

Experimental Spectrum Colour Code:

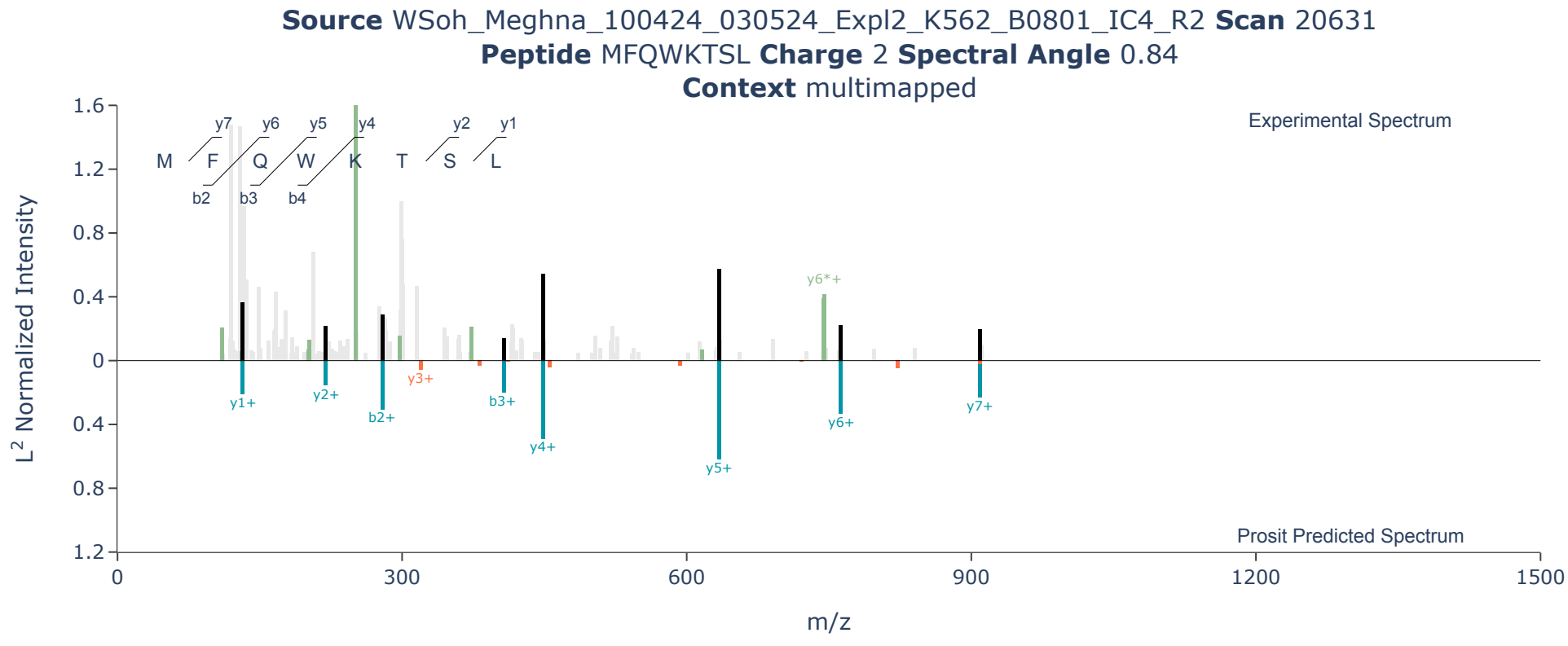
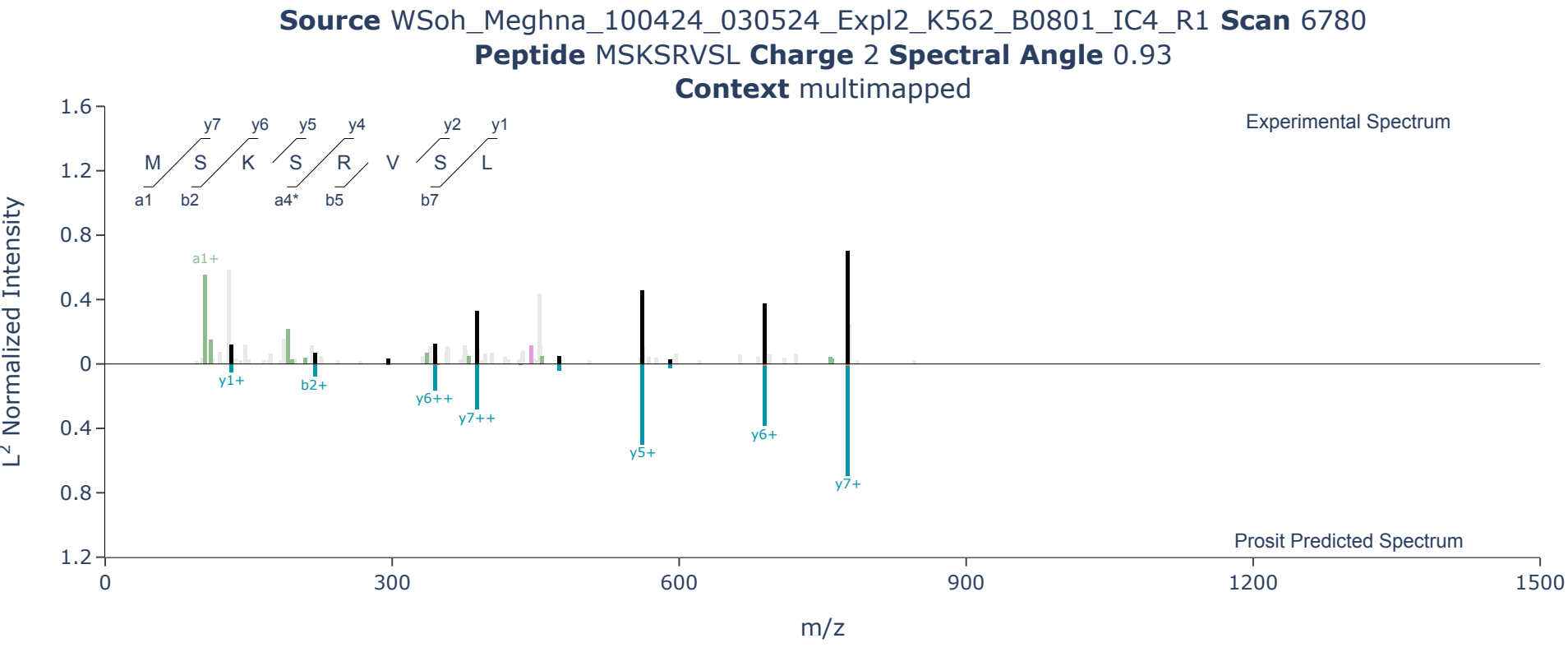
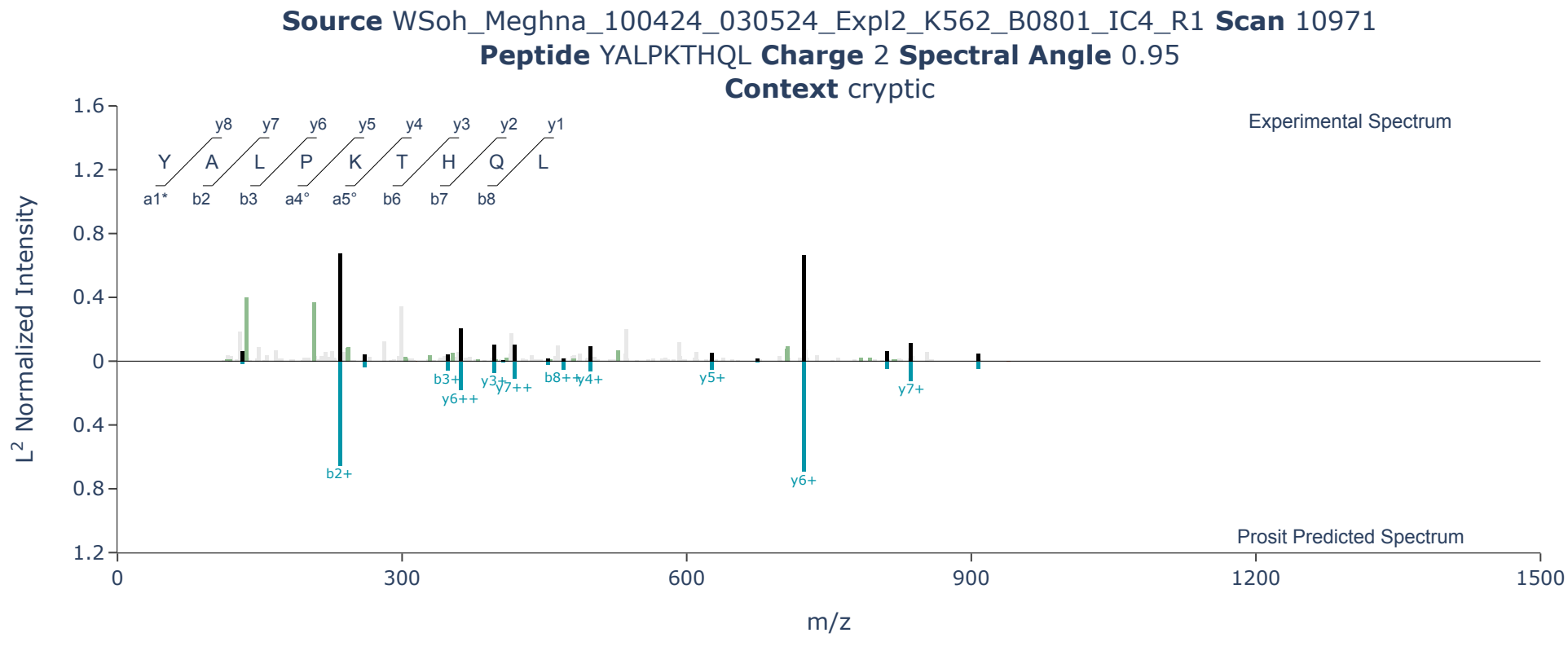
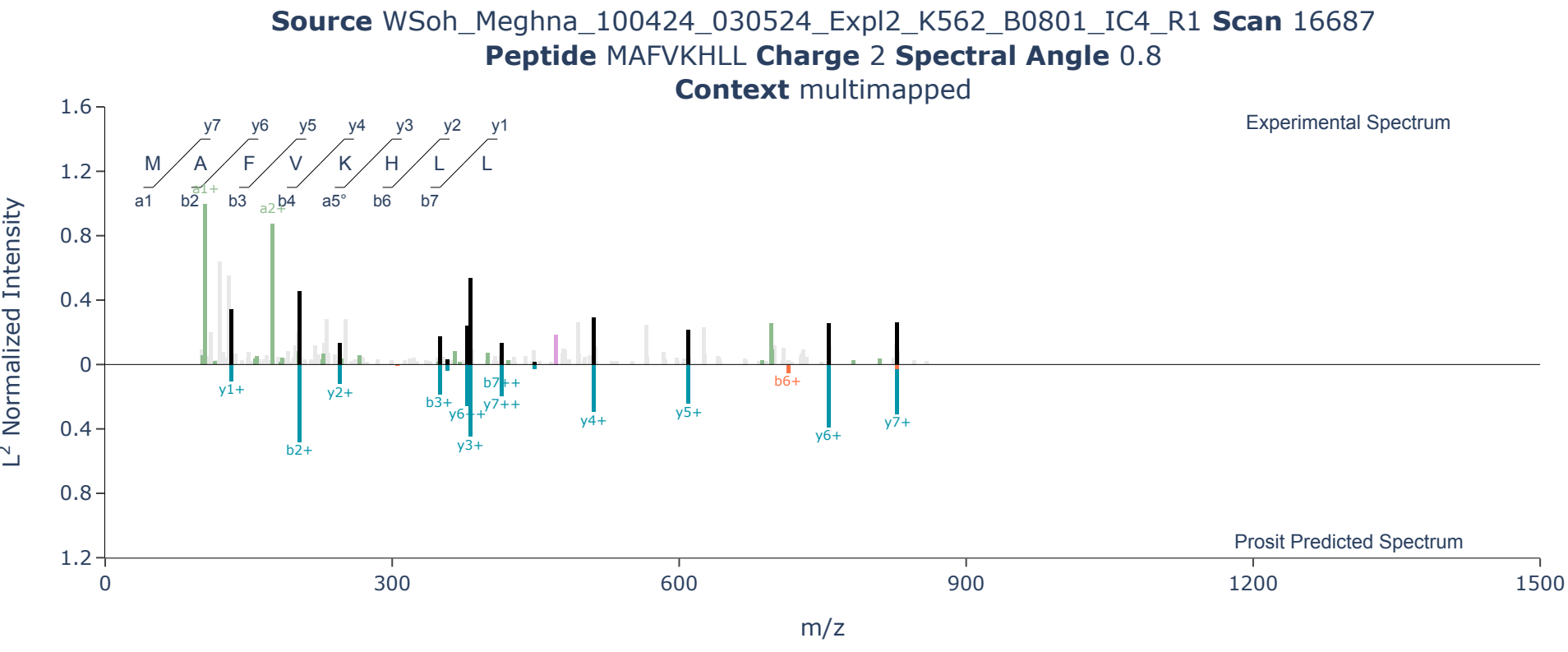
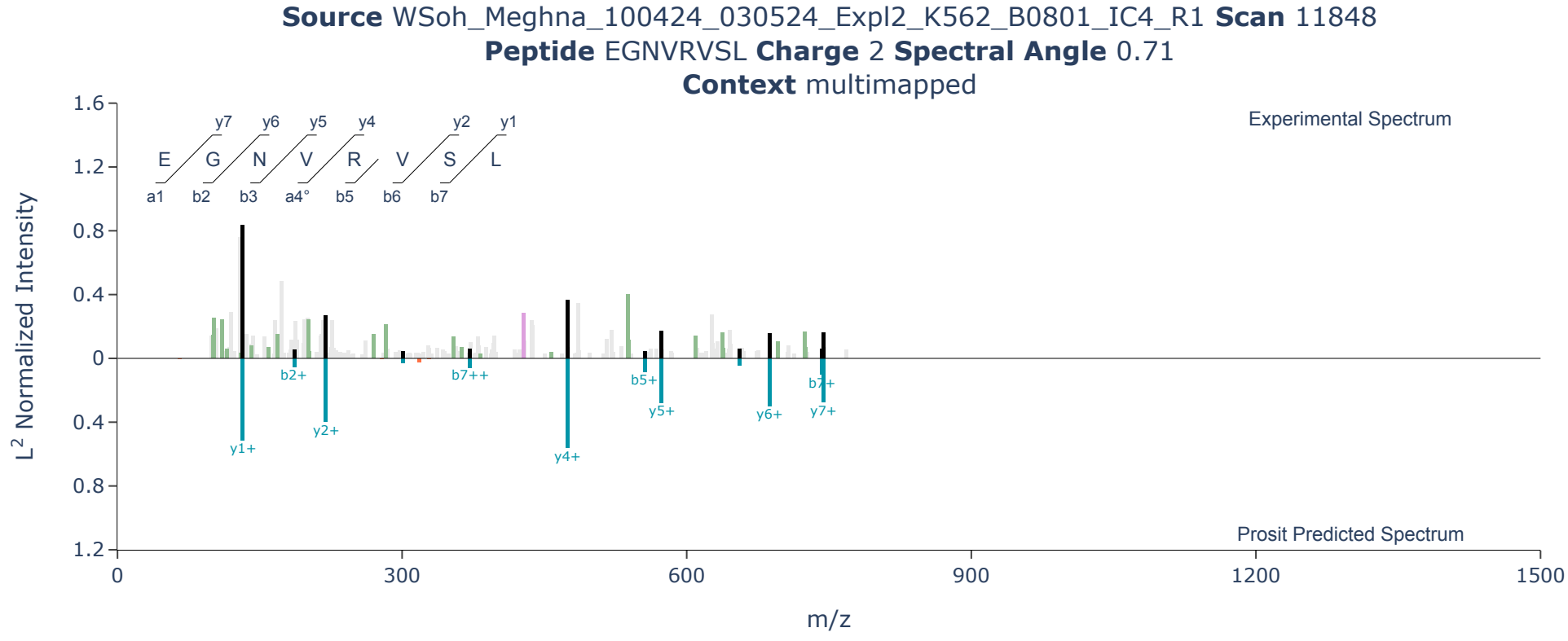
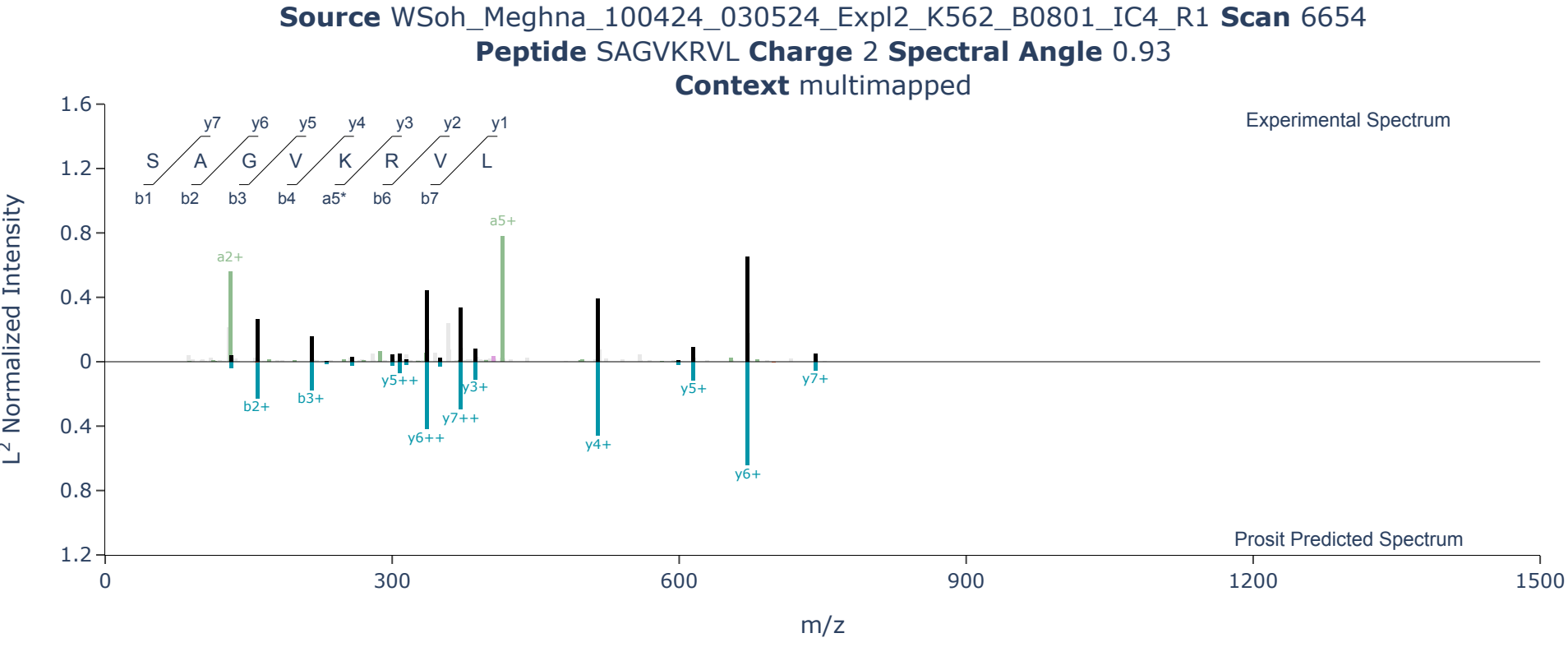
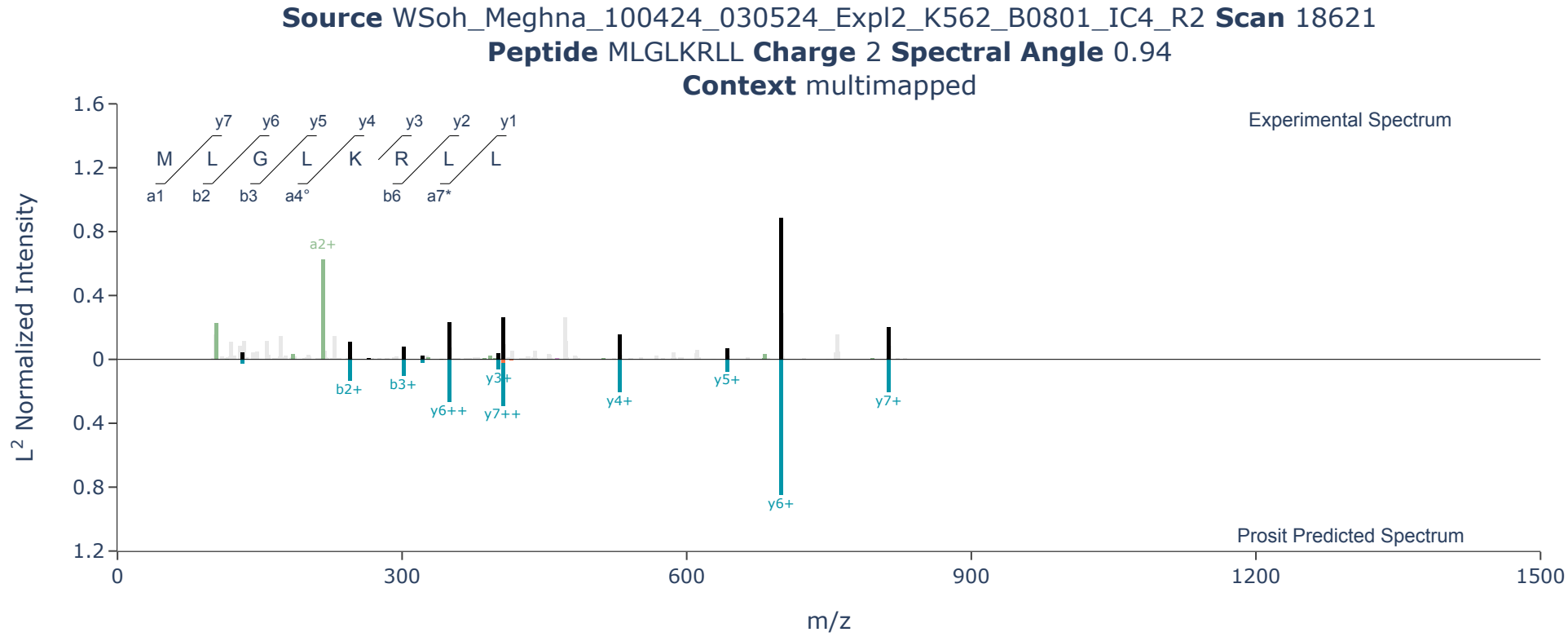
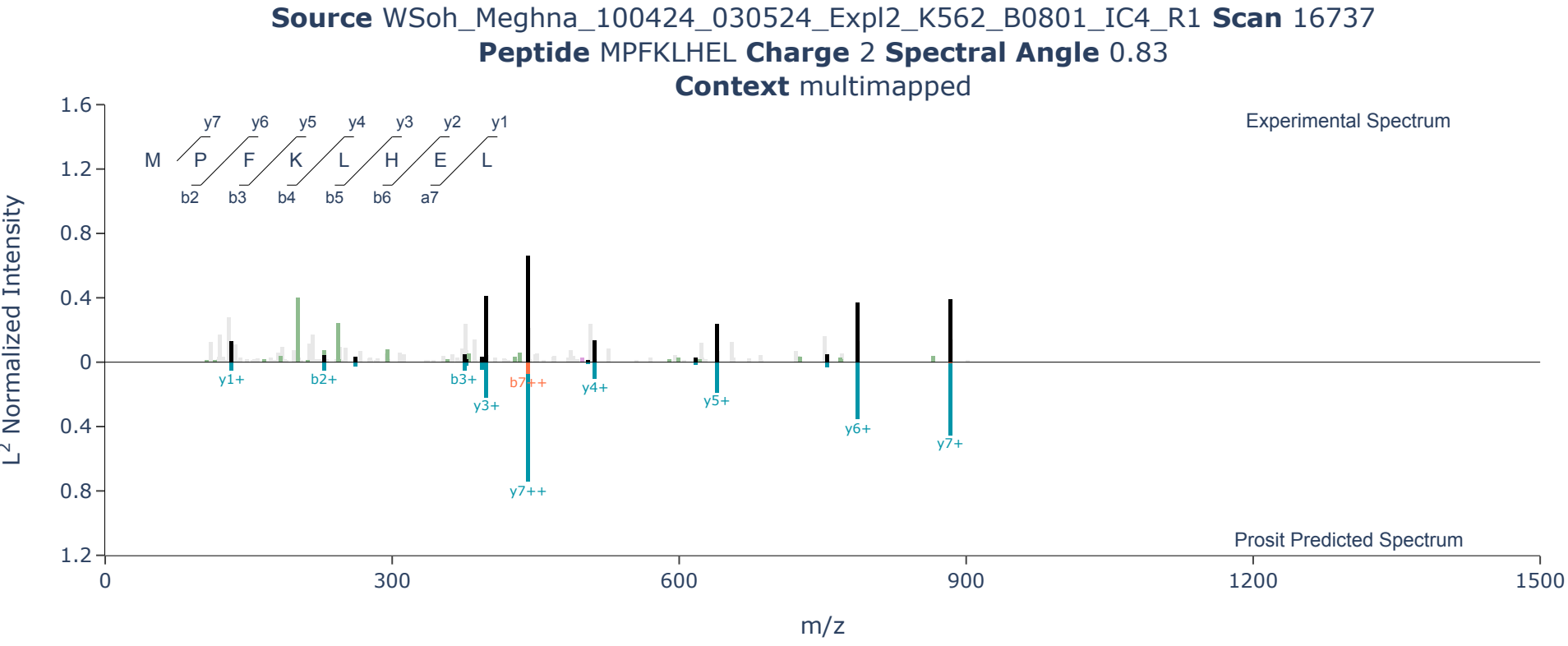
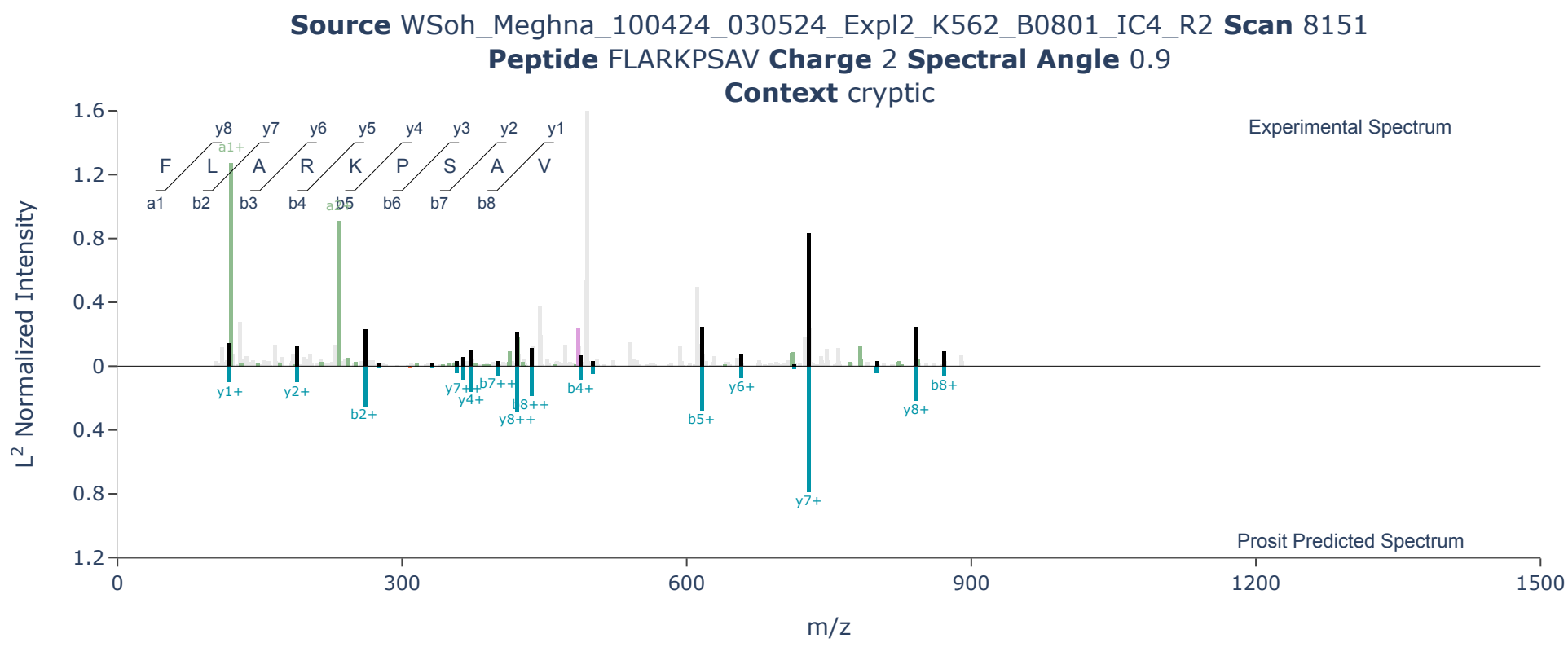
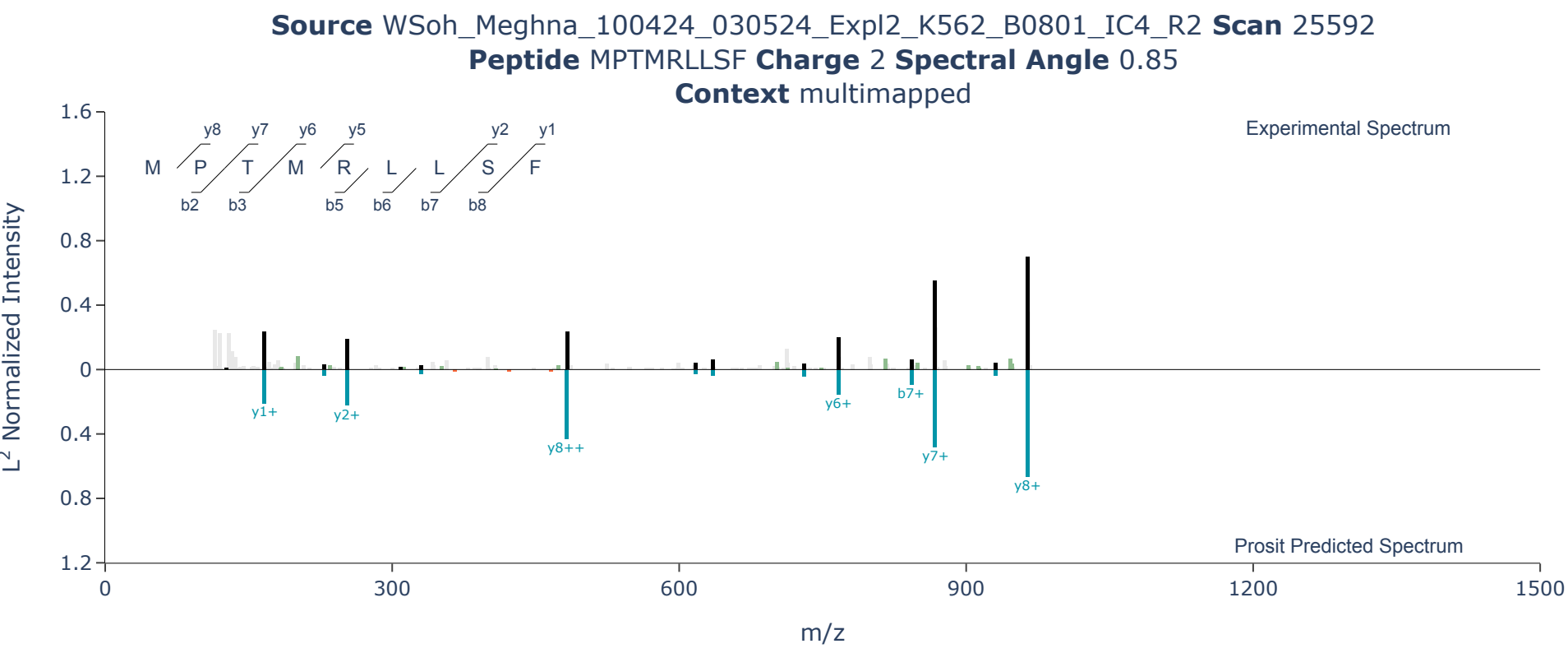
- Experimental peak matched to a Prosit predicted peak.
- Possible ion unknown to Prosit.
- Precursor matched peak.
- Experimental peak not matched to any potential ion.

