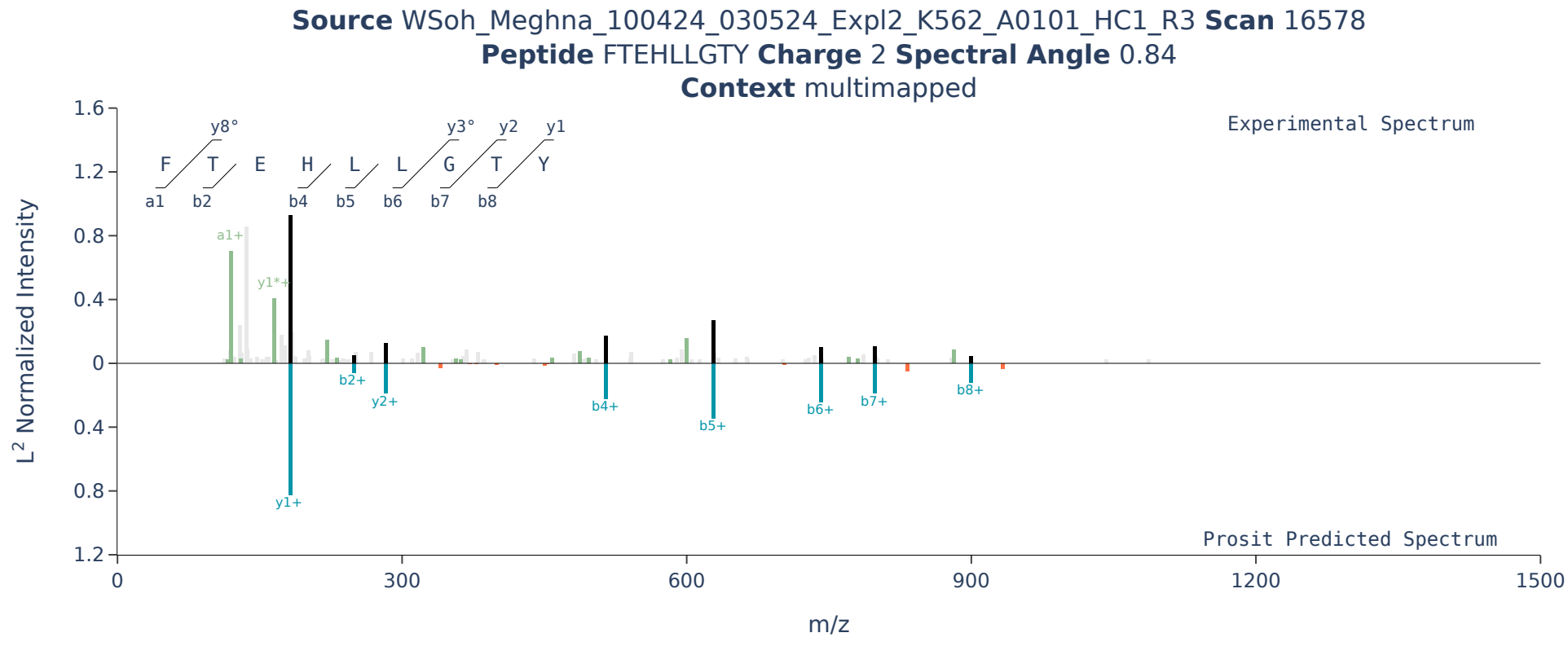
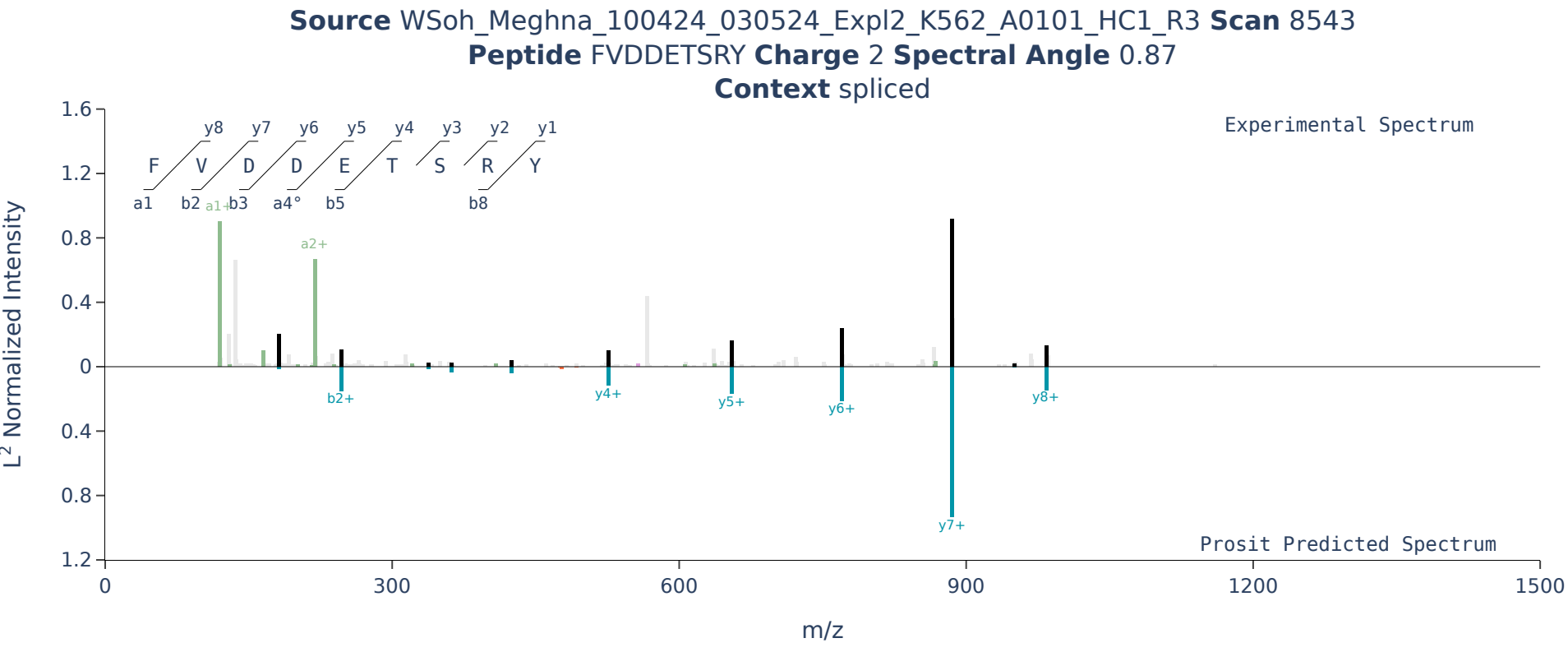
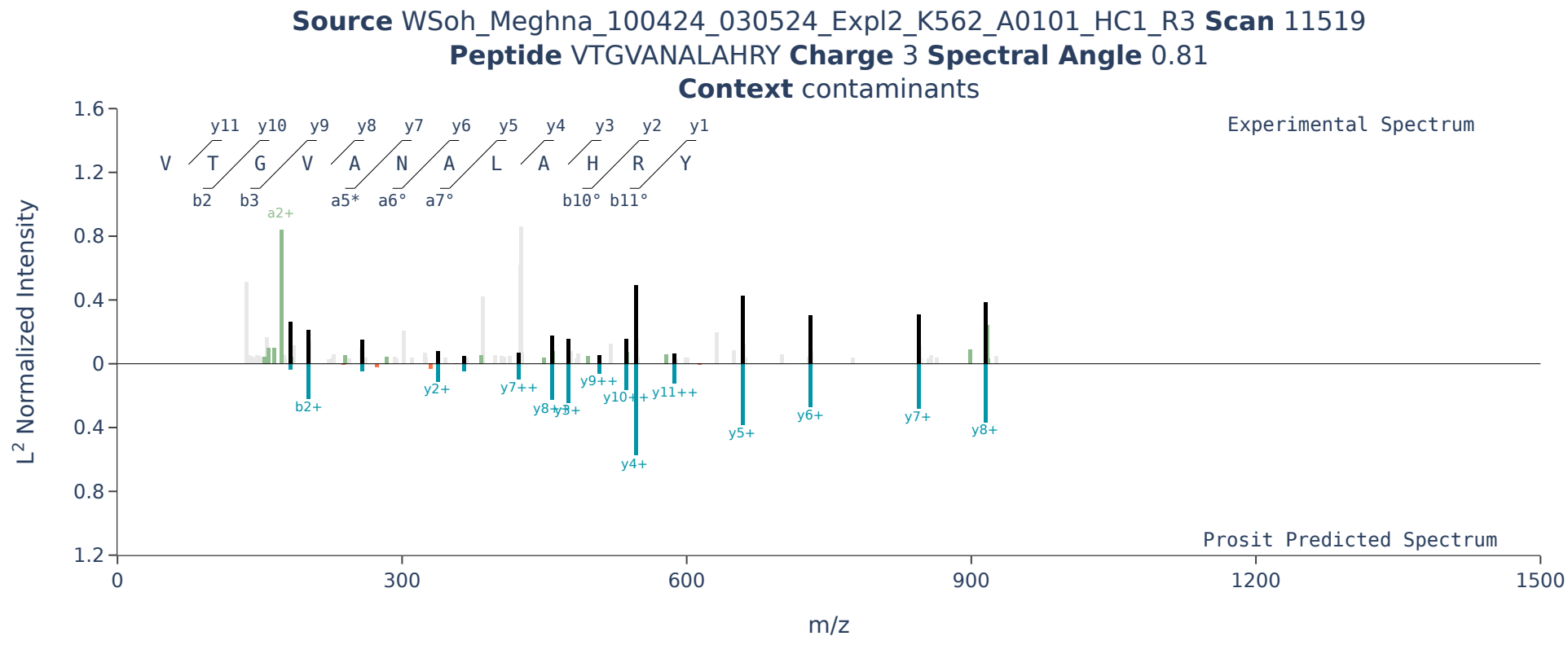
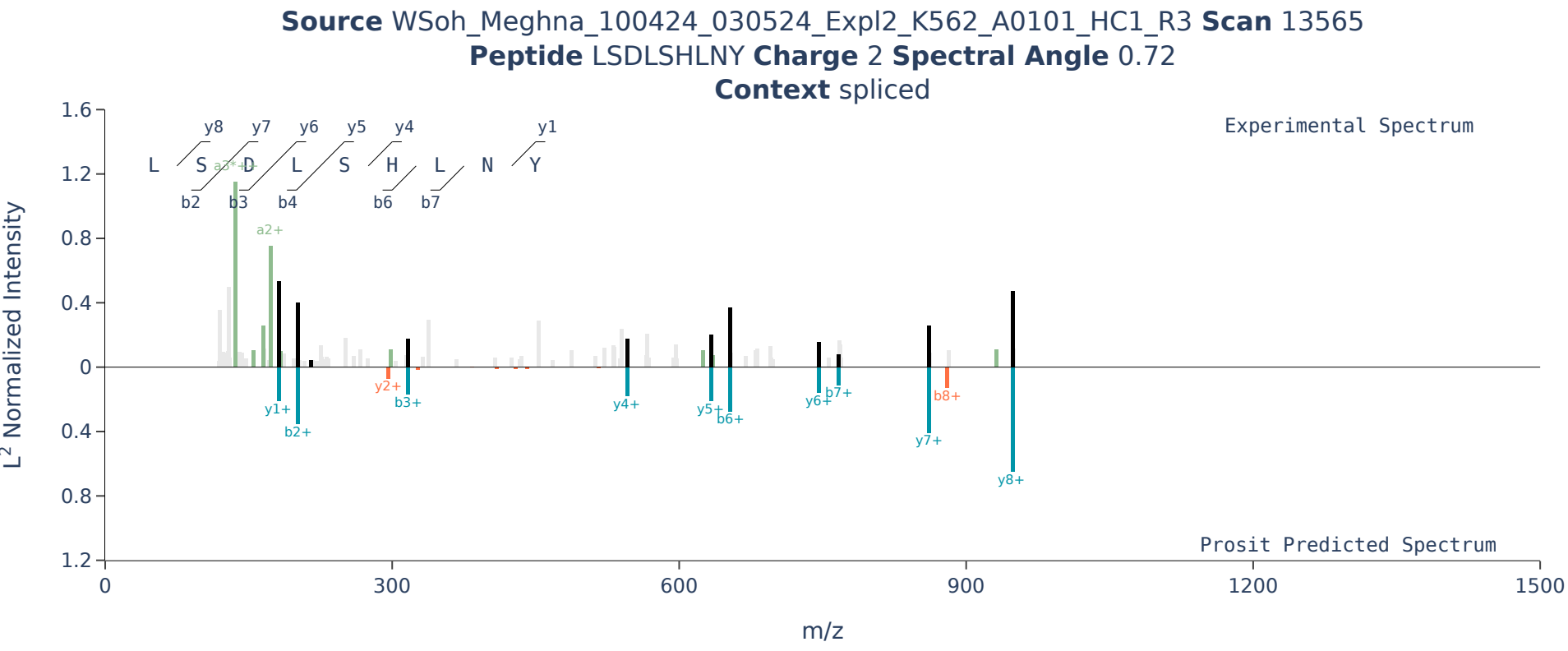
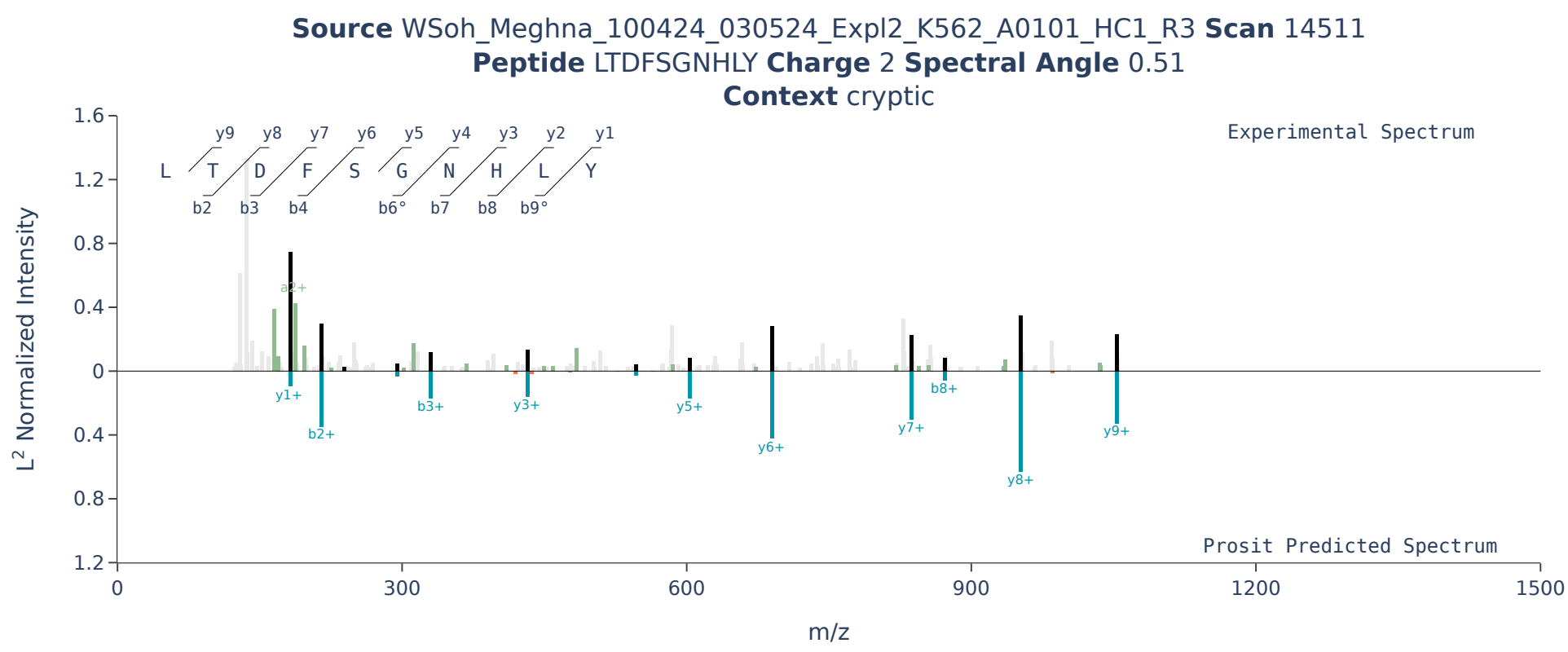
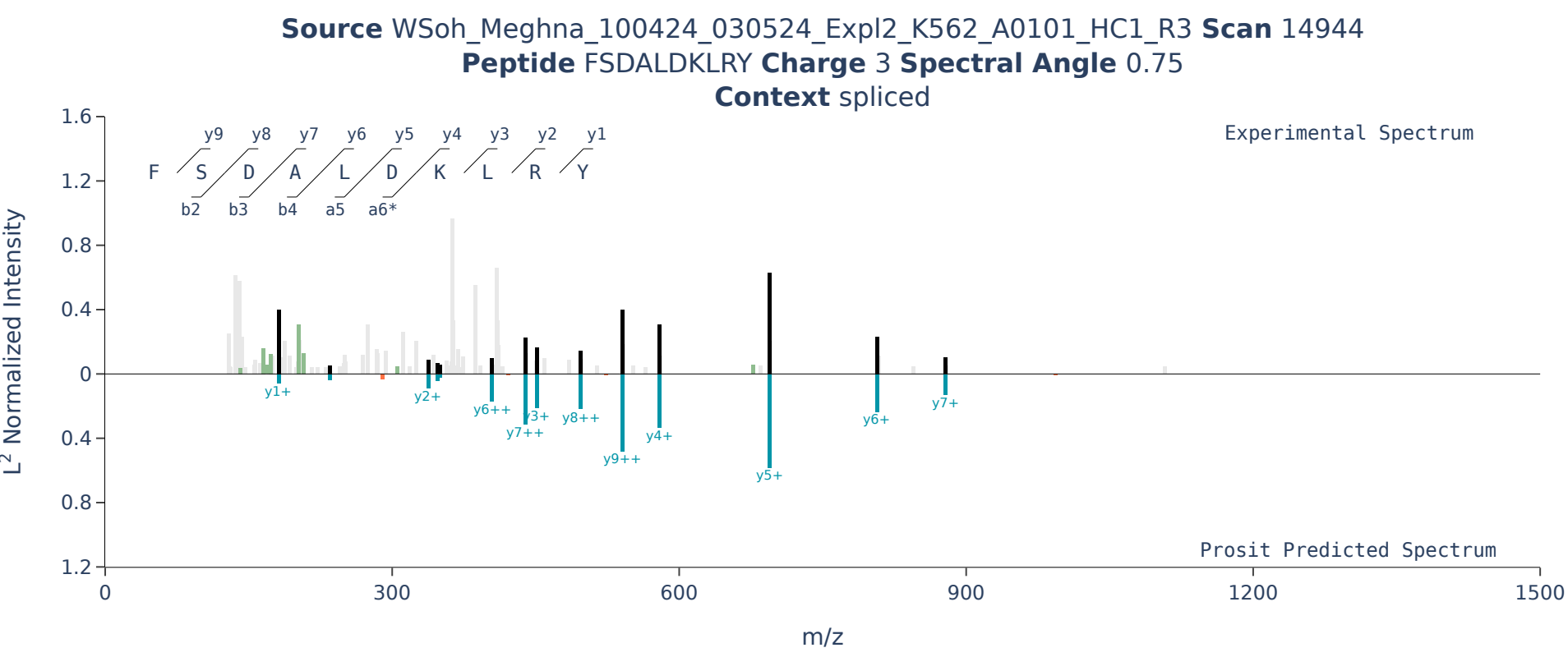


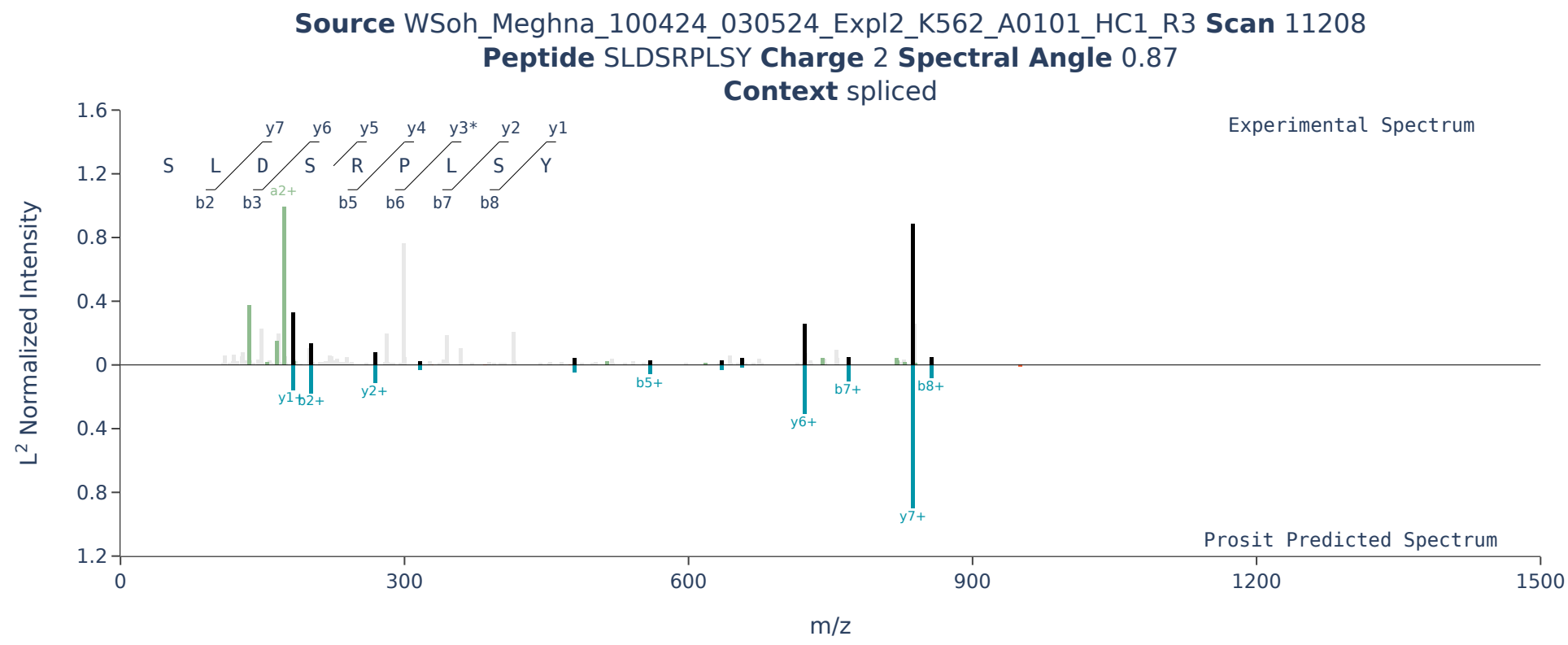
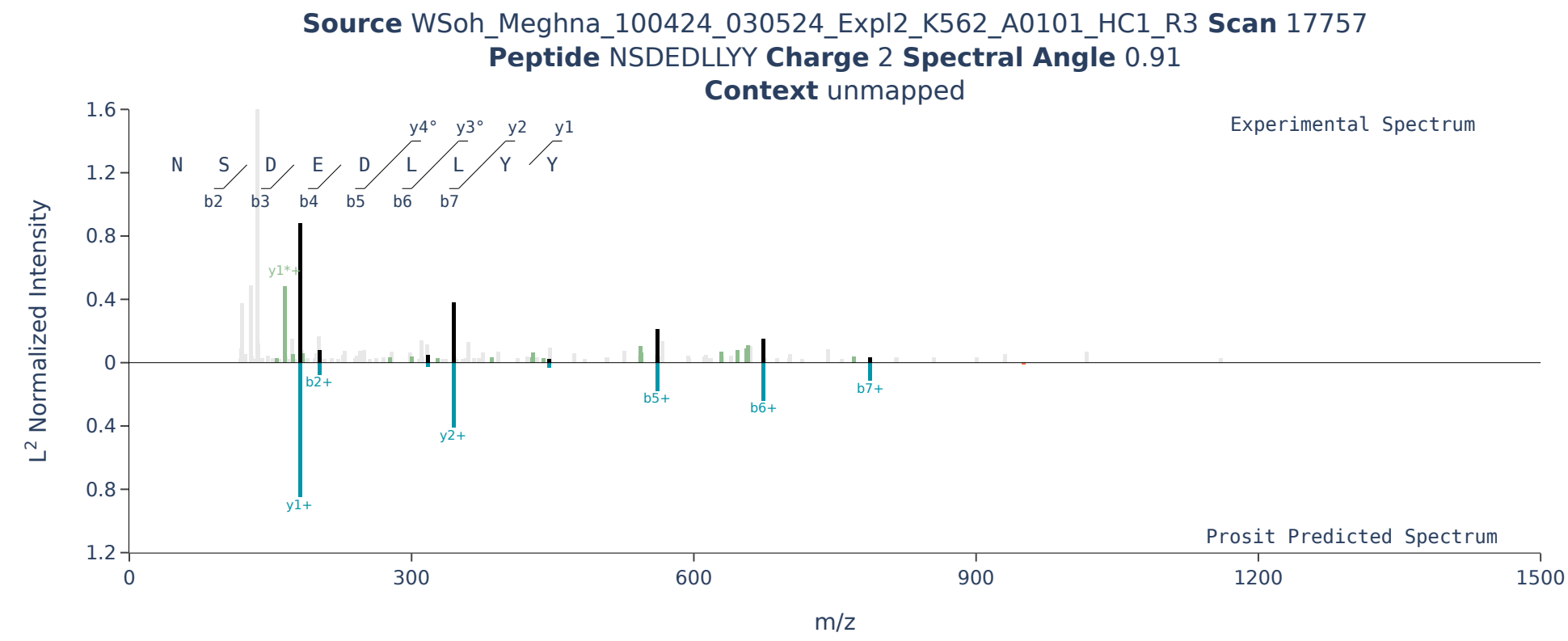
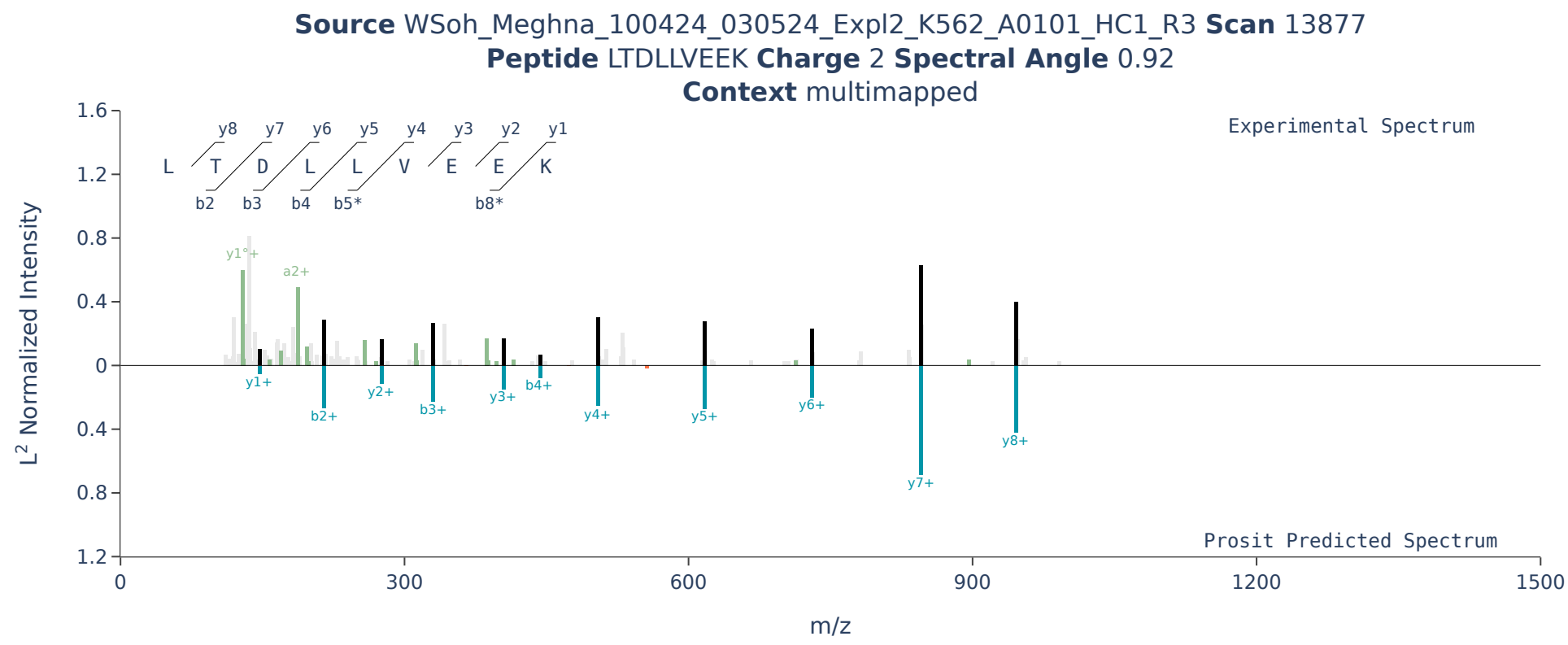
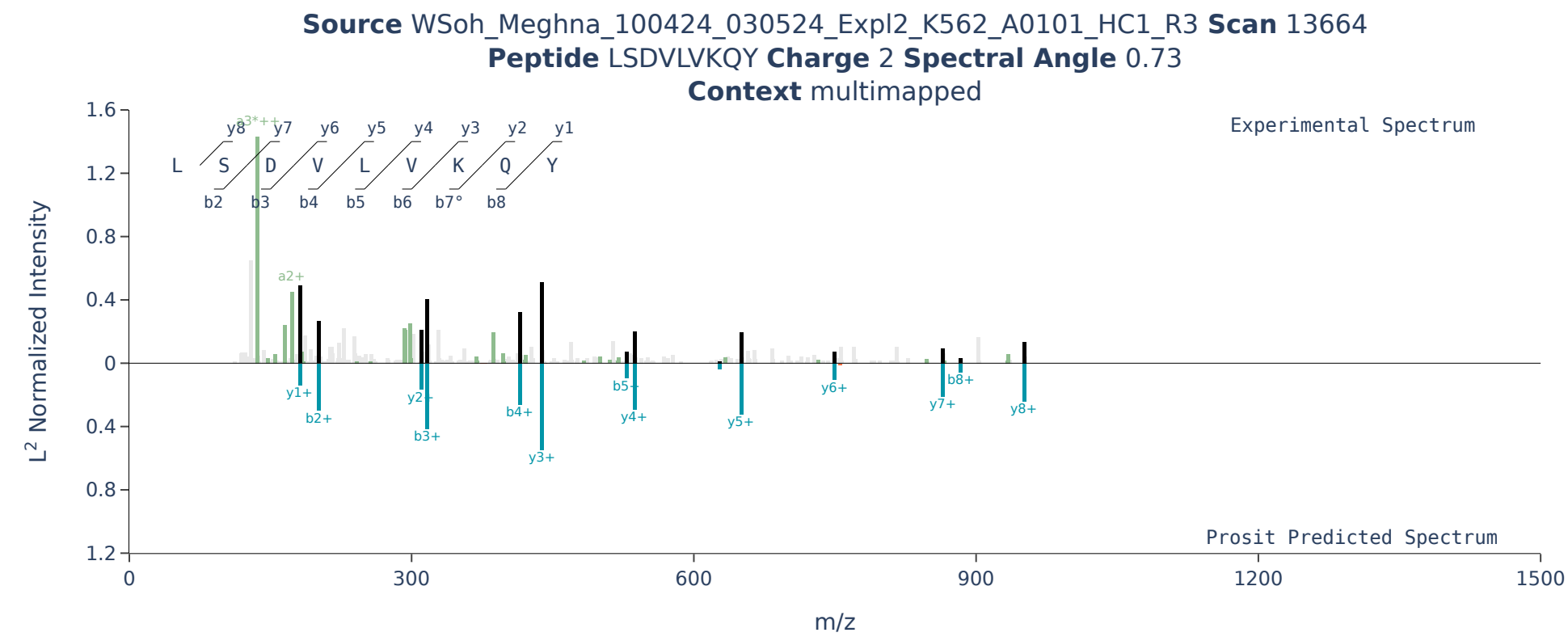
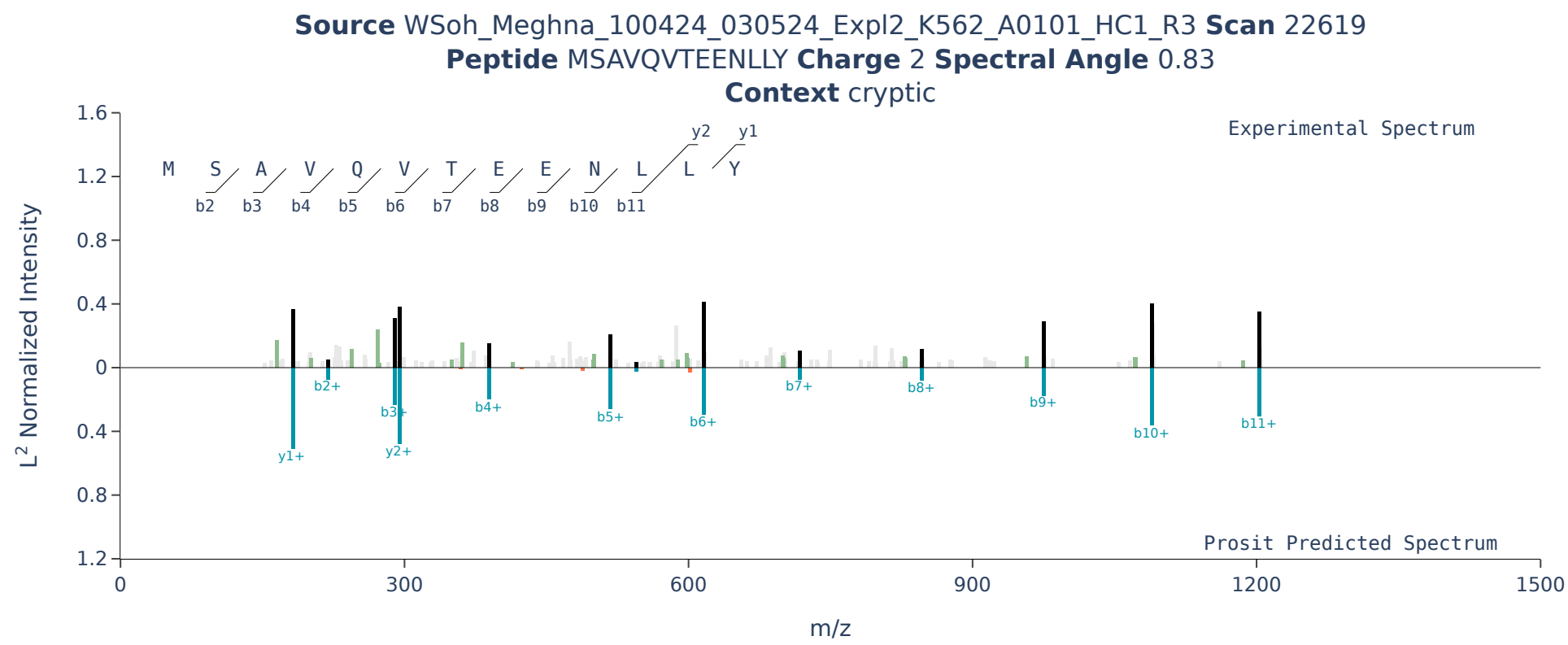
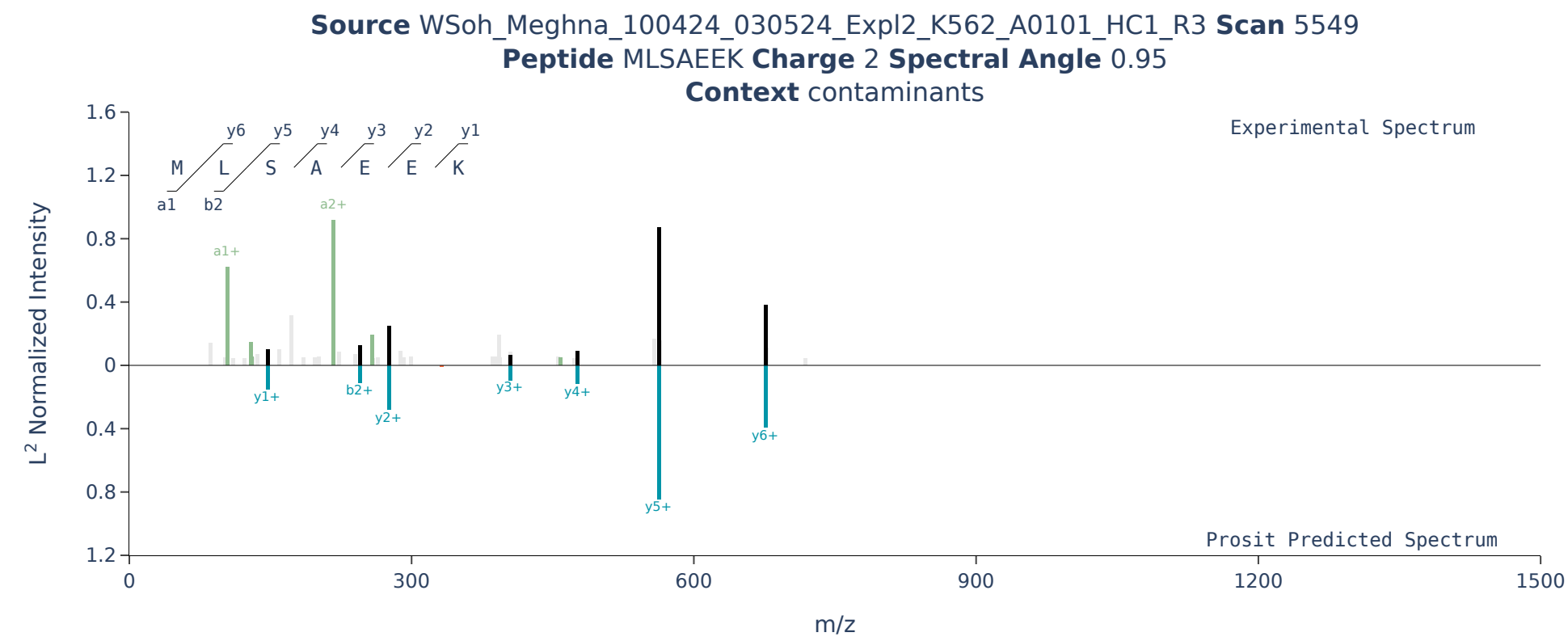
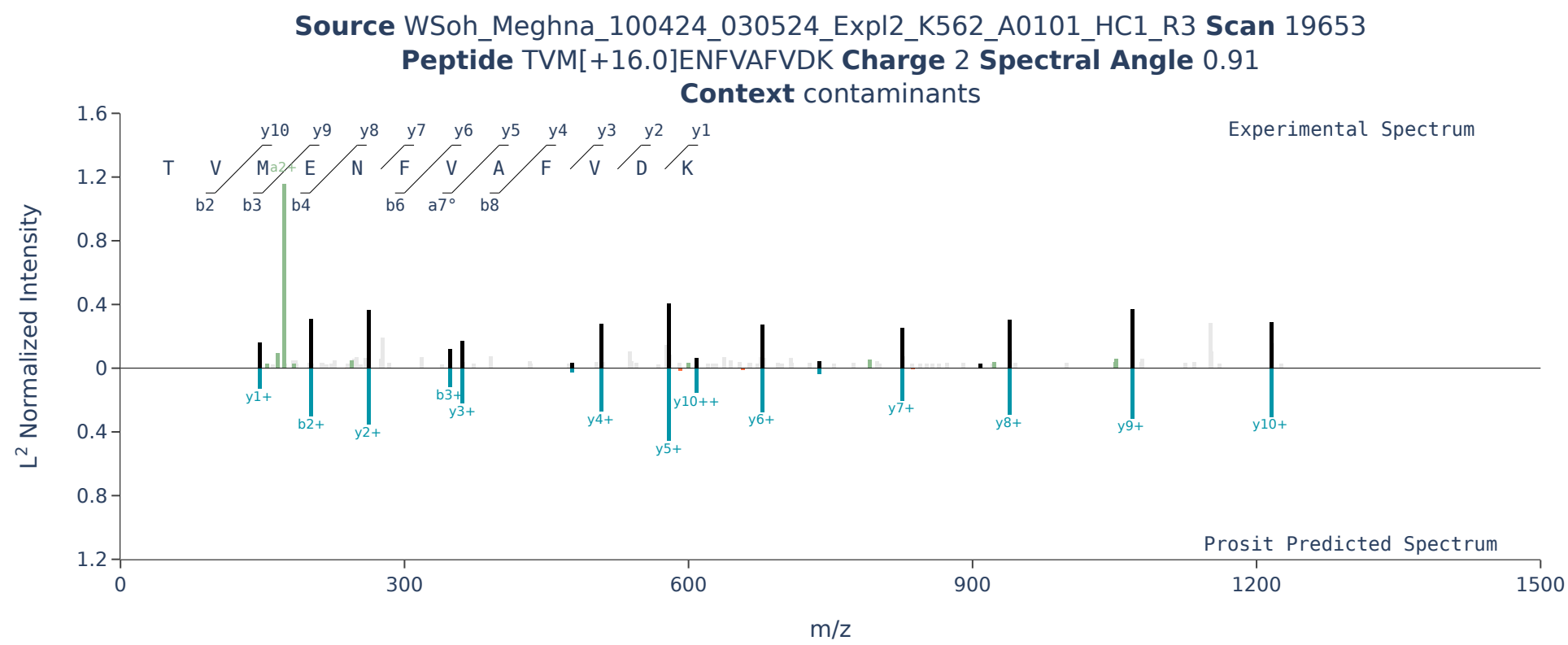
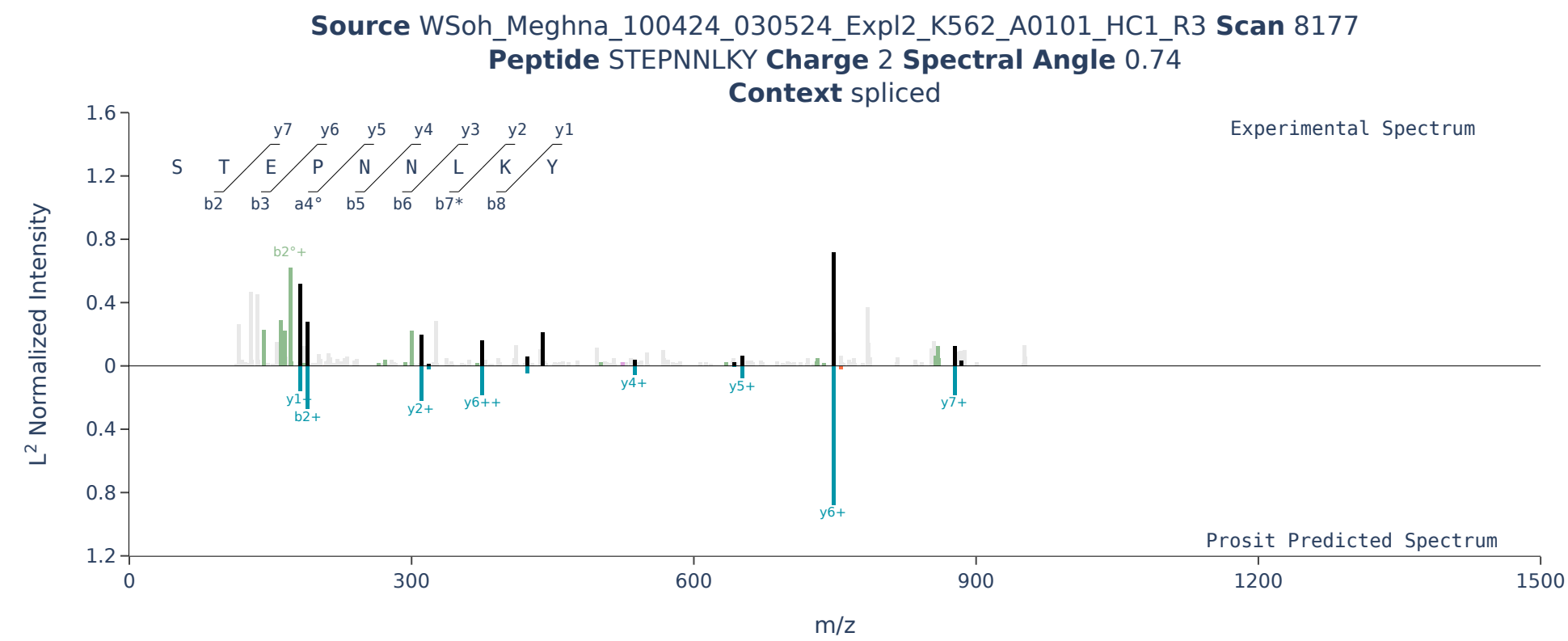
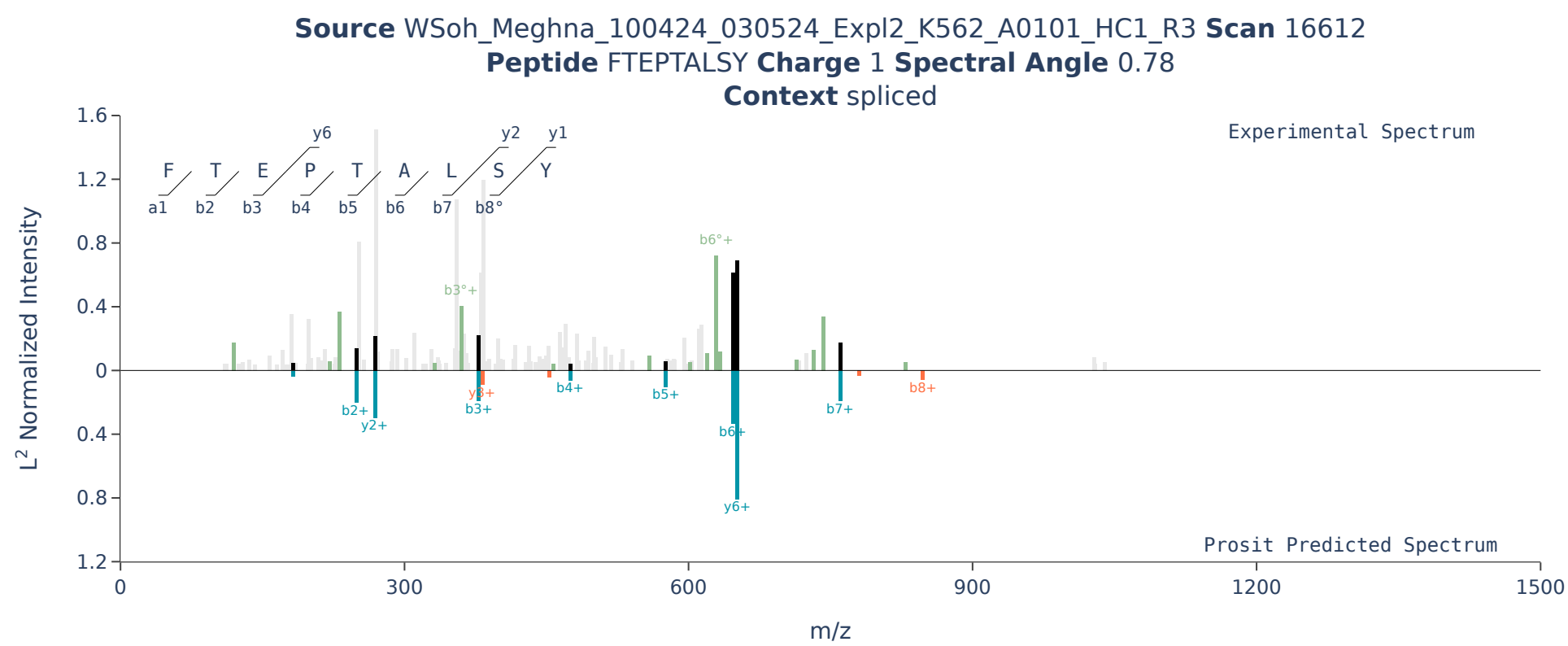
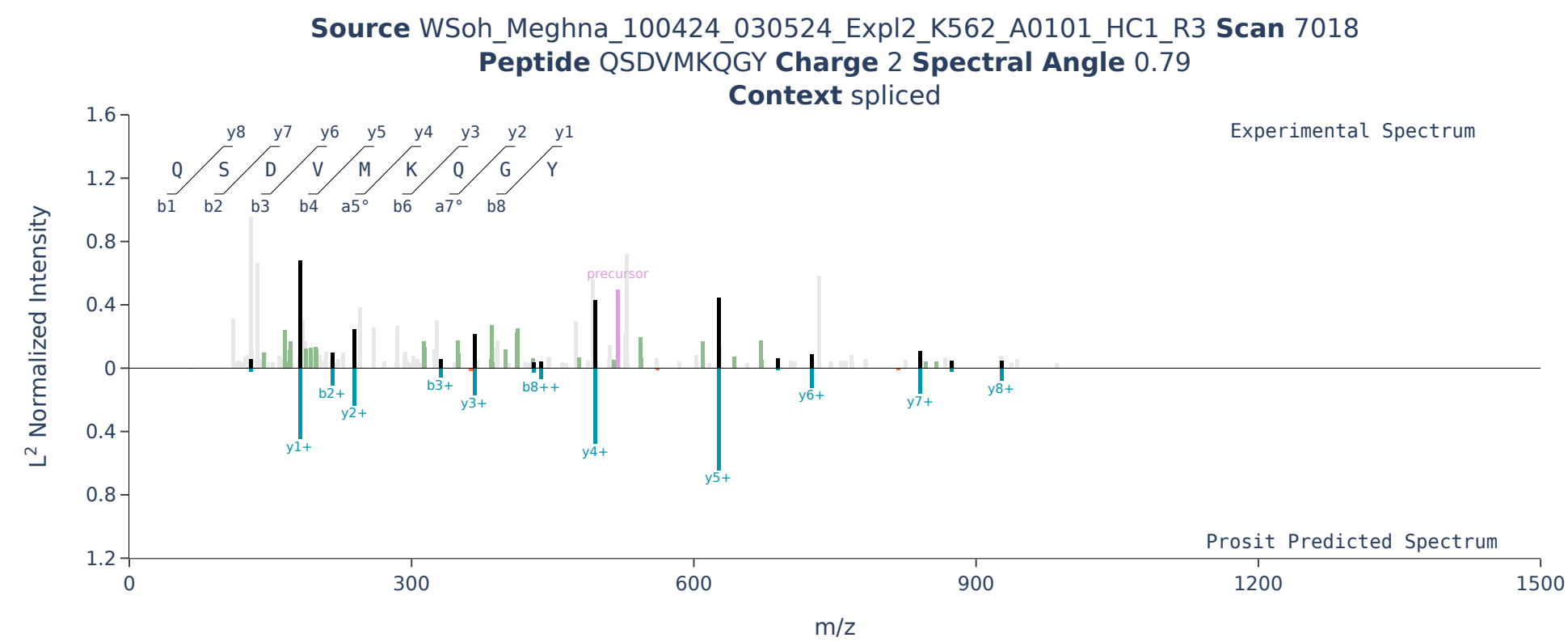
Peptide RFDQI TVVT **Charge** 2 **Spectral Angle** 0.92
Context multimapped