Prosit Spectrum Colour Code:

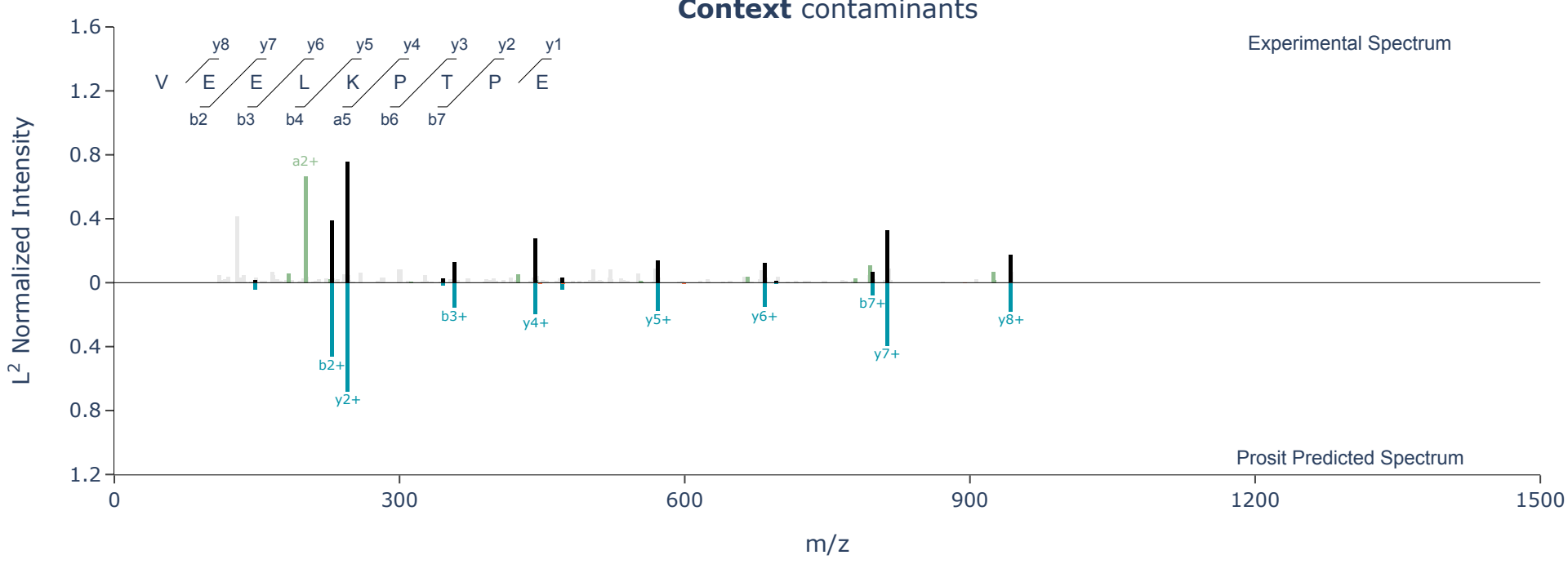
- Prosit predicted peak matched to experimental spectrum.
- Prosit predicted peak not matched to experimental spectrum.

Additional Notes:

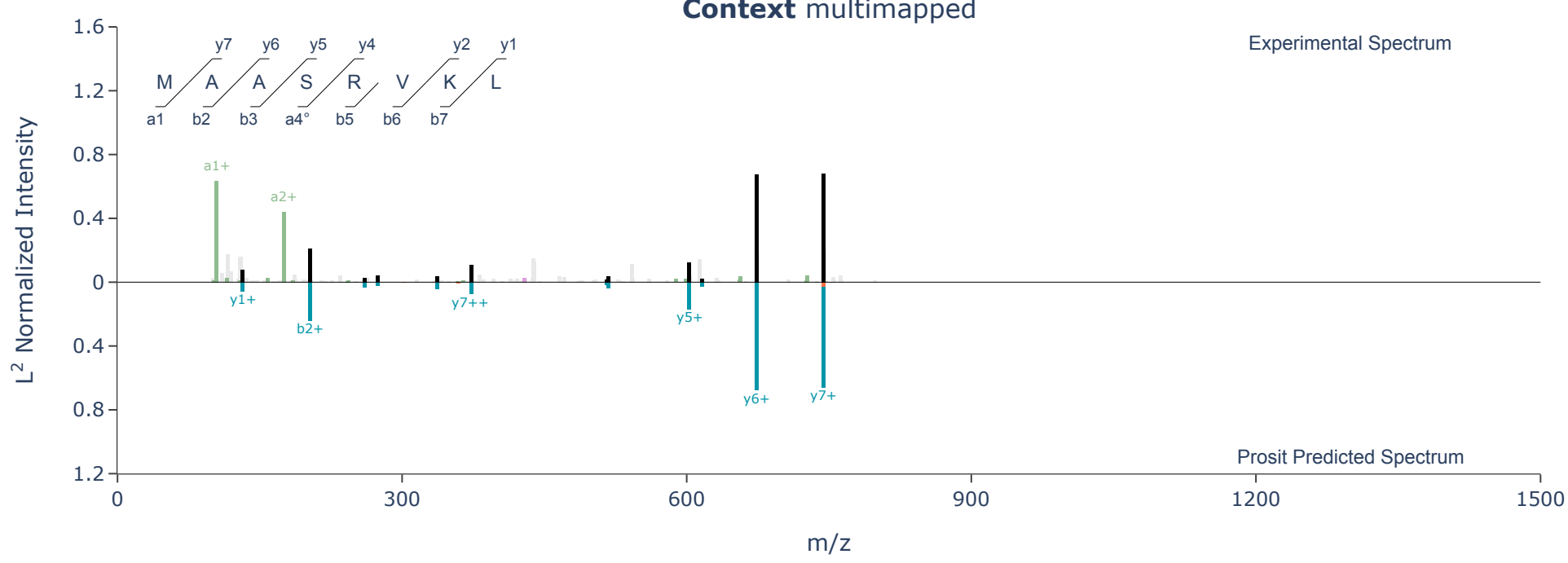
- ° indicates an ion with loss of H₂O.
- * indicates an ion with loss of NH₃.



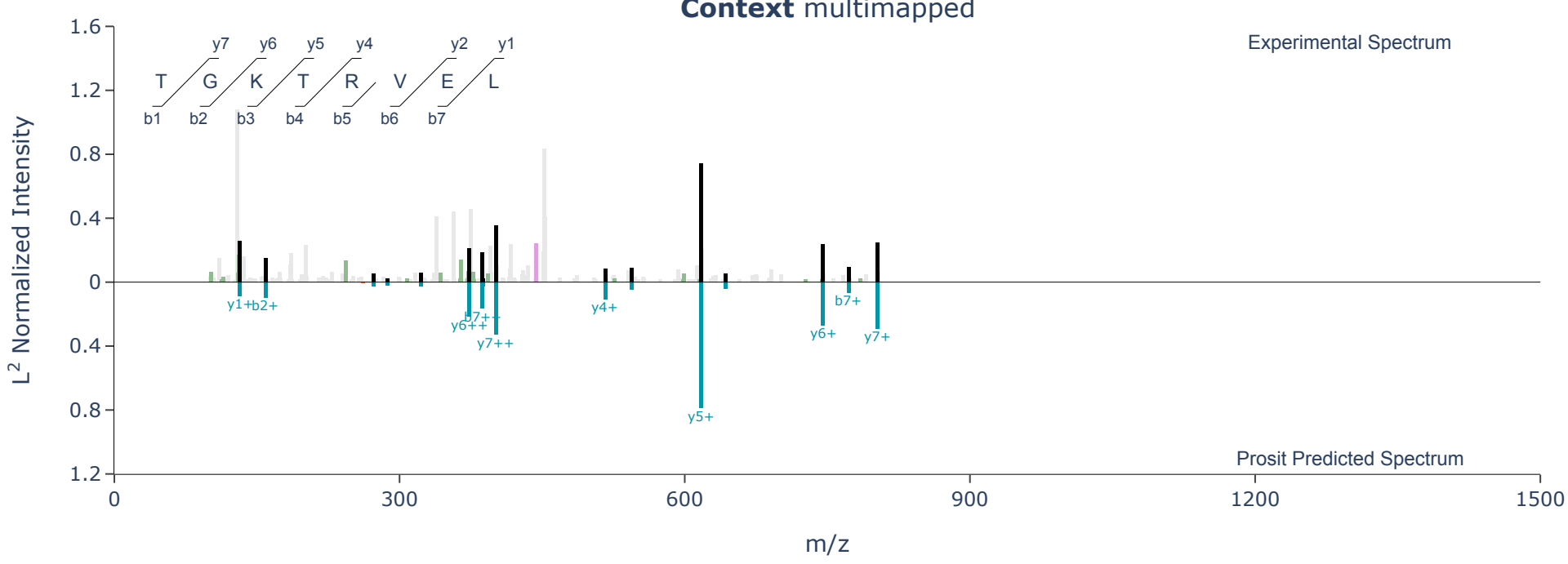
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Peptide VEELKPTPE Charge 2 Spectral Angle 0.9



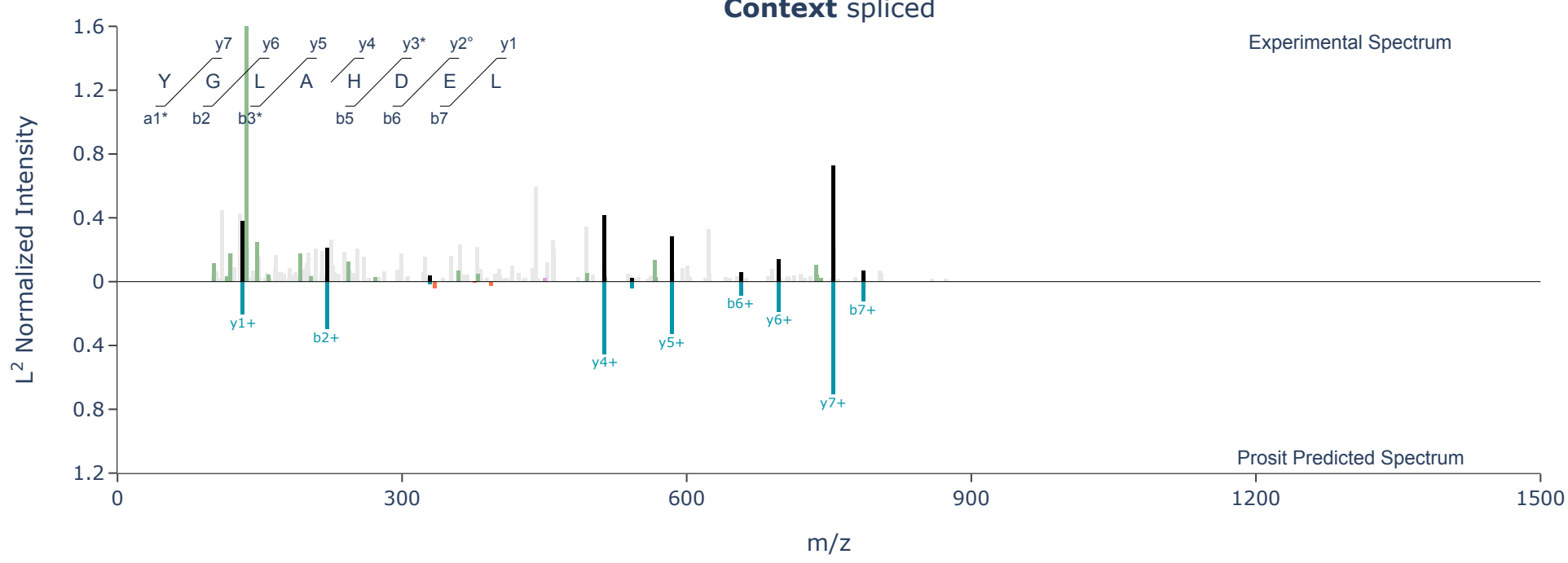
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R2 Scan 8325
Peptide MAASRVKL Charge 2 Spectral Angle 0.95



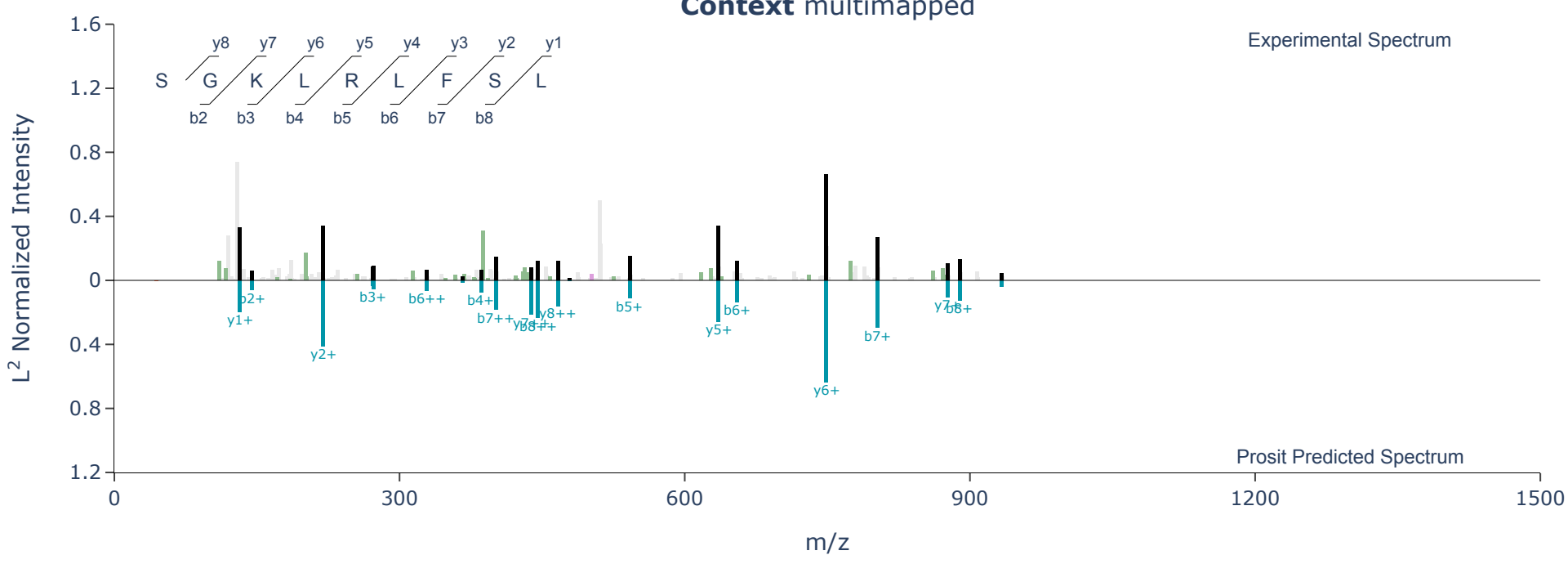
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R1 Scan 6949
Peptide TGKTRVEL Charge 2 Spectral Angle 0.87



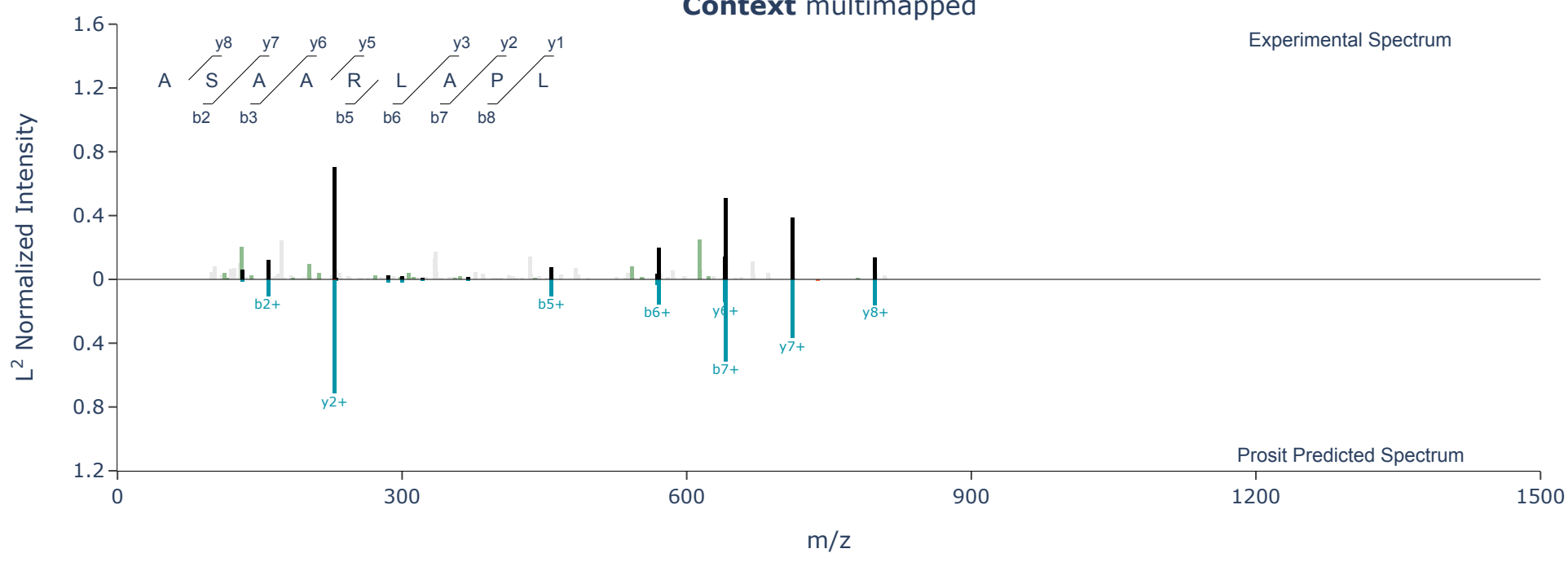
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Peptide YGLAHDEL Charge 2 Spectral Angle 0.86



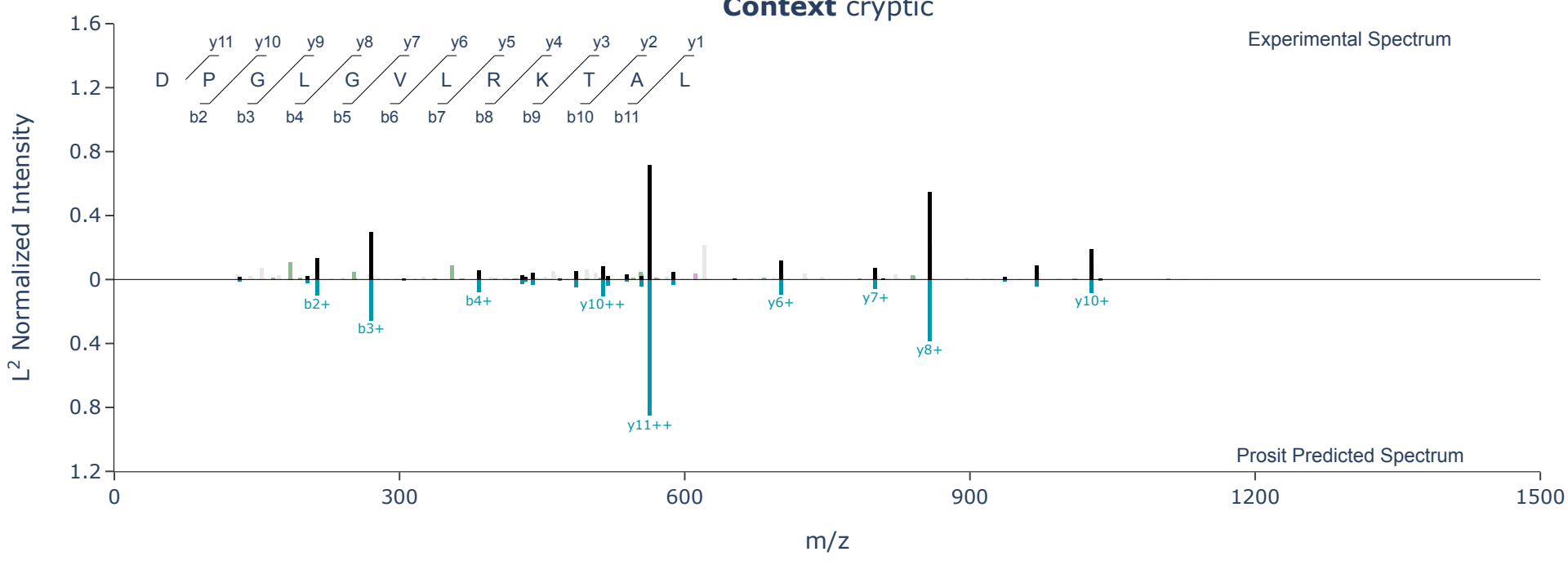
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Peptide SGKLRFLSL Charge 2 Spectral Angle 0.83



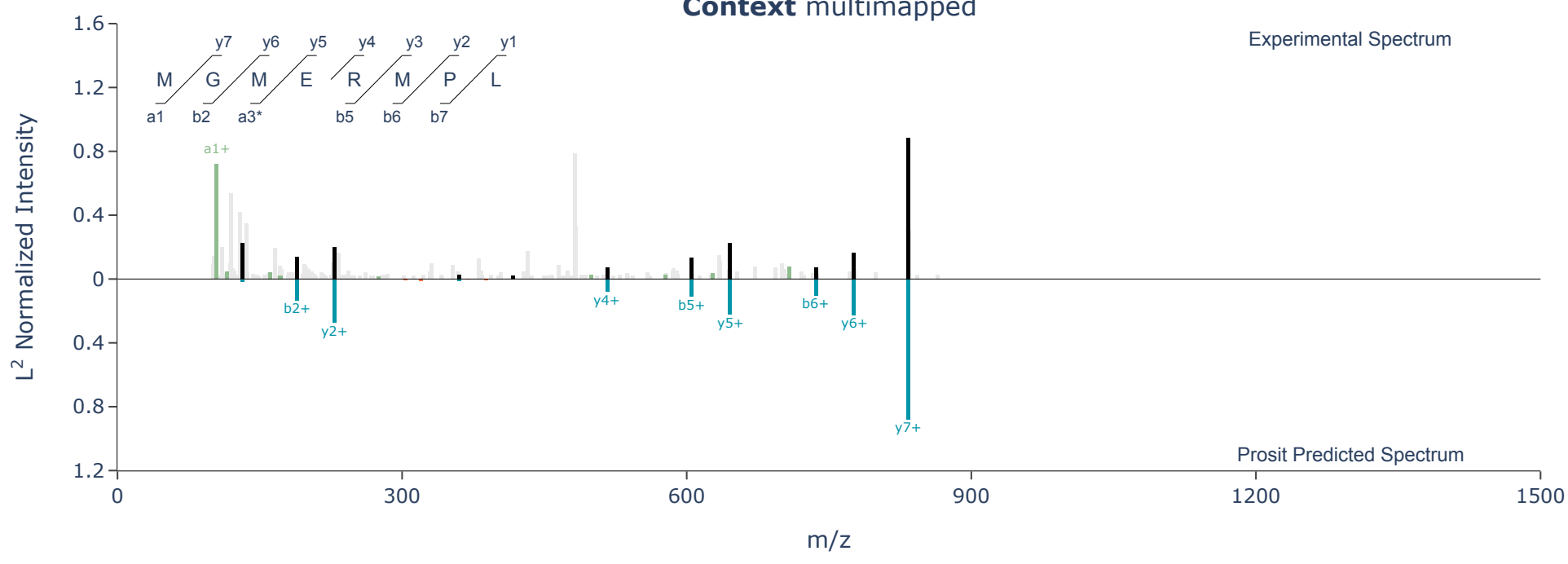
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Peptide ASARLAPL Charge 2 Spectral Angle 0.95



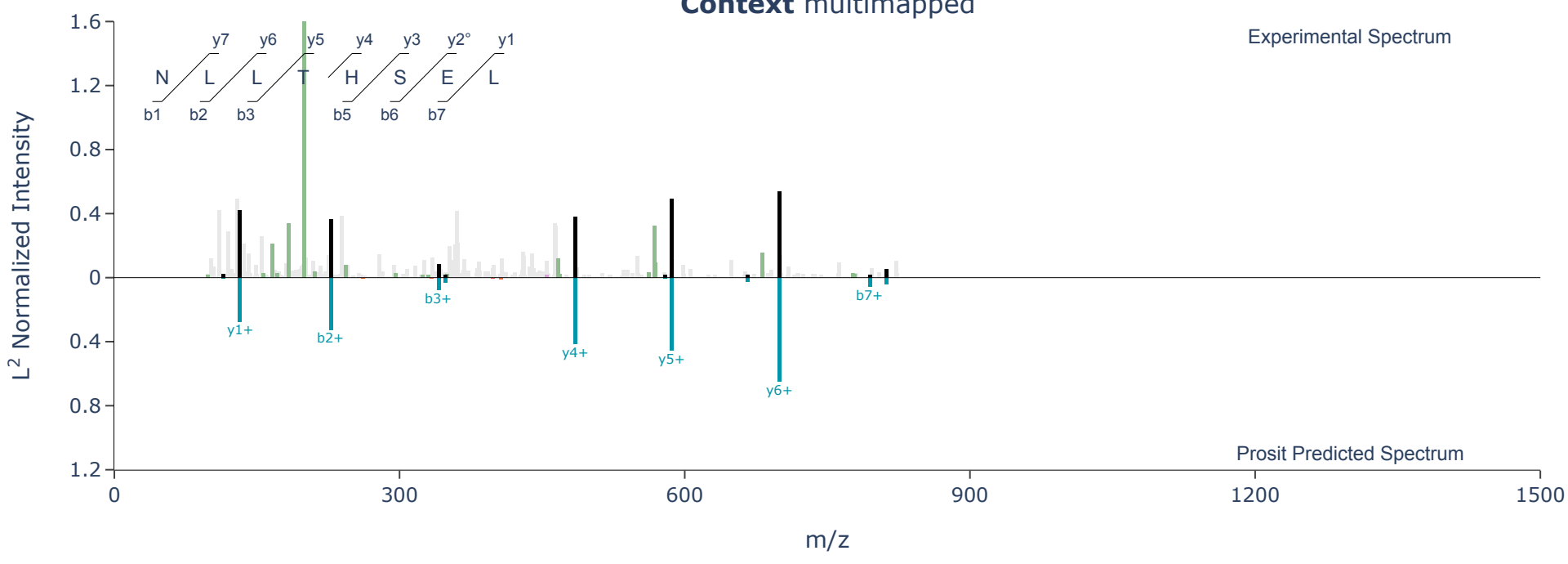
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Peptide DPLGLVRKTAL Charge 2 Spectral Angle 0.84