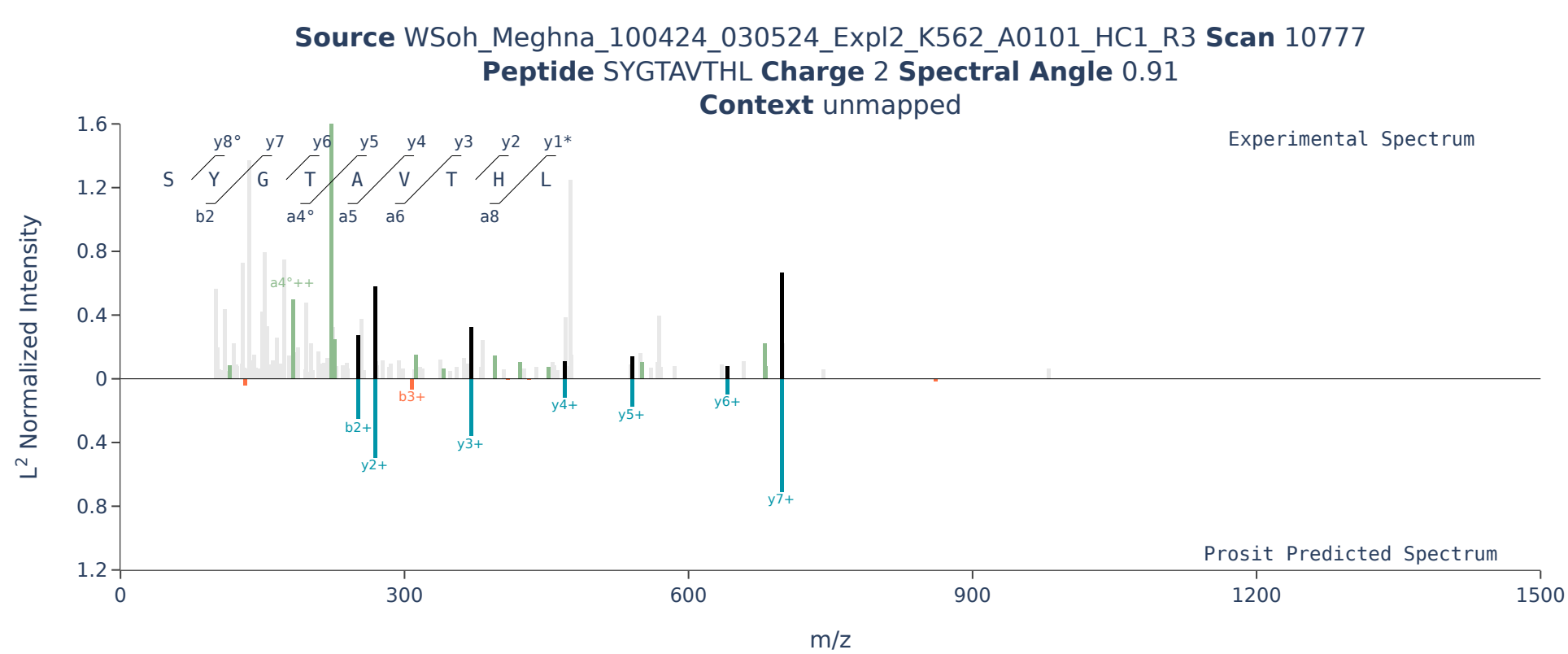
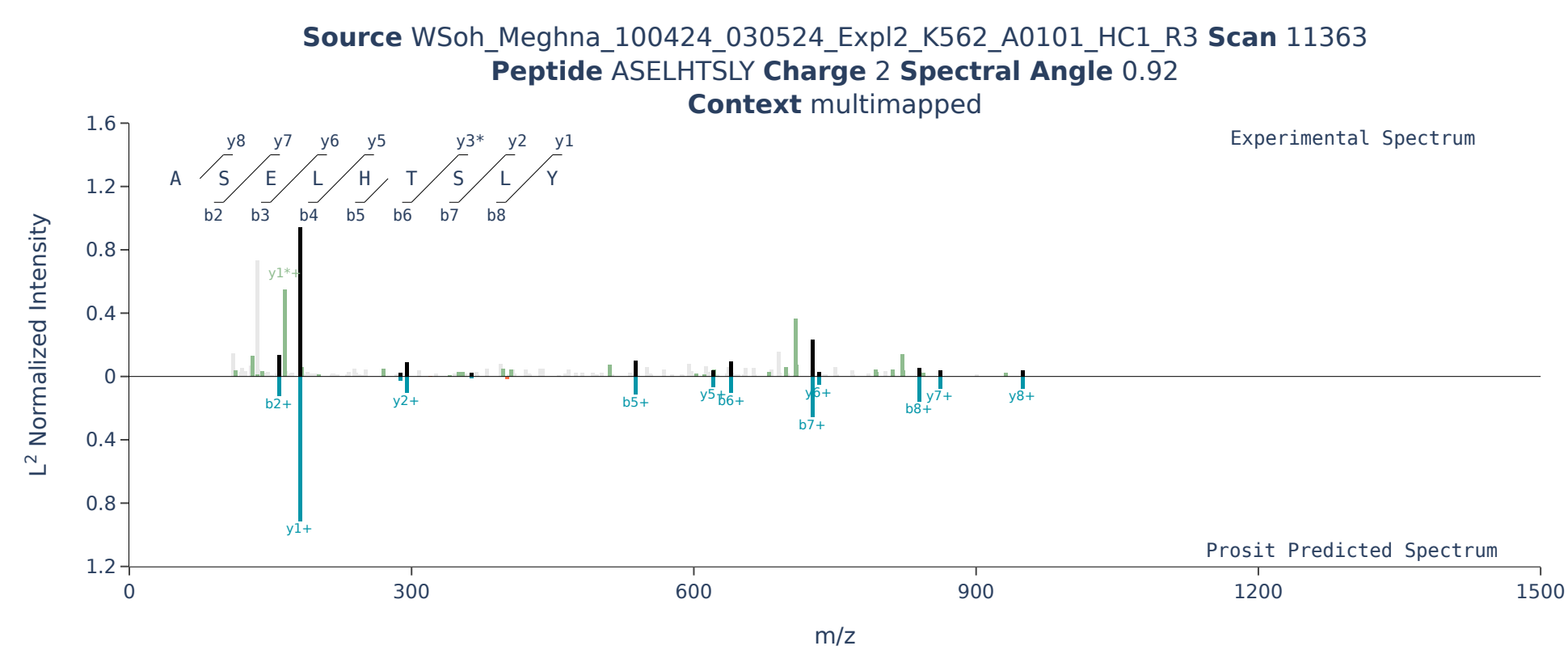
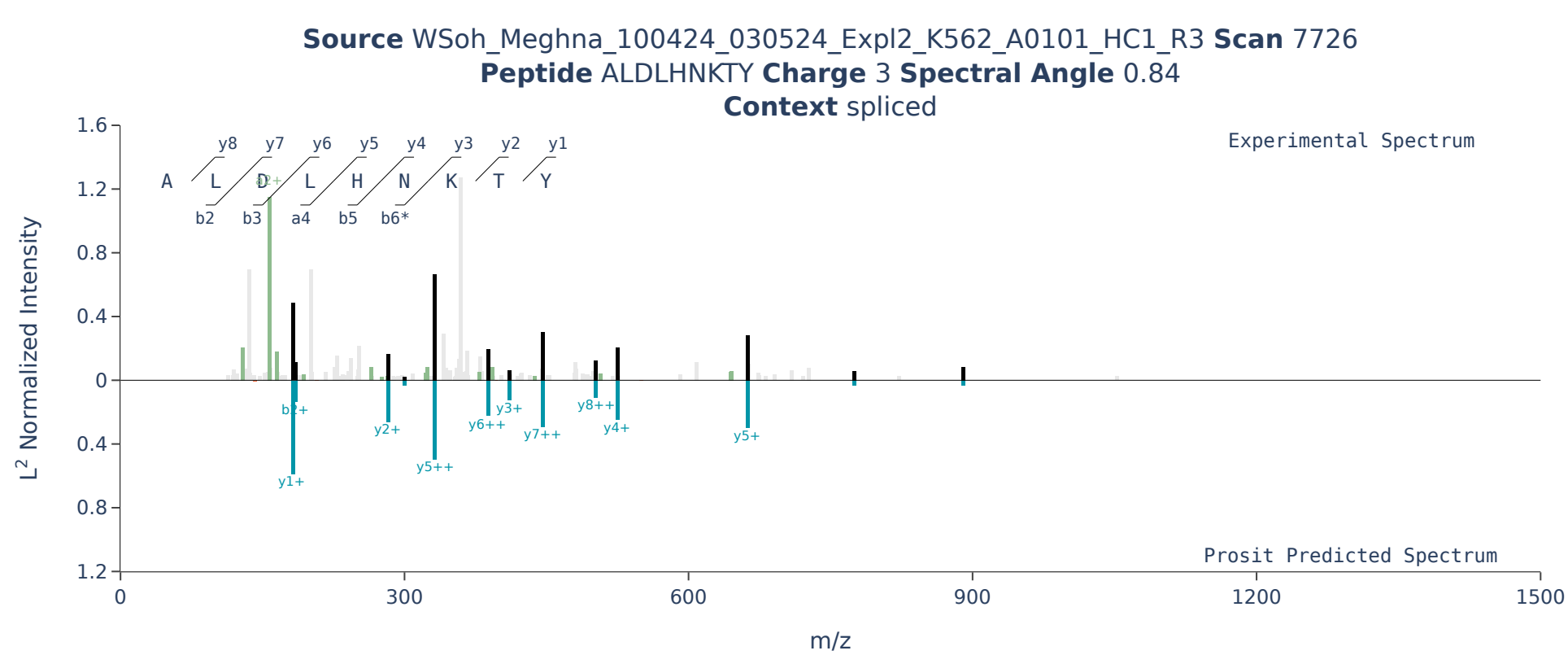
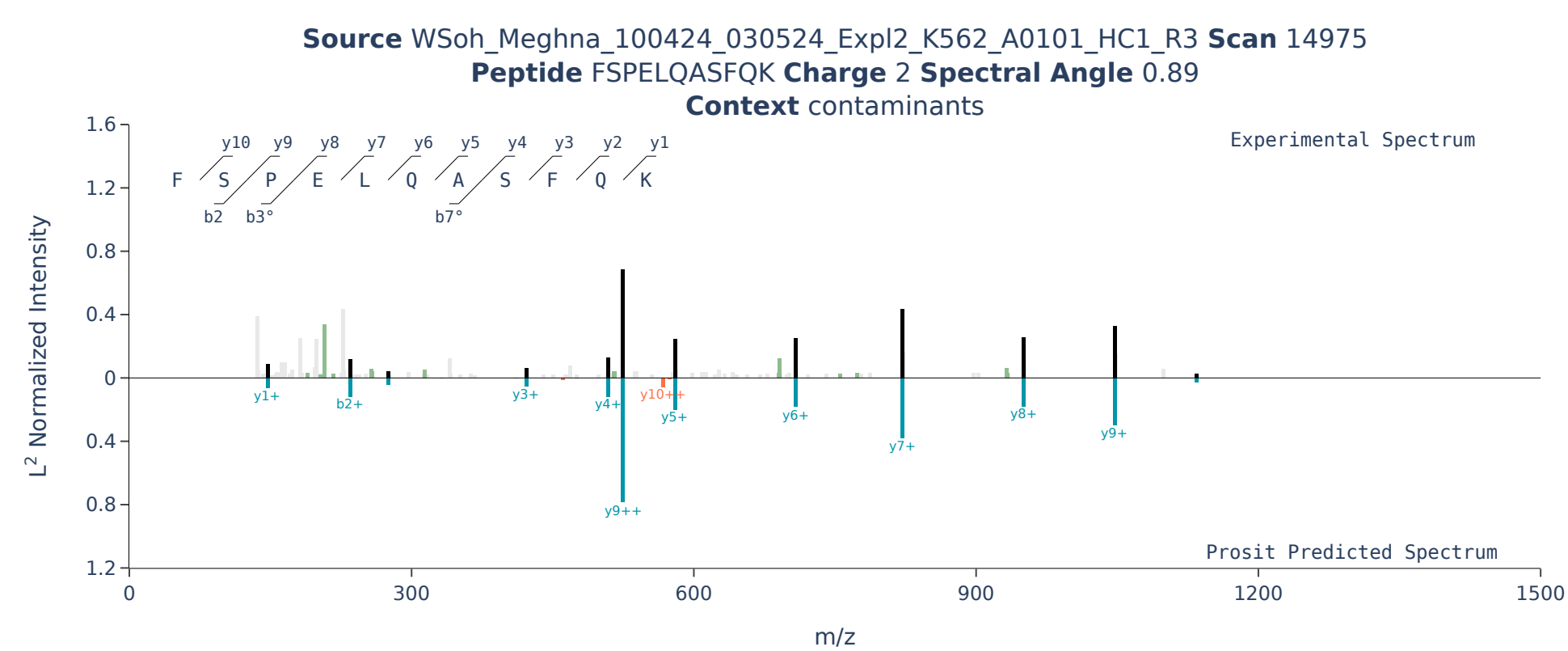
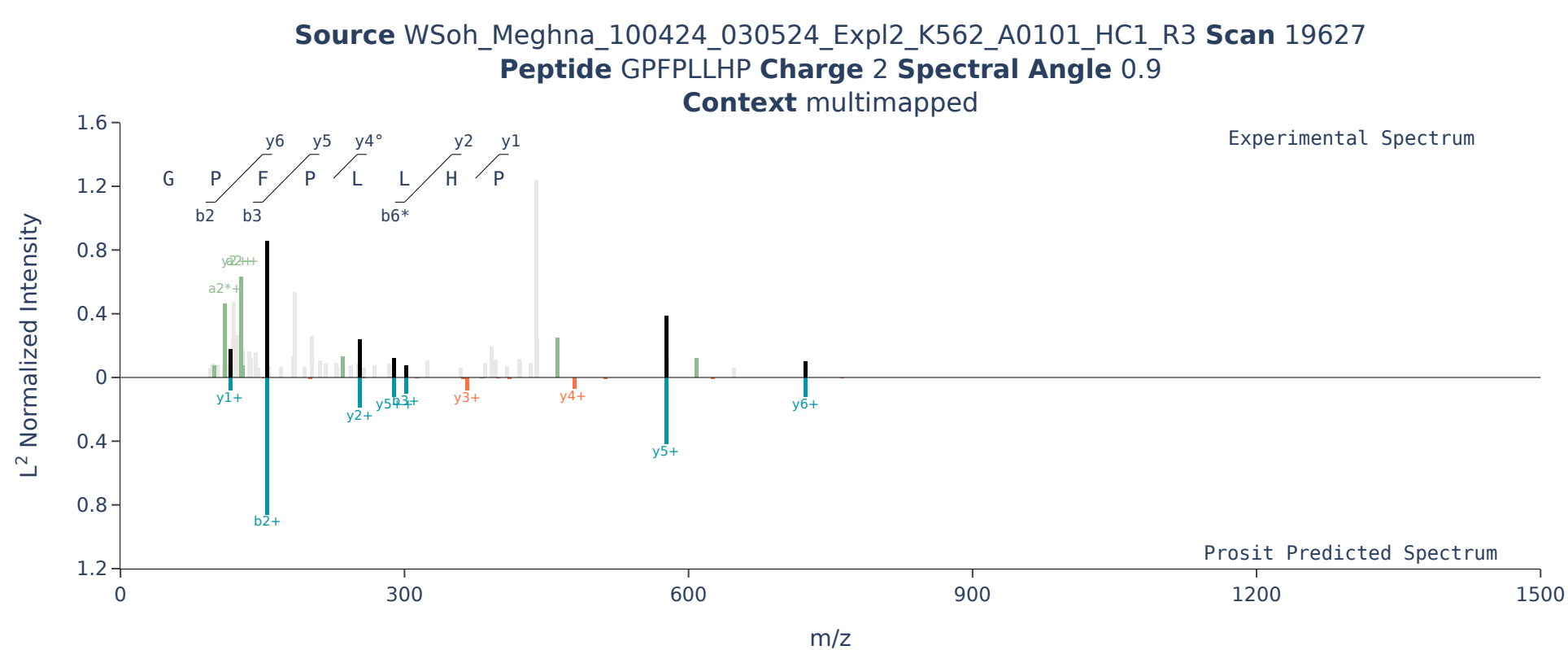
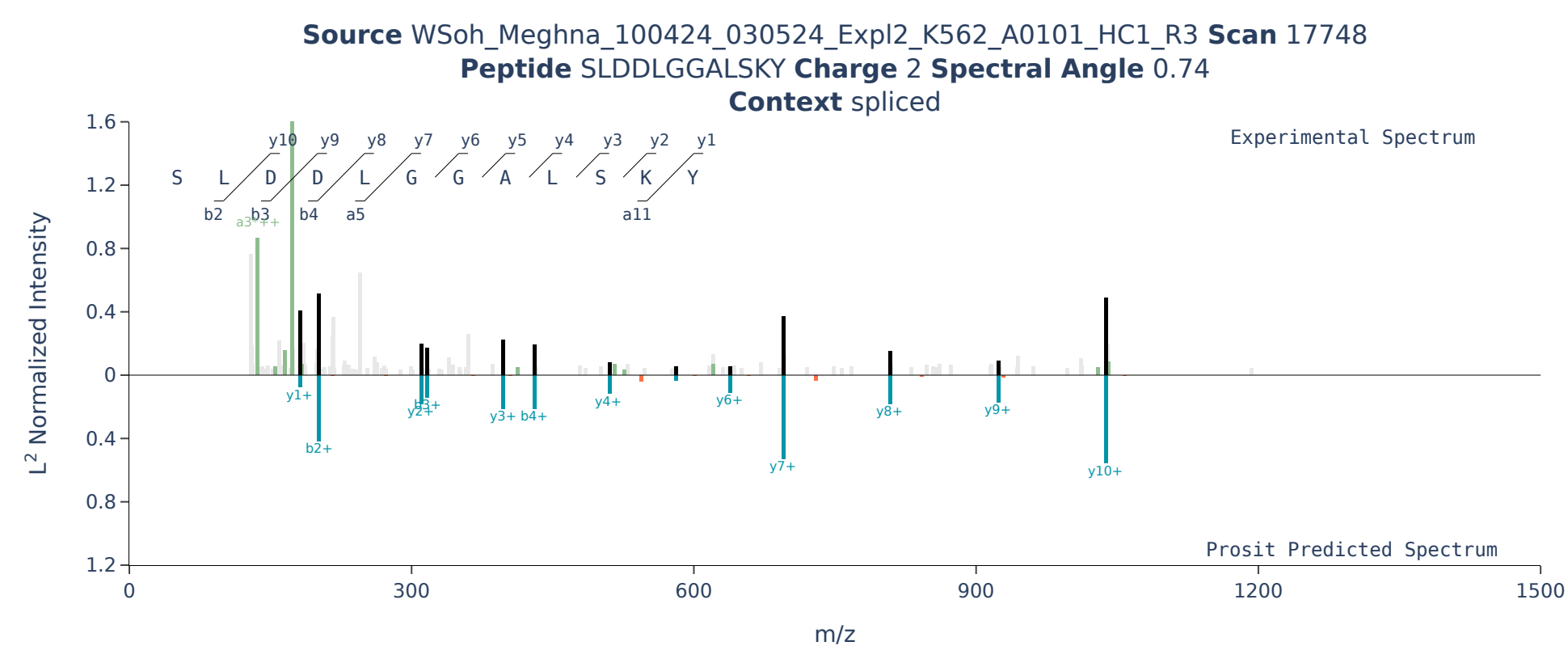
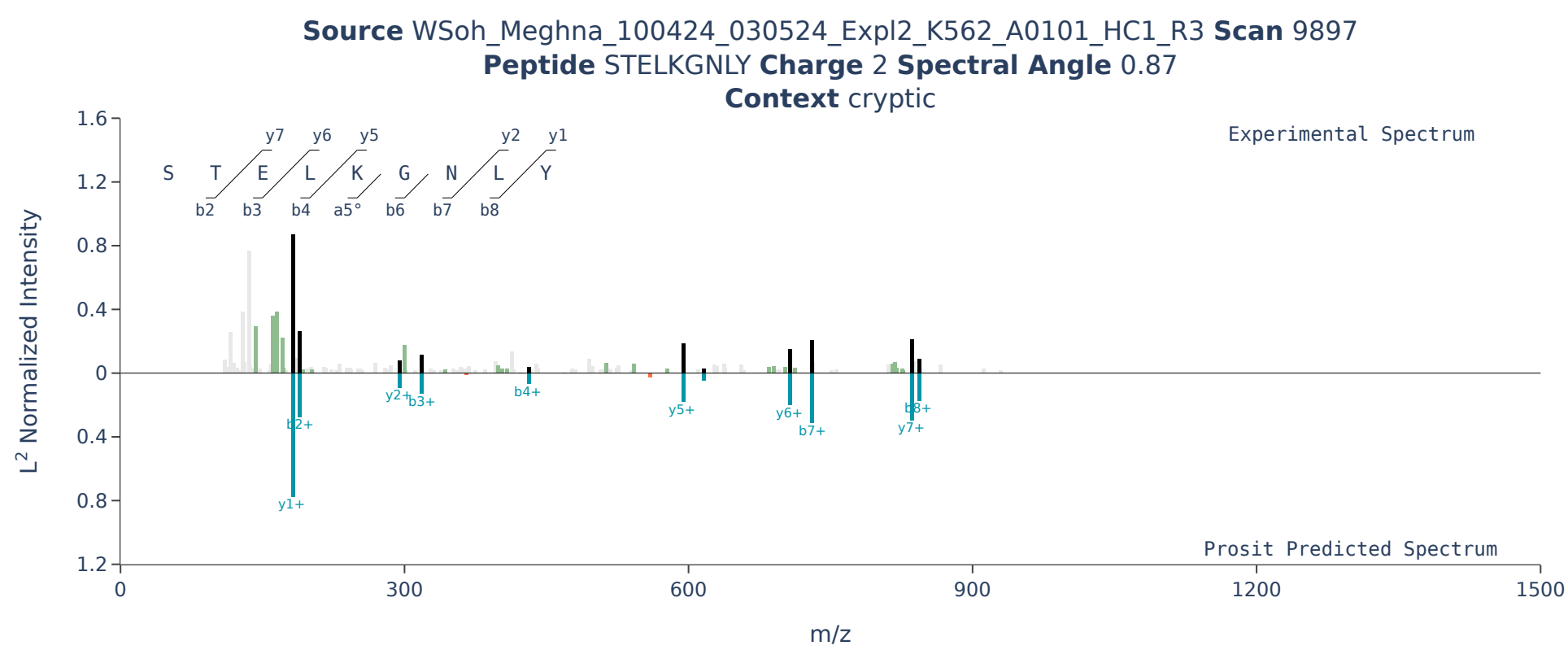
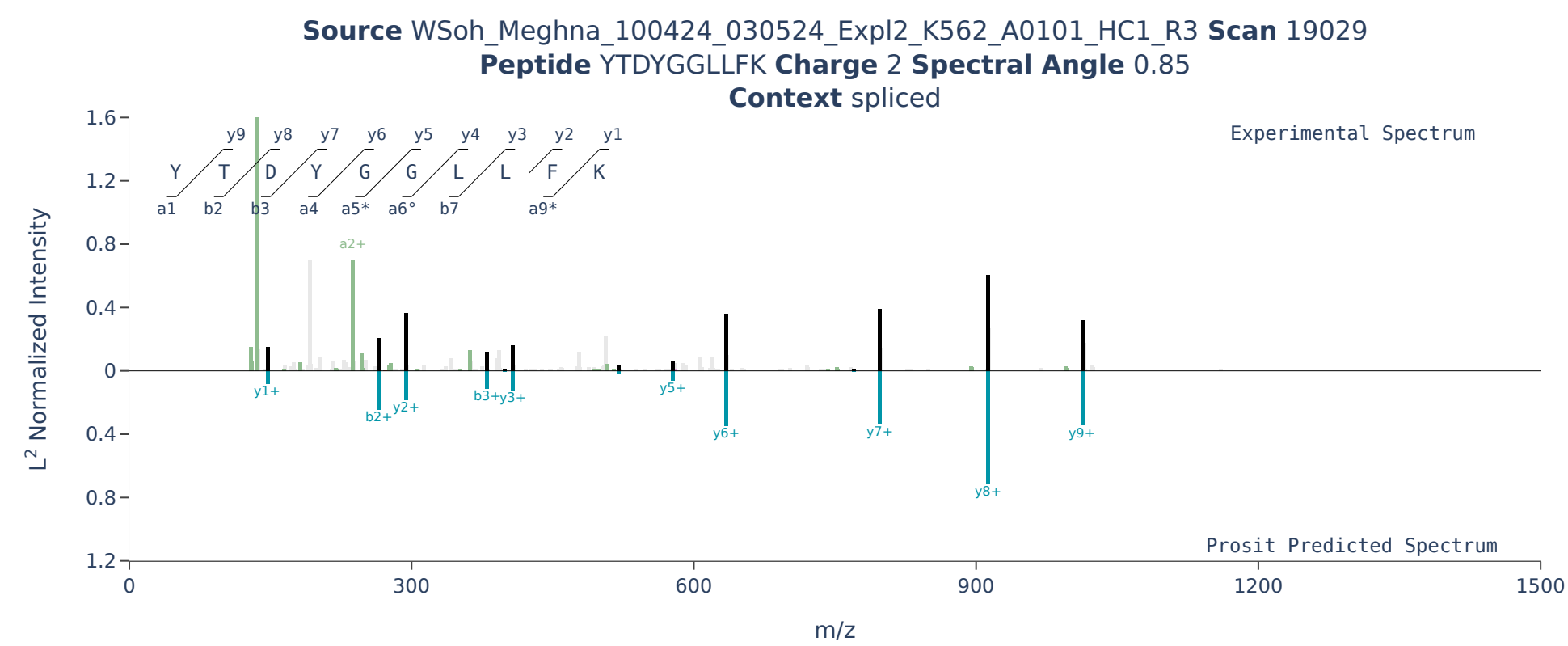
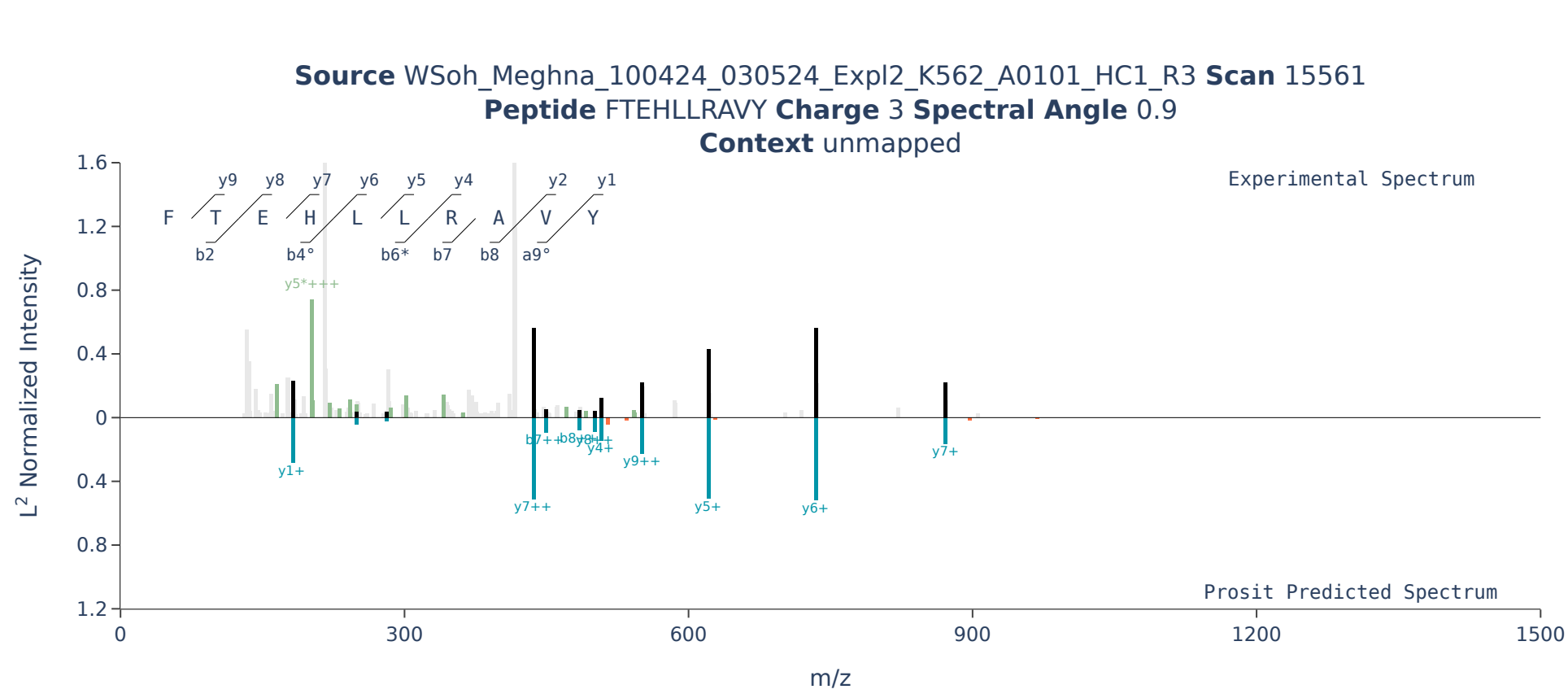
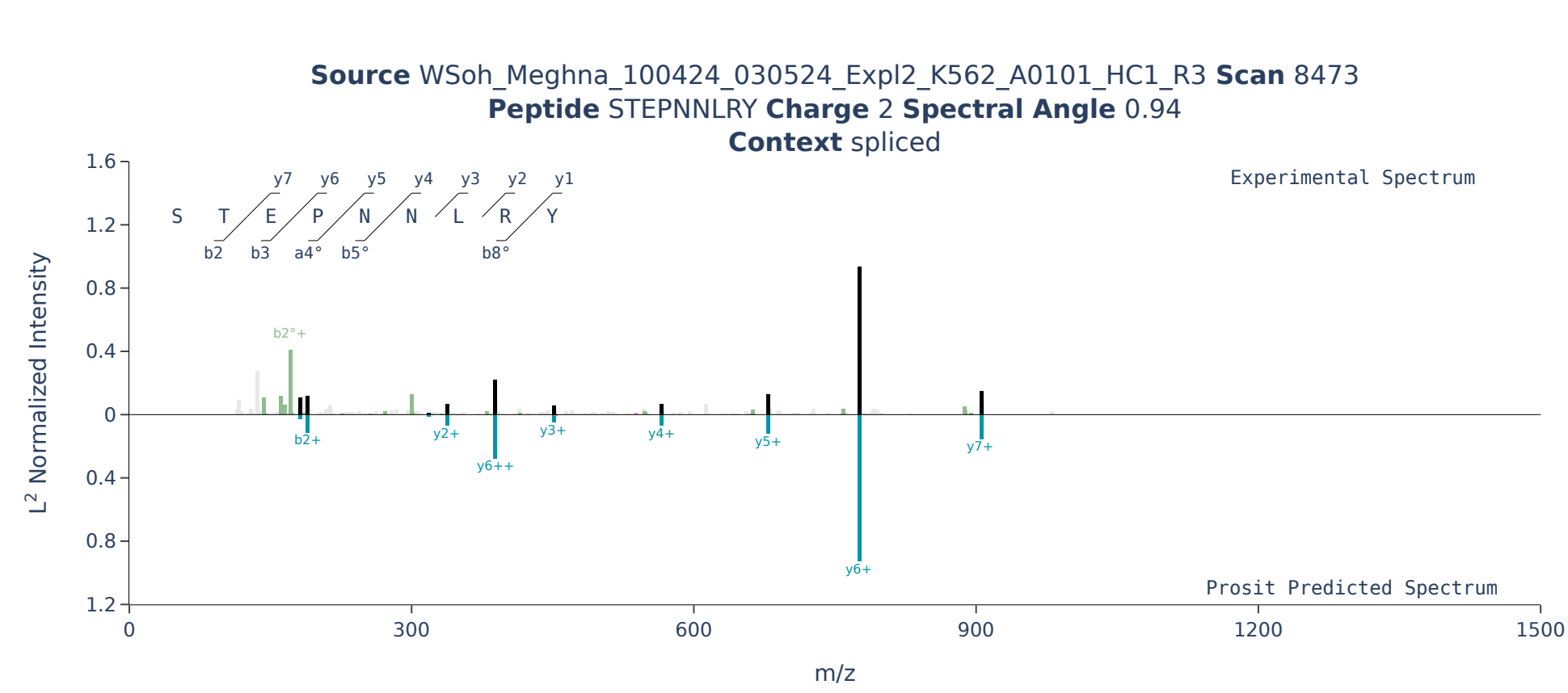


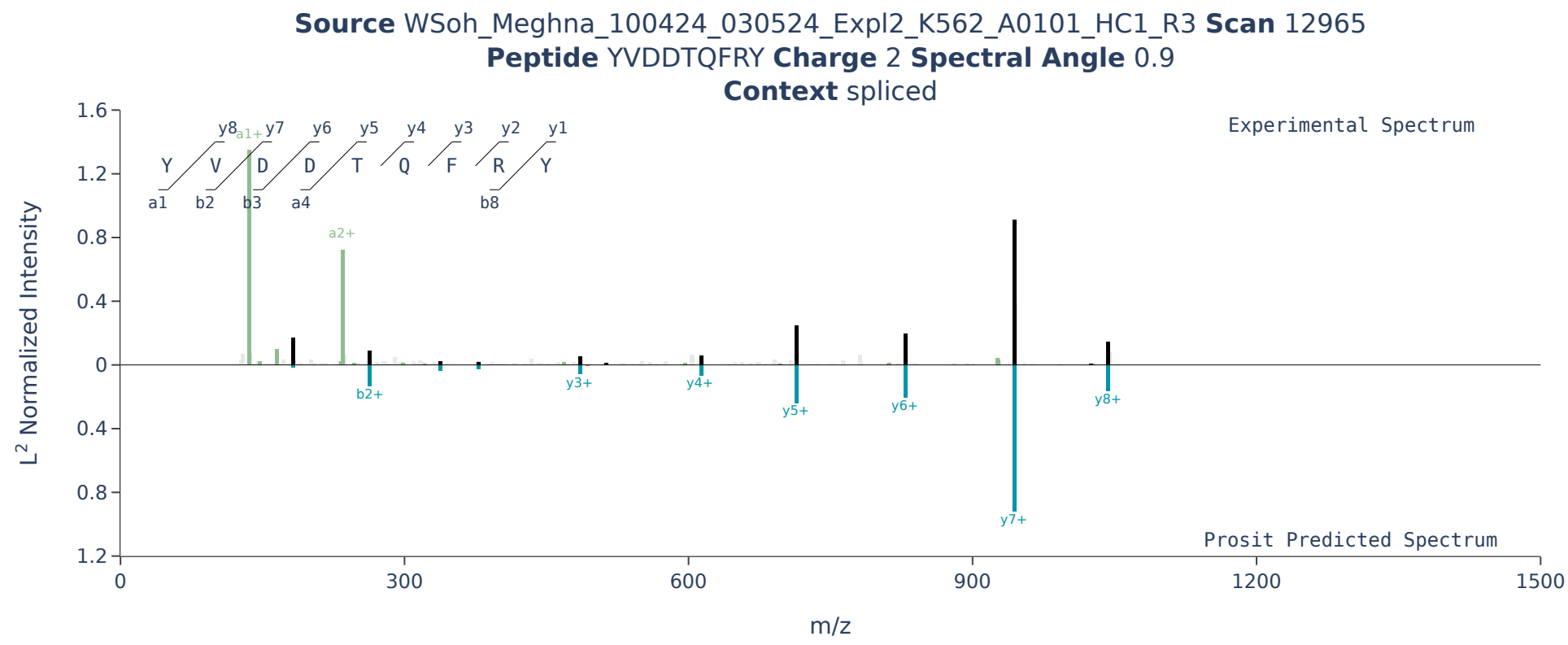
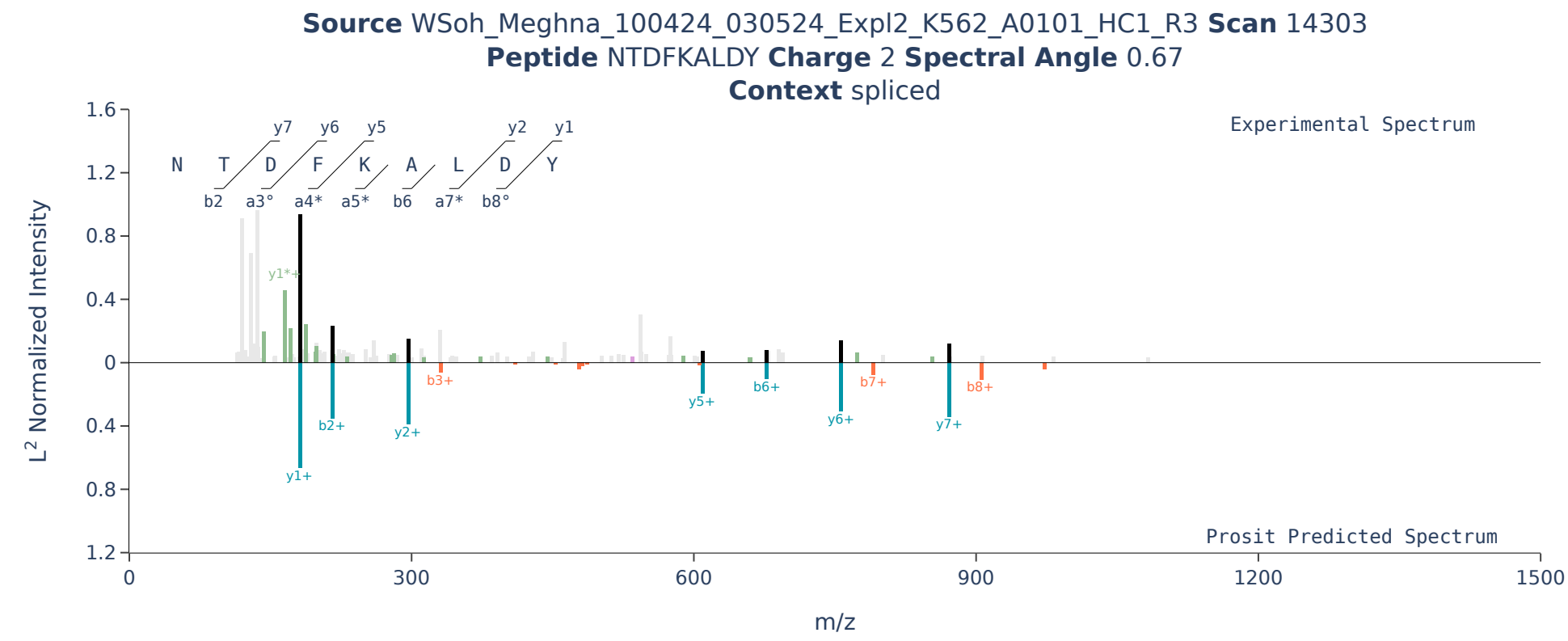
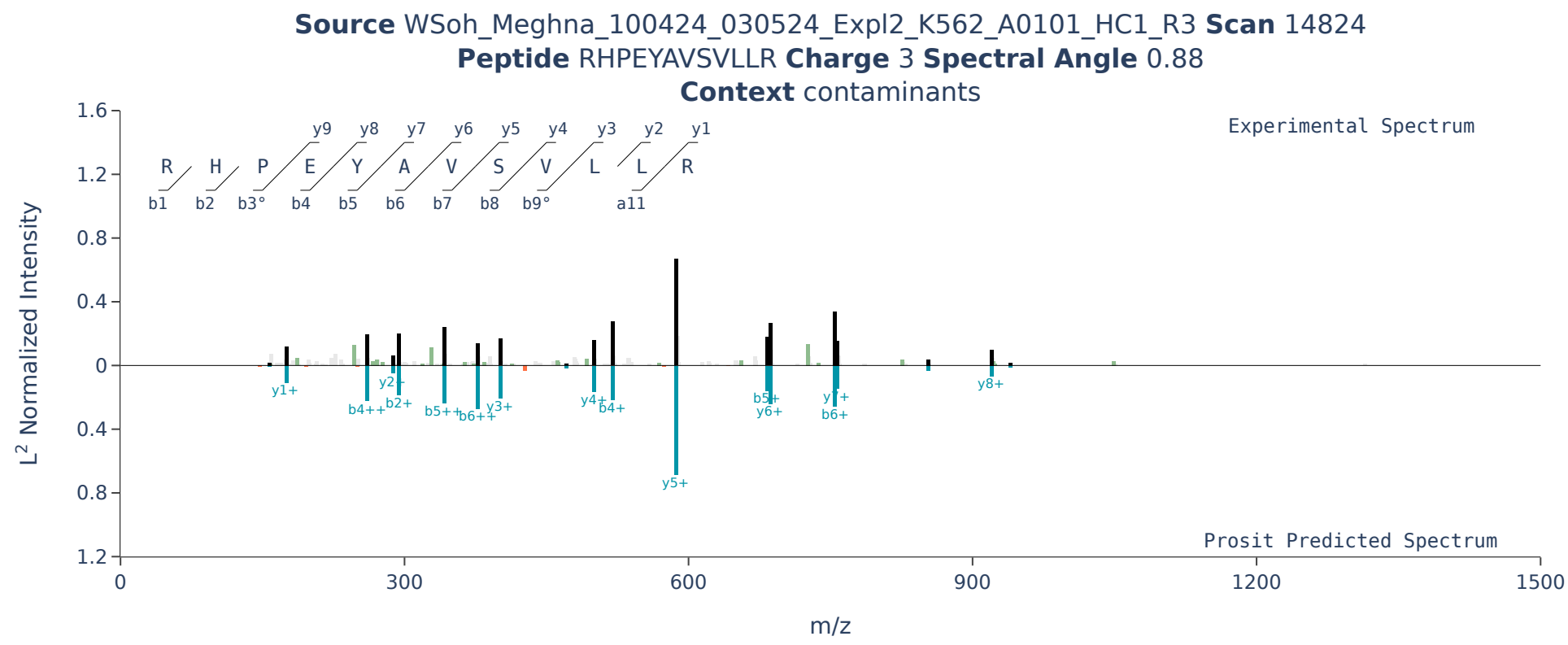
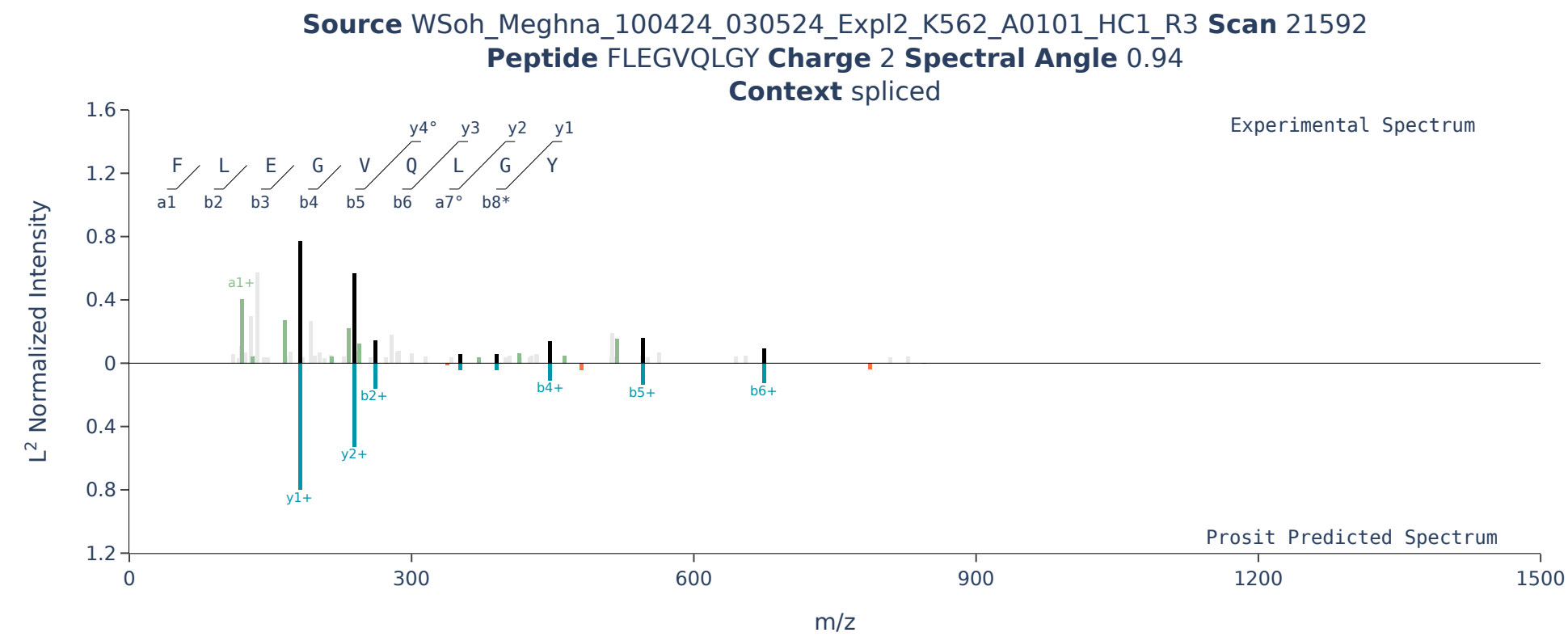
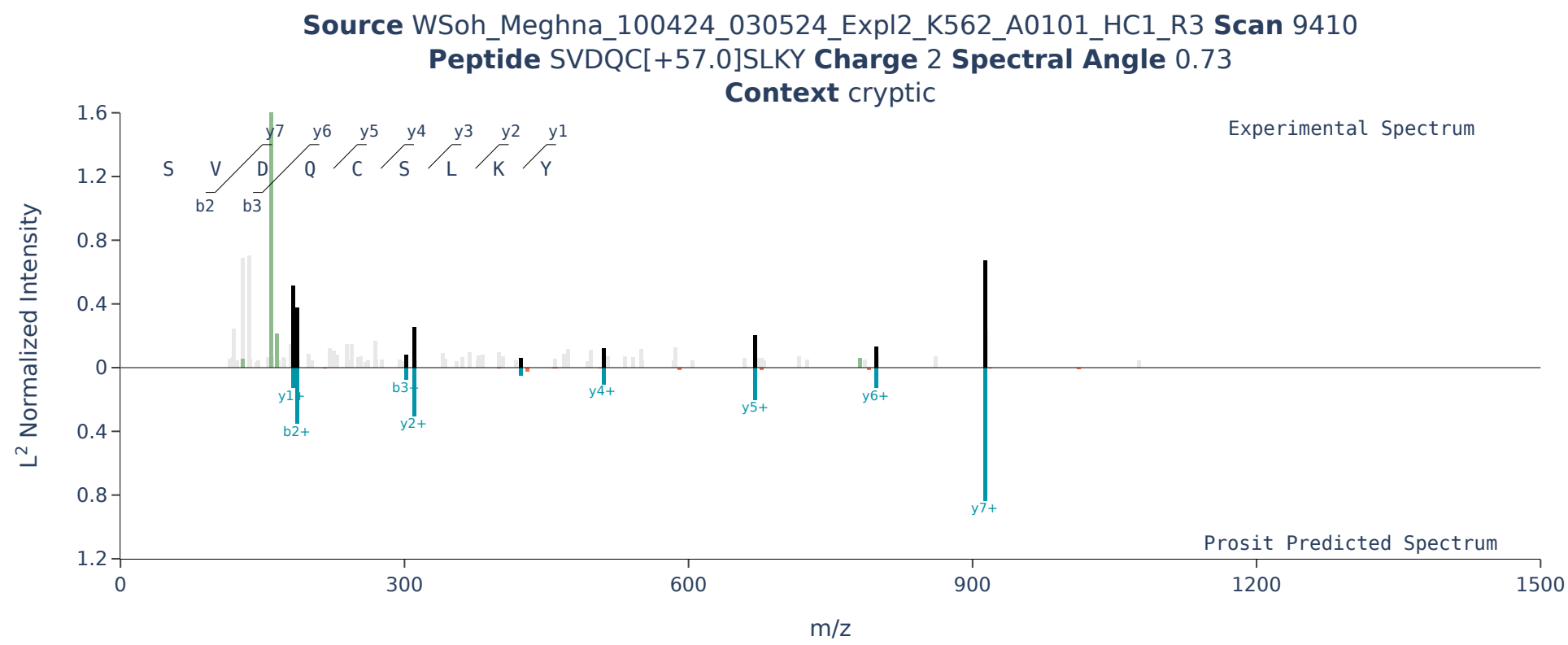
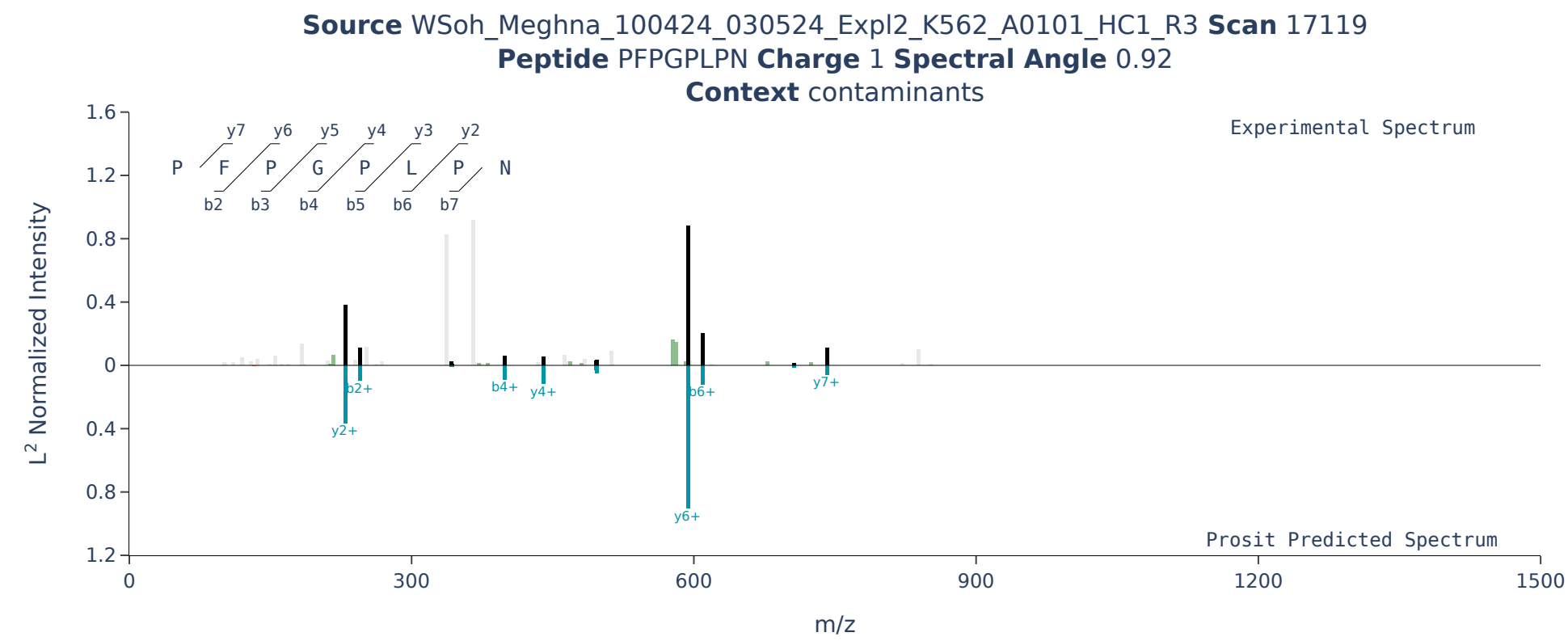
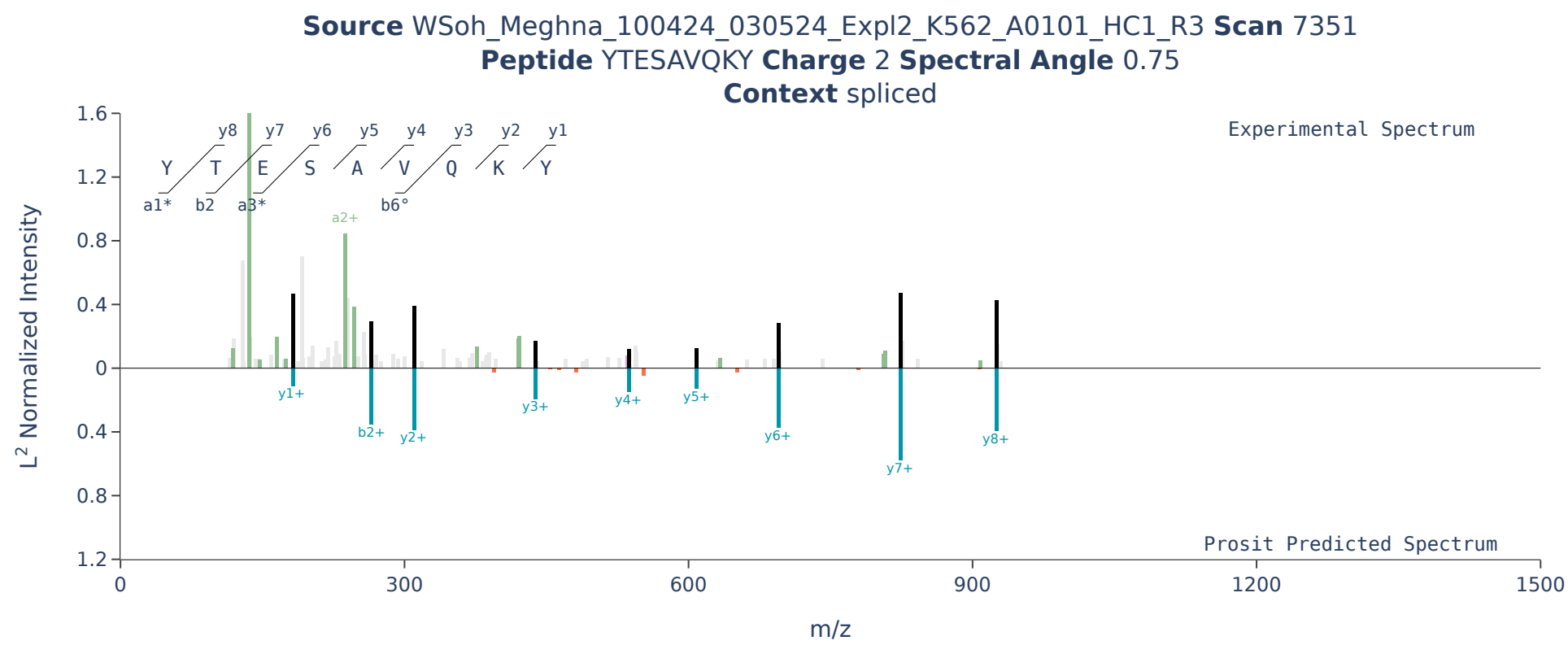
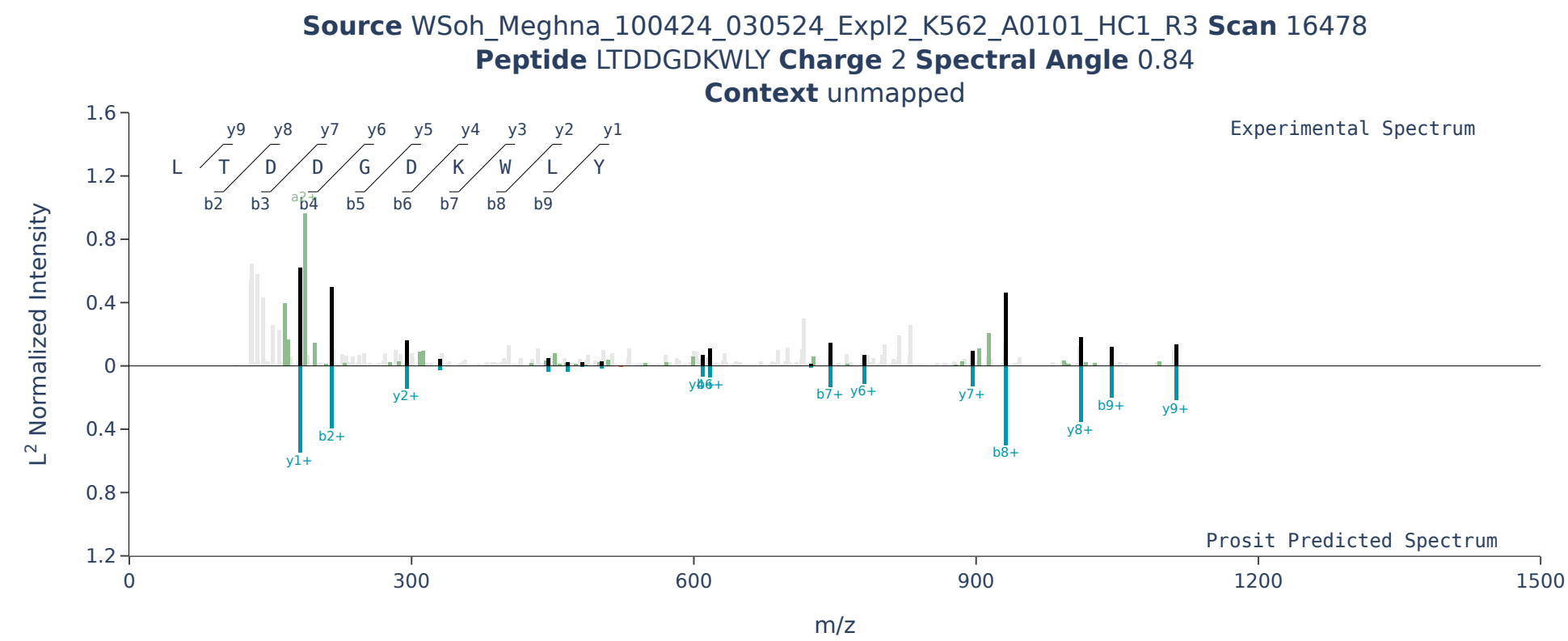
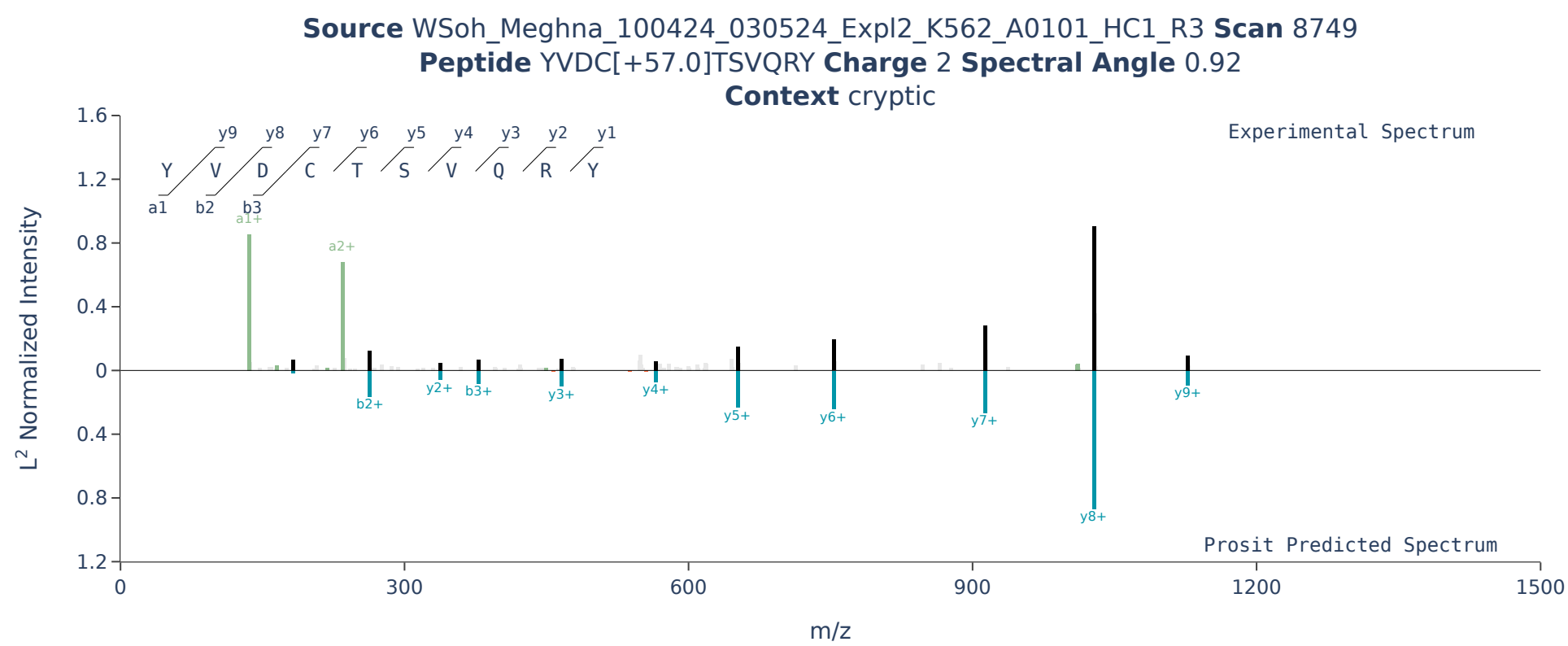
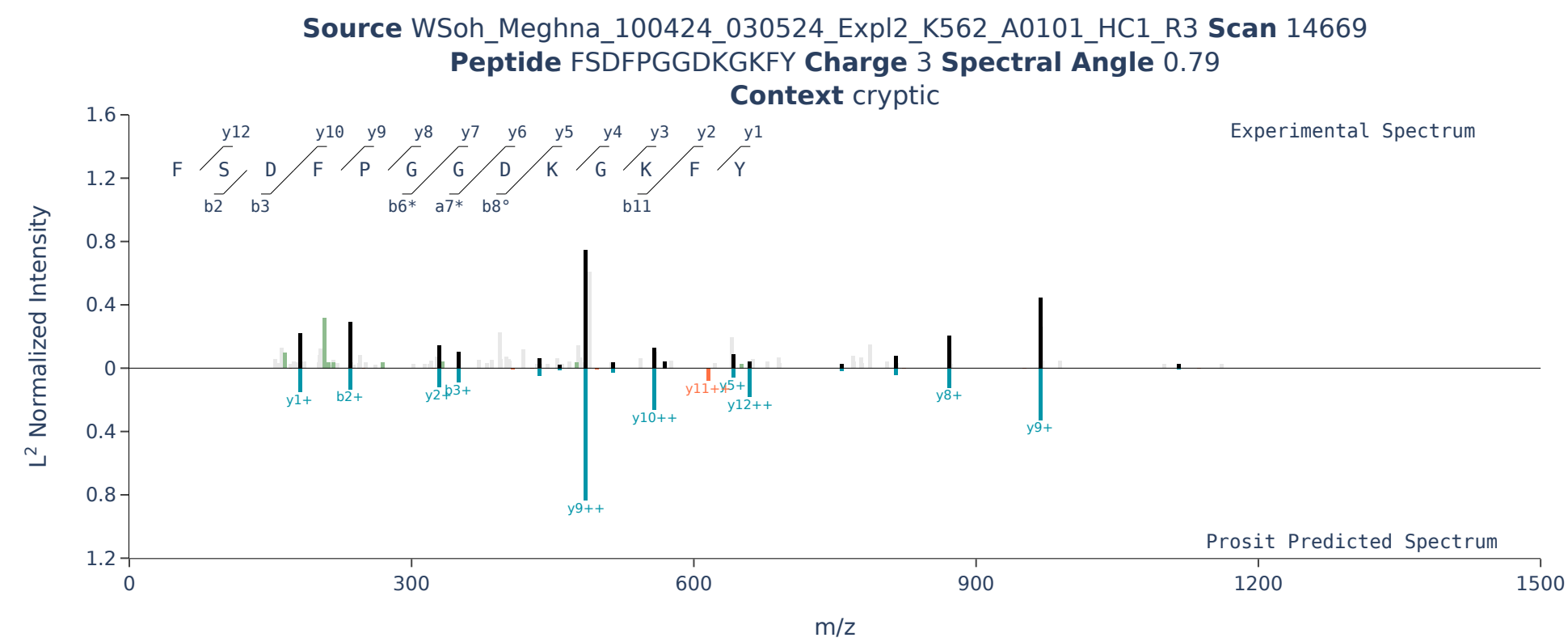