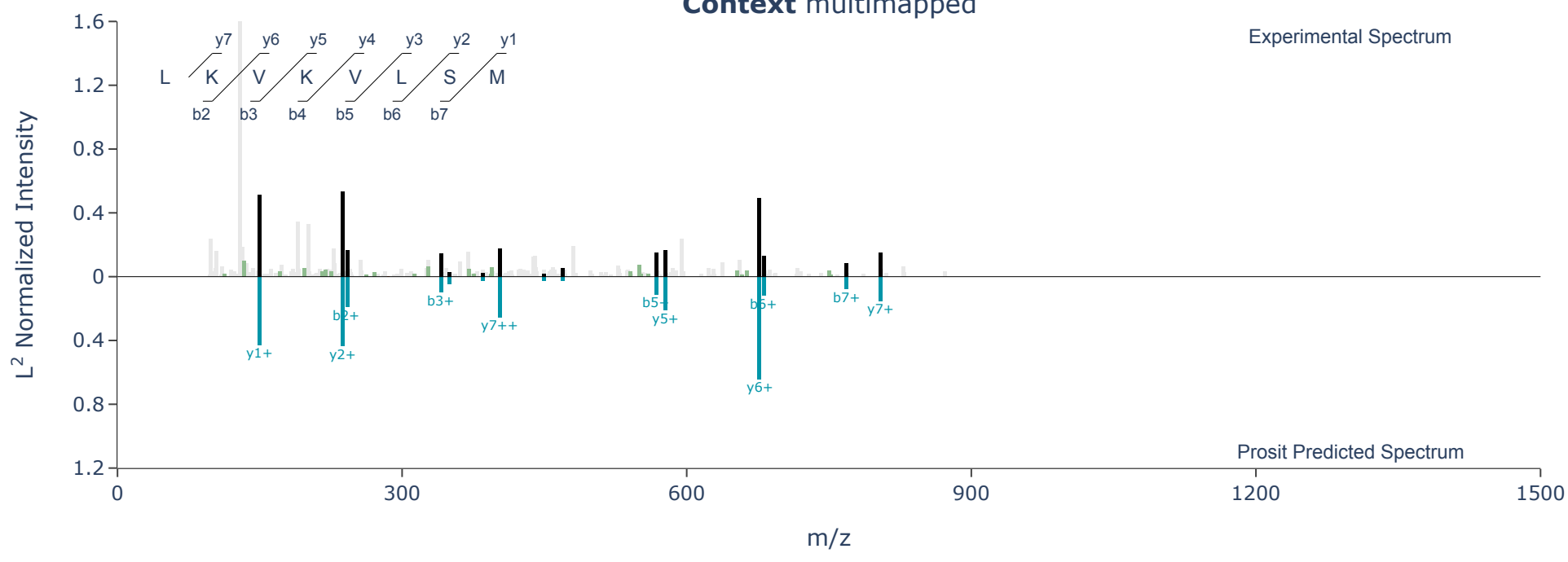
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Peptide MGMERMLP Charge 2 Spectral Angle 0.85

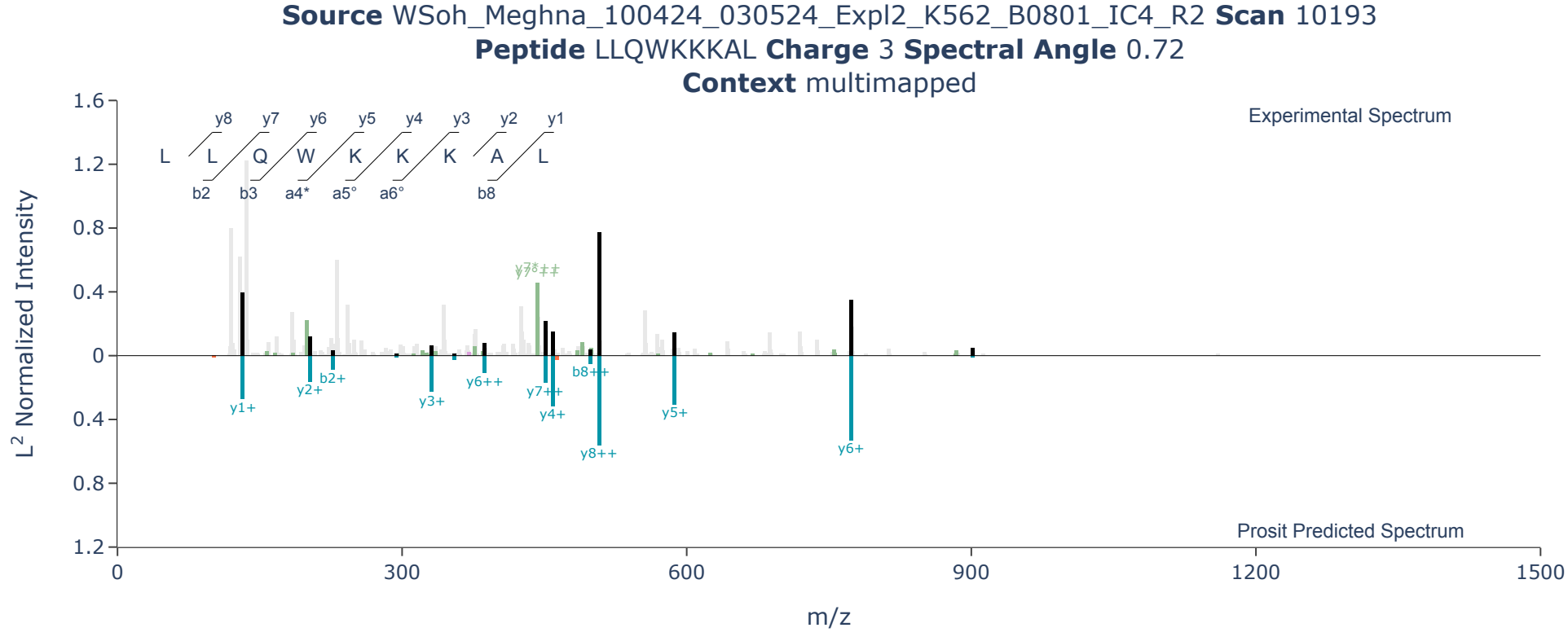
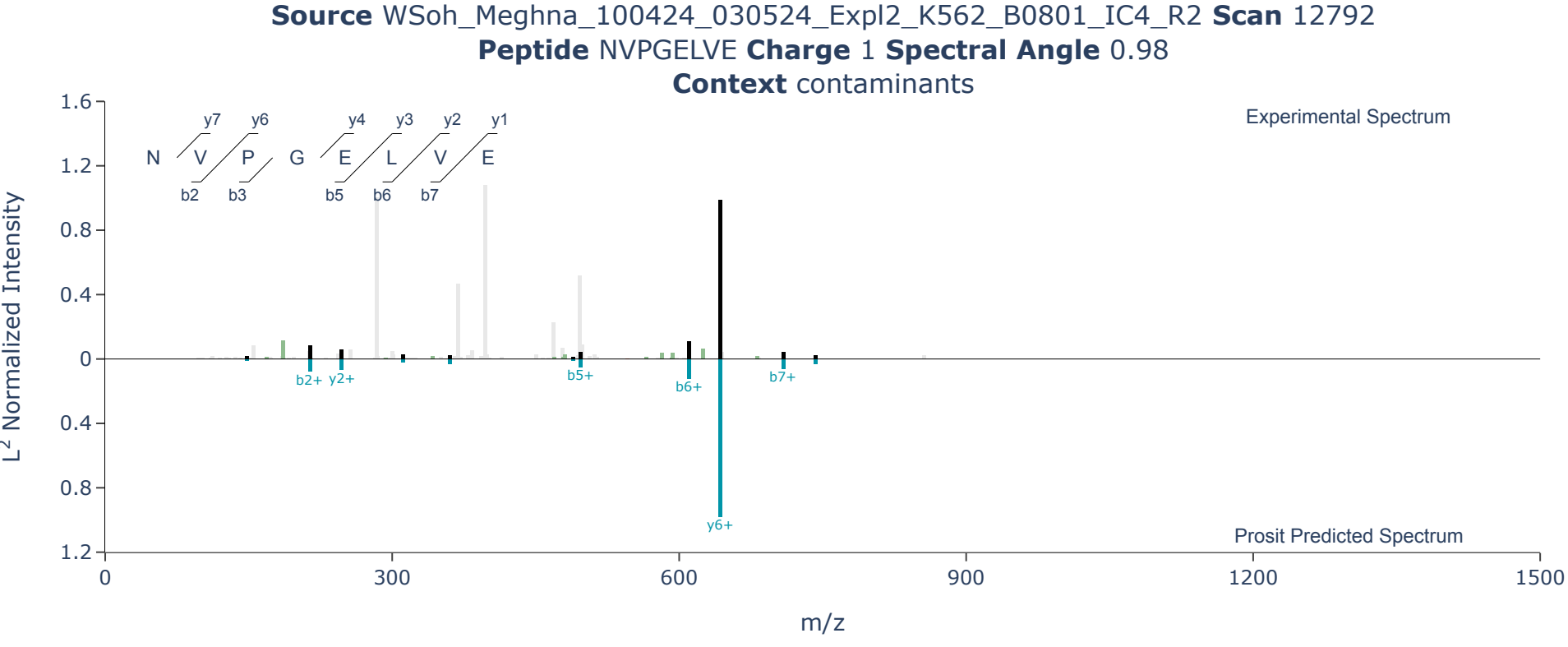
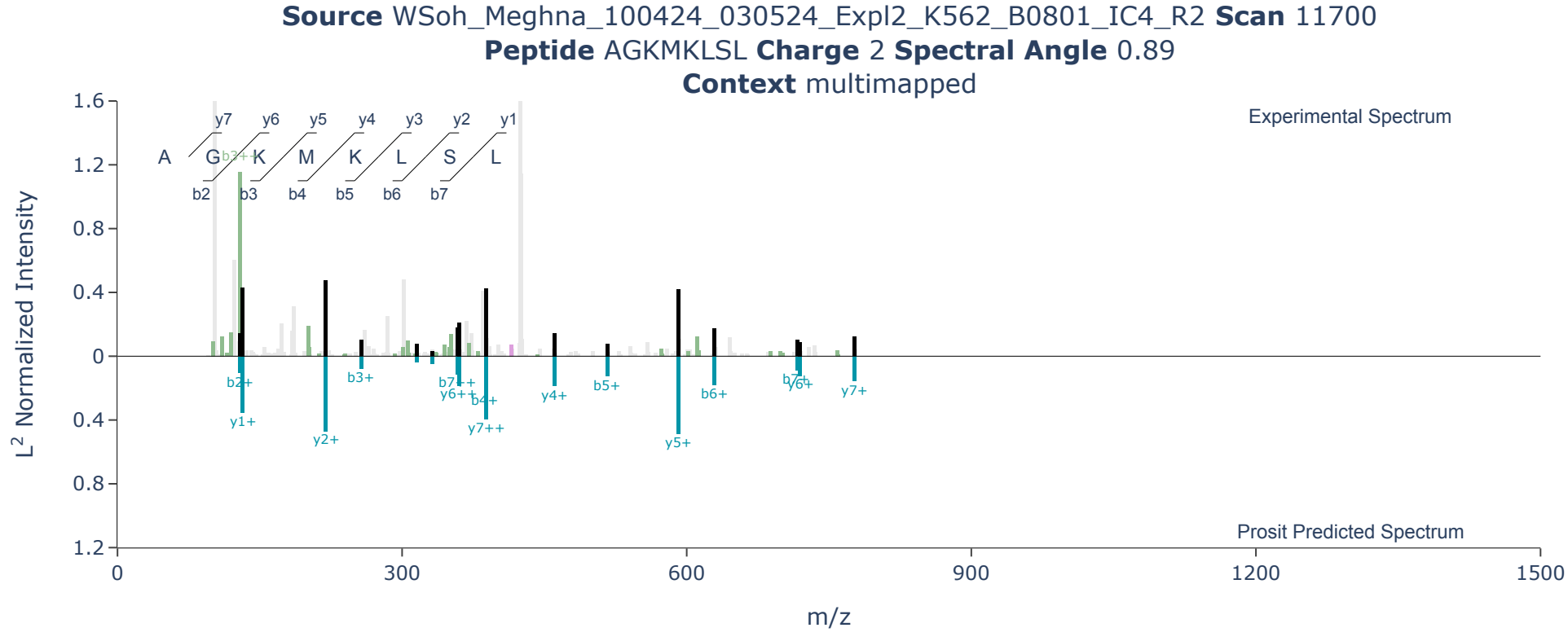
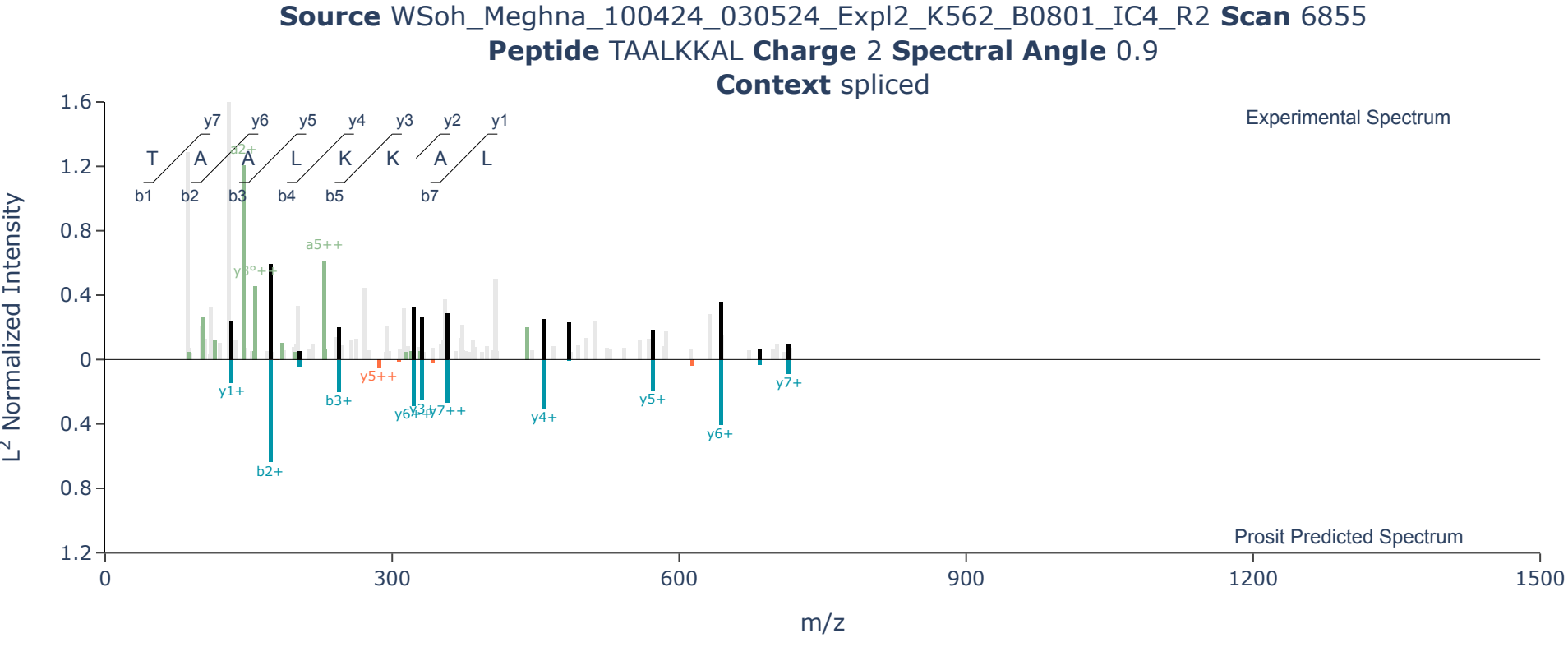
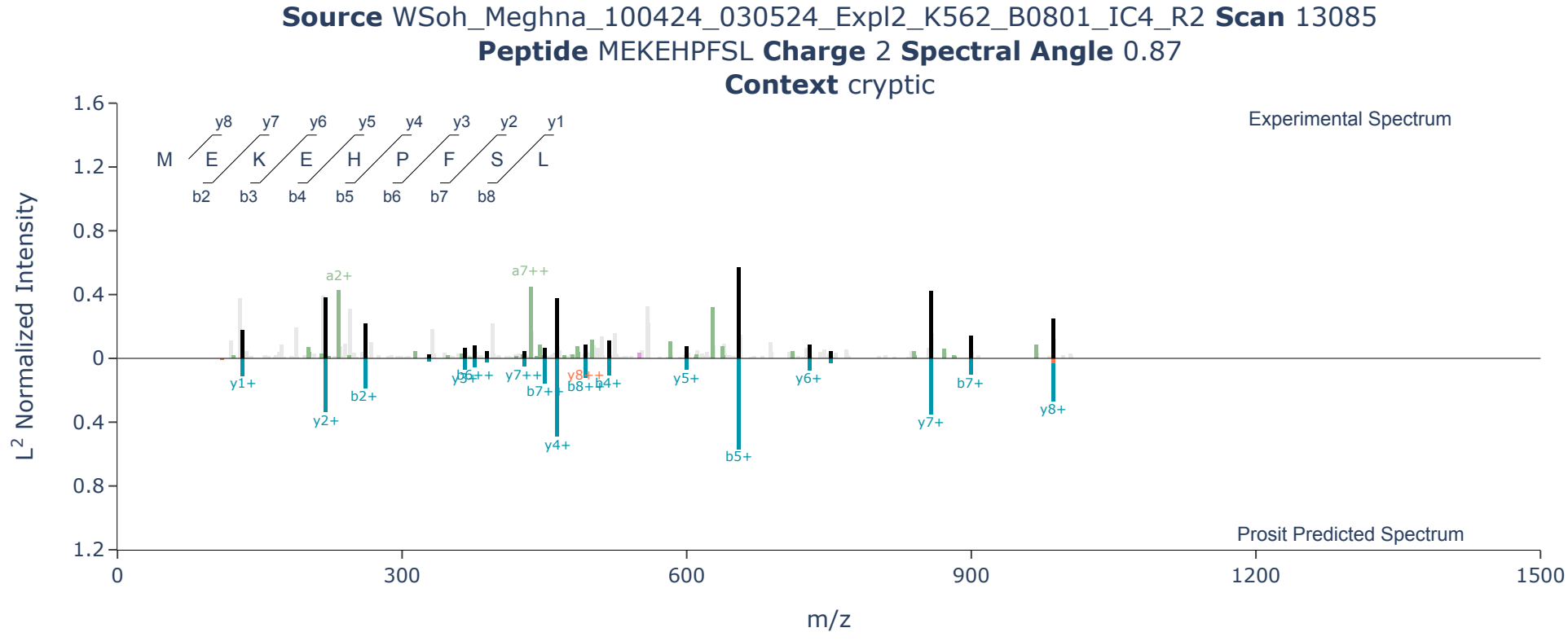
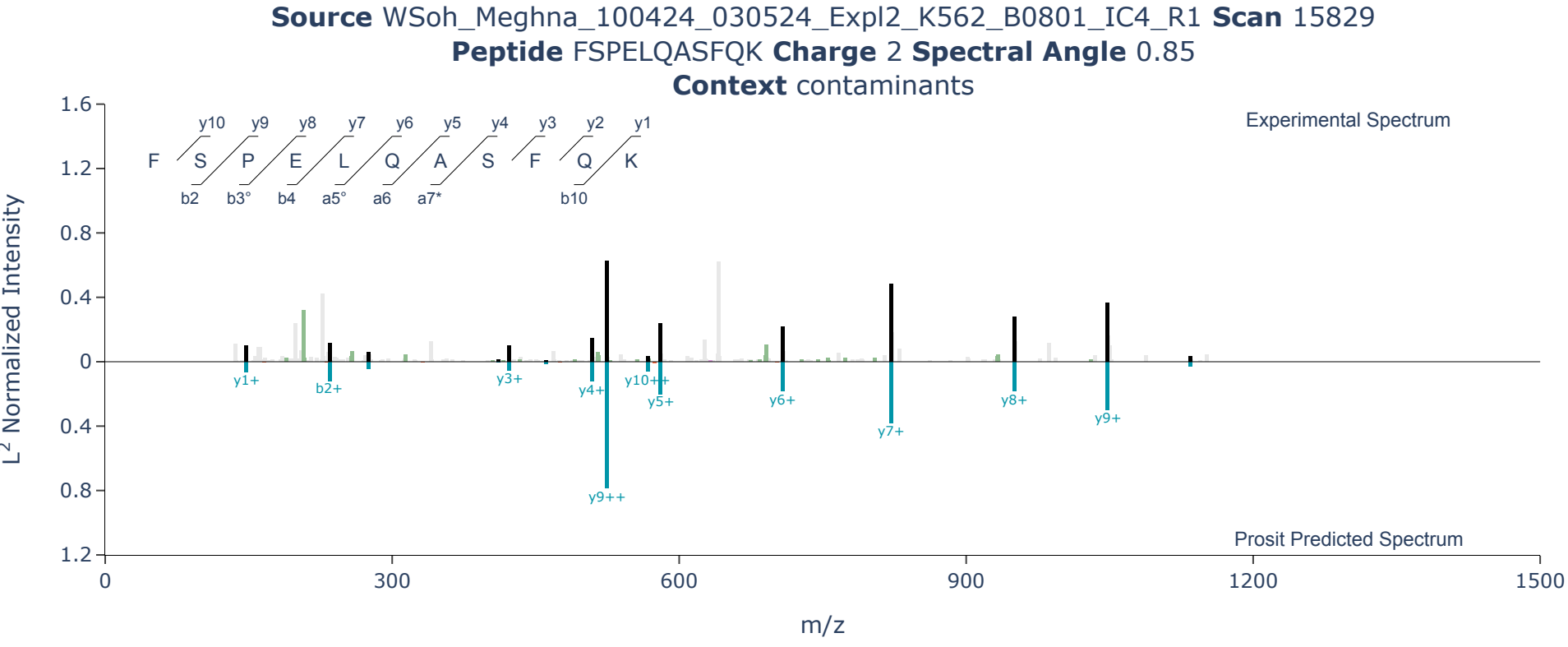
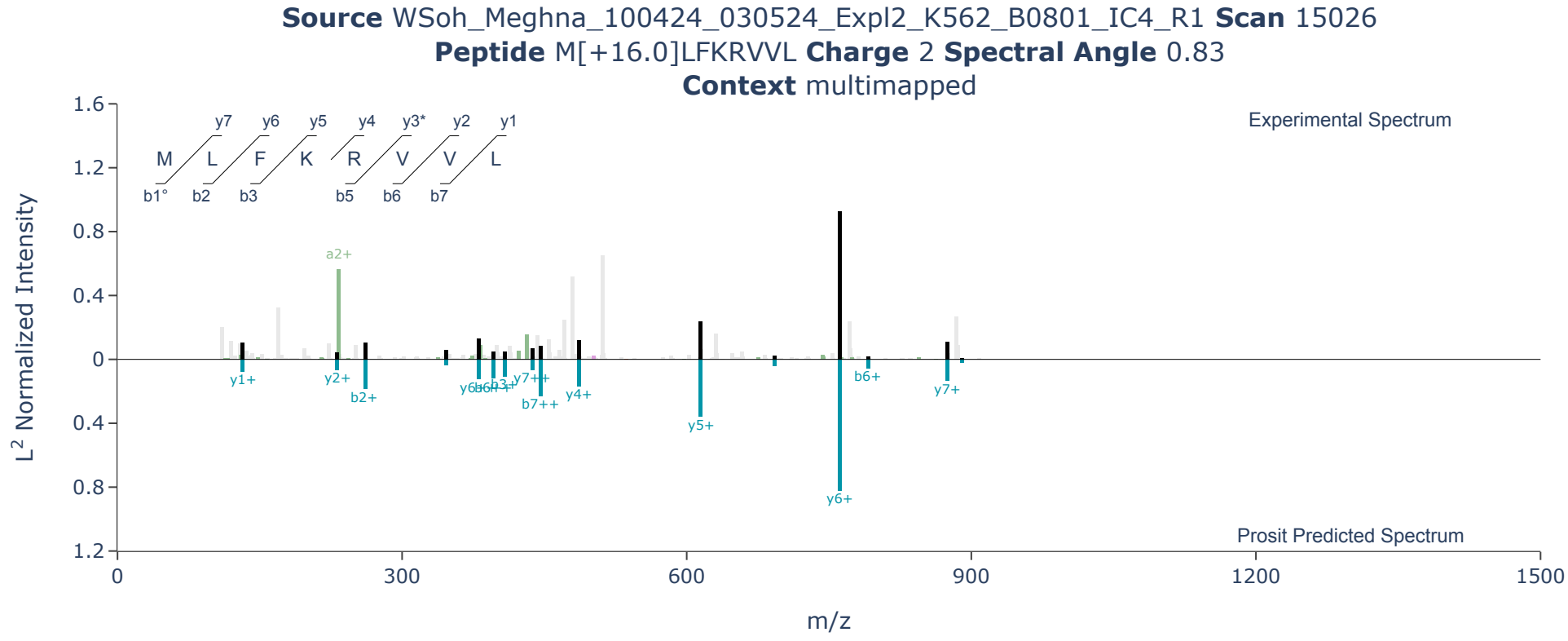
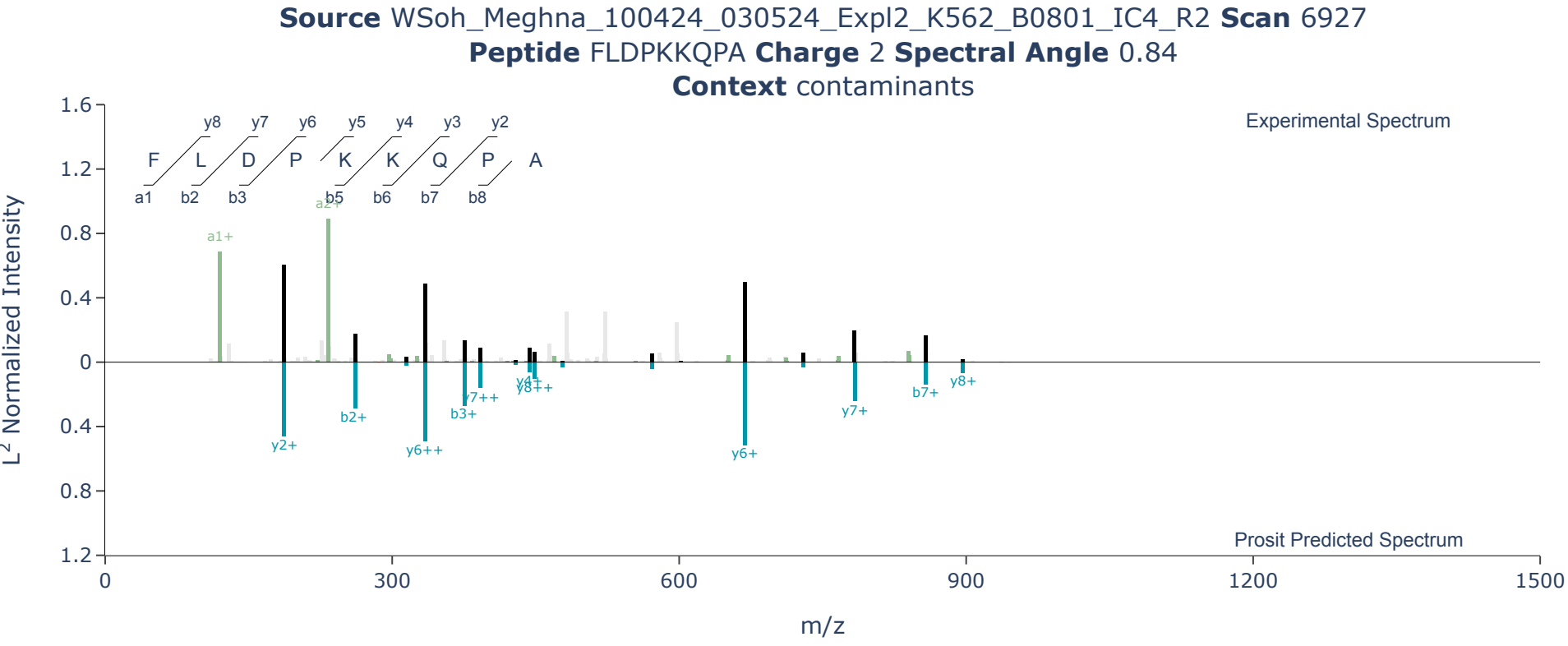
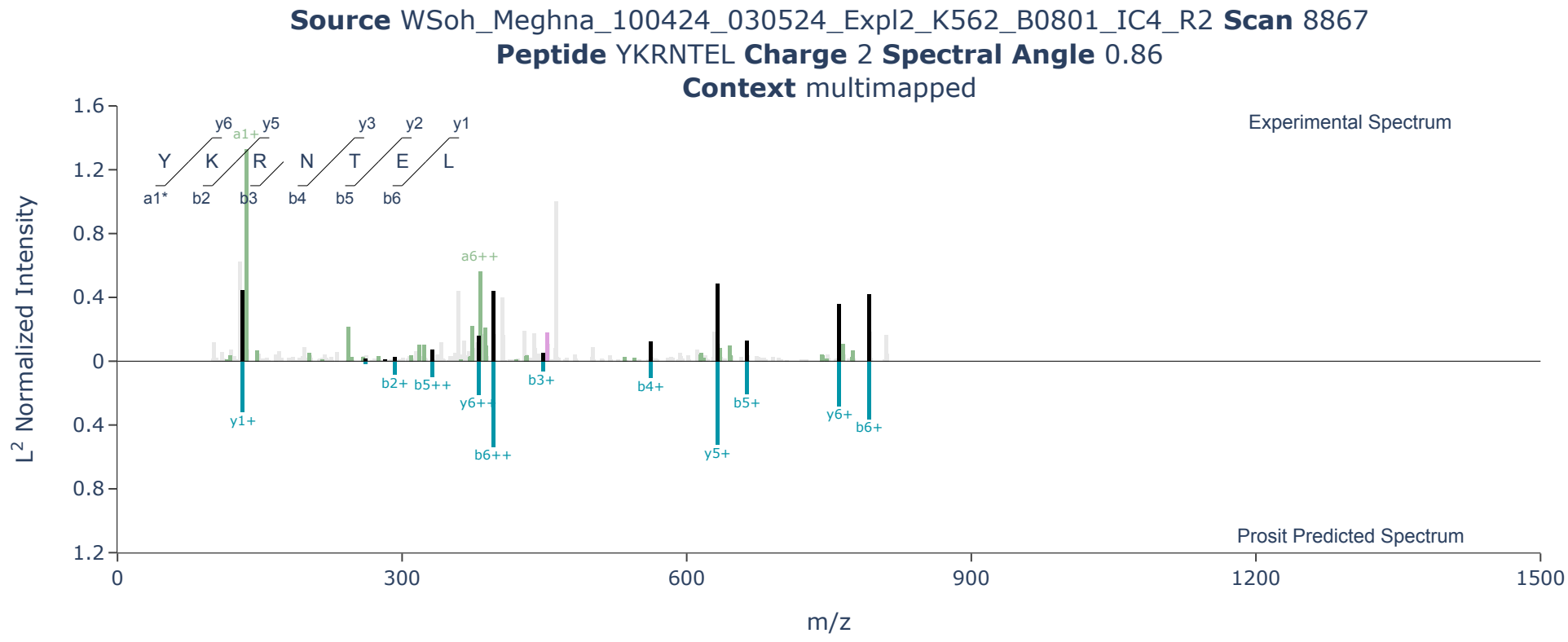
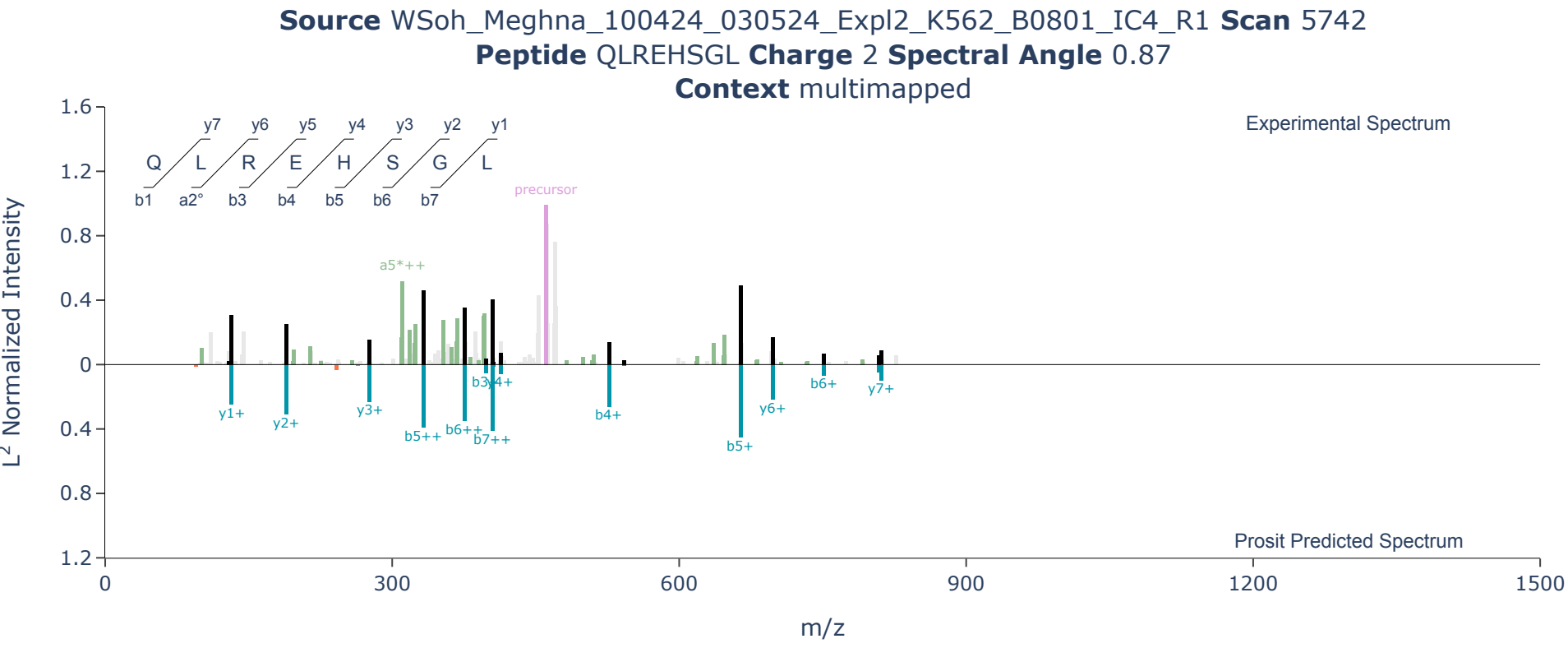