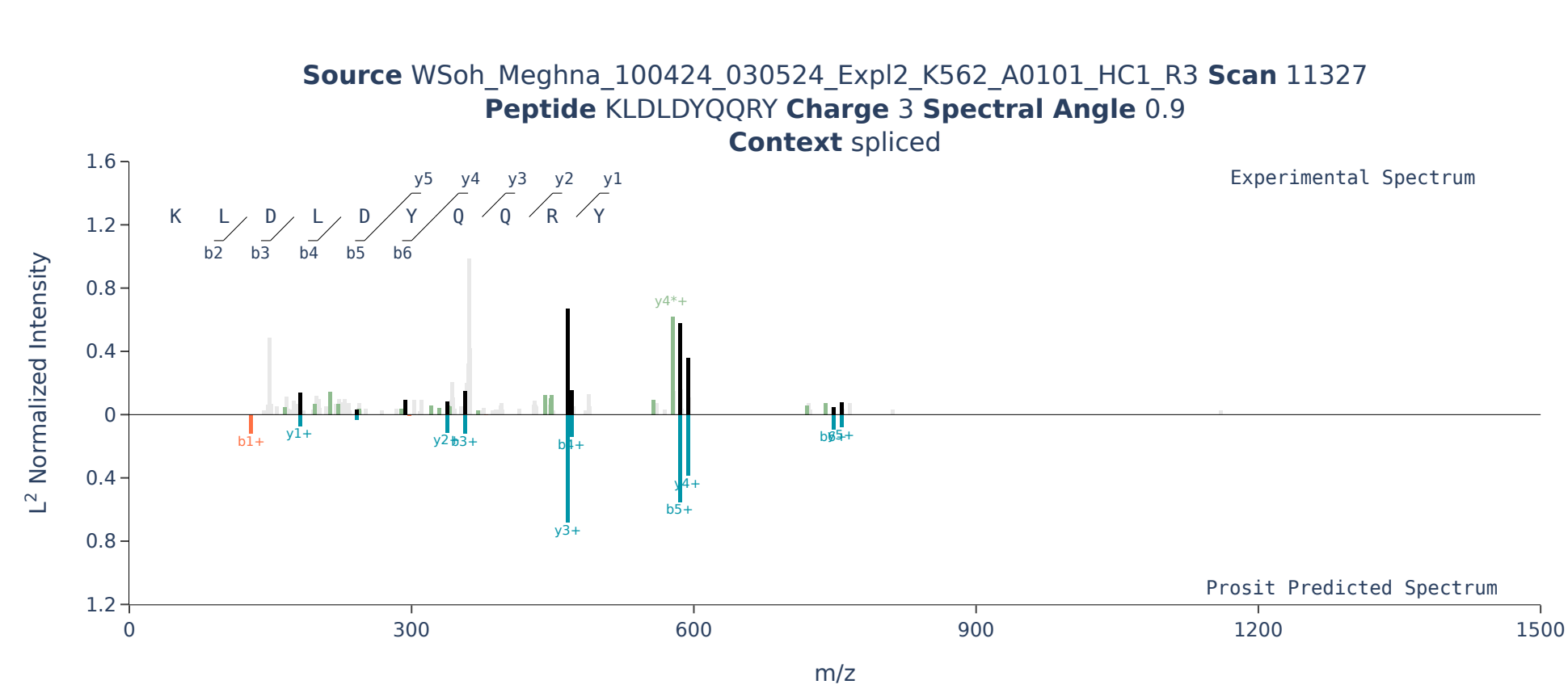


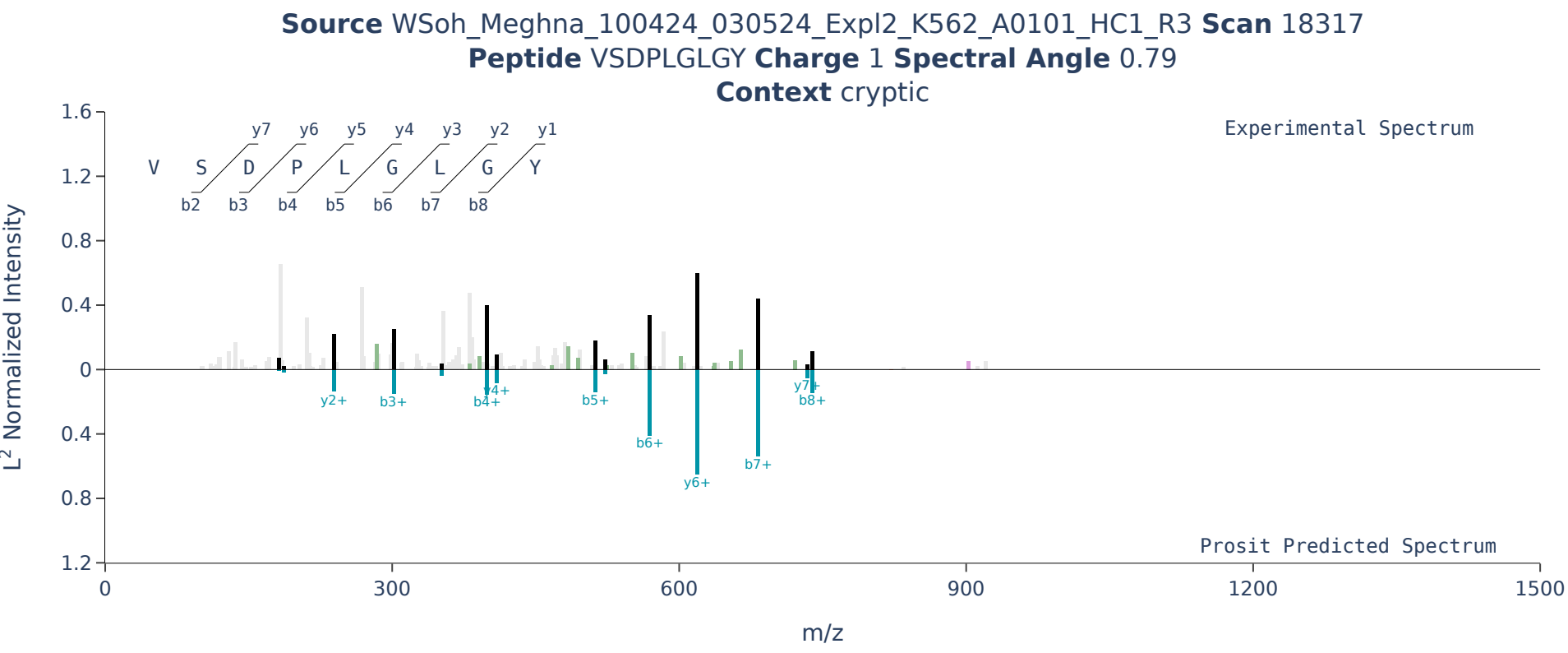


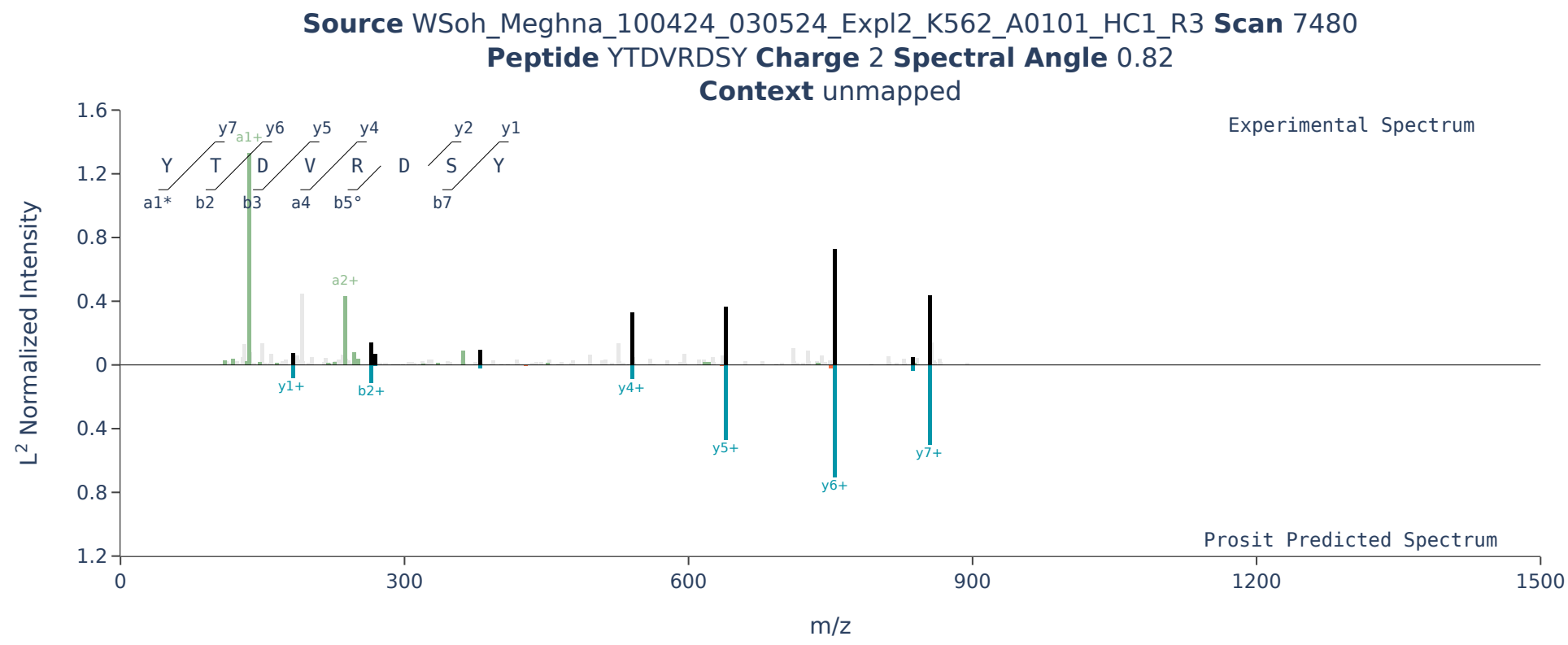
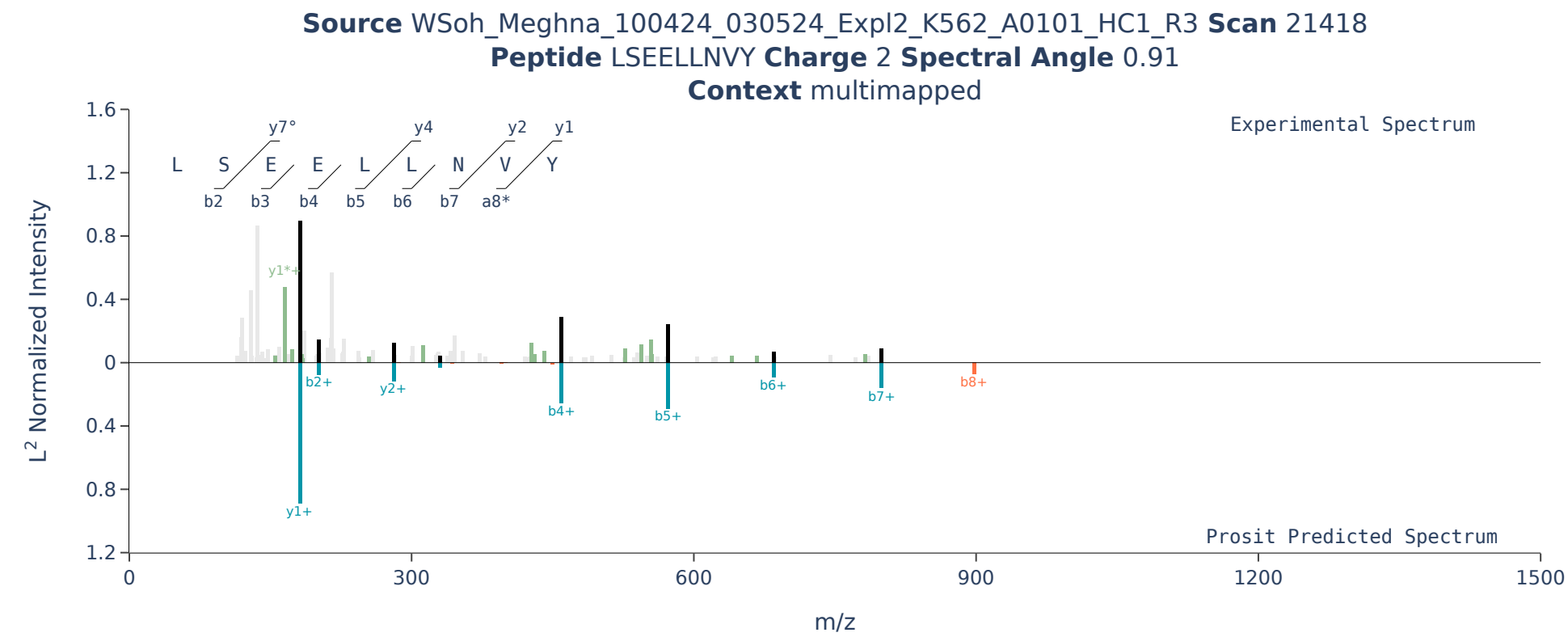
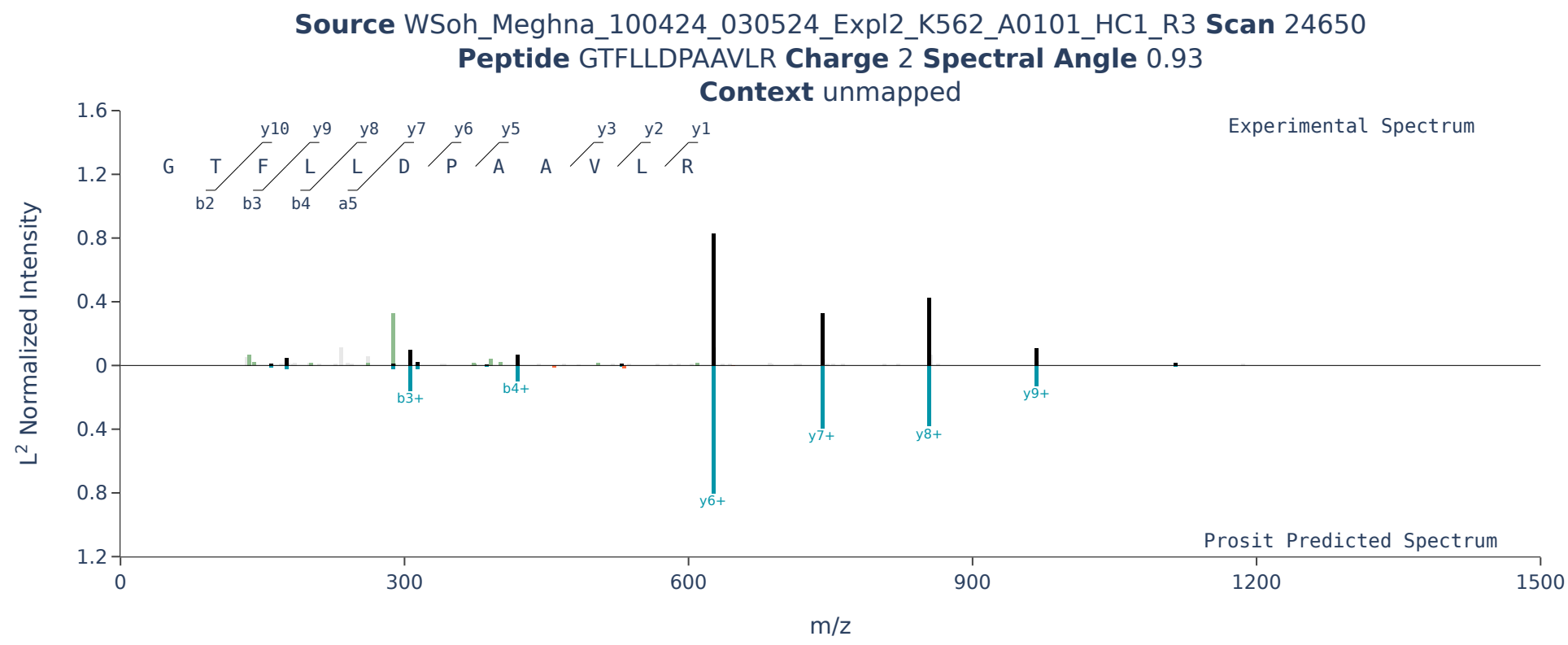
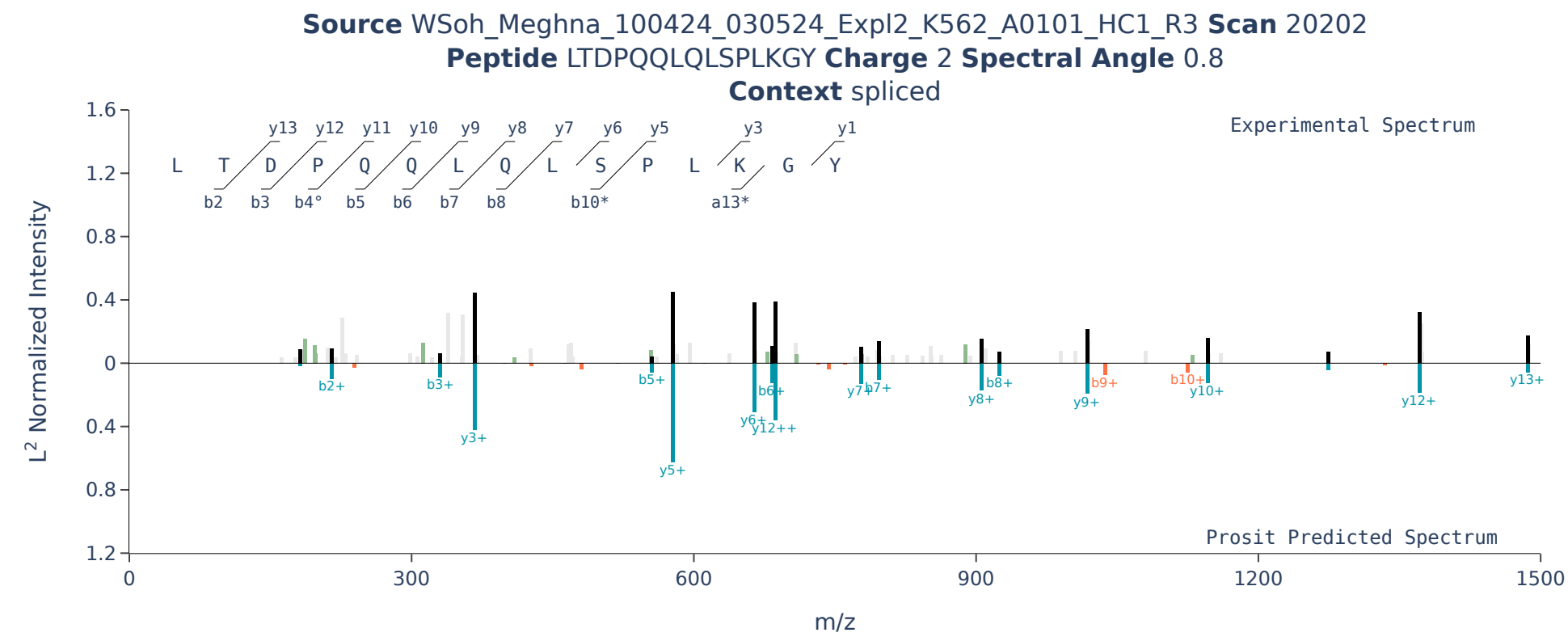
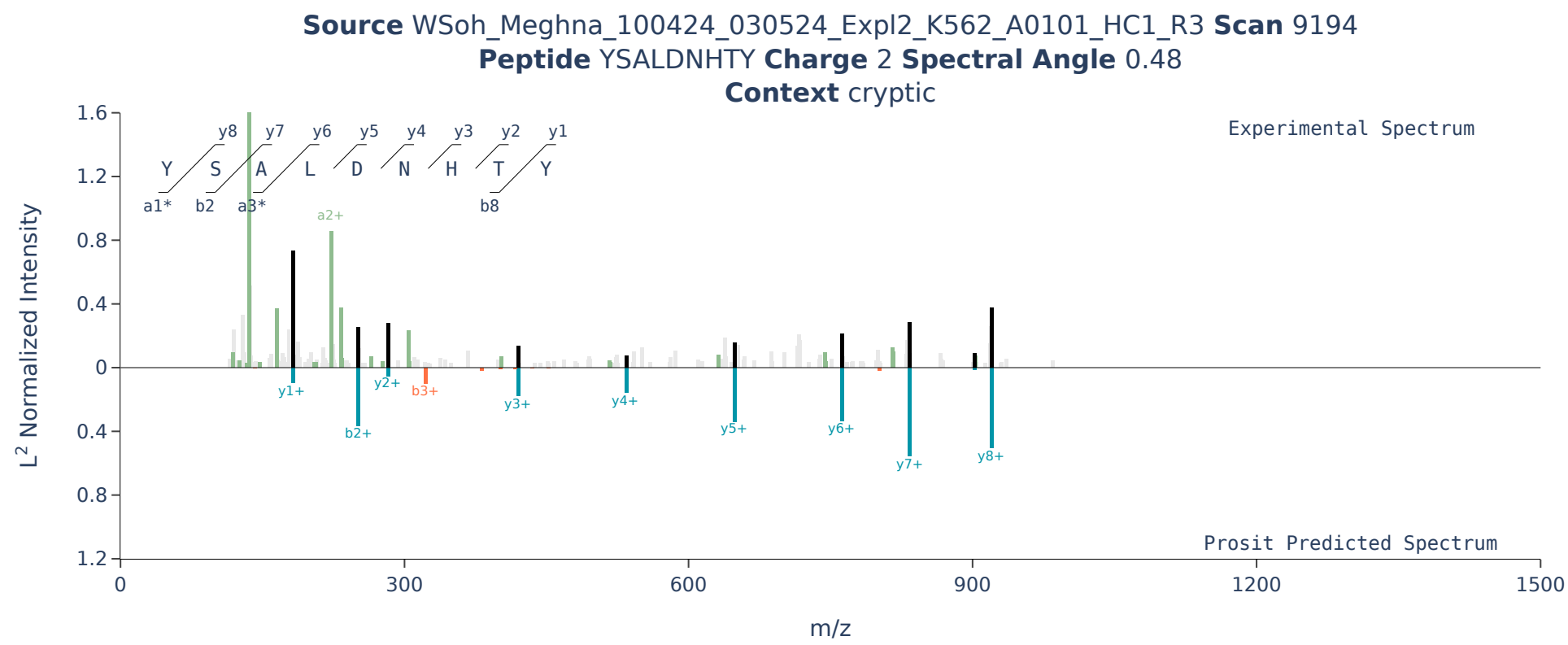
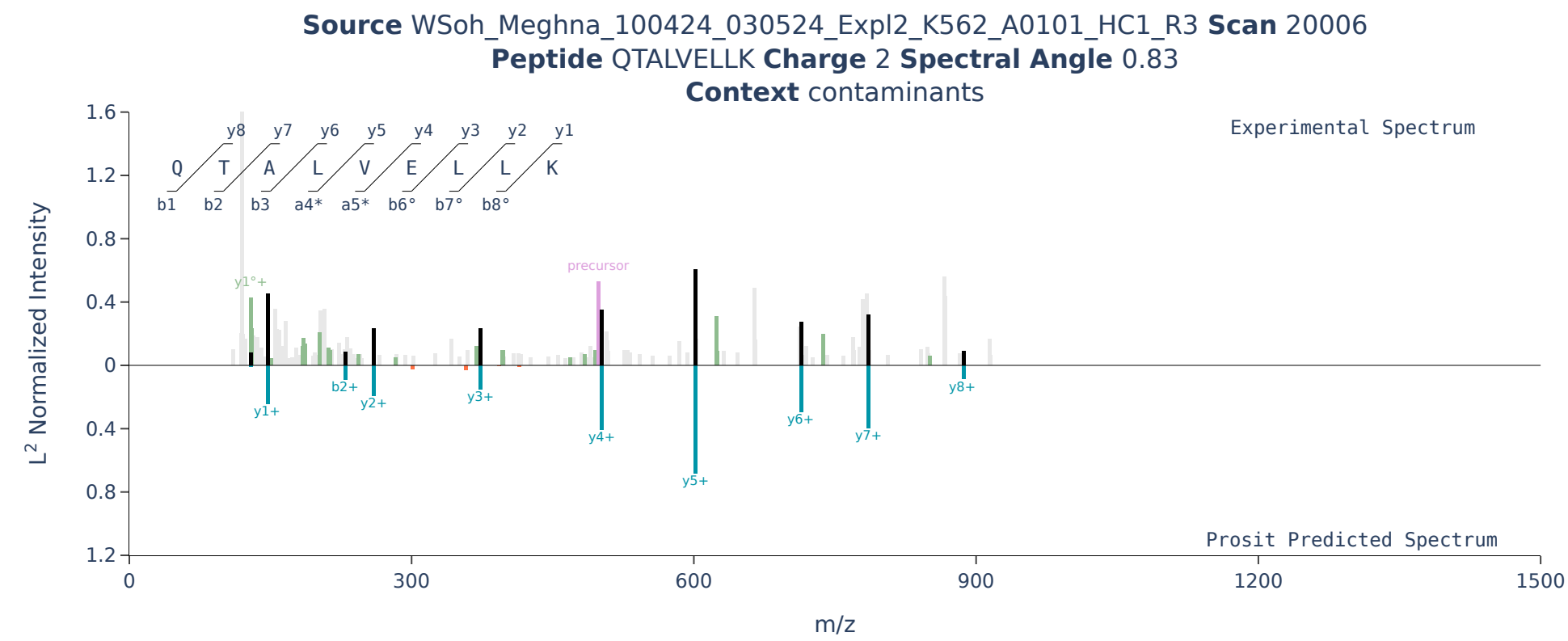
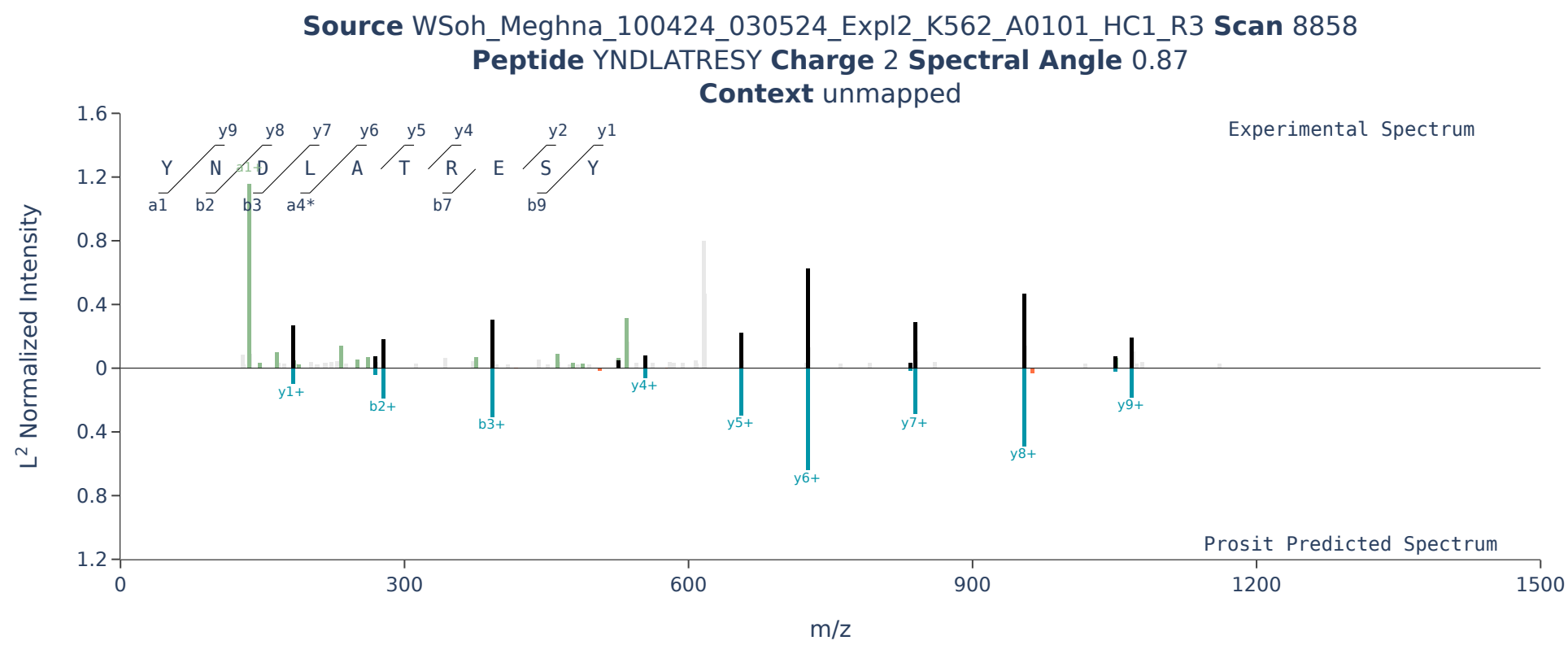
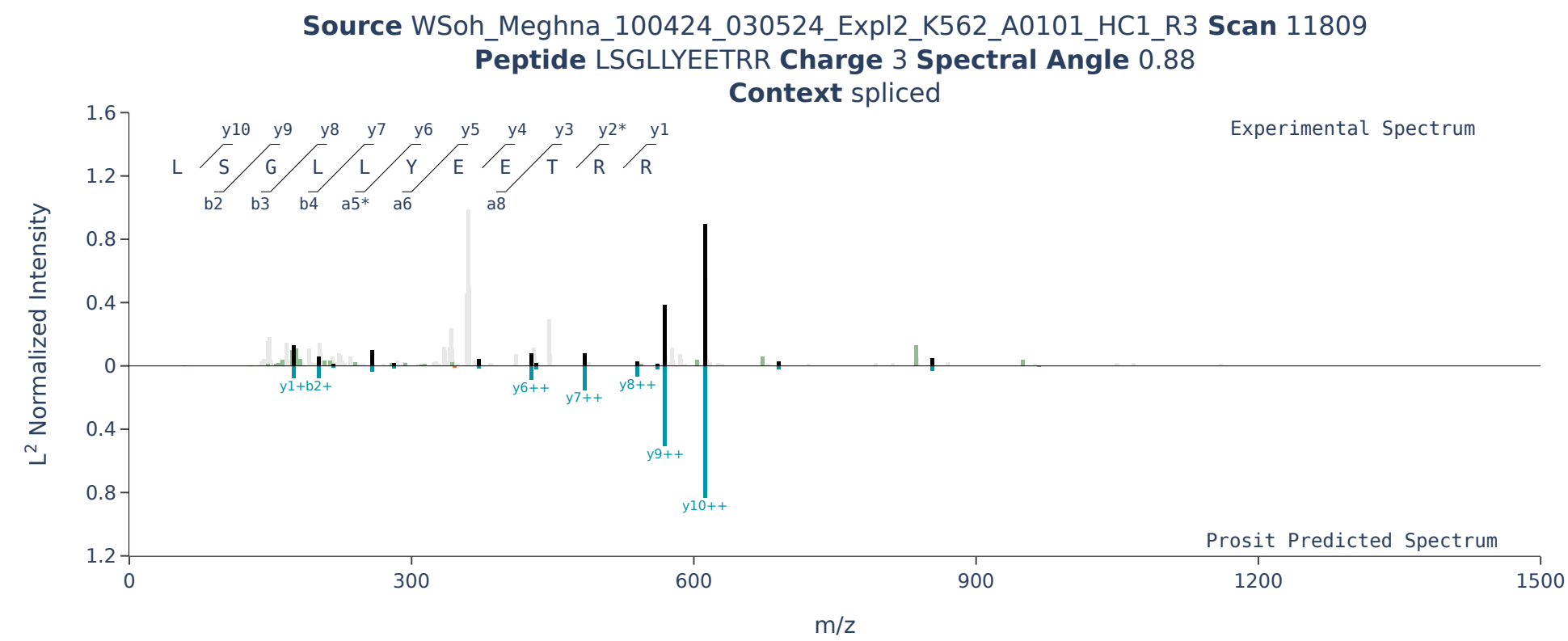
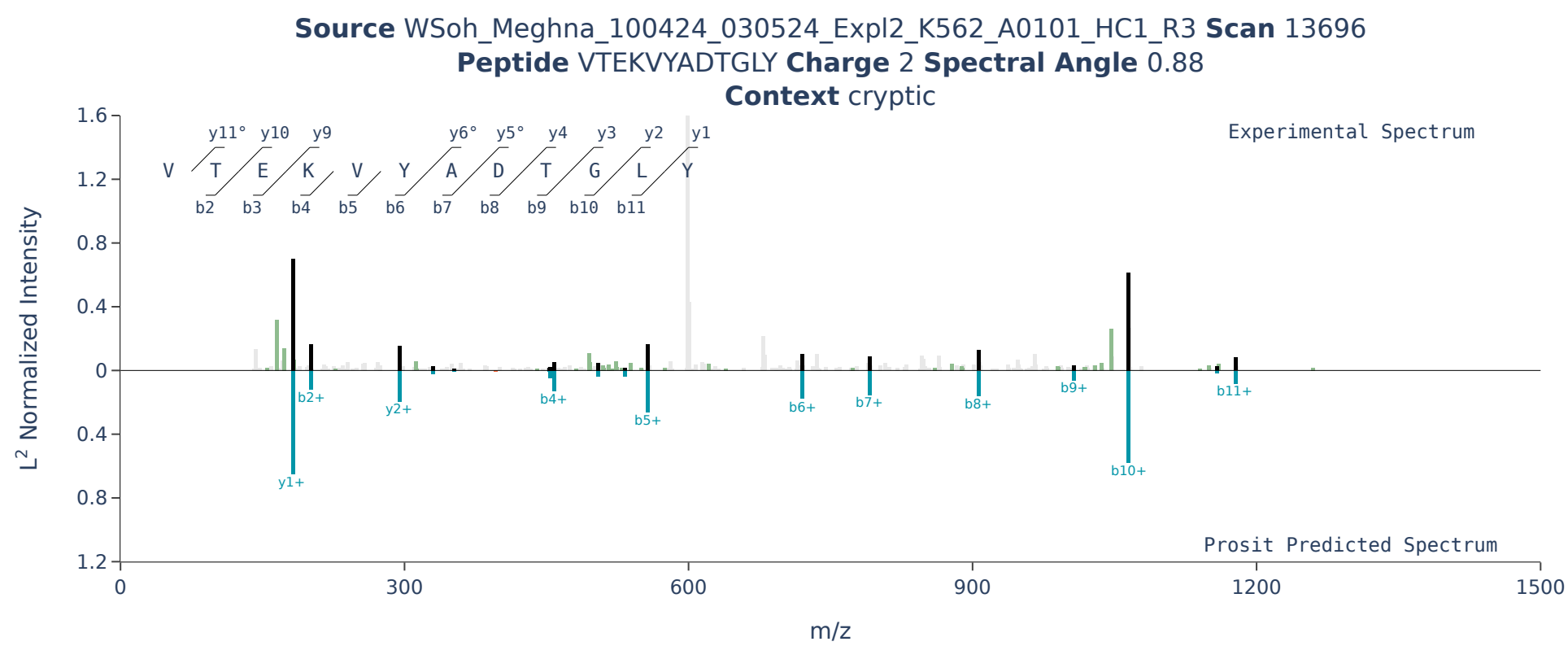
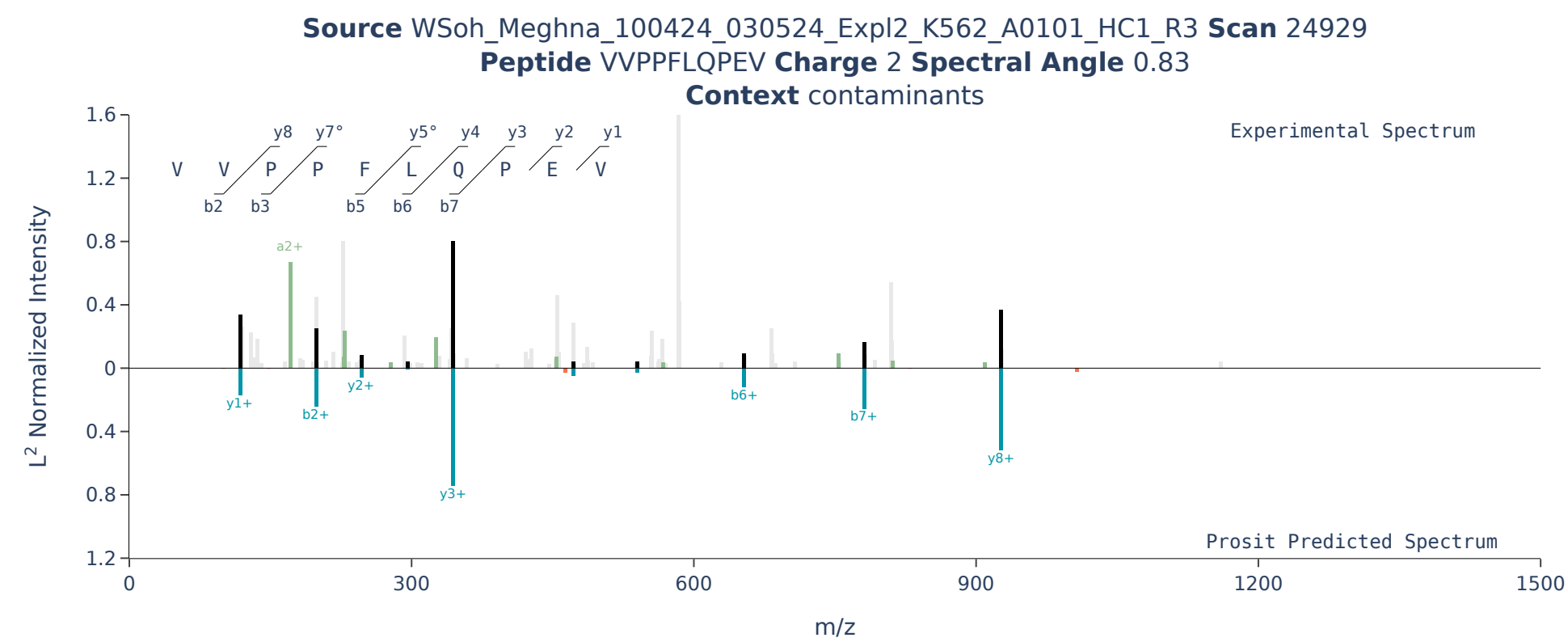


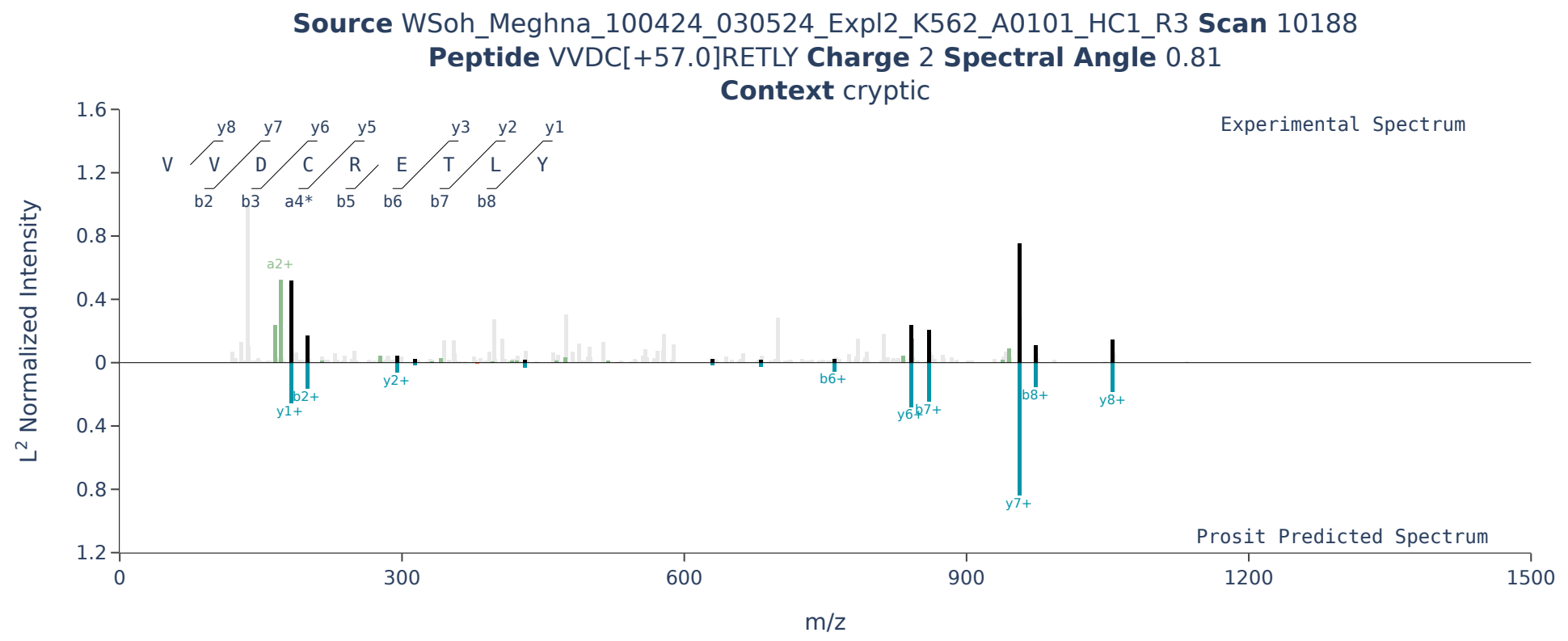
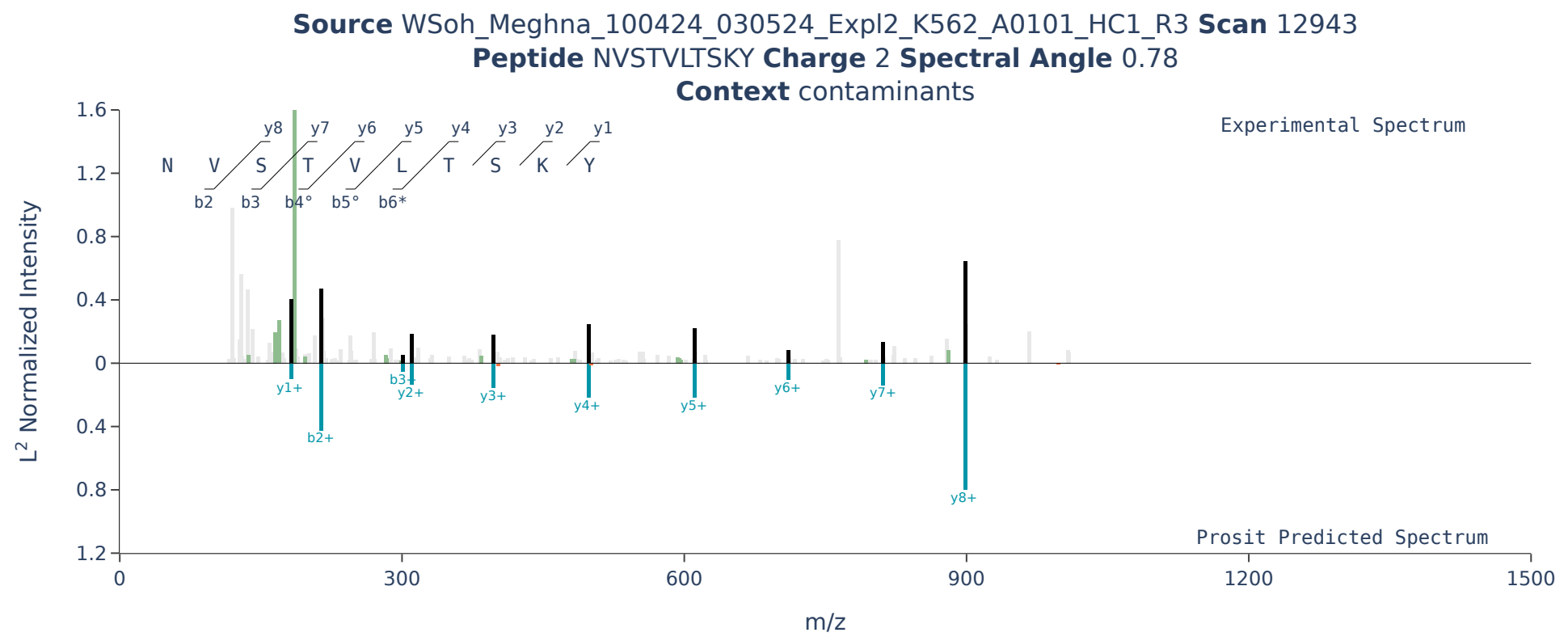
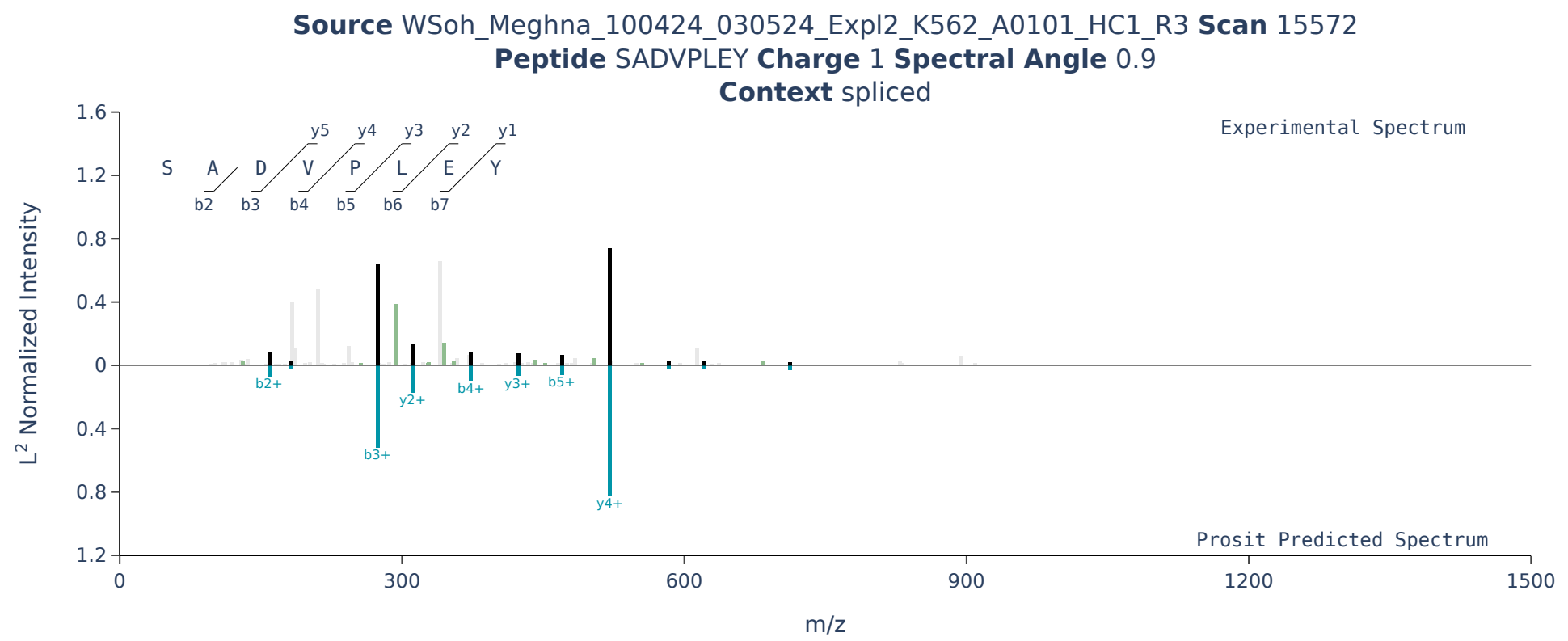
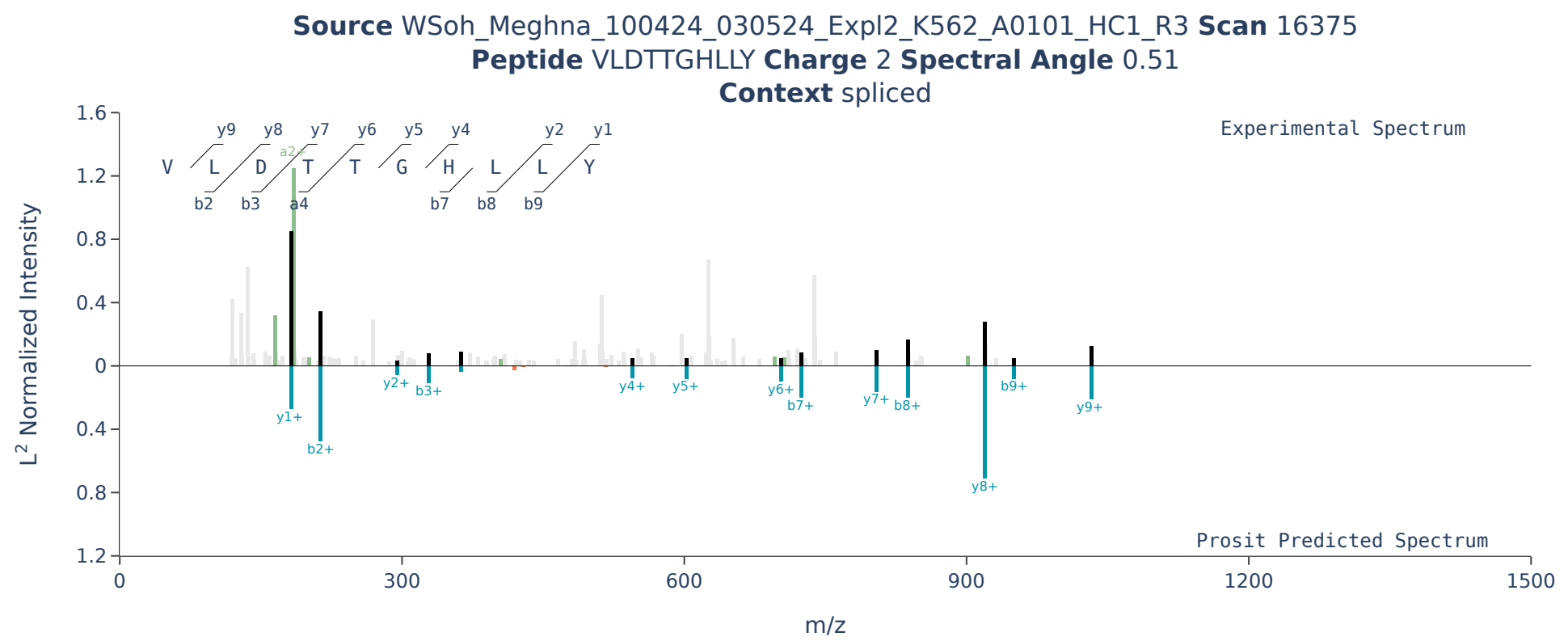
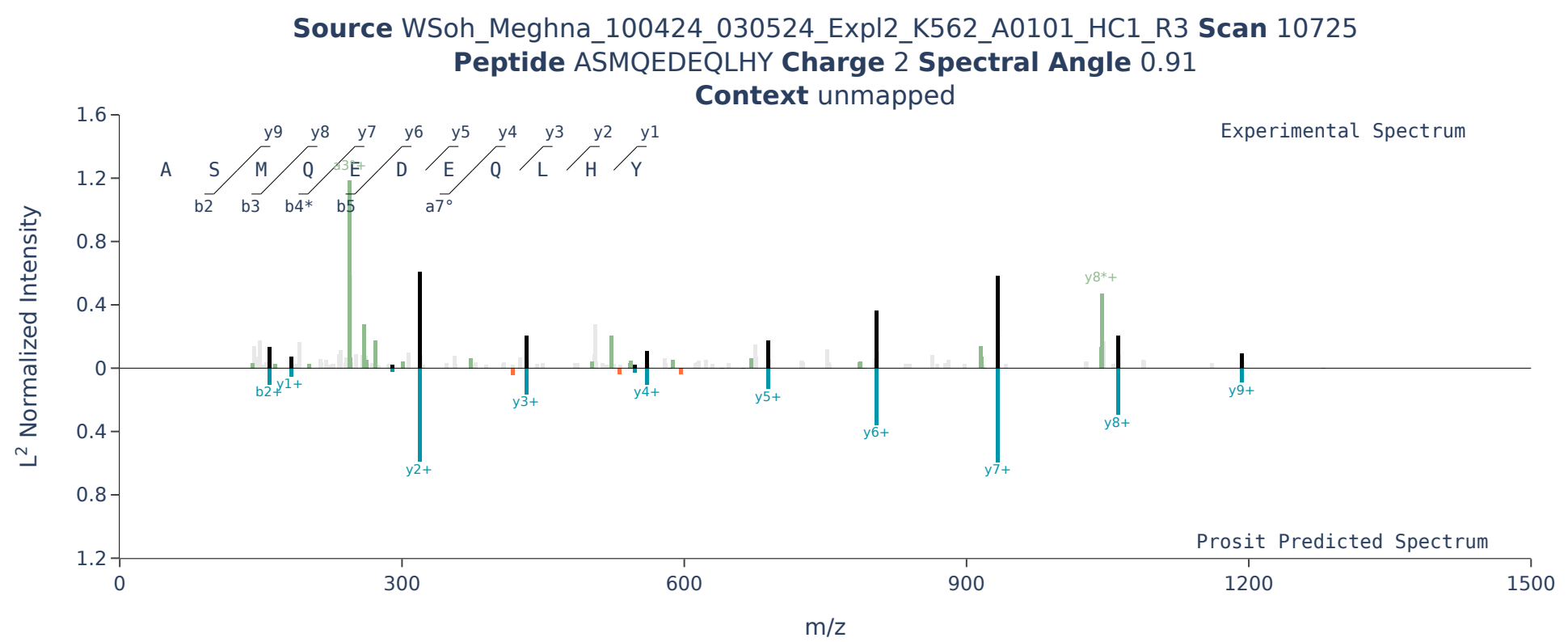