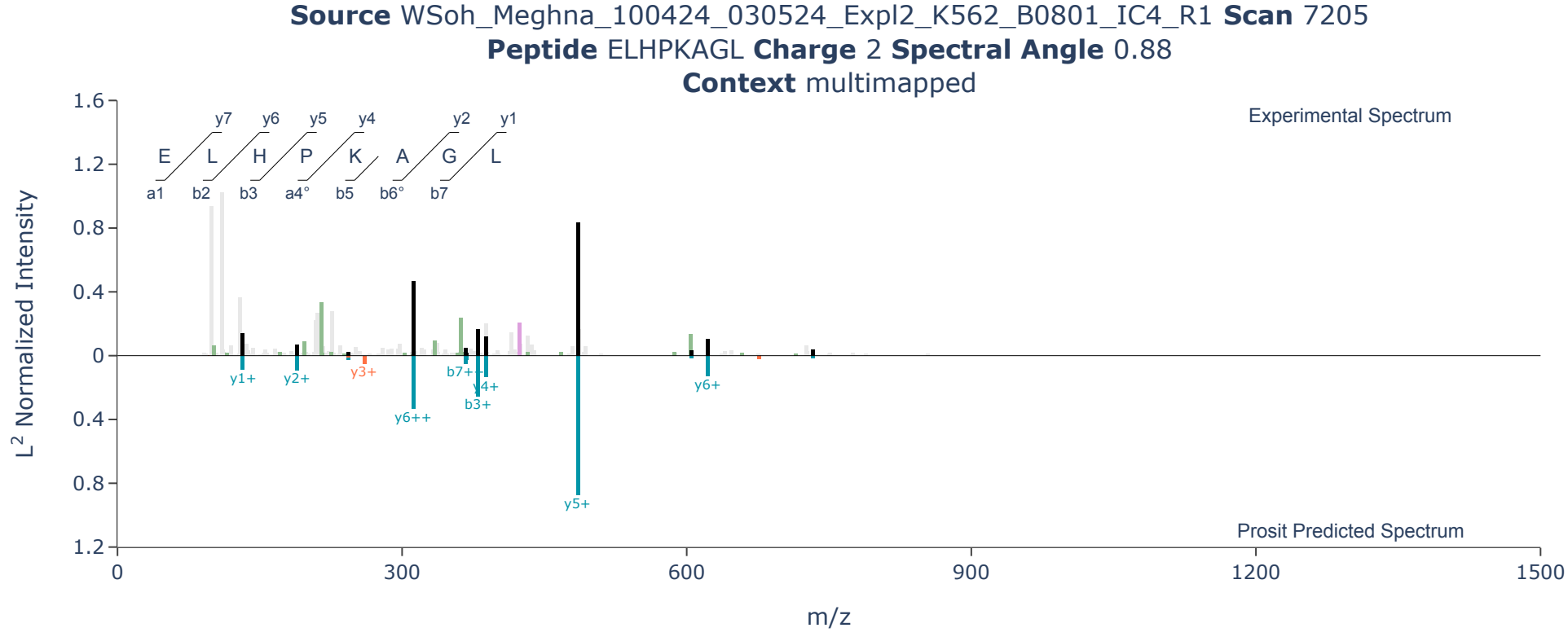
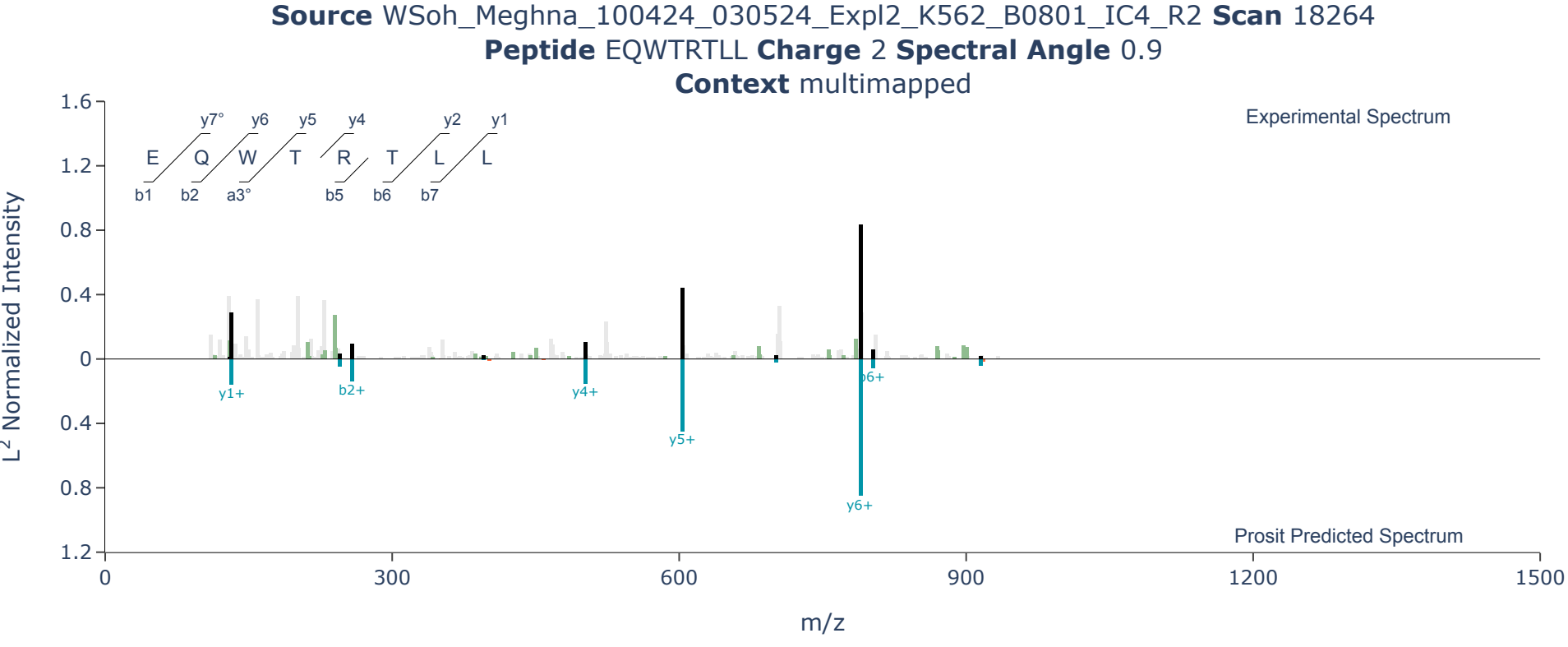
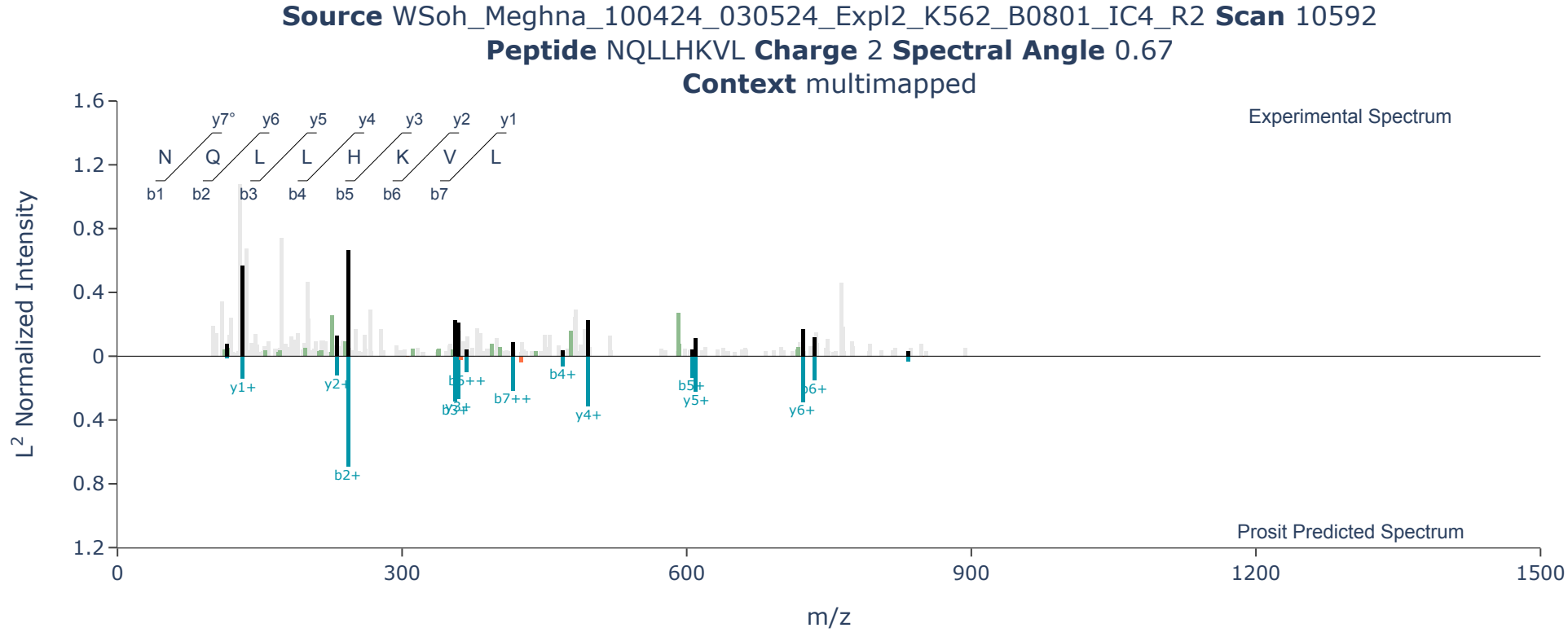
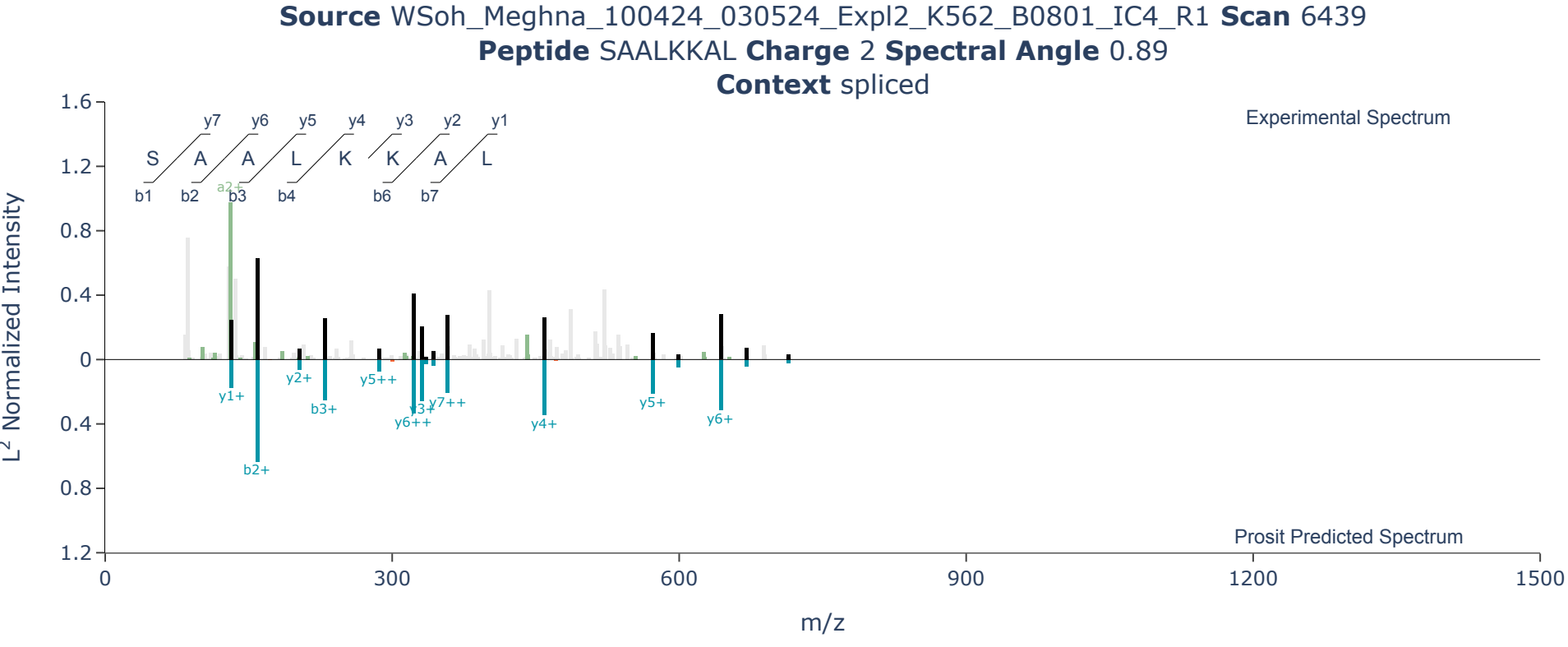
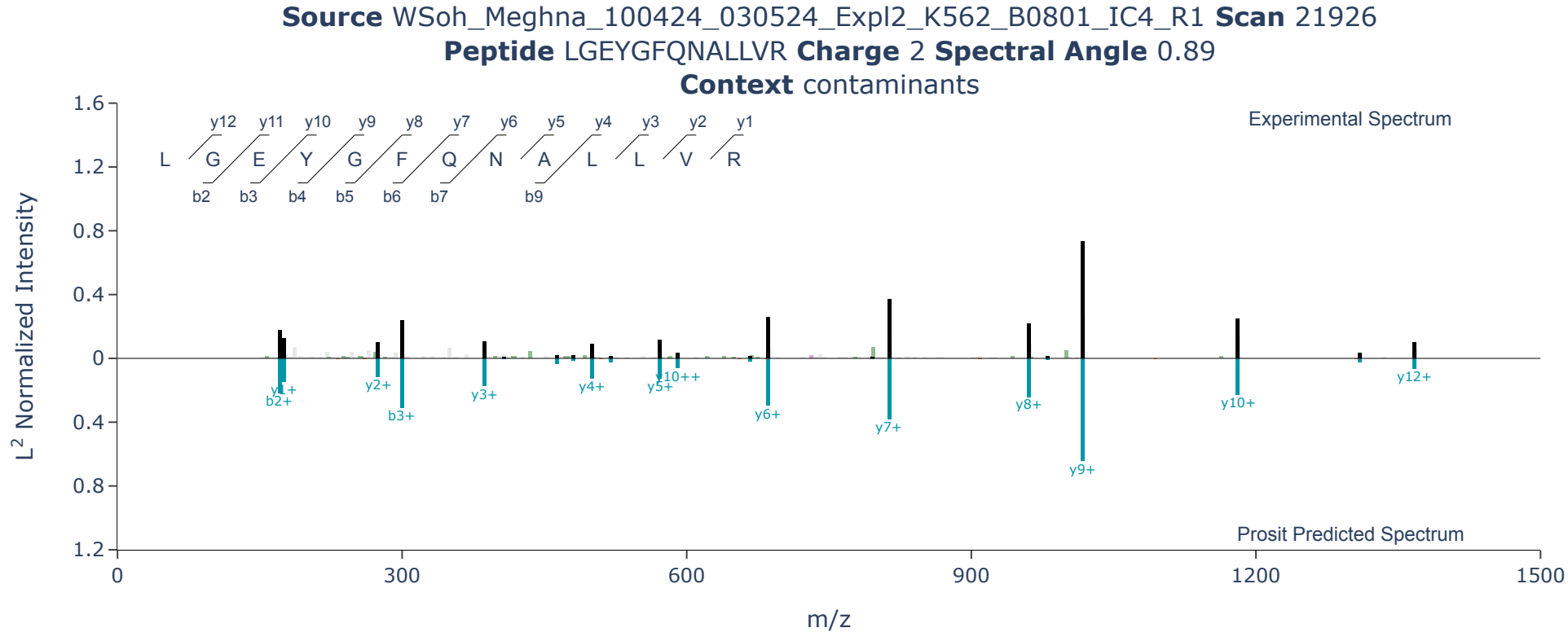
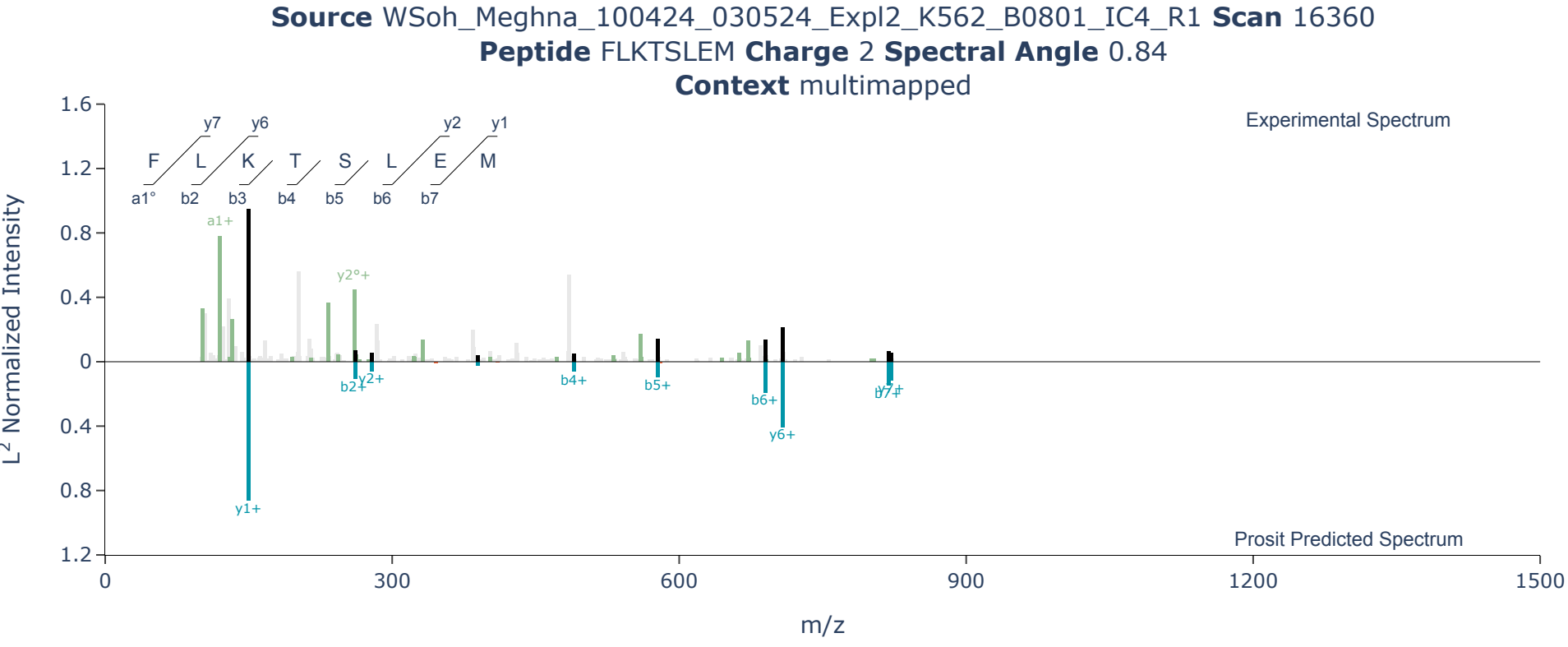
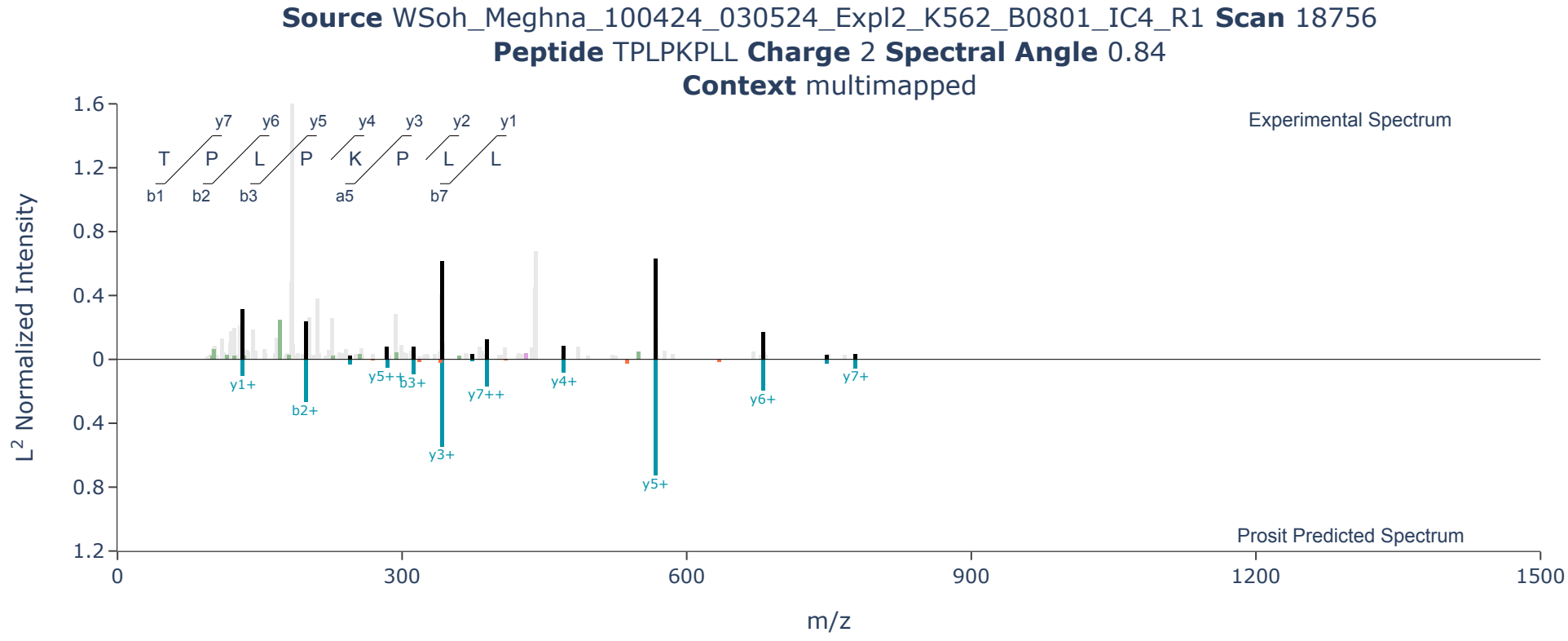
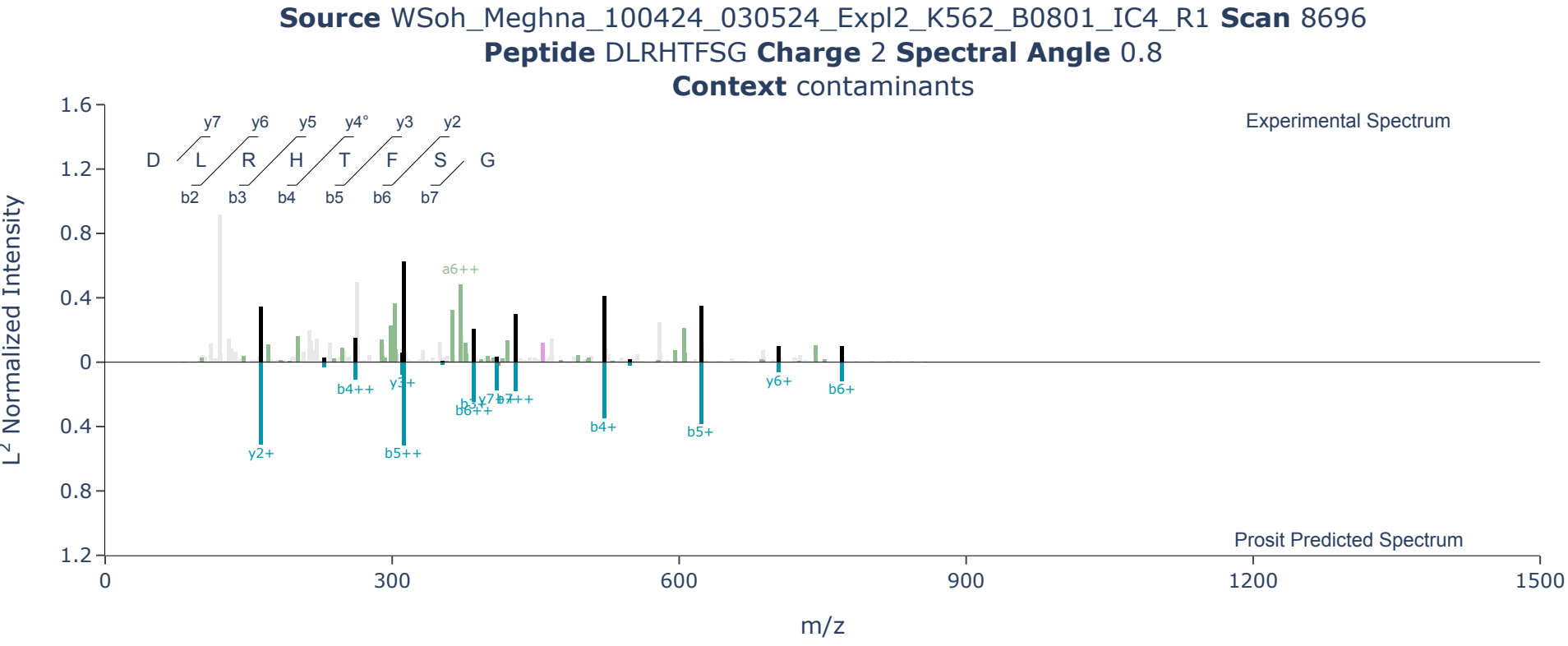
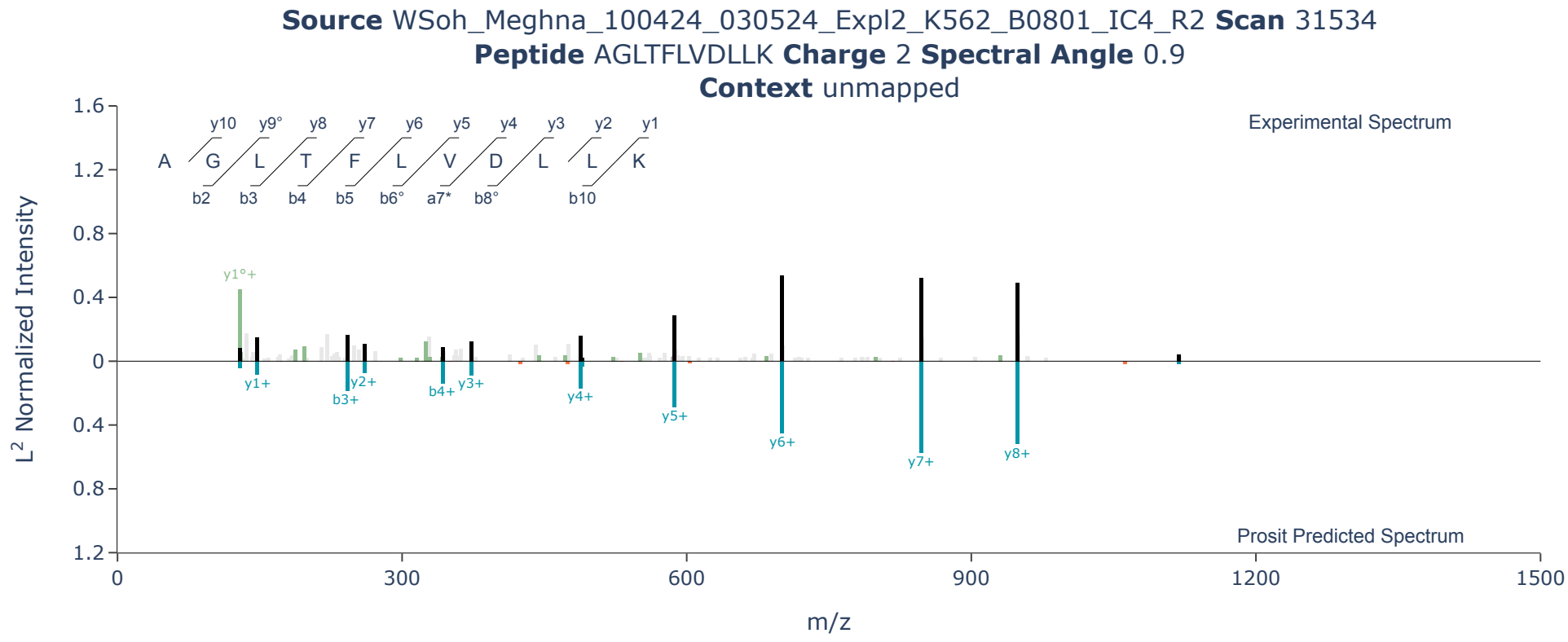
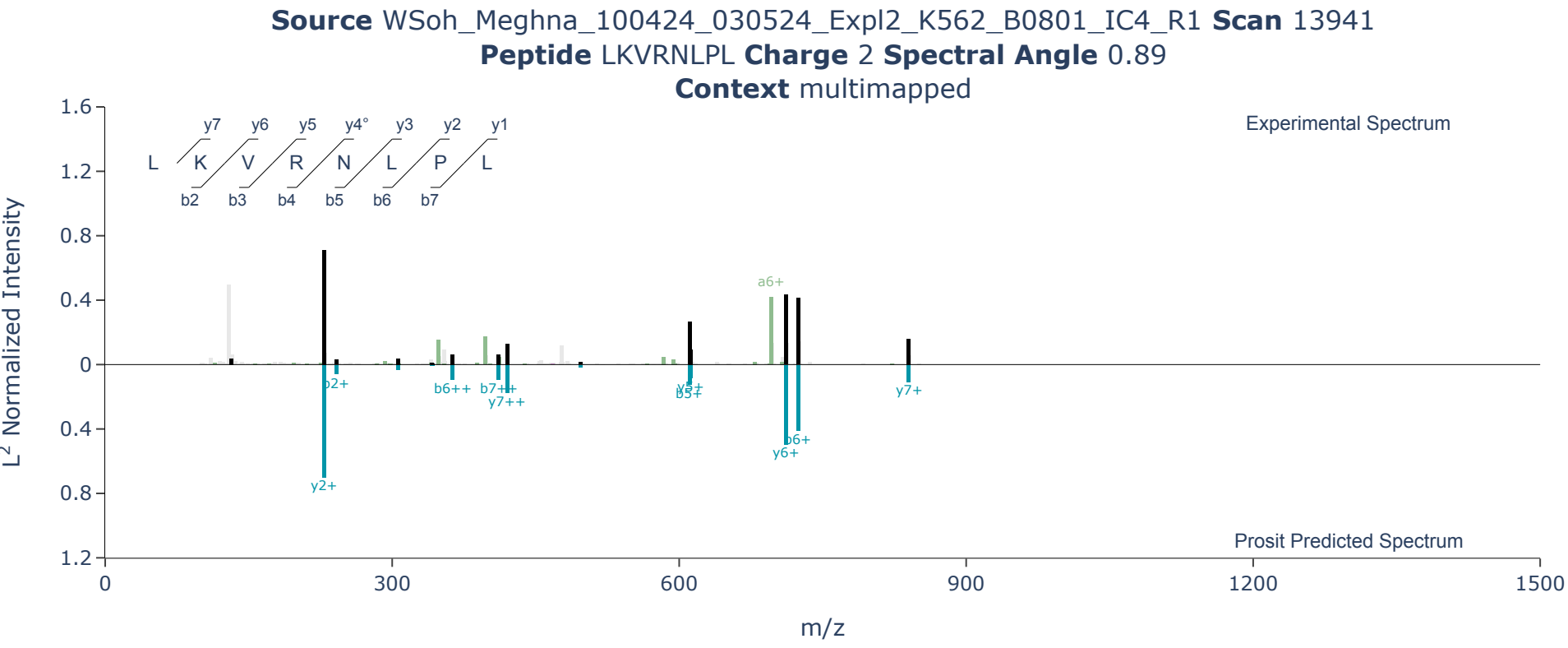
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Peptide NLLTHSEL Charge 2 Spectral Angle 0.87

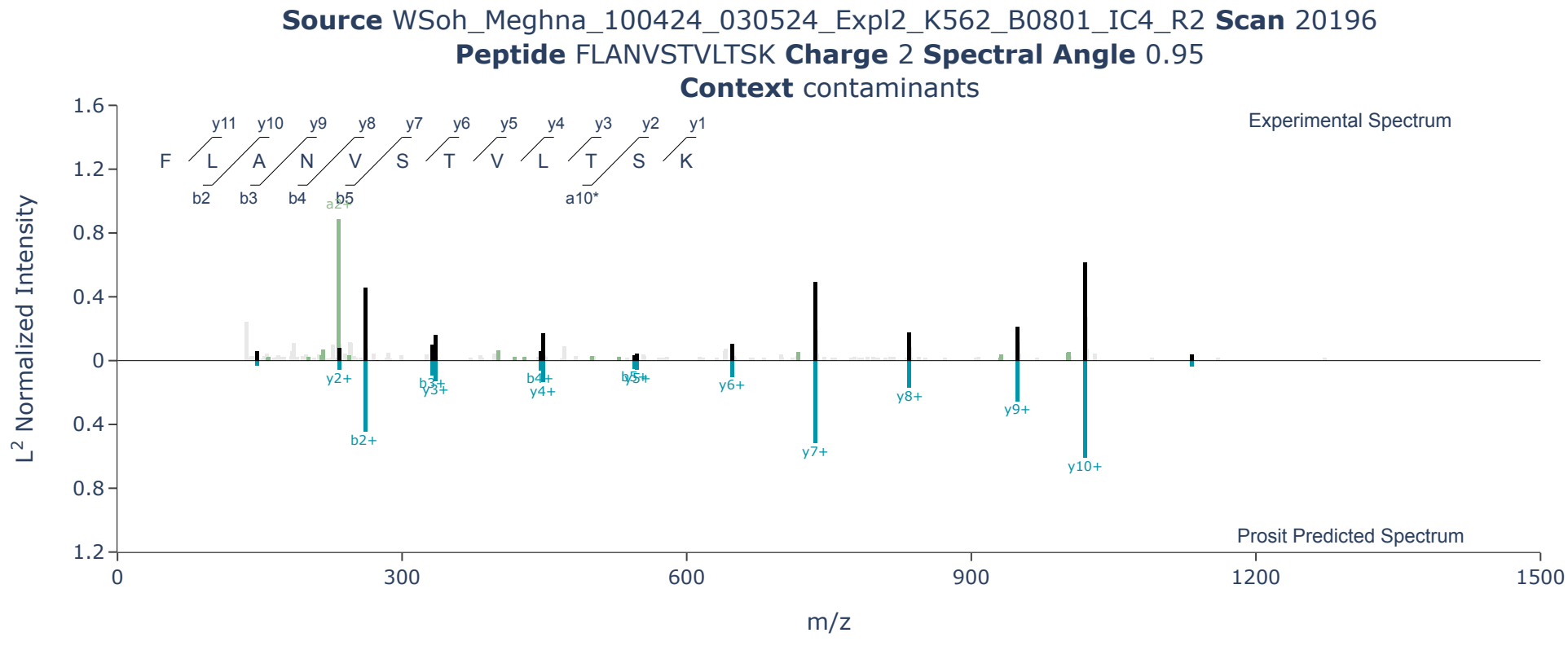
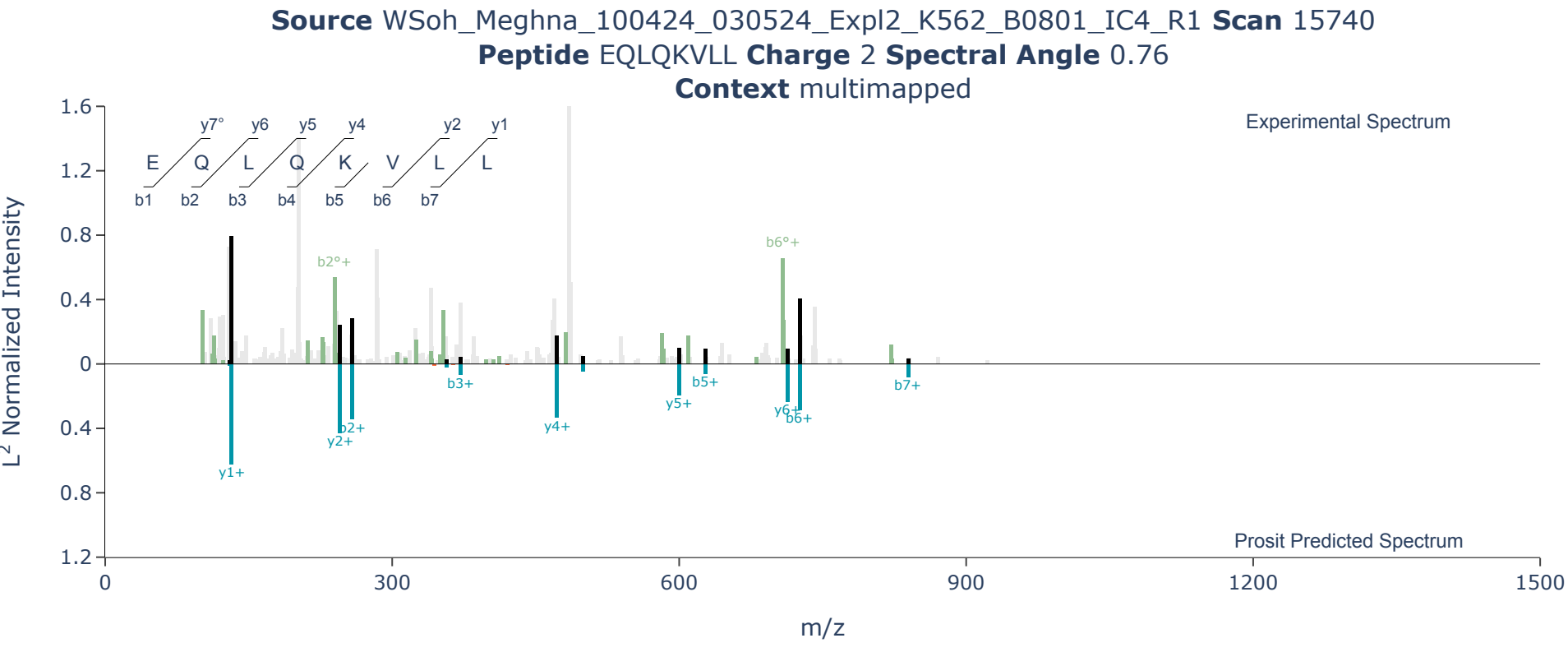
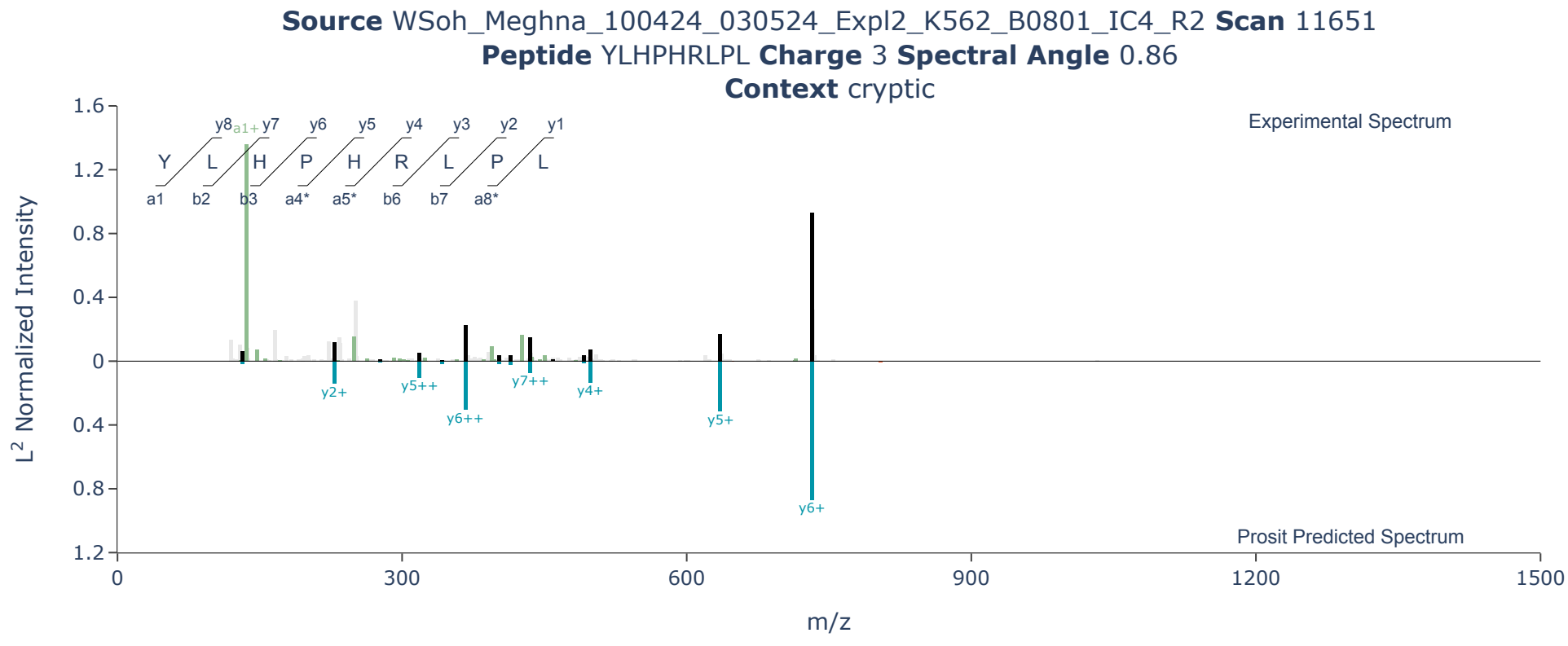
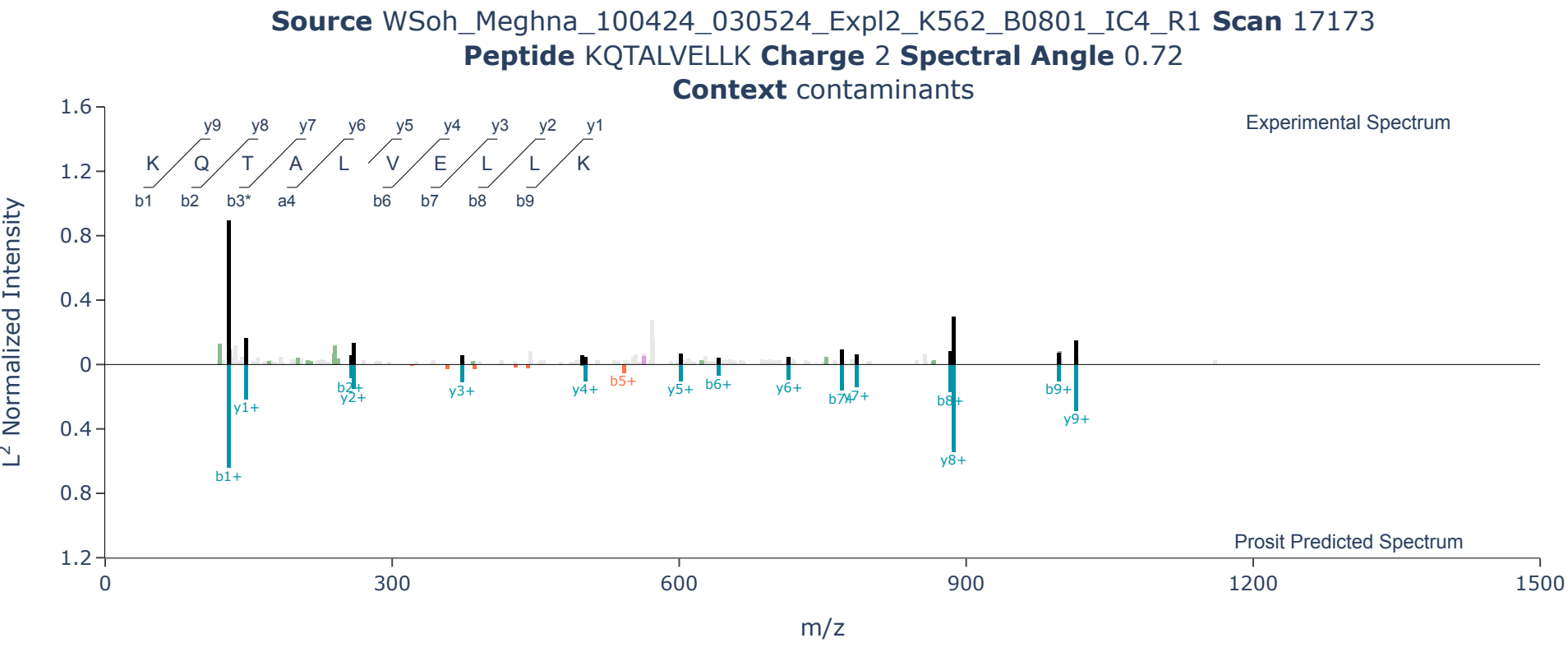
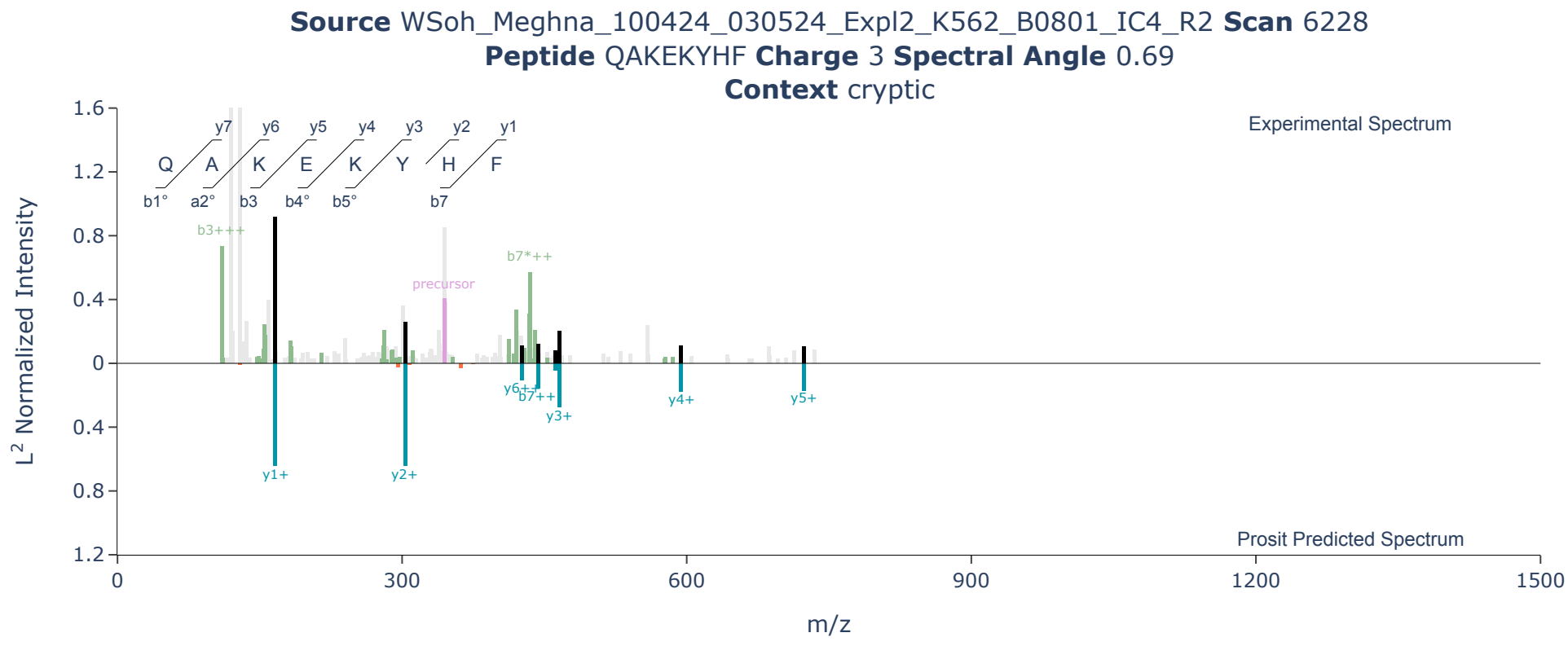
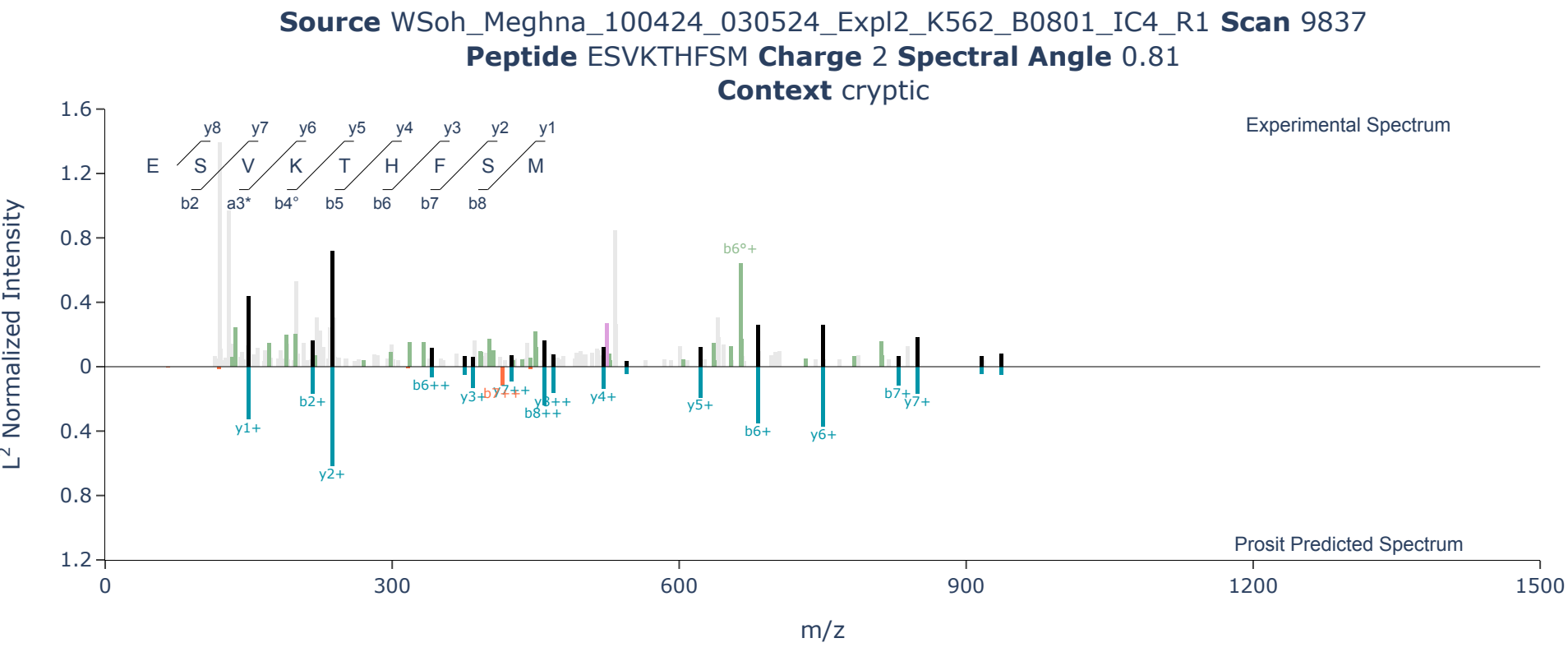
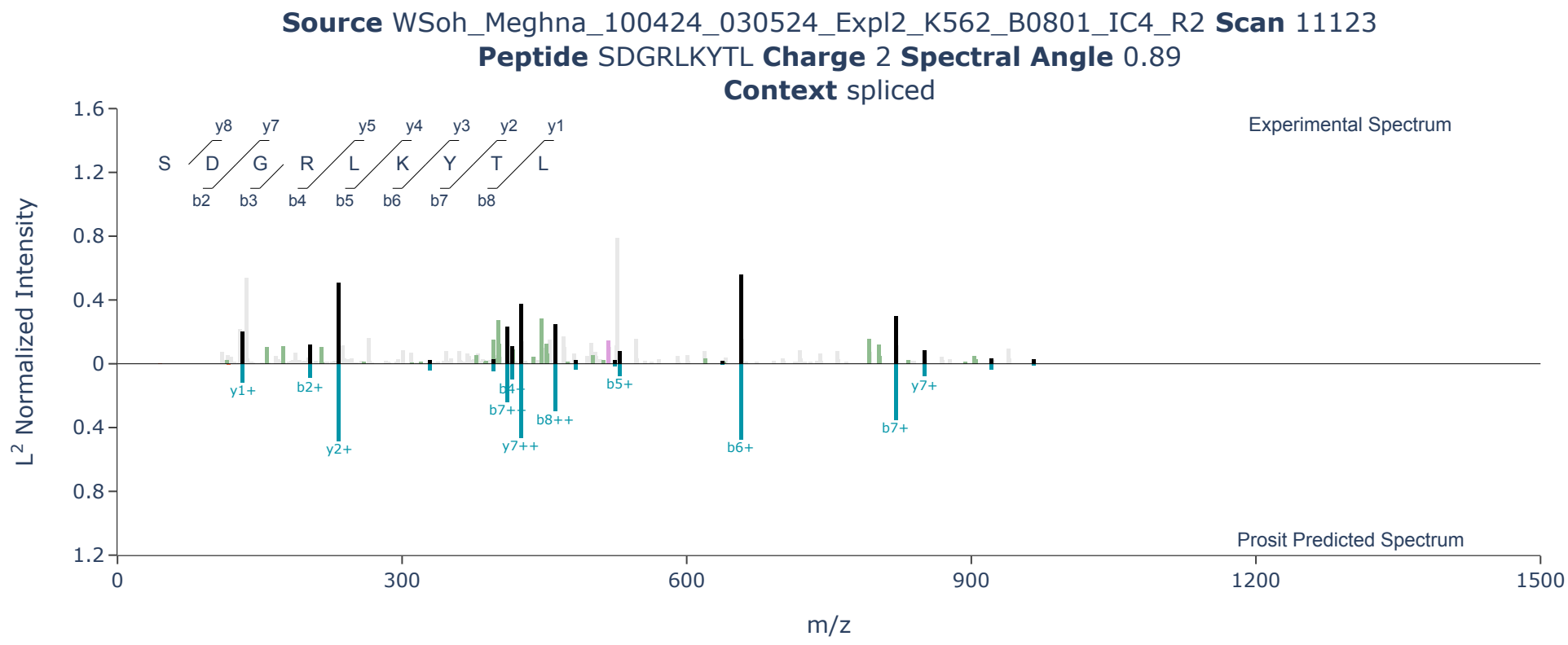
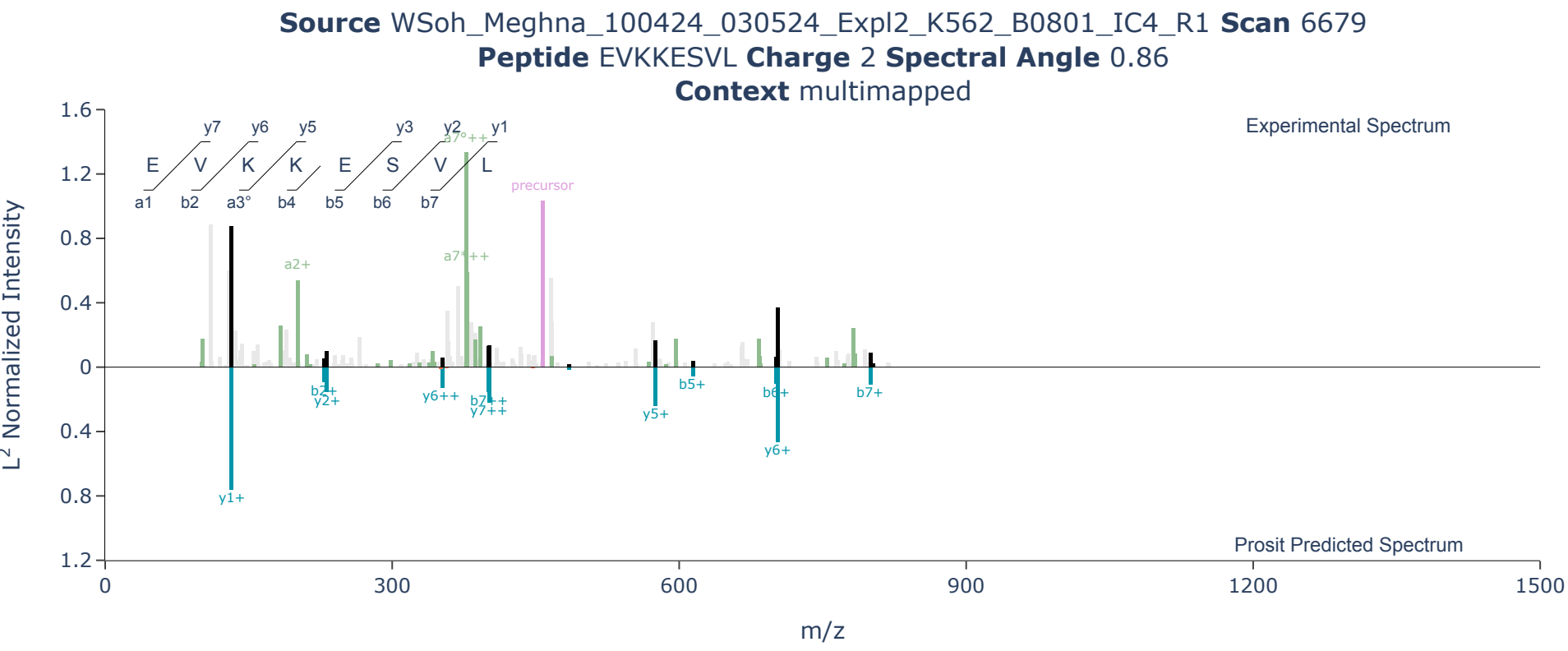
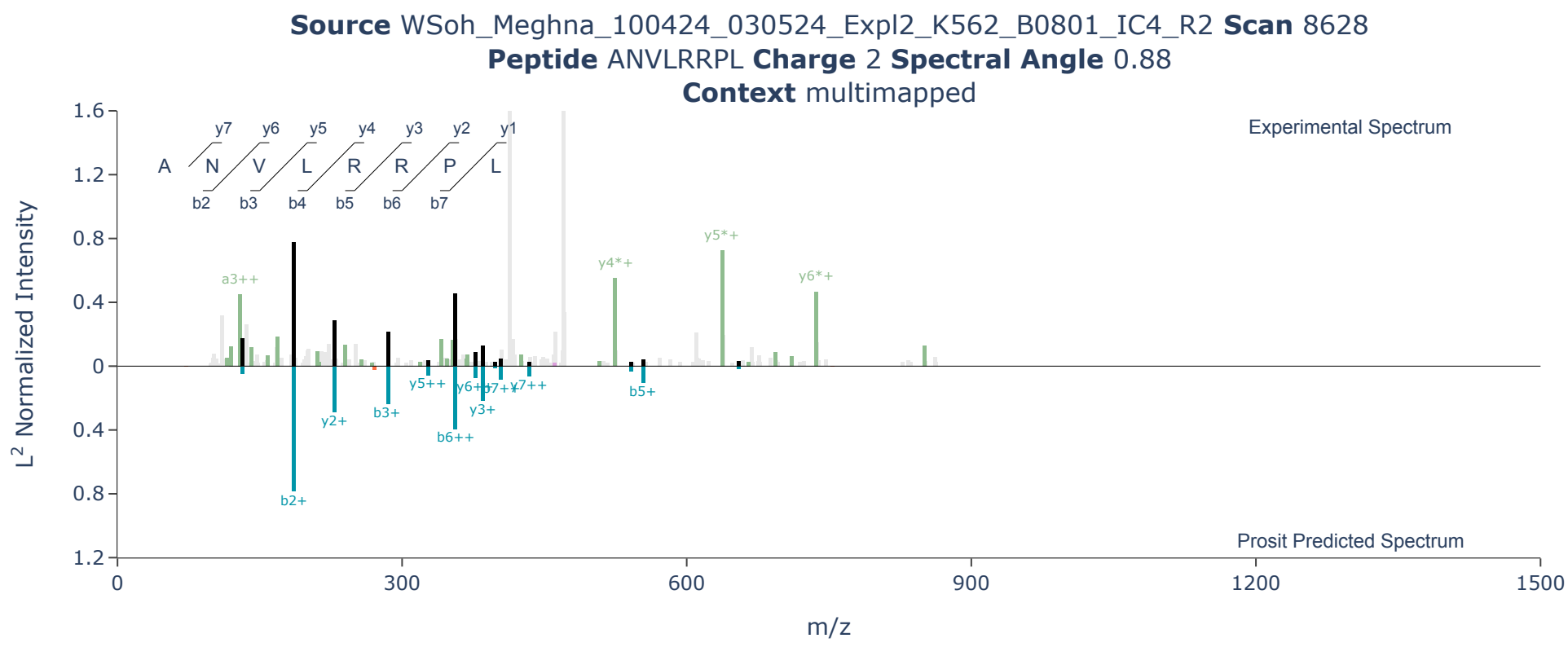
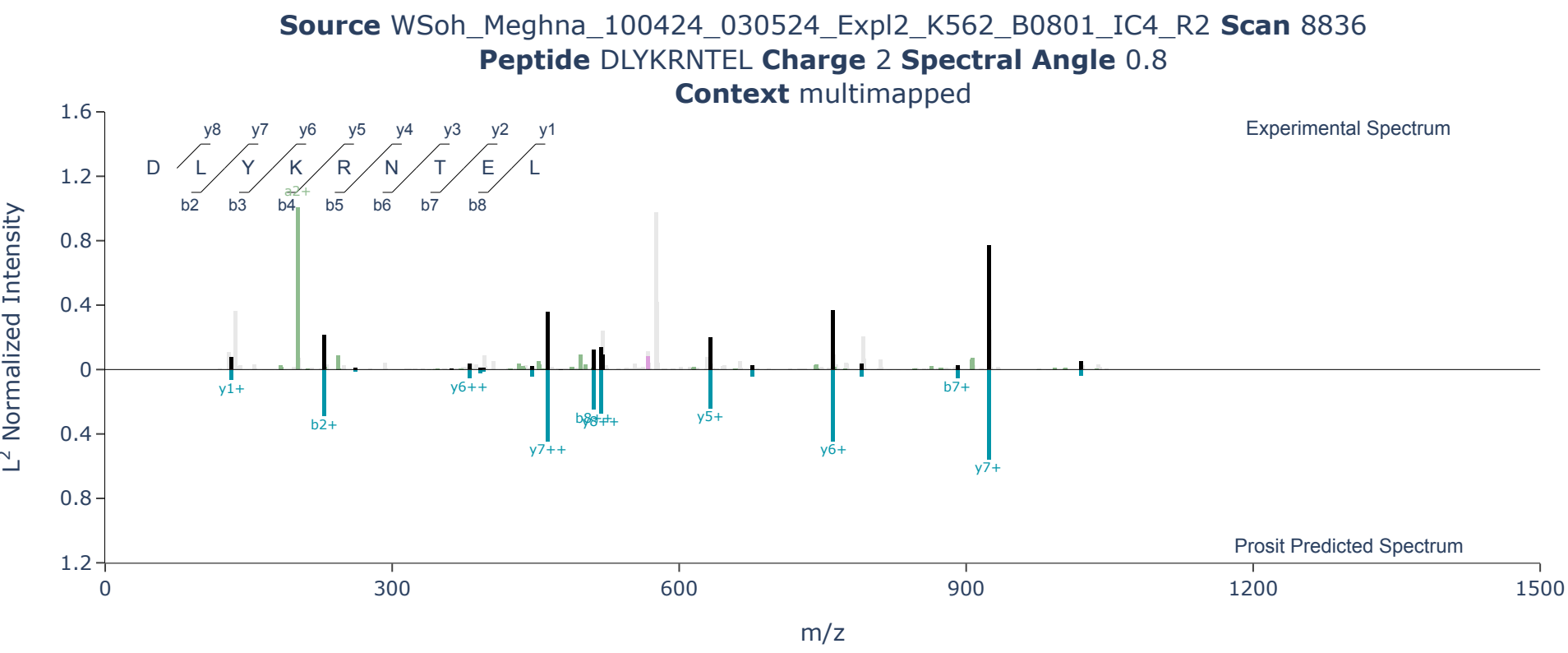


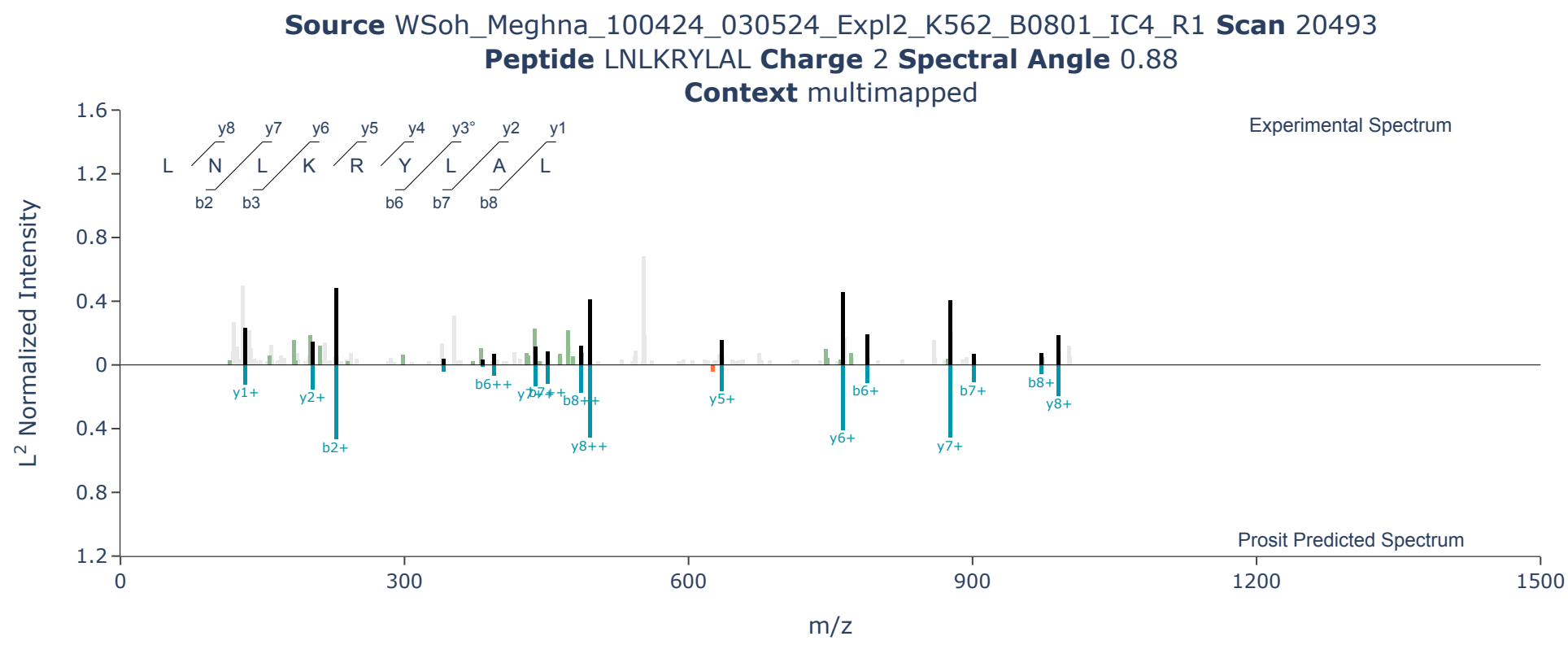
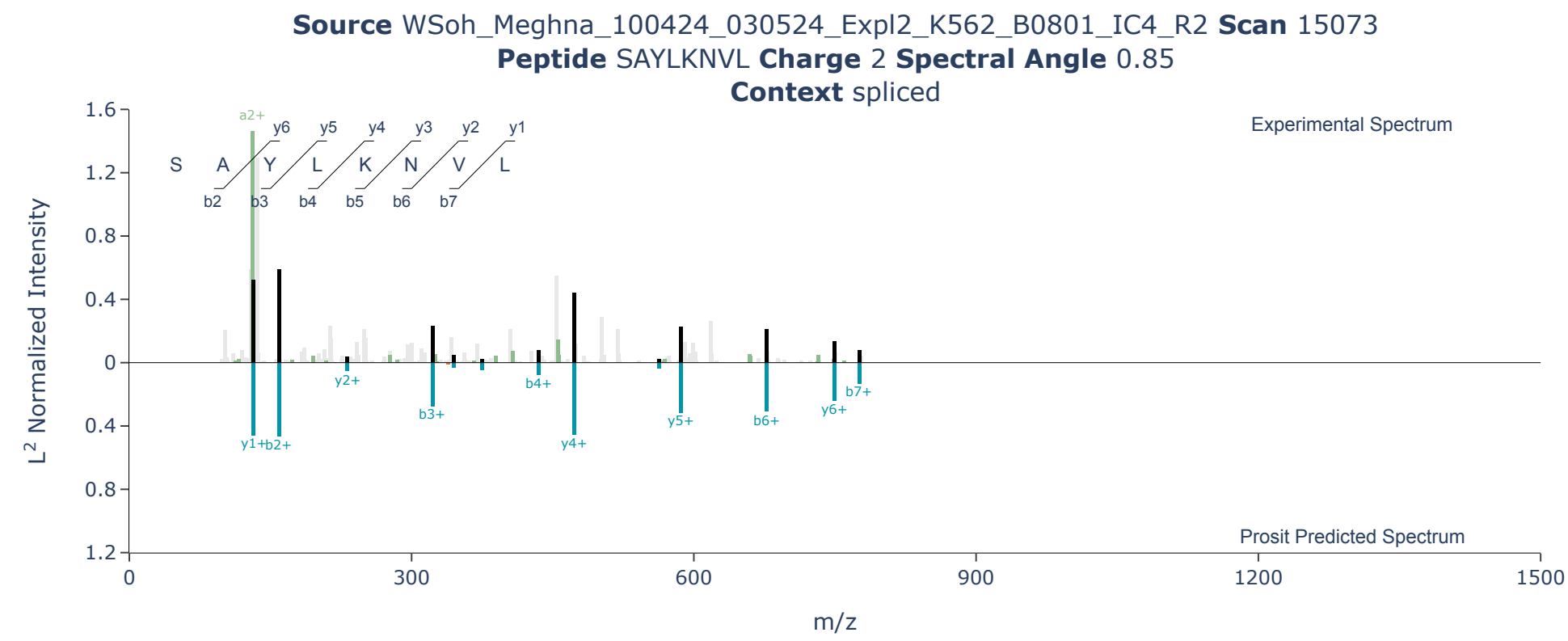
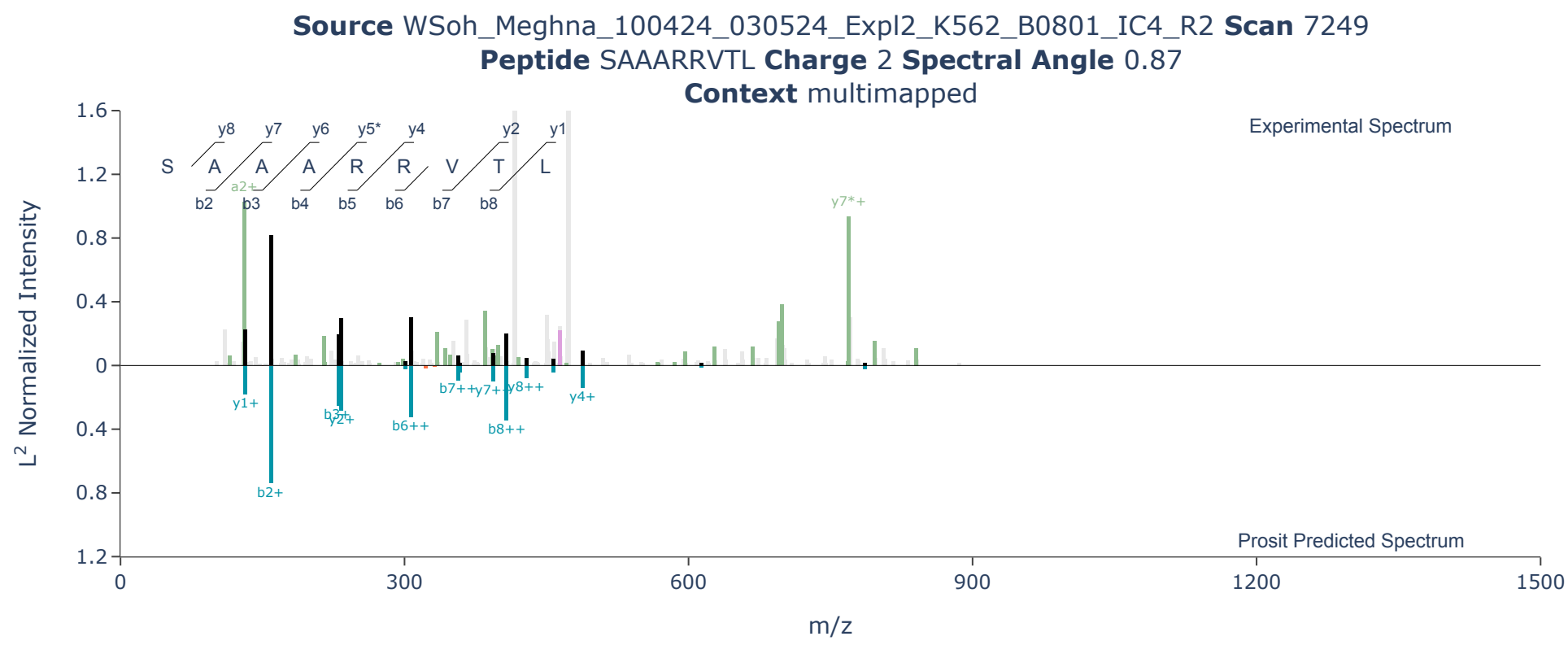
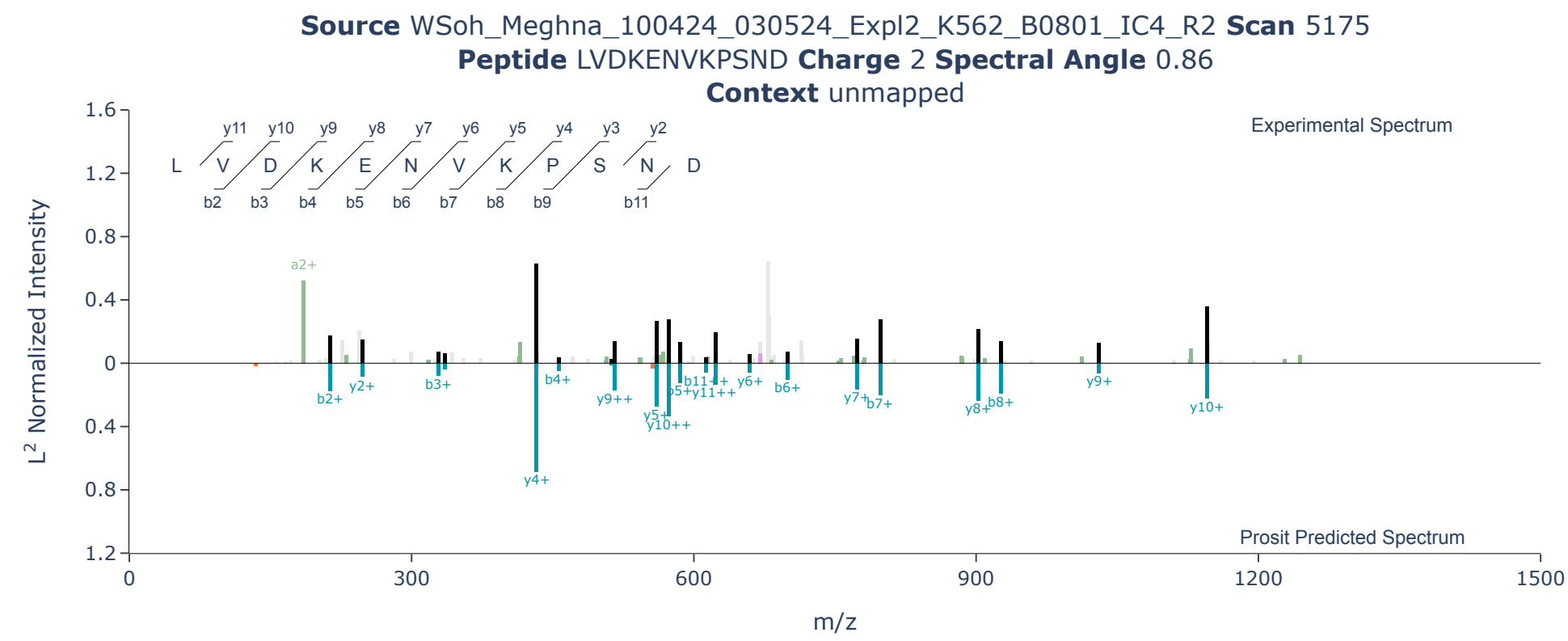
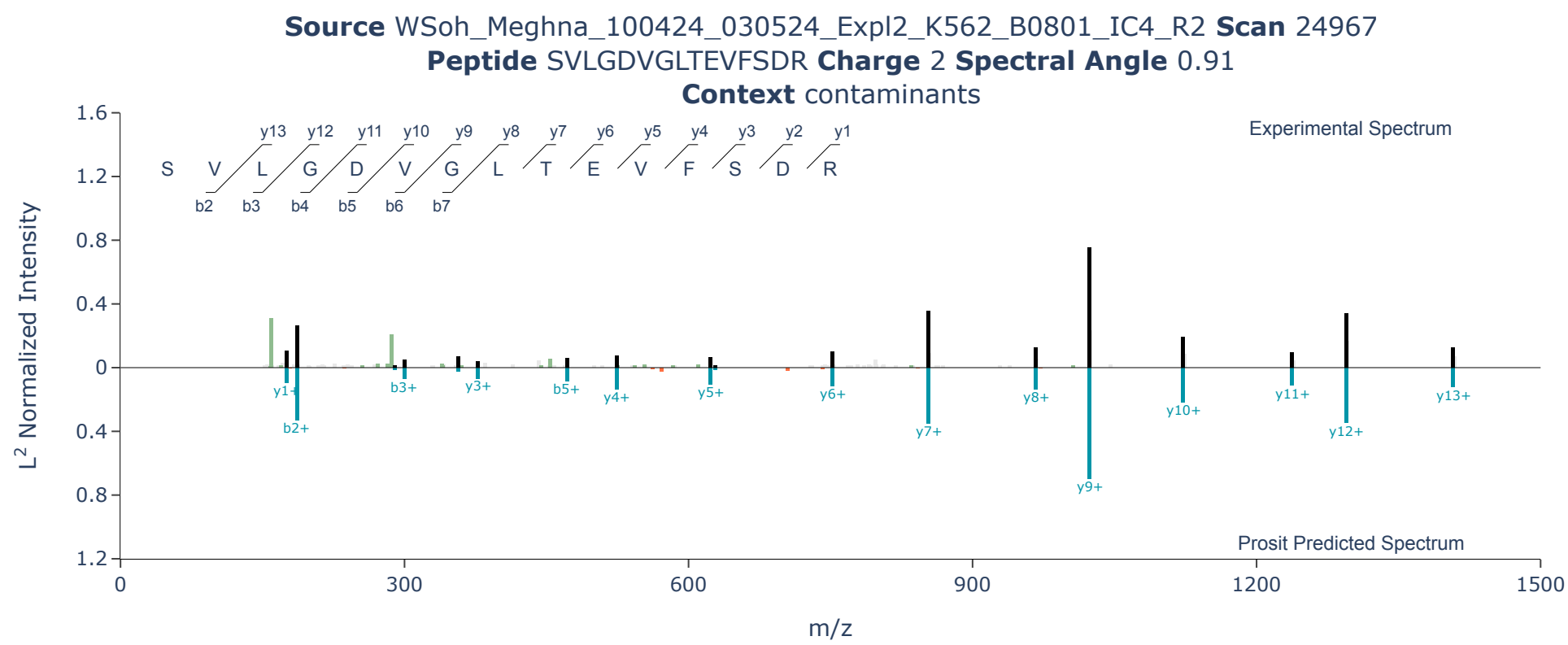
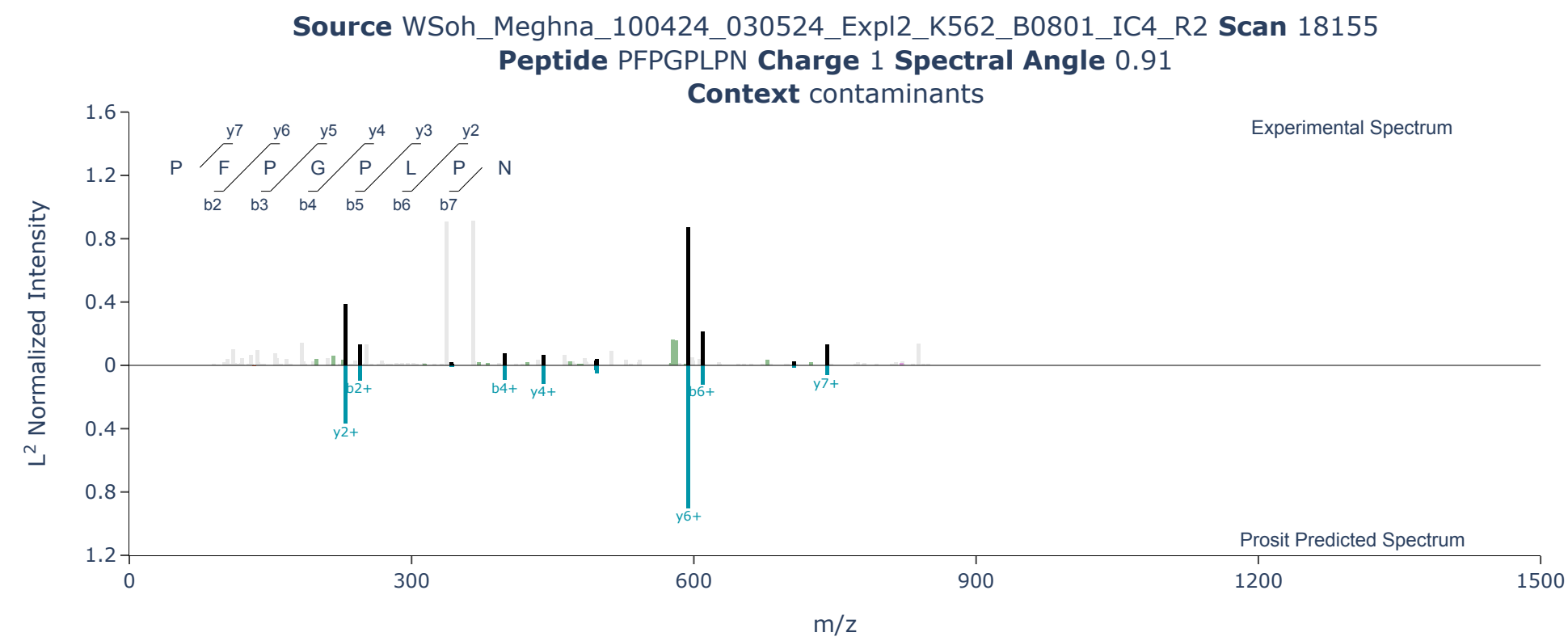
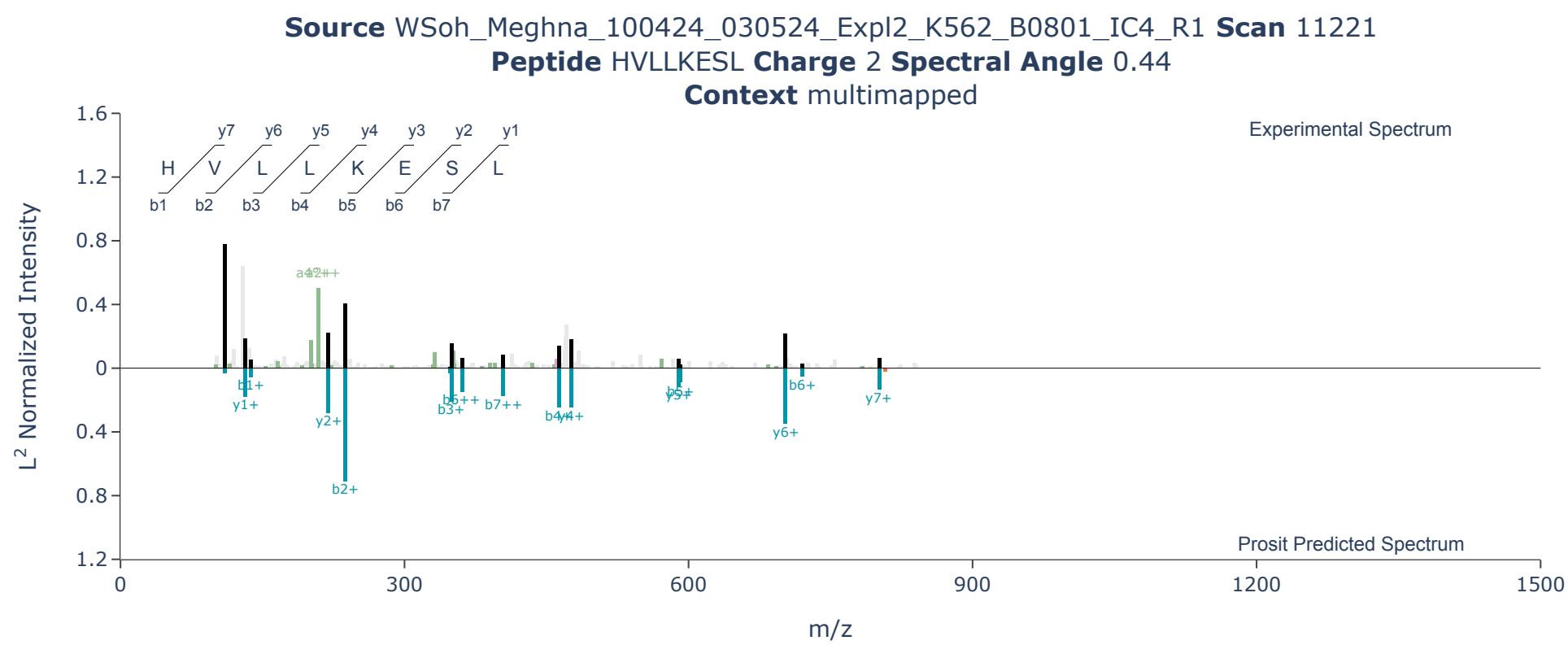
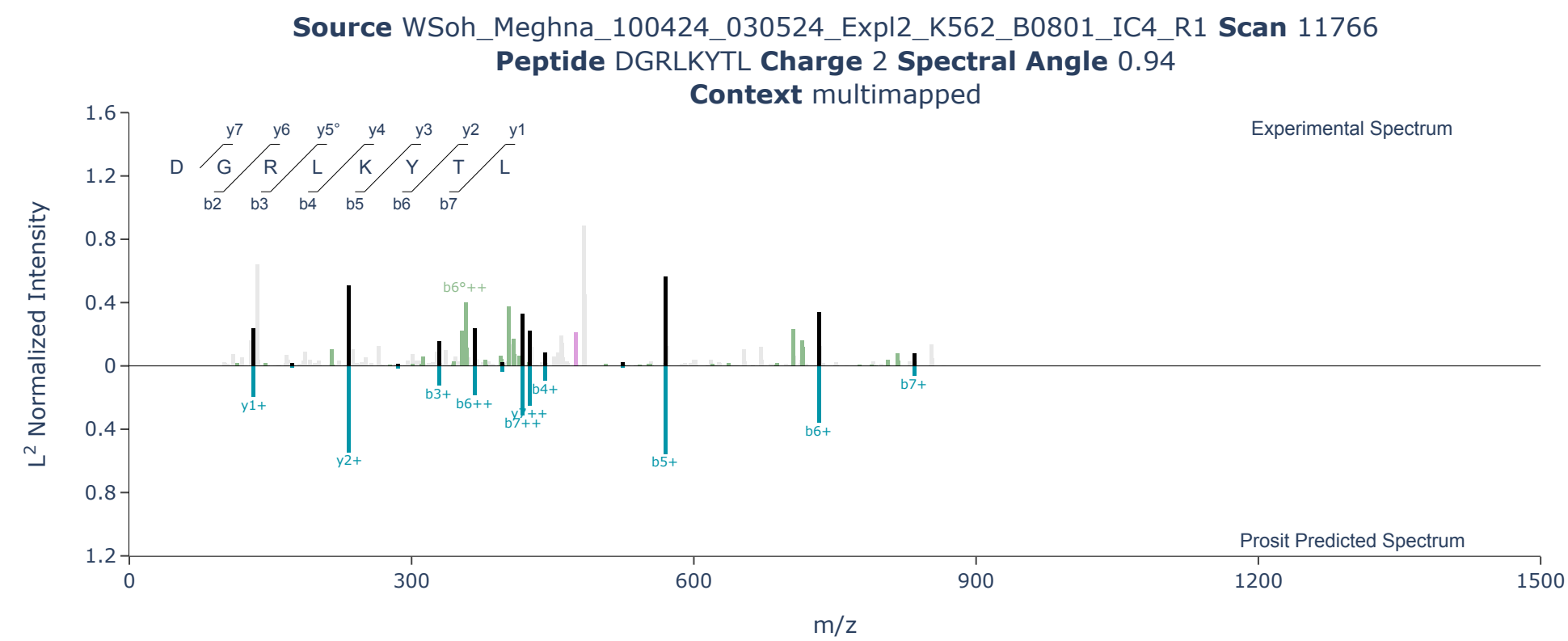
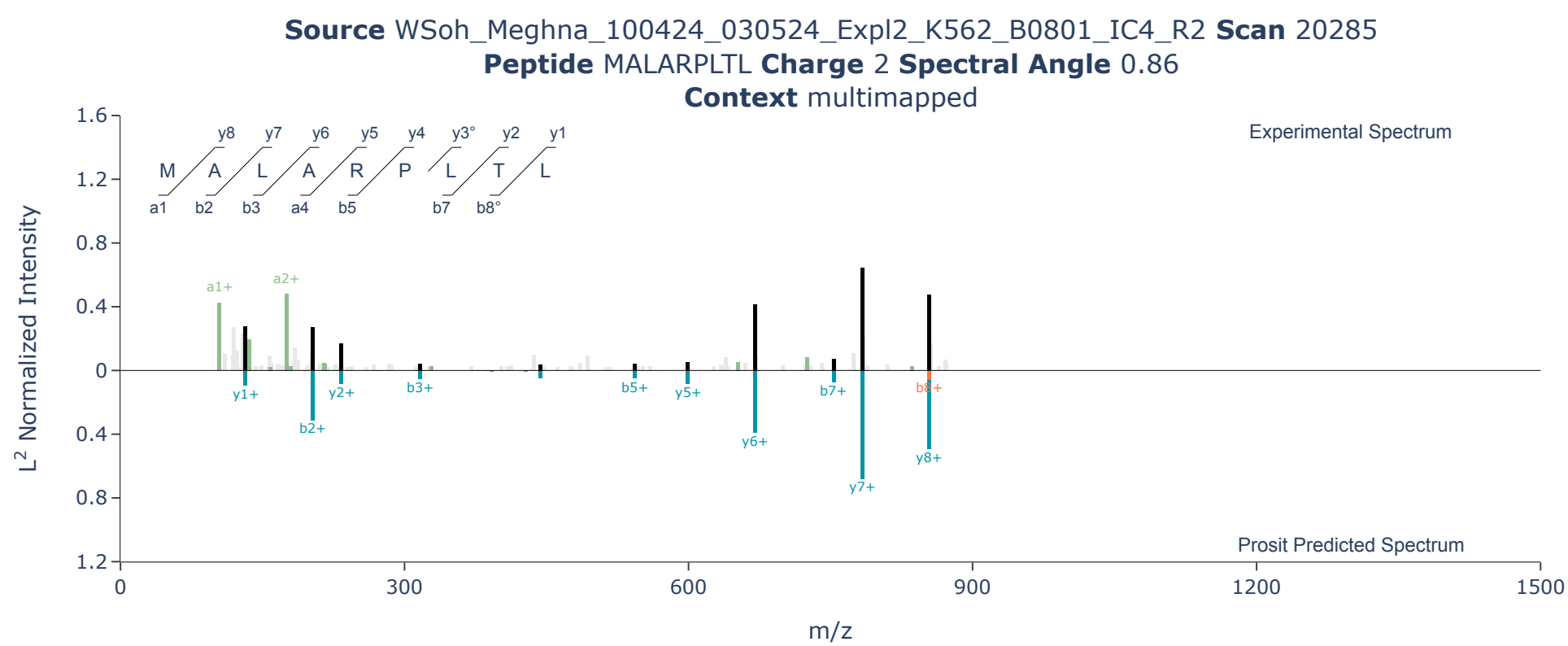
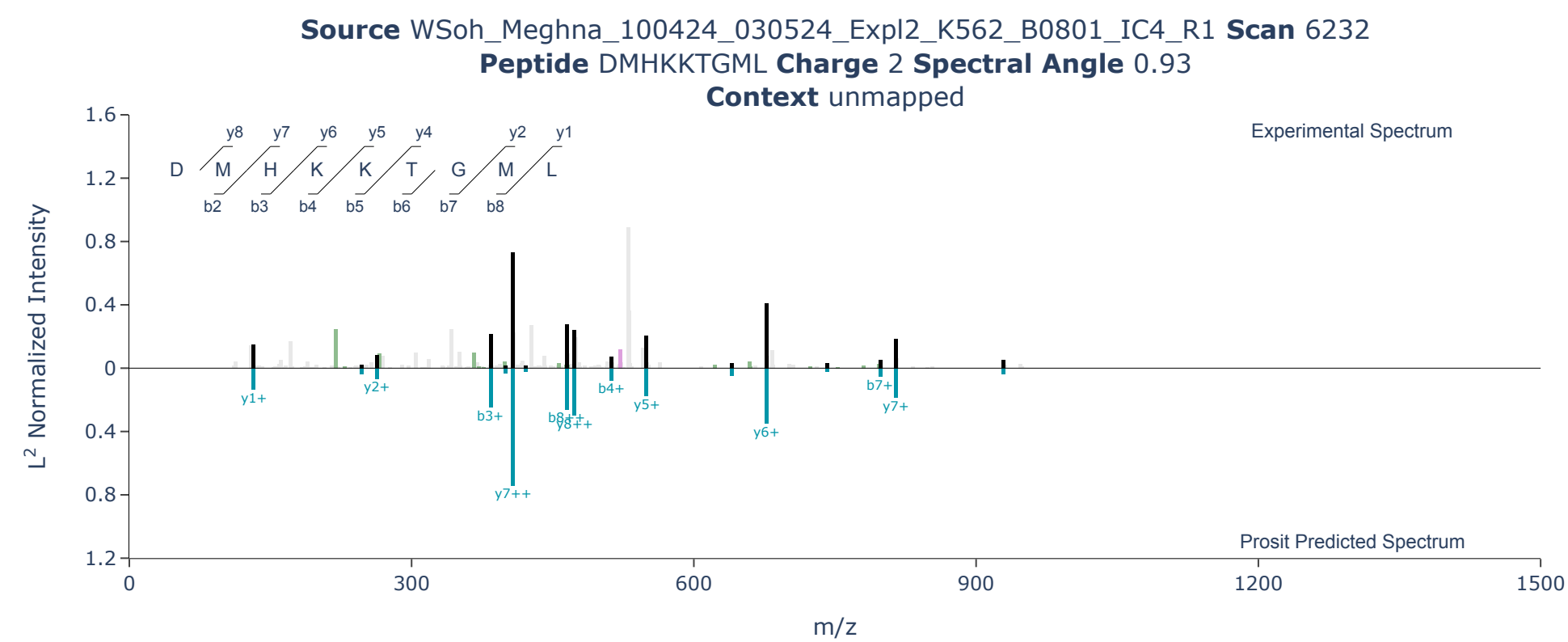
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R1 Scan 13957
Peptide LKVKVLSM Charge 2 Spectral Angle 0.85

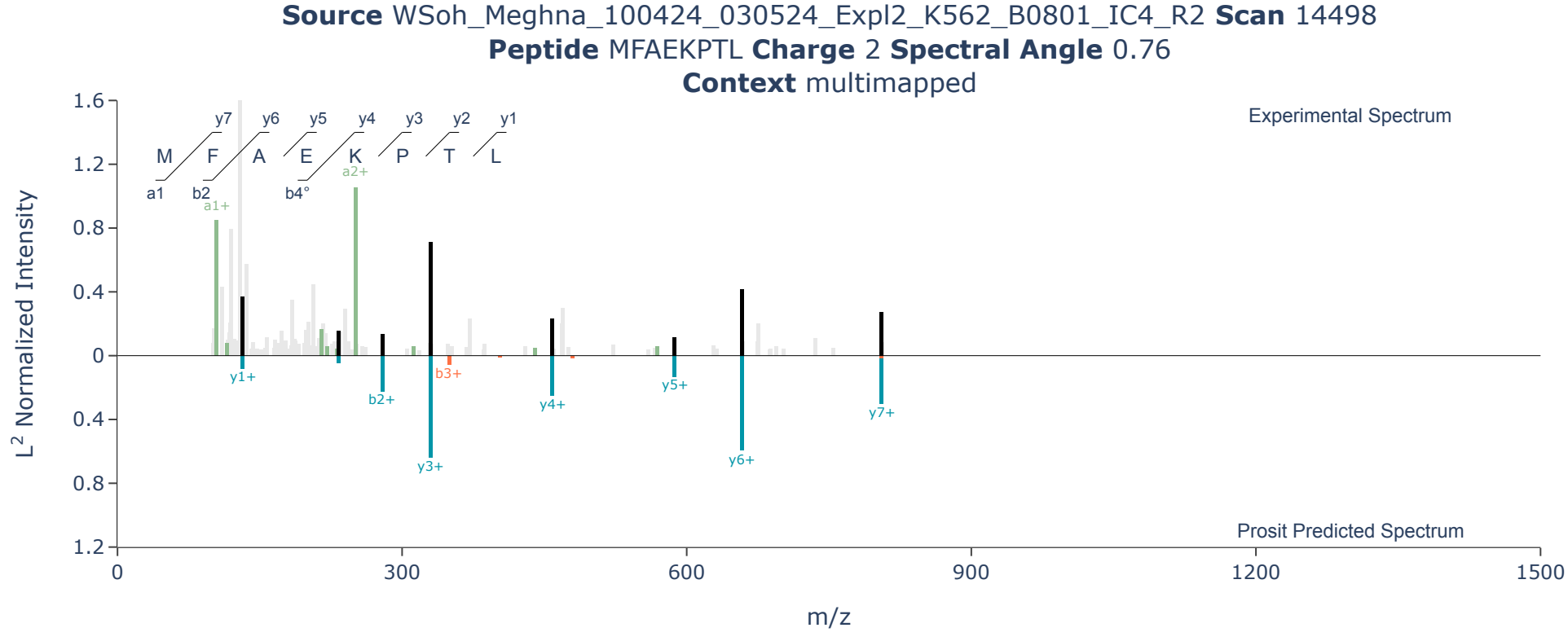
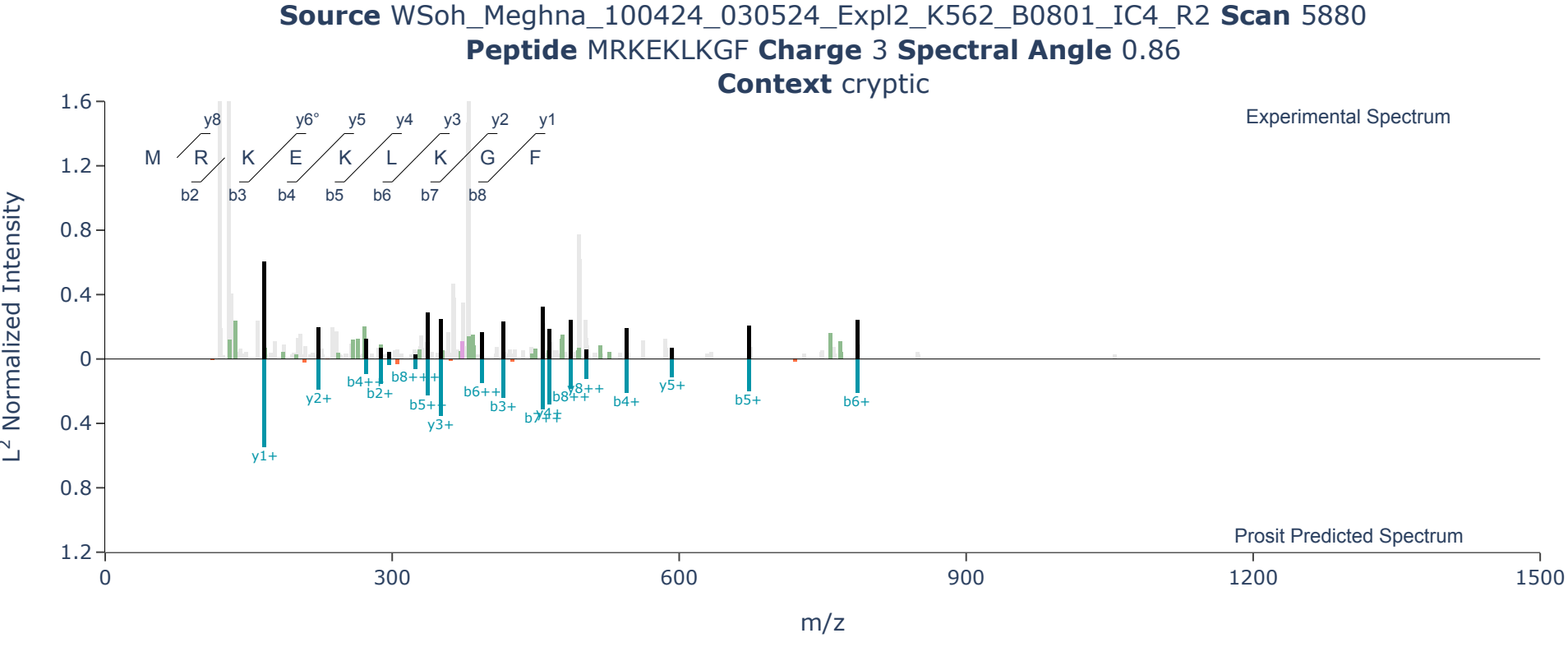
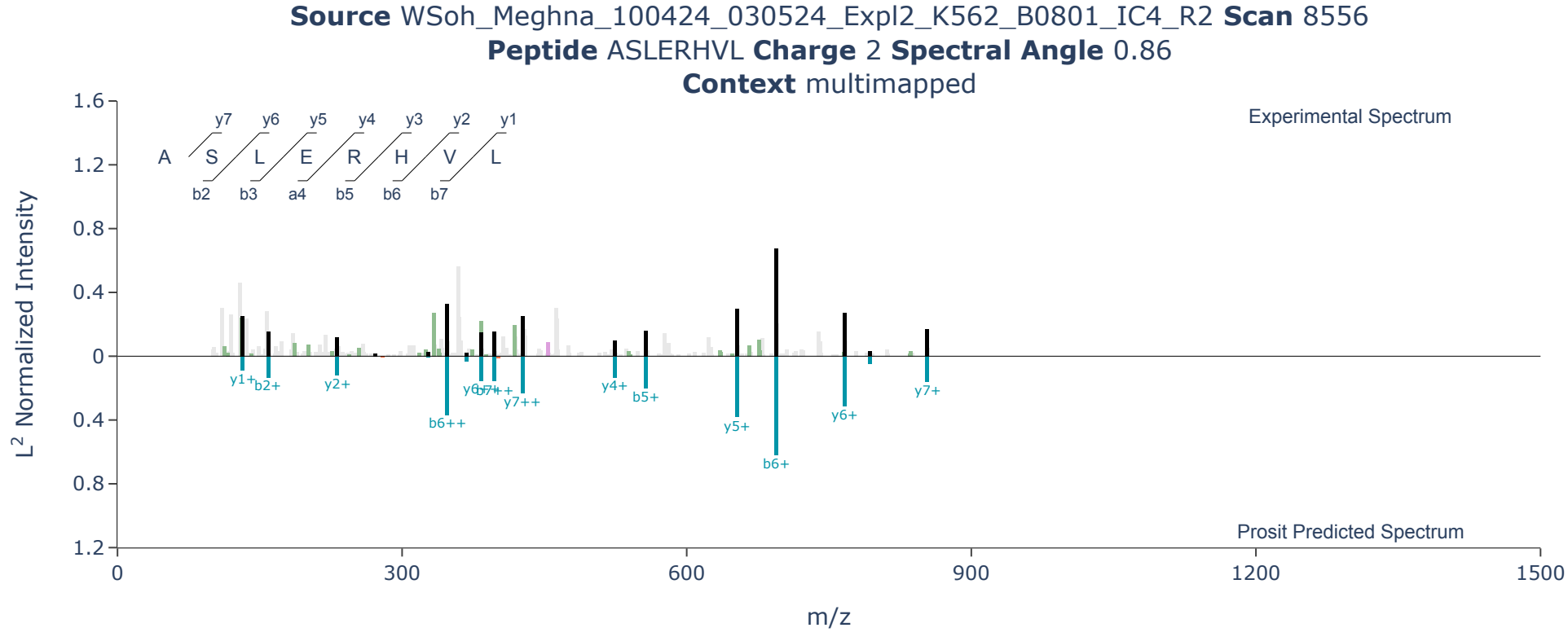
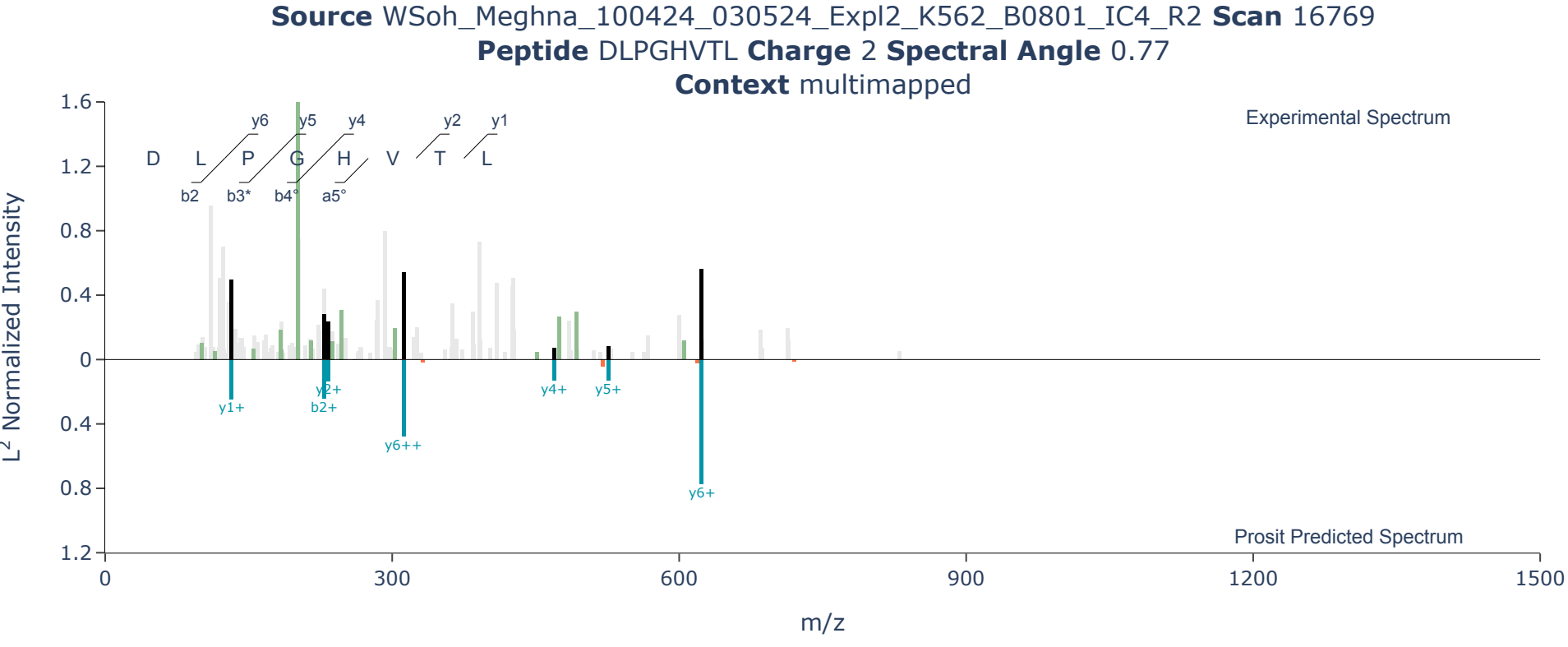
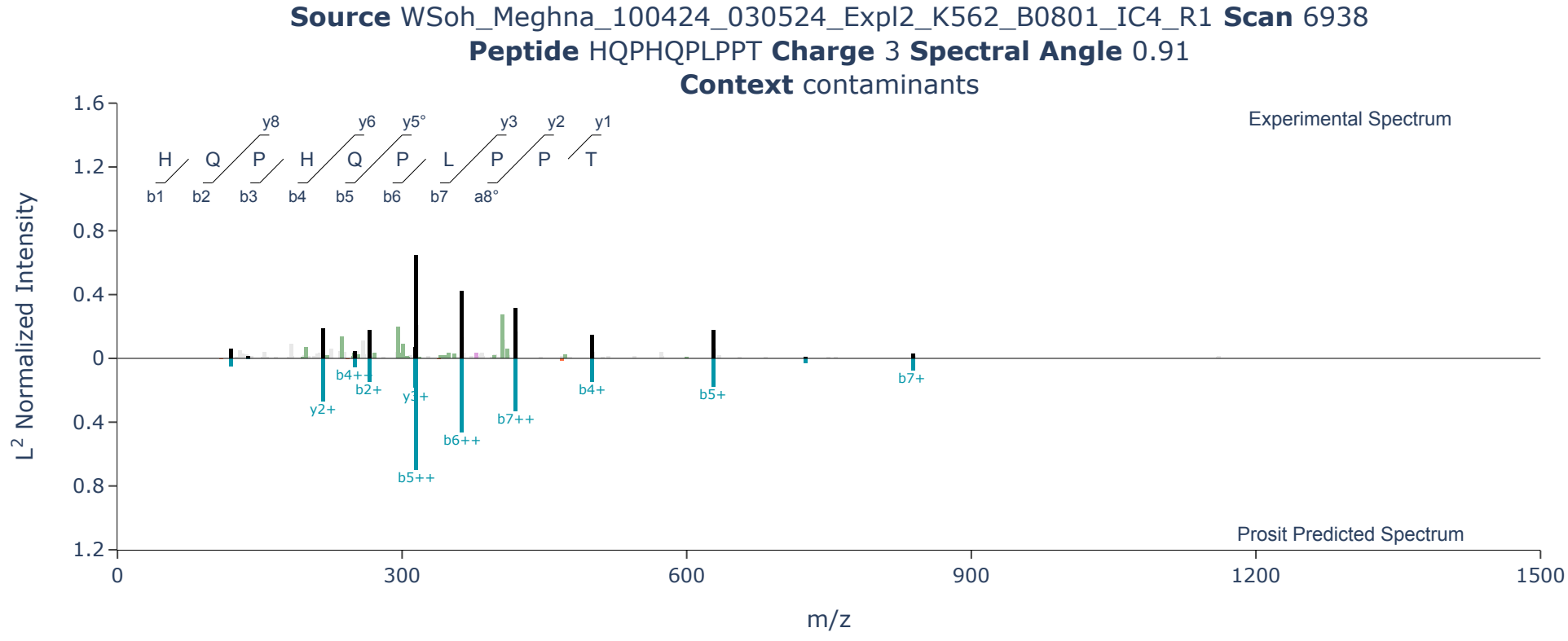
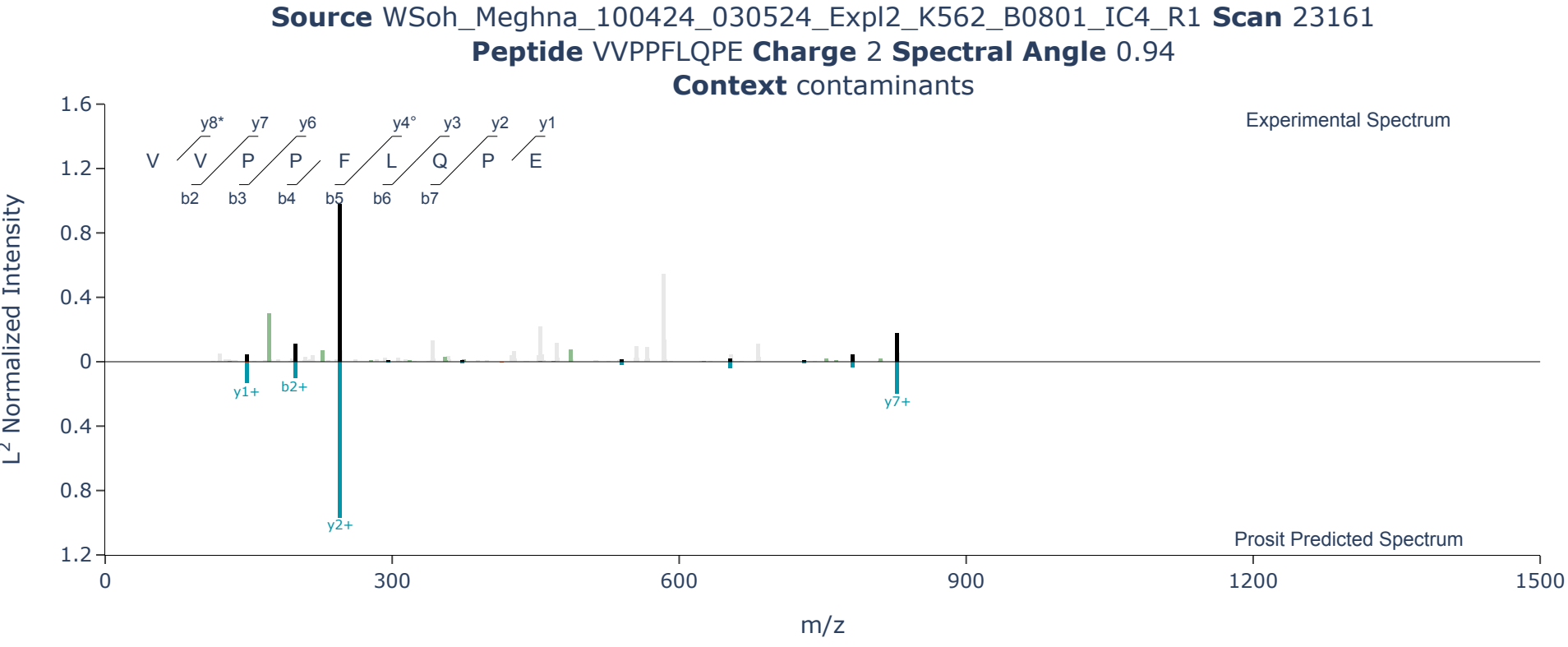
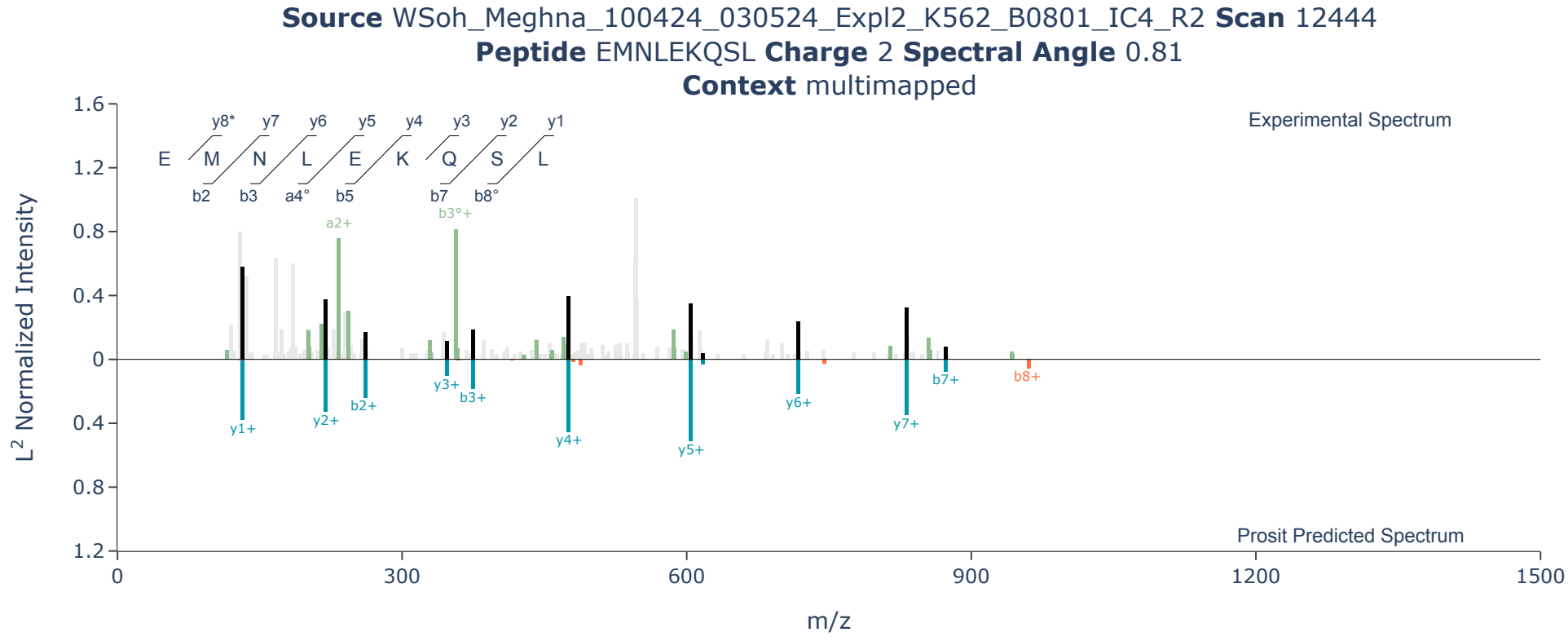
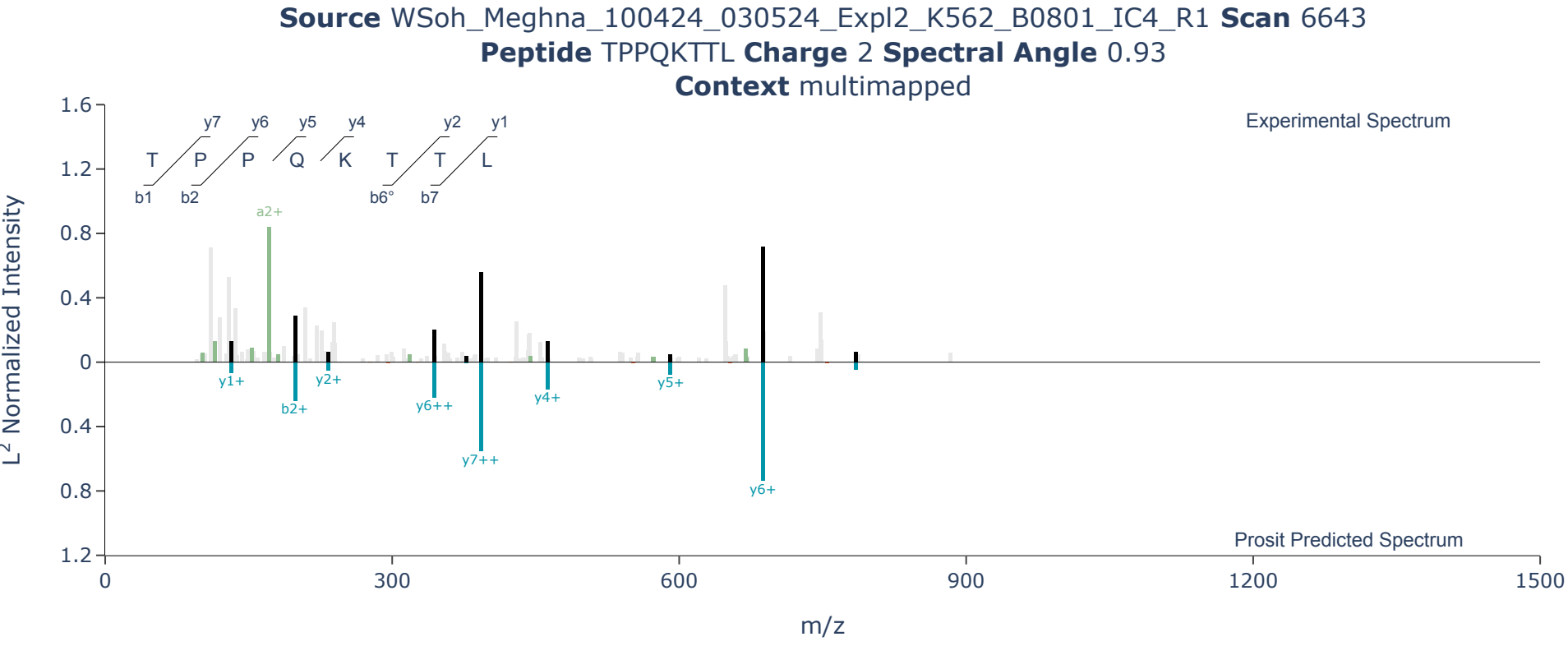
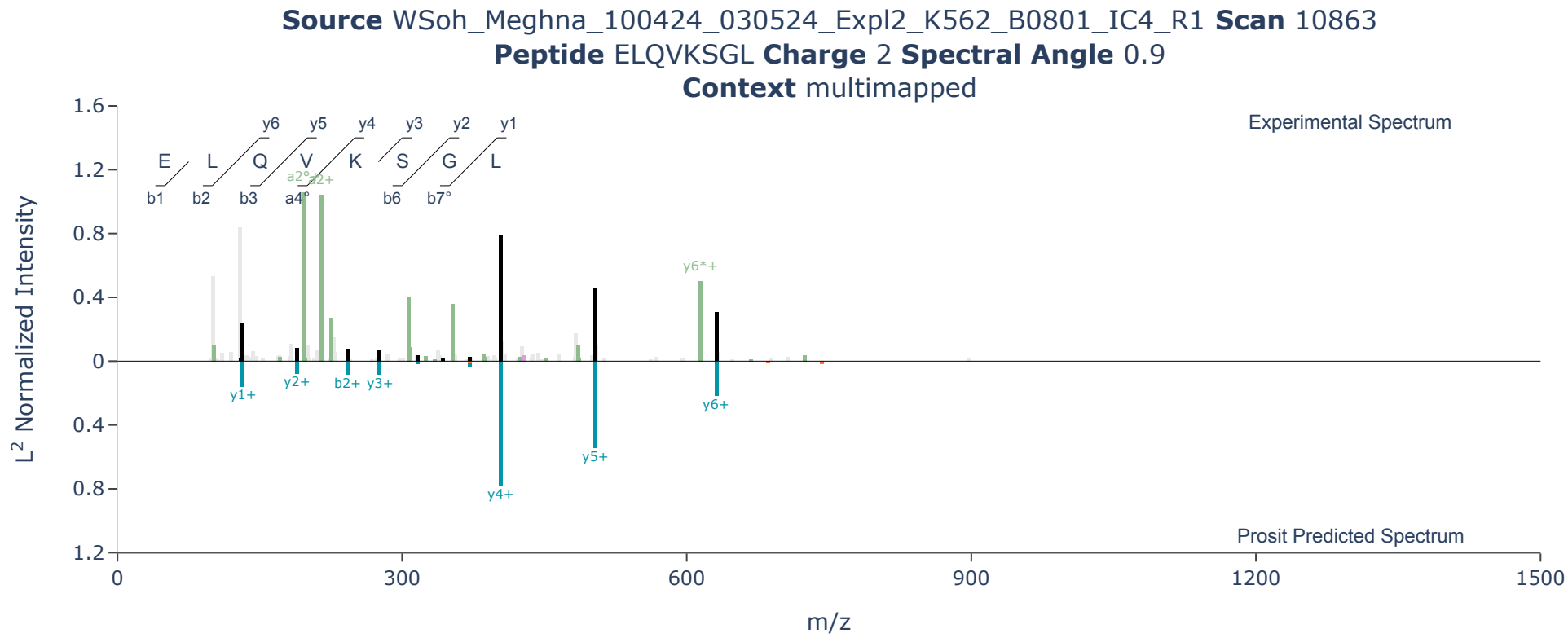
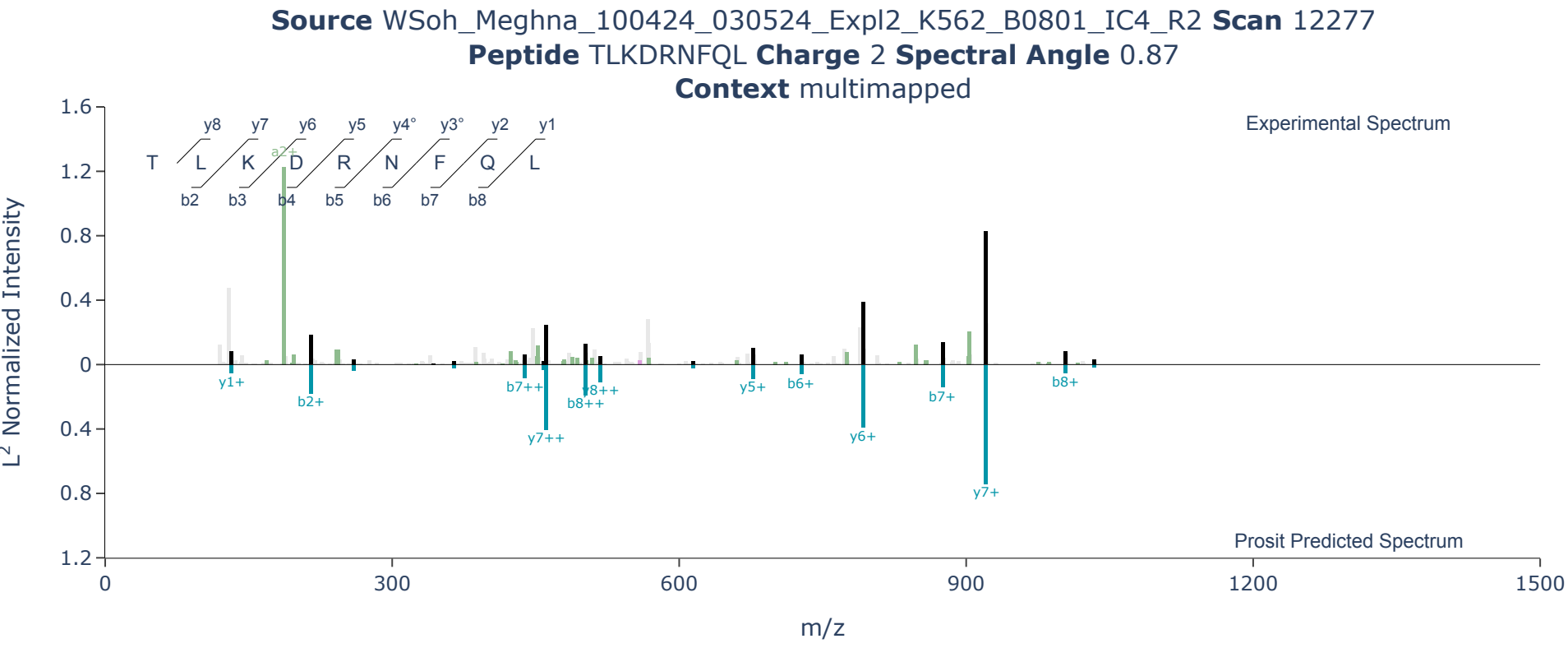


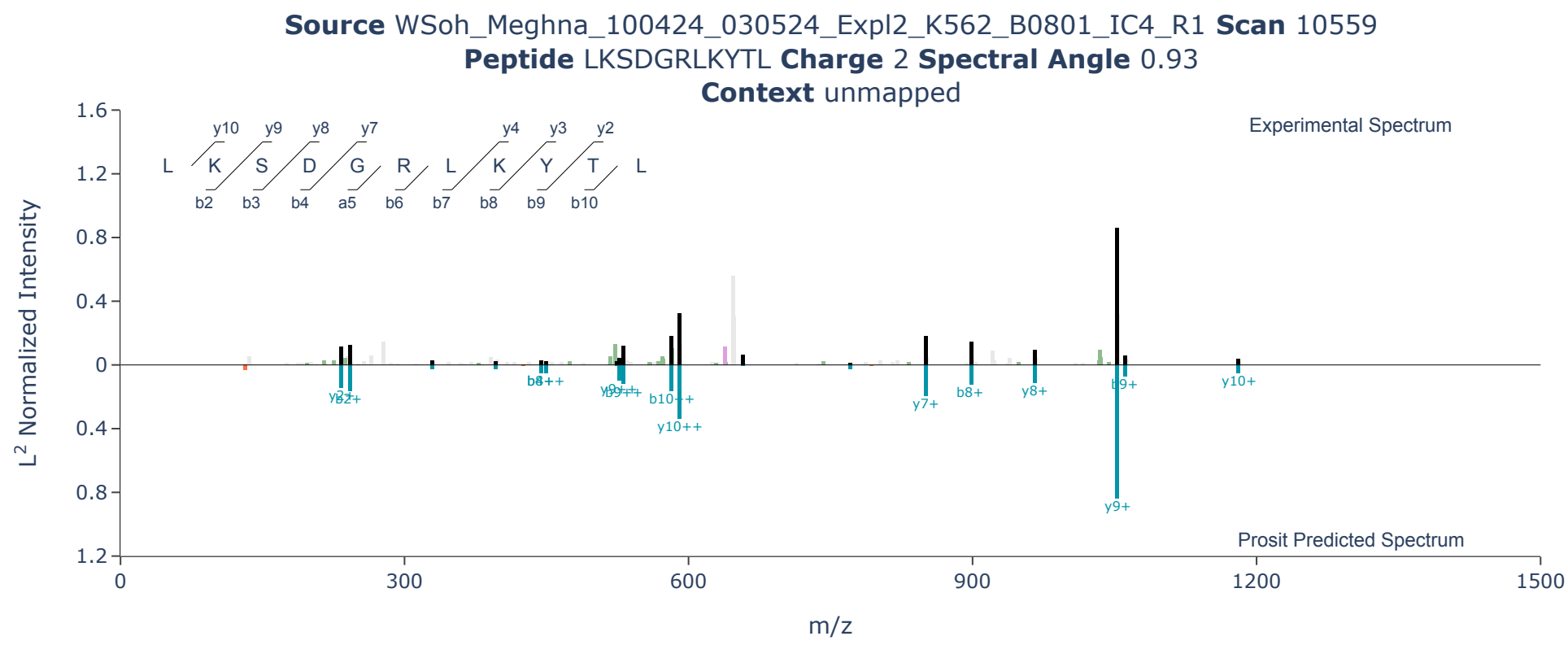
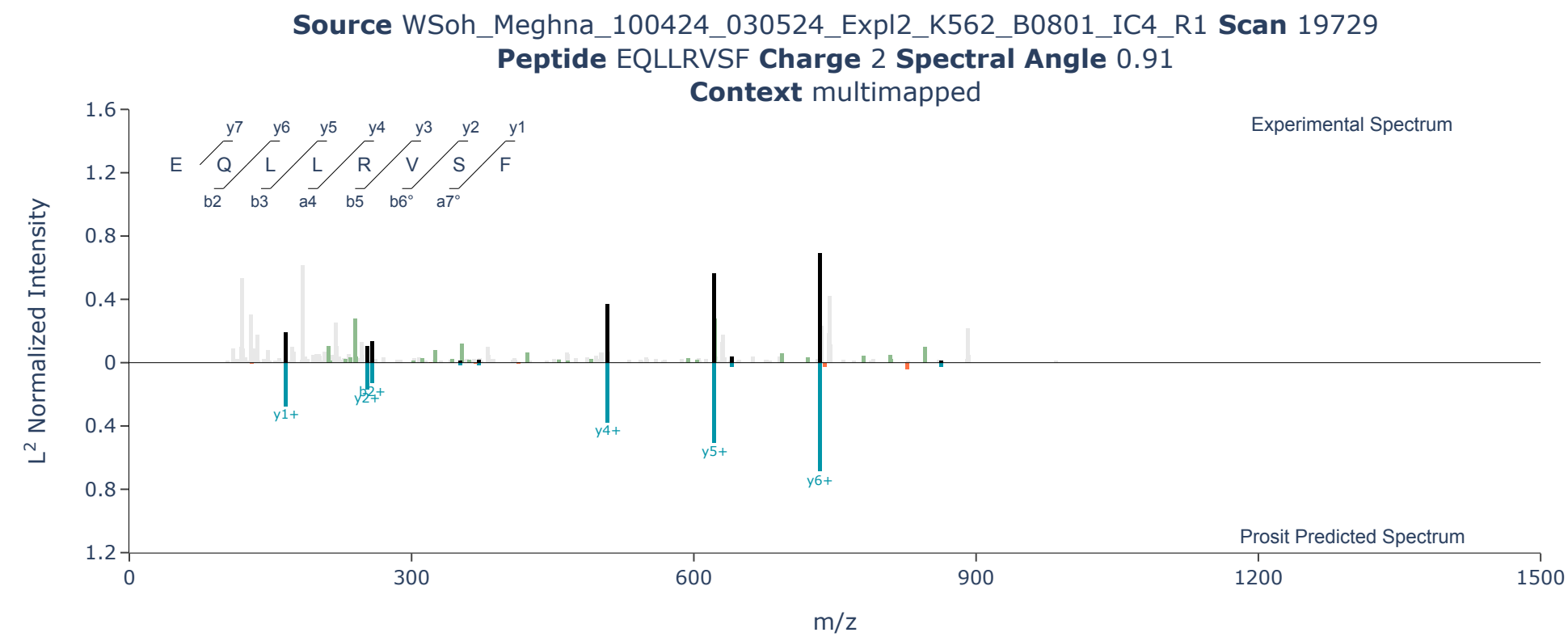
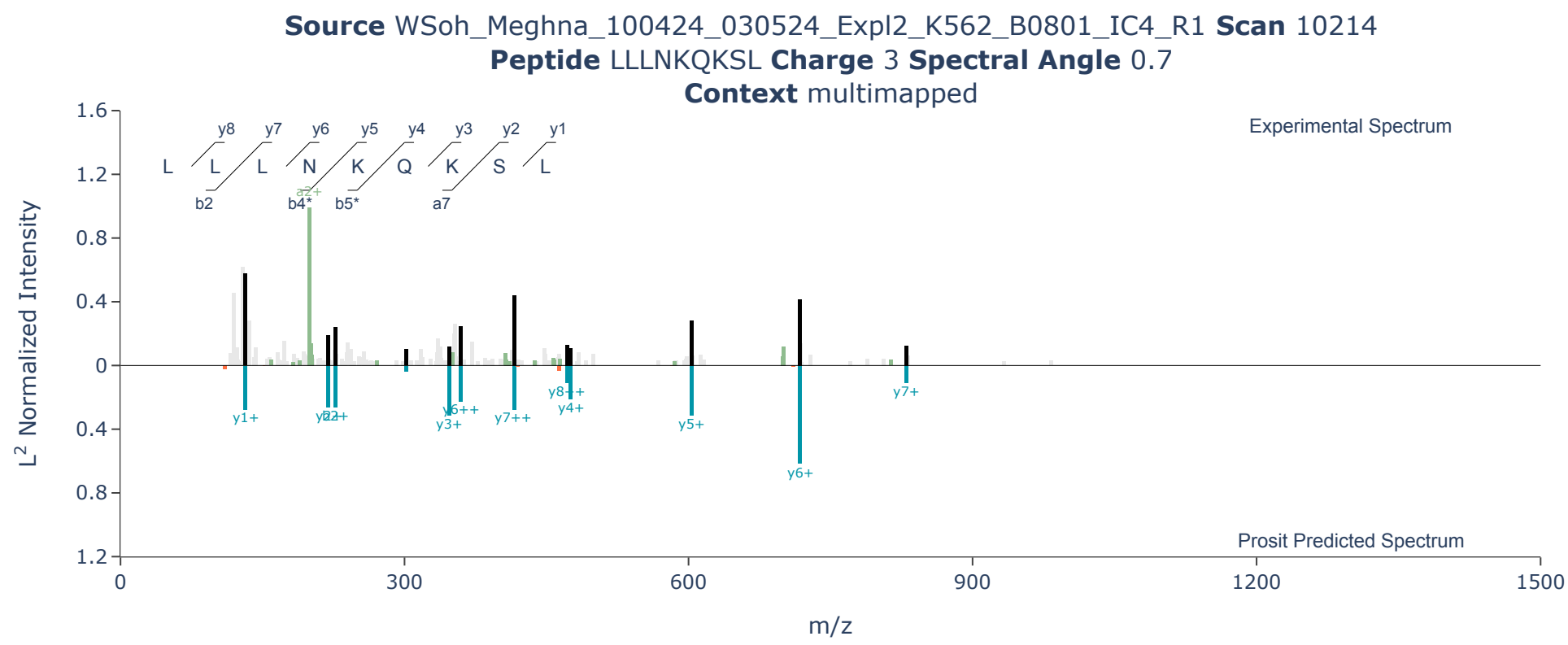
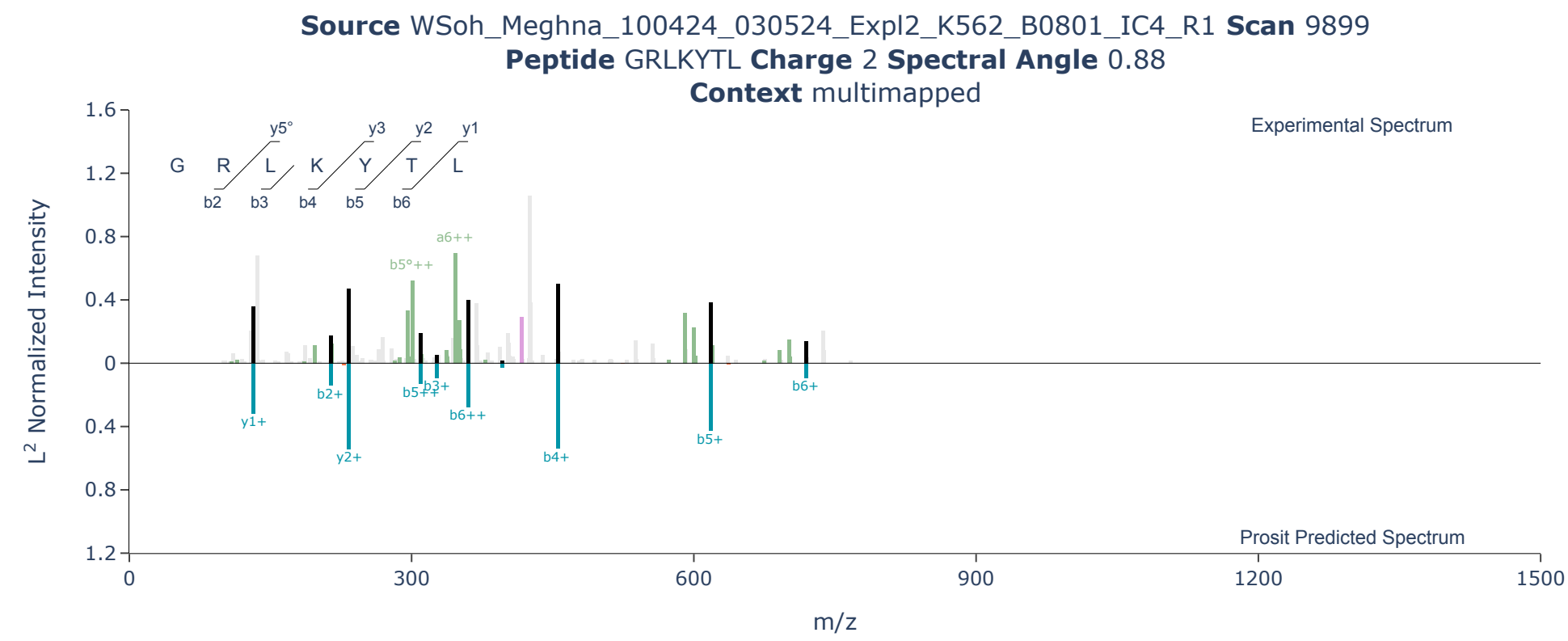
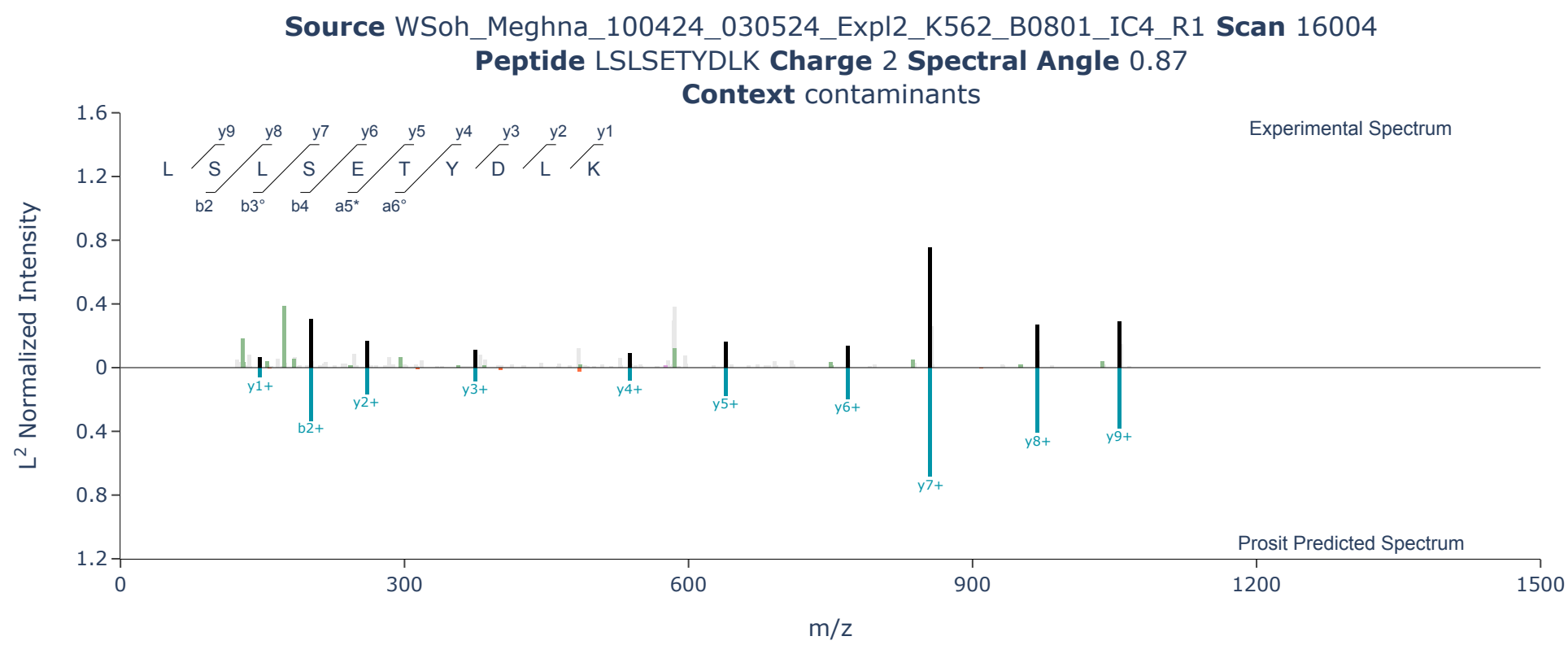