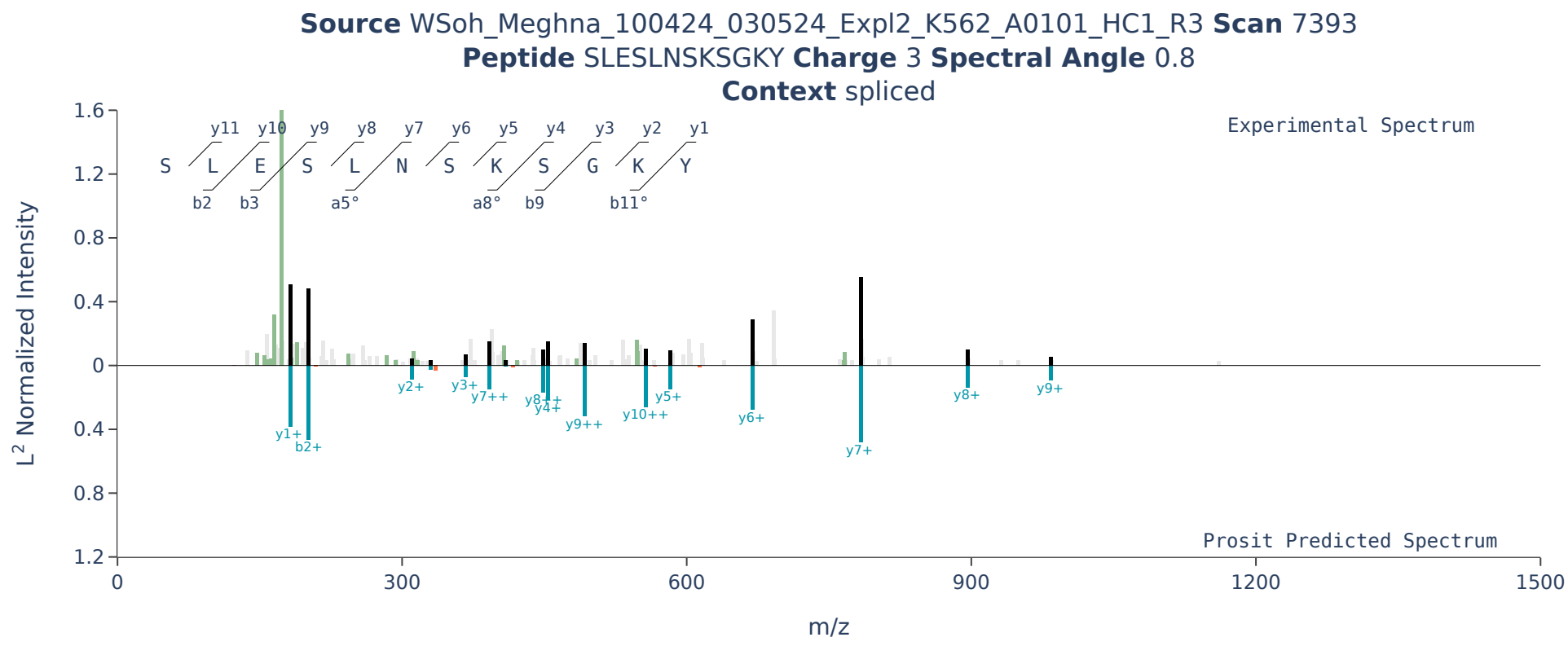
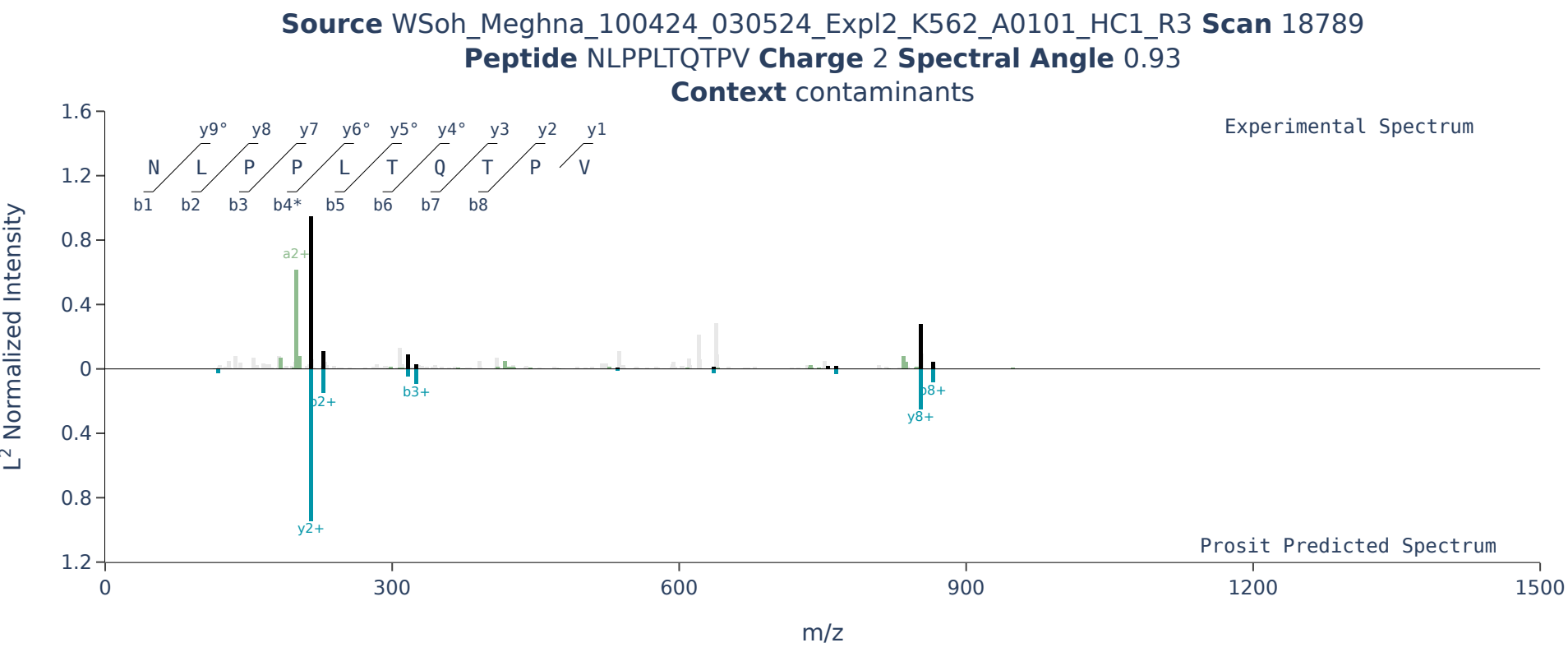
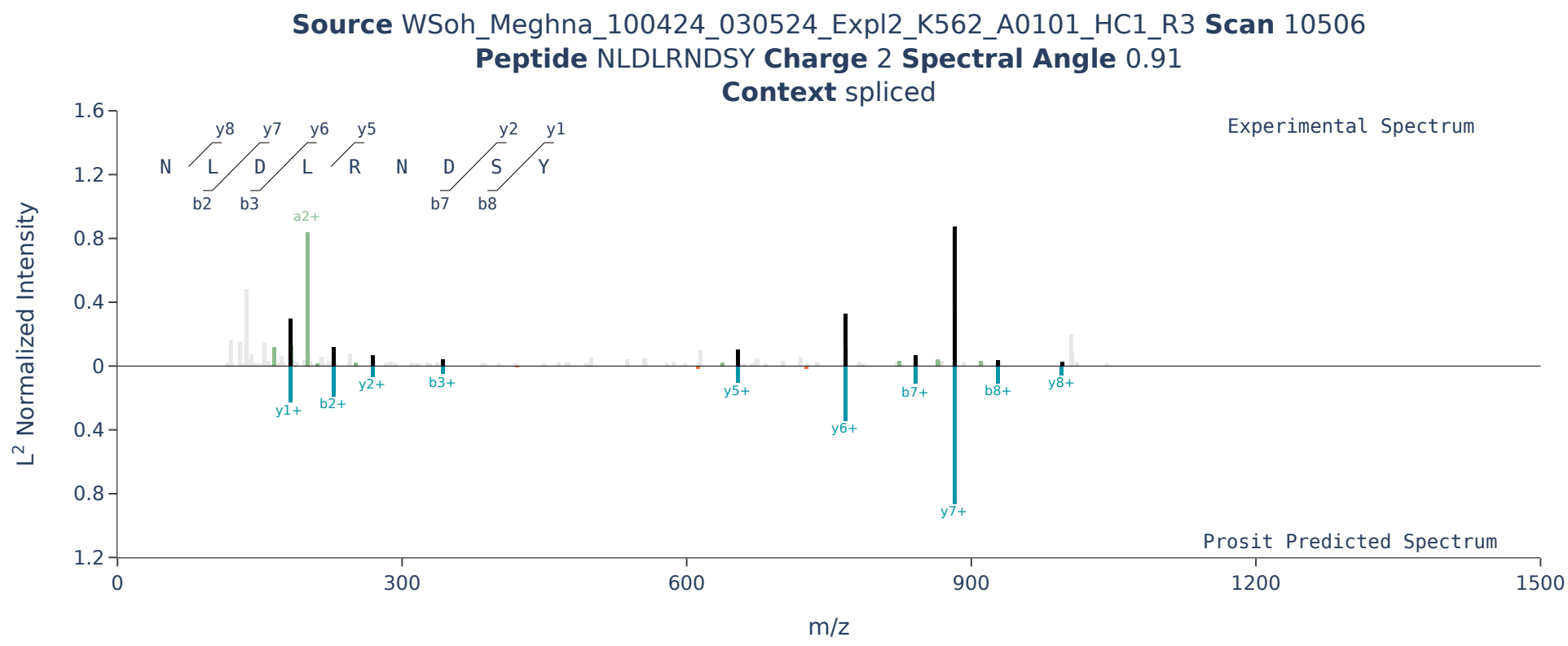
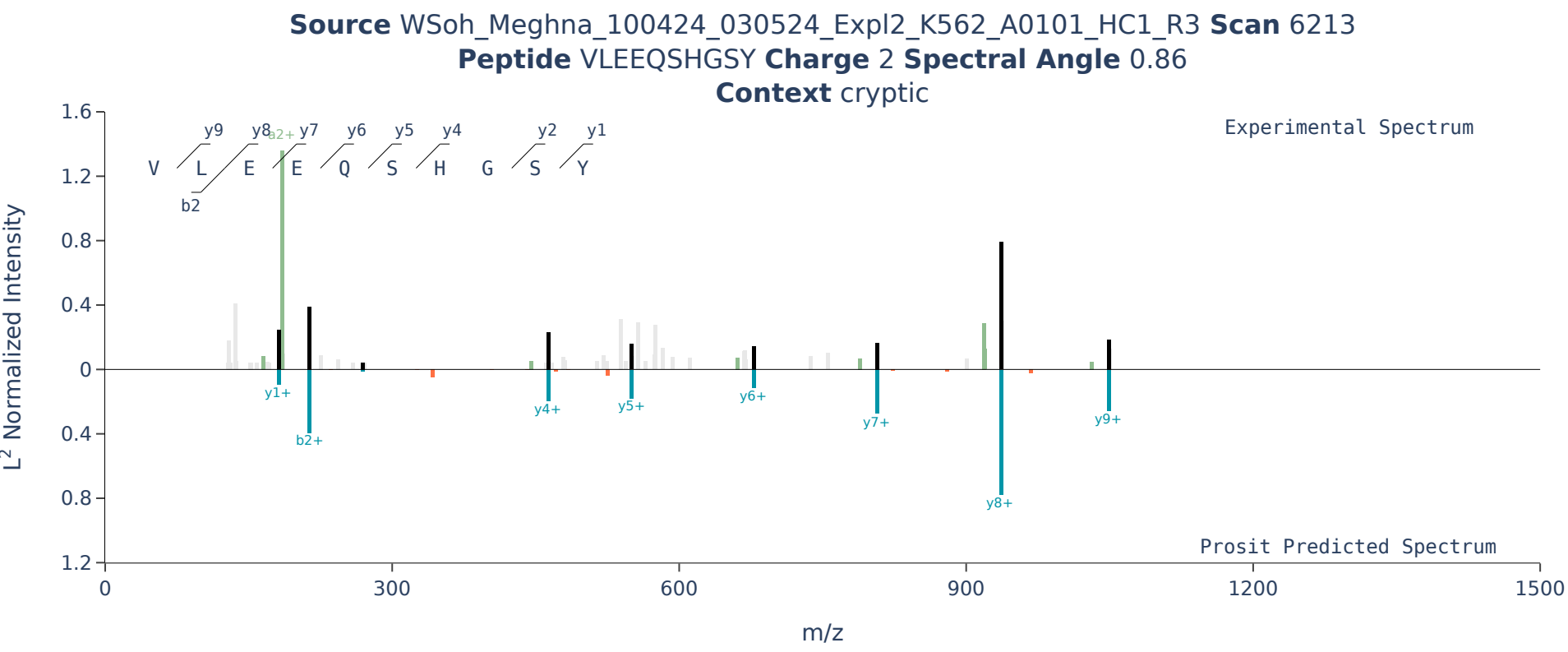
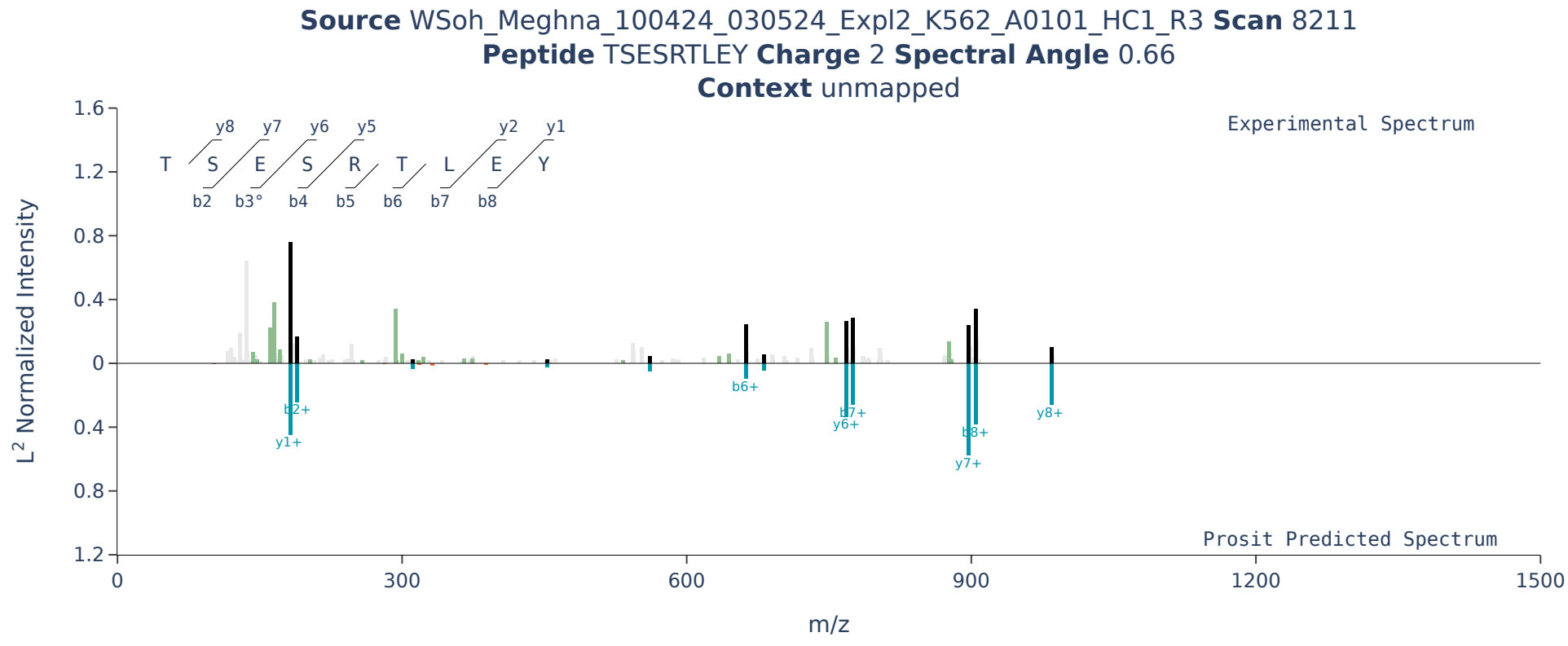
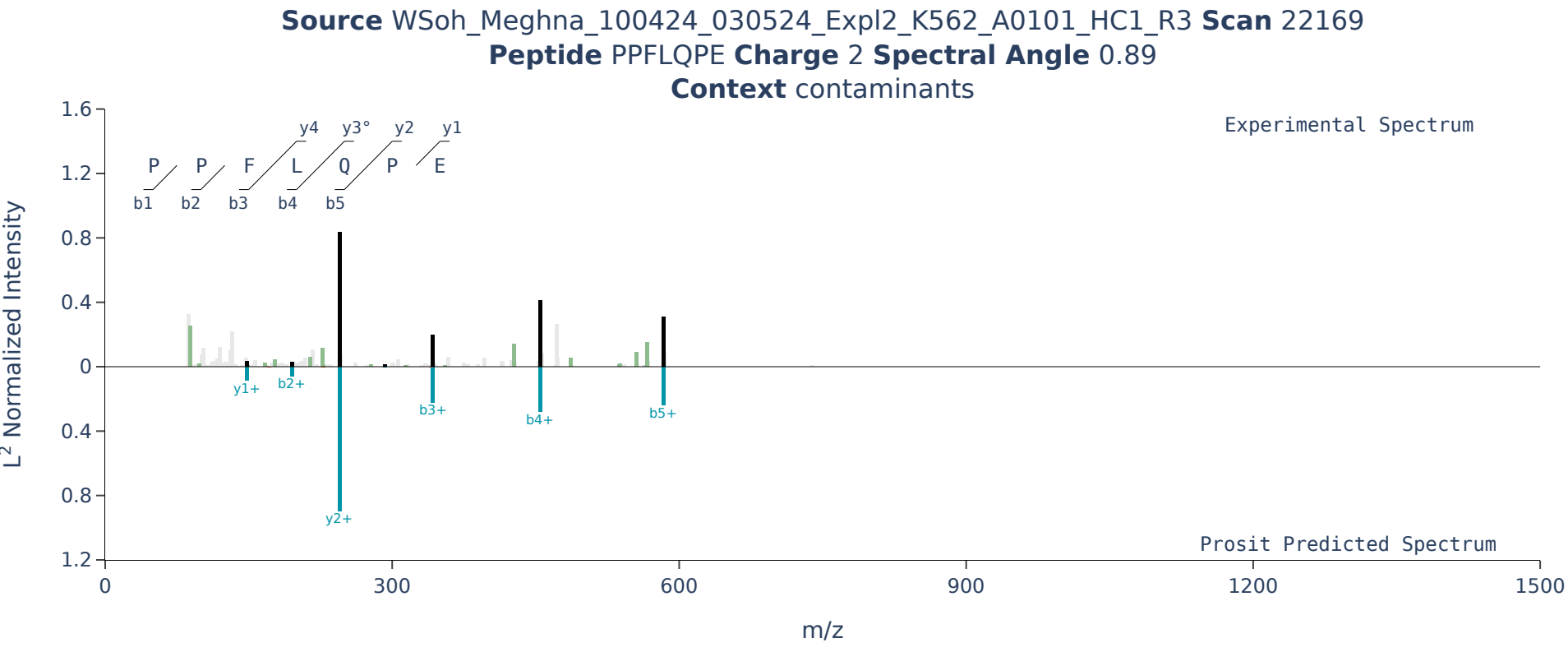
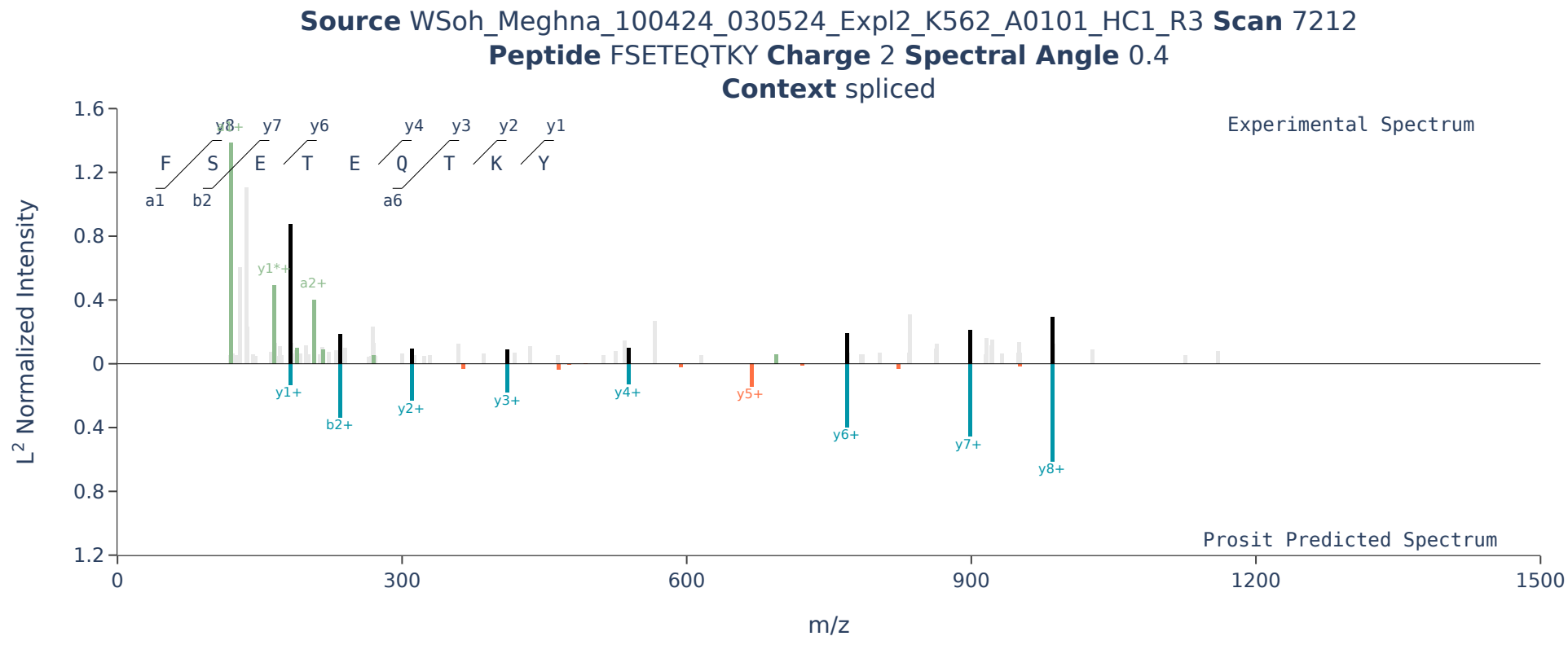
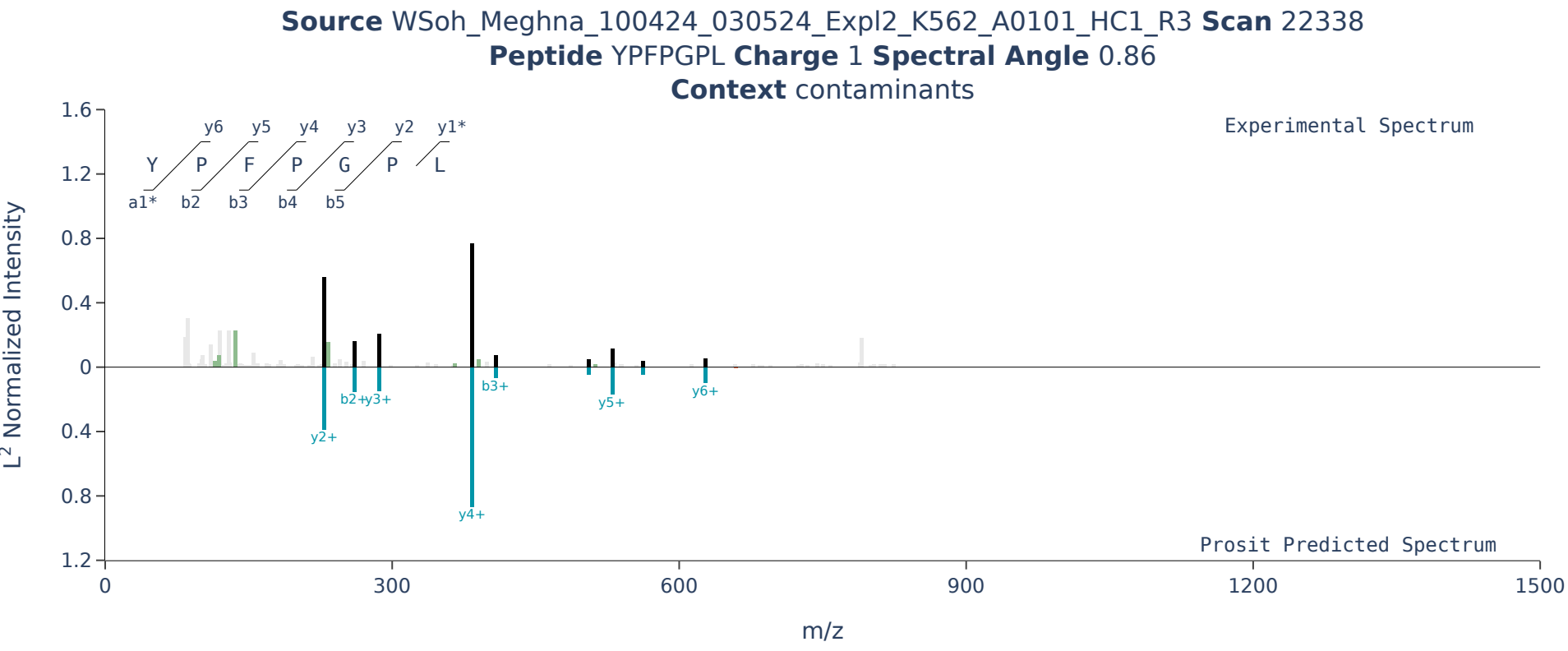
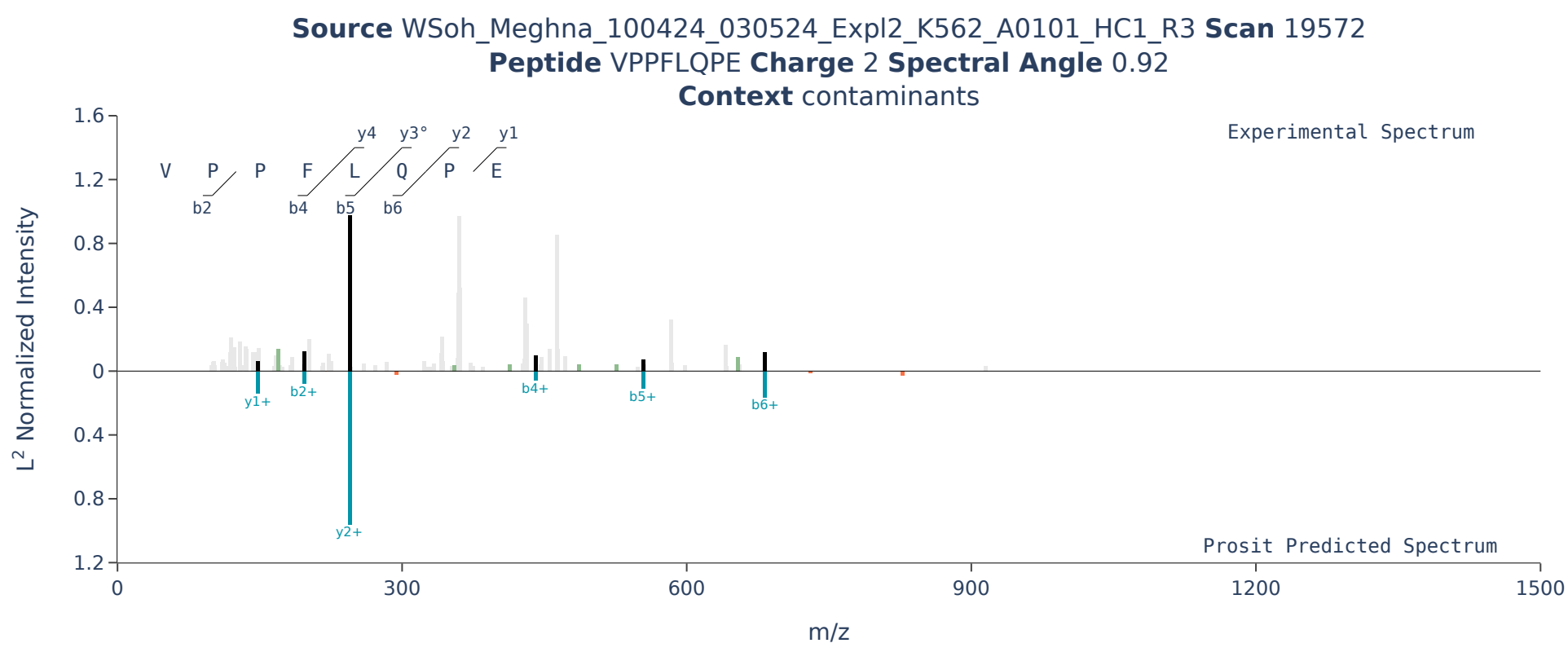
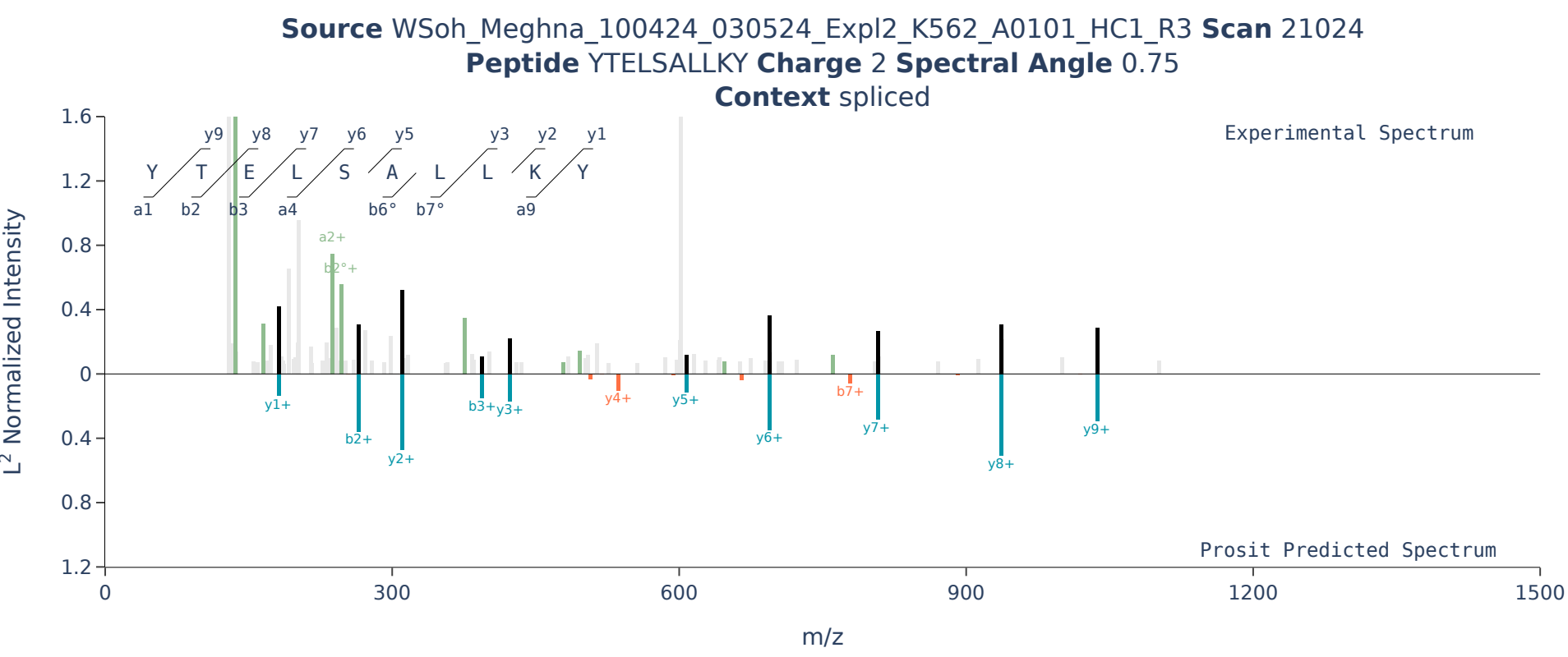


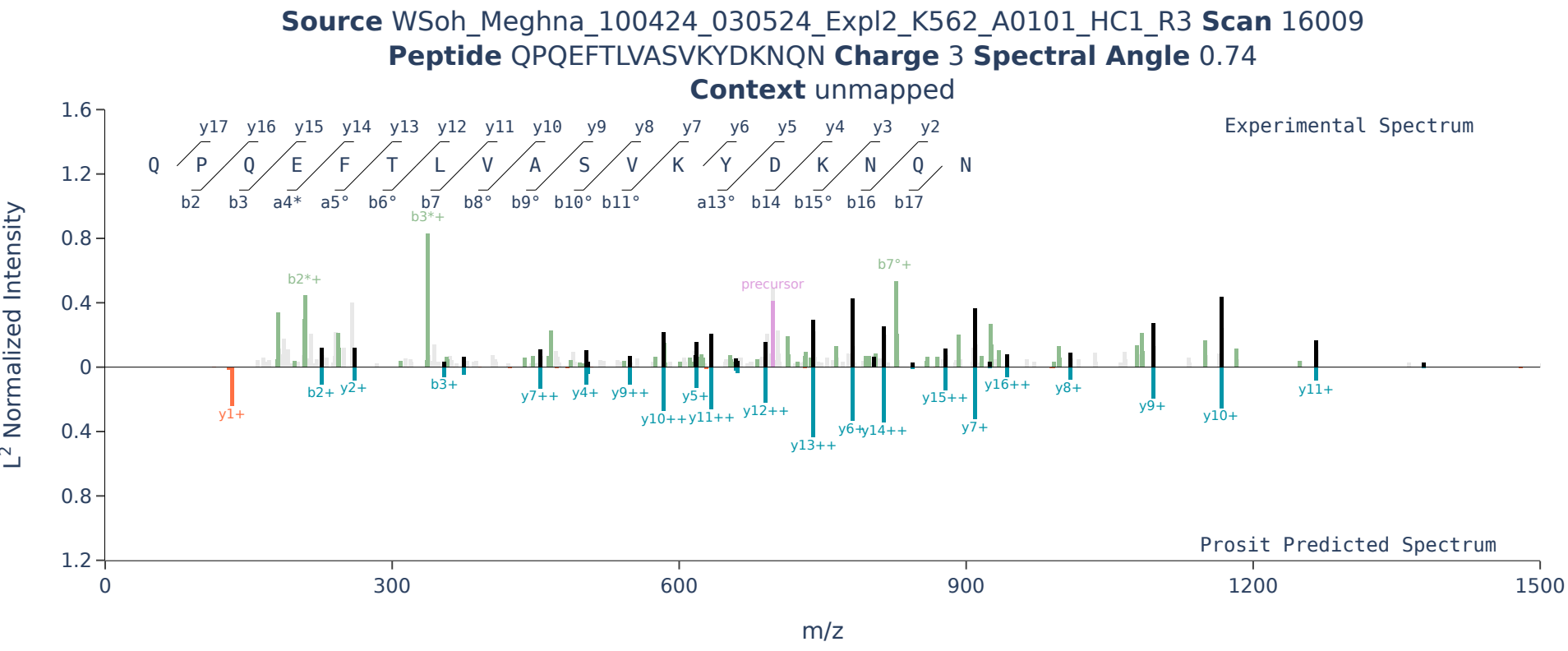
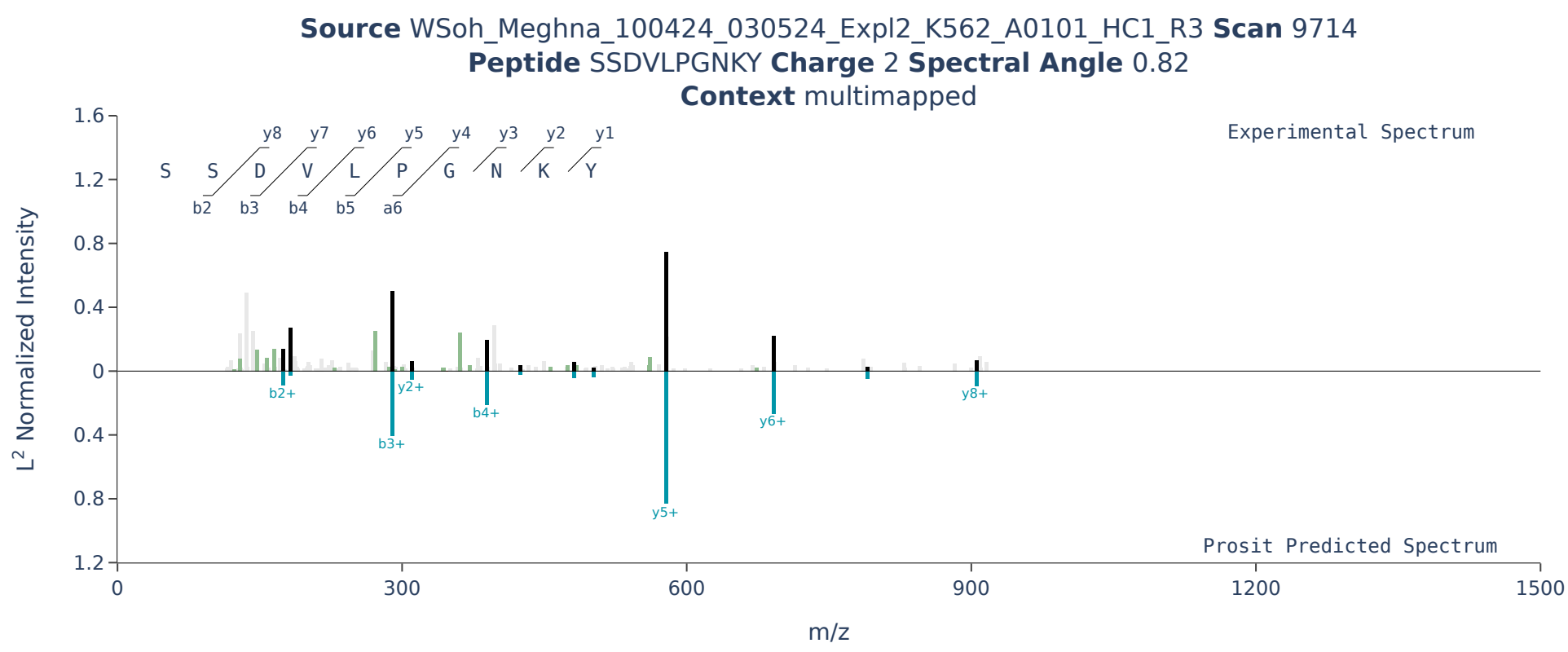
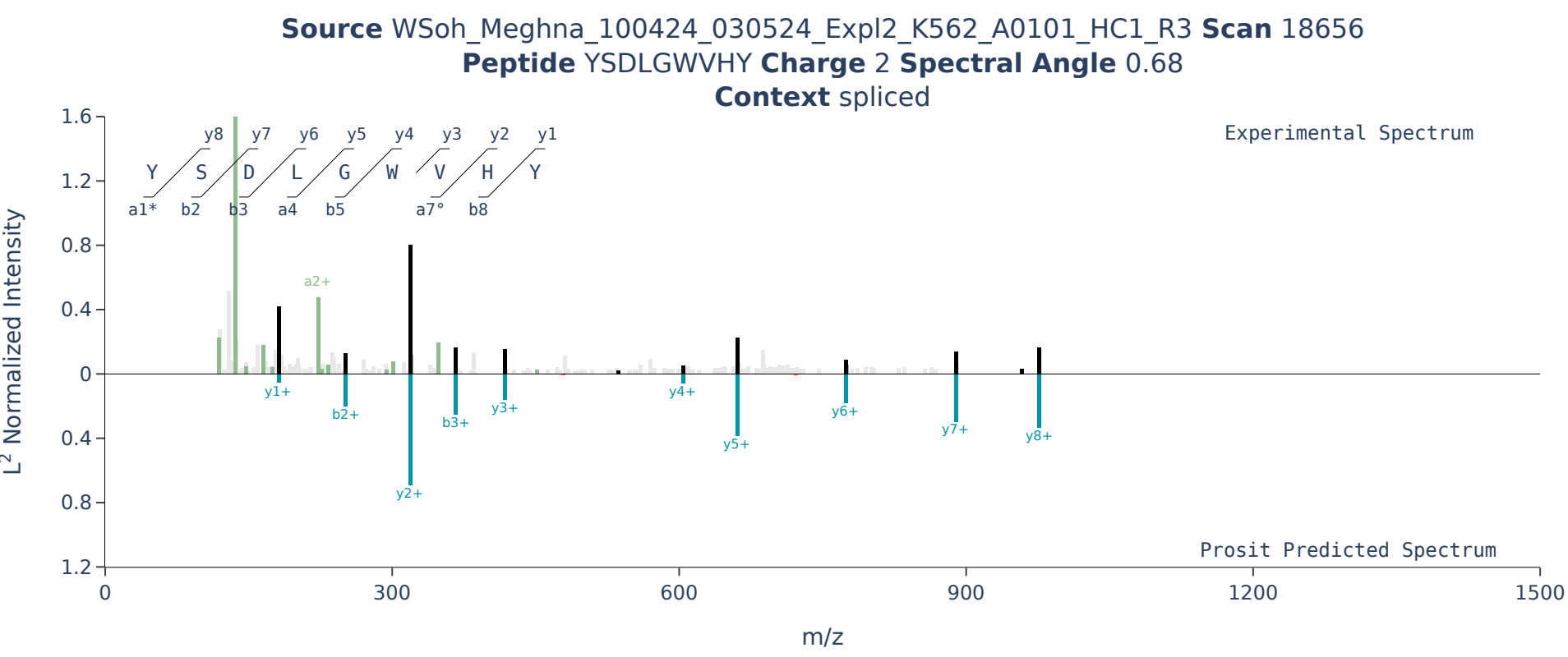




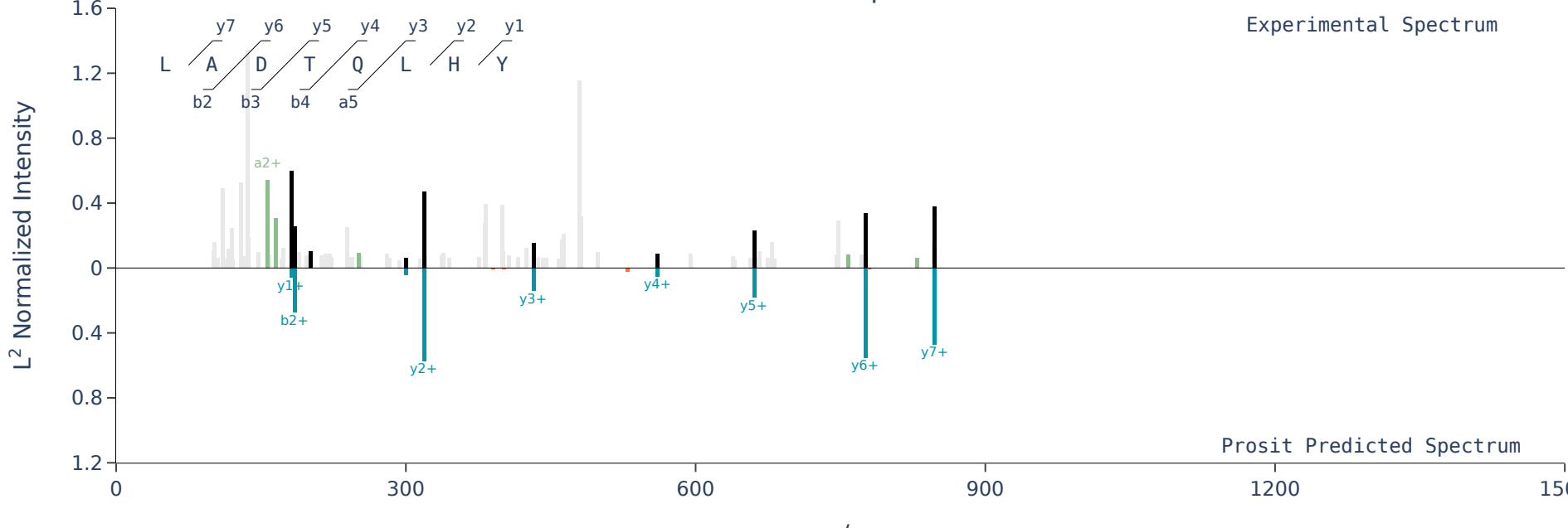




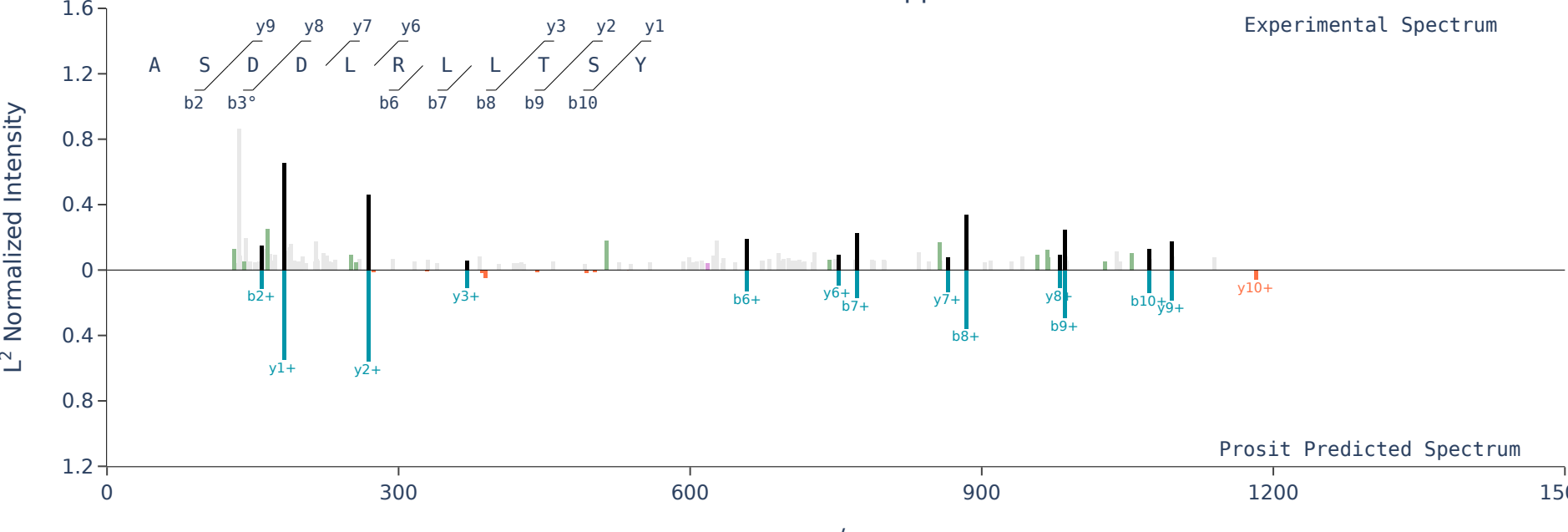




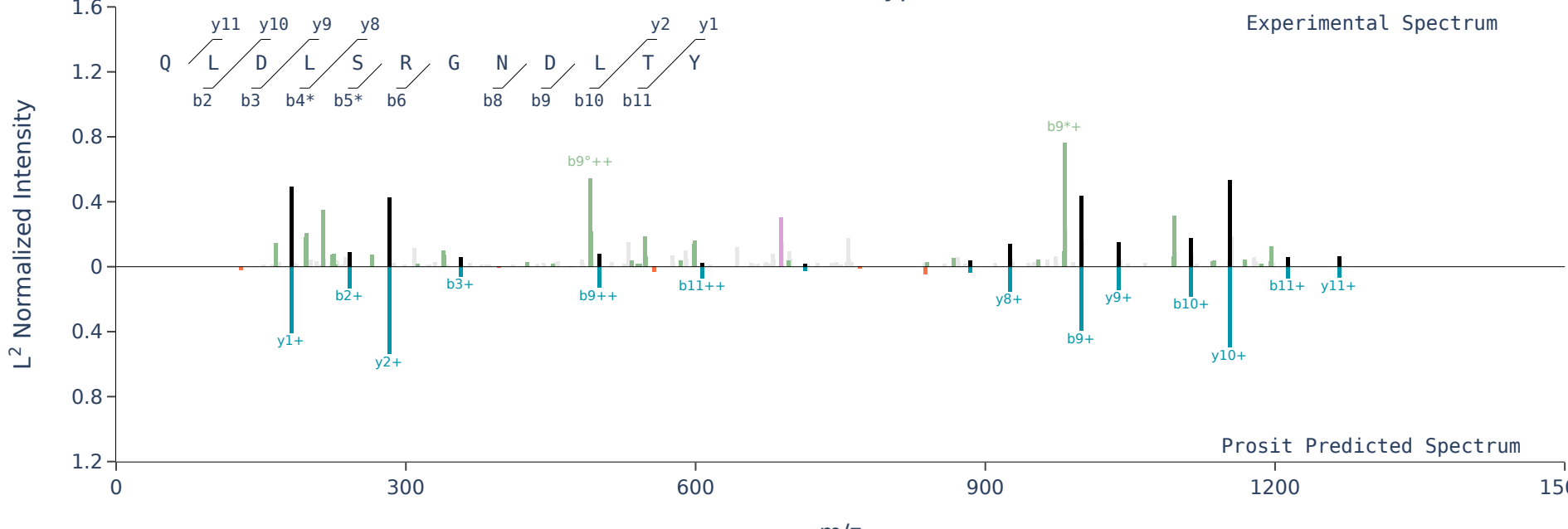
Peptide LADTQLHY Charge 2 Spectral Angle 0.61



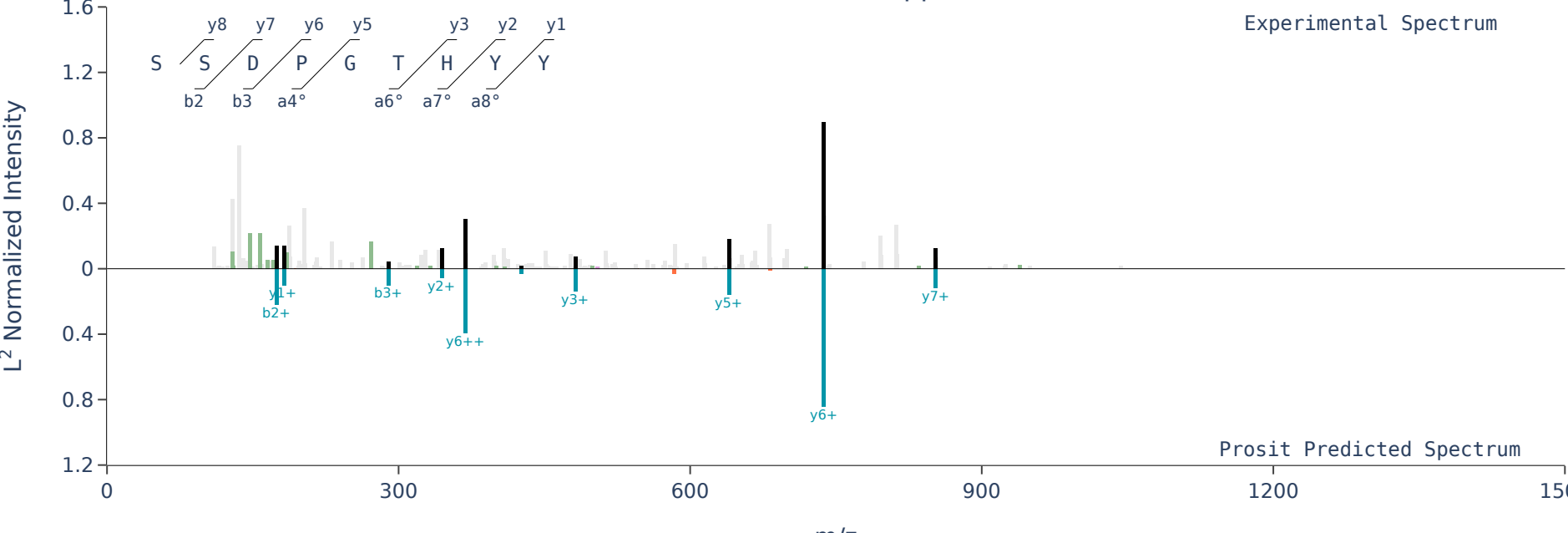
Peptide ASDDLRLTSY Charge 2 Spectral Angle 0.86



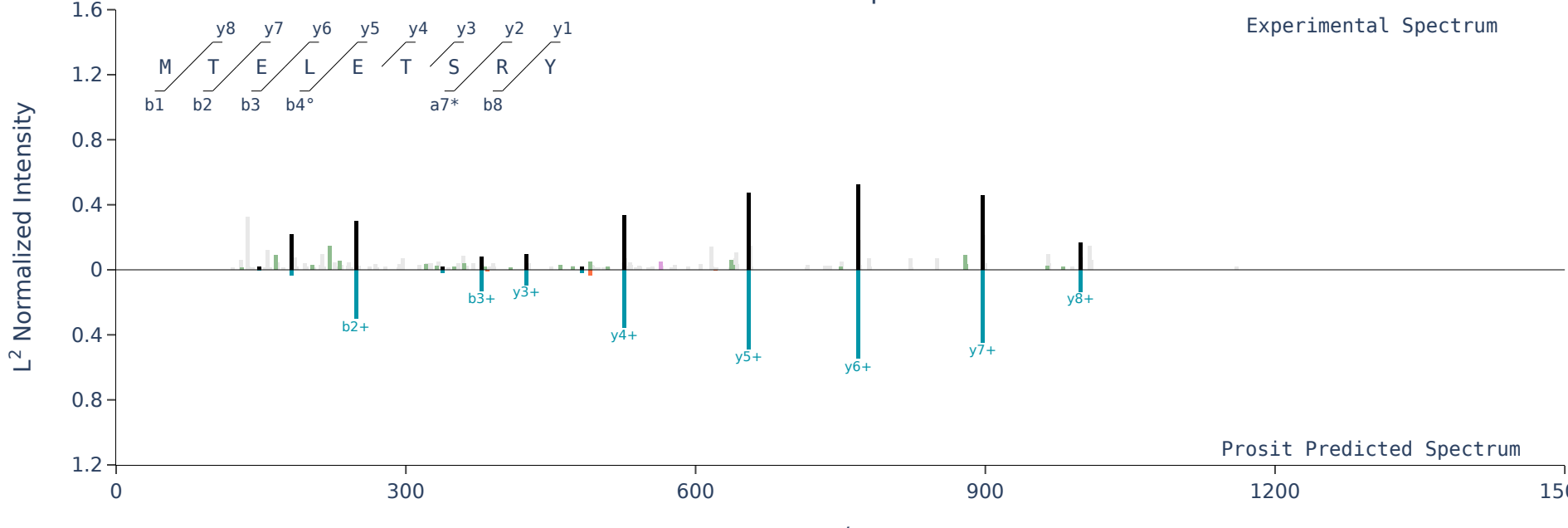
Peptide QLDLSRGNDLTY Charge 2 Spectral Angle 0.88



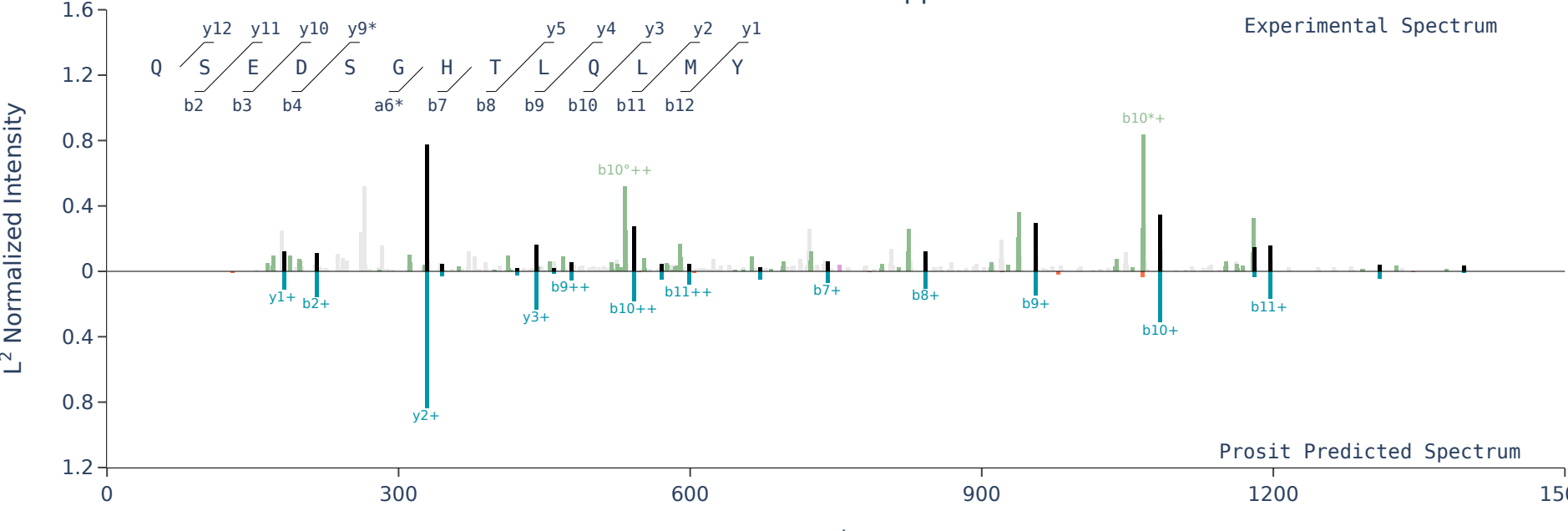
Peptide SSDPGTHYY Charge 2 Spectral Angle 0.88



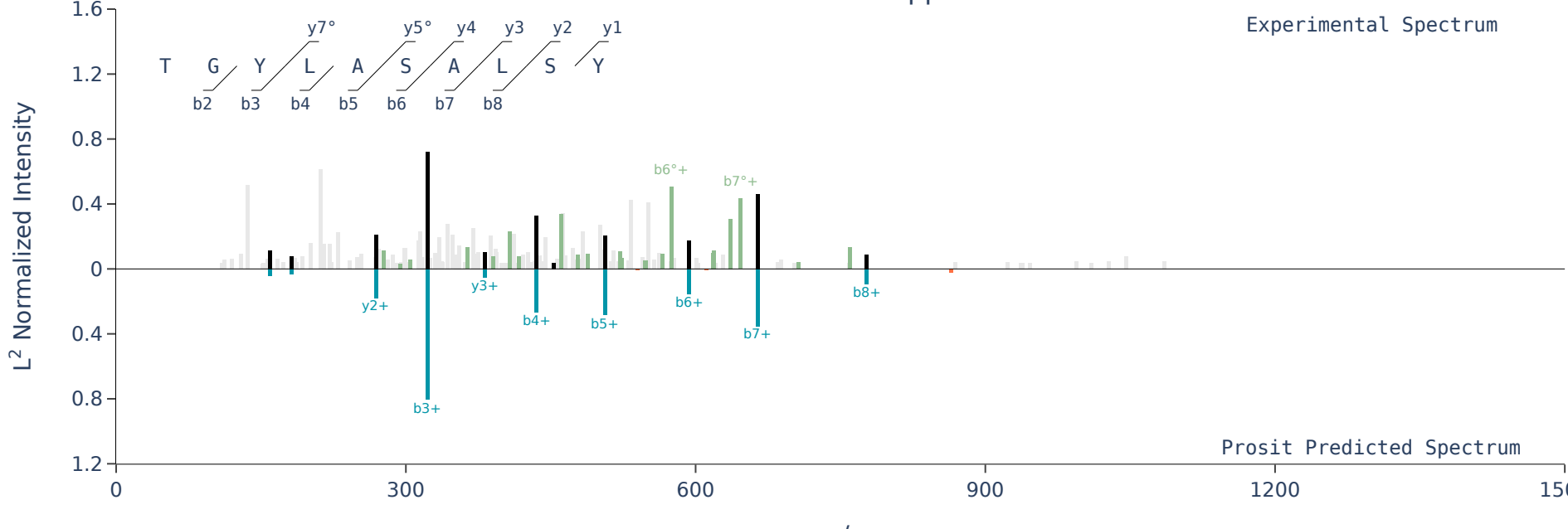
Peptide M[+16.0]TELETSRY **Charge** 2 **Spectral Angle** 0.87



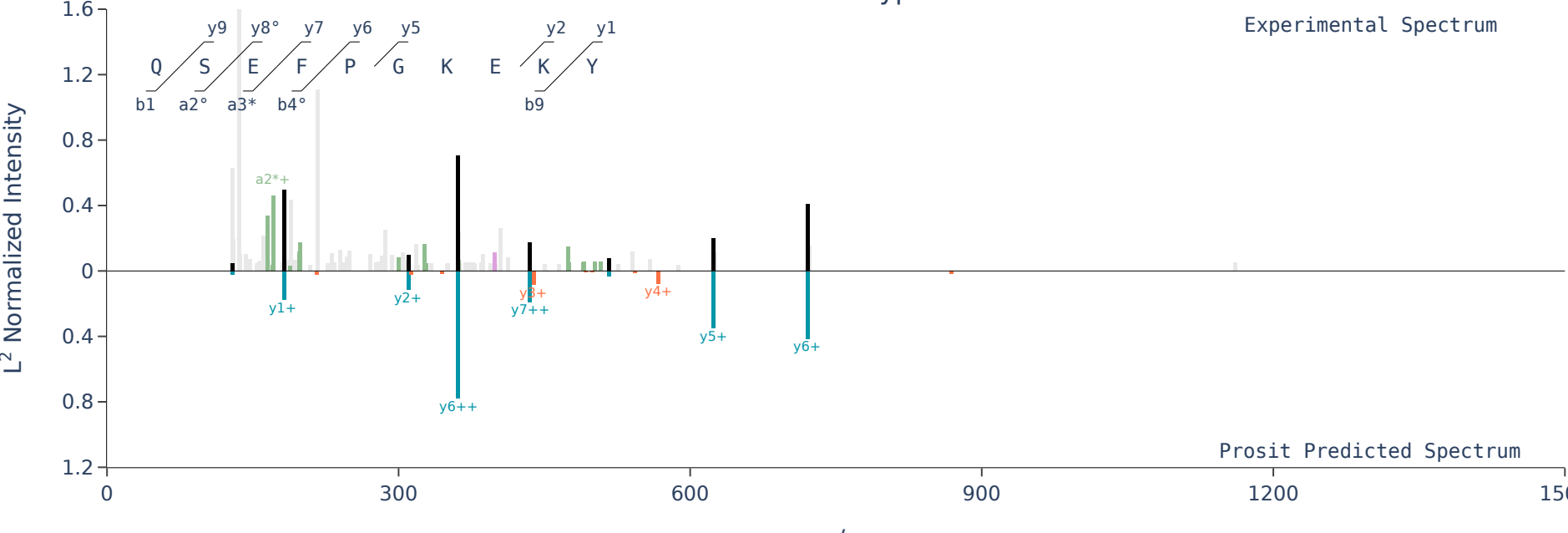
Peptide QSEDSGHTLQLM[+16.0]Y **Charge** 2 **Spectral Angle** 0.84



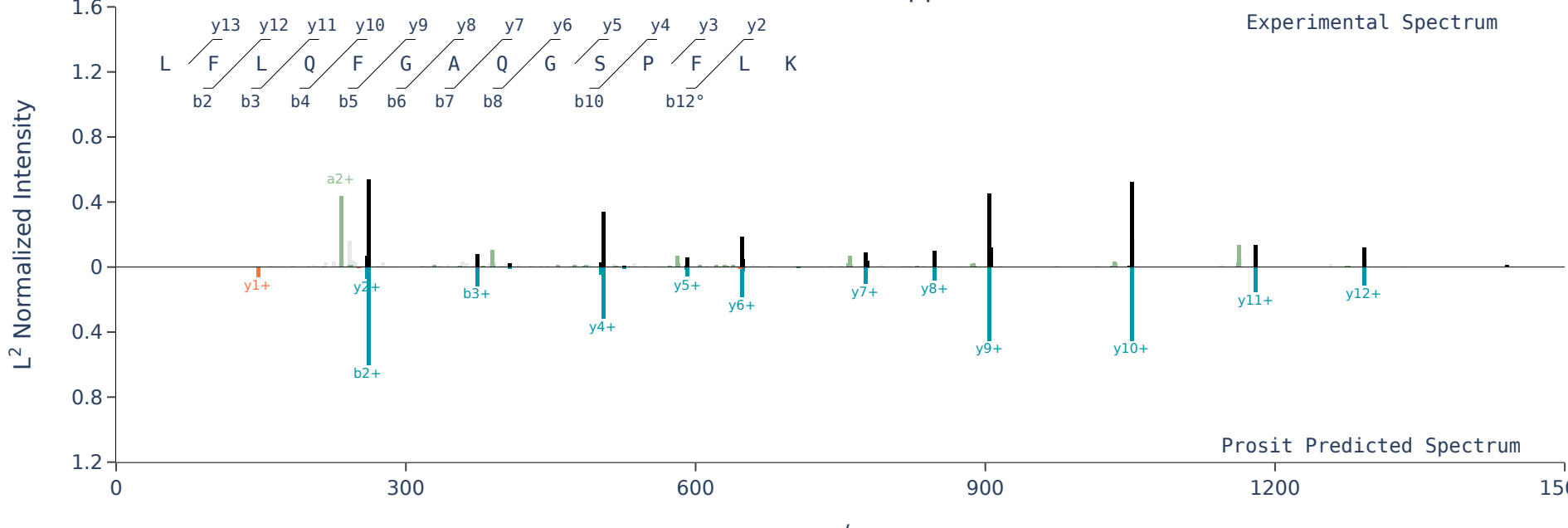
Peptide TGYLASALSY Charge 1 Spectral Angle 0.87



Peptide QSEFPGKEY **Charge** 3 **Spectral Angle** 0.75



Peptide LFLQFGAQGSPFLK Charge 2 Spectral Angle 0.92

Peptide MSEPHNYSLN^y Charge 2 Spectral Angle 0.71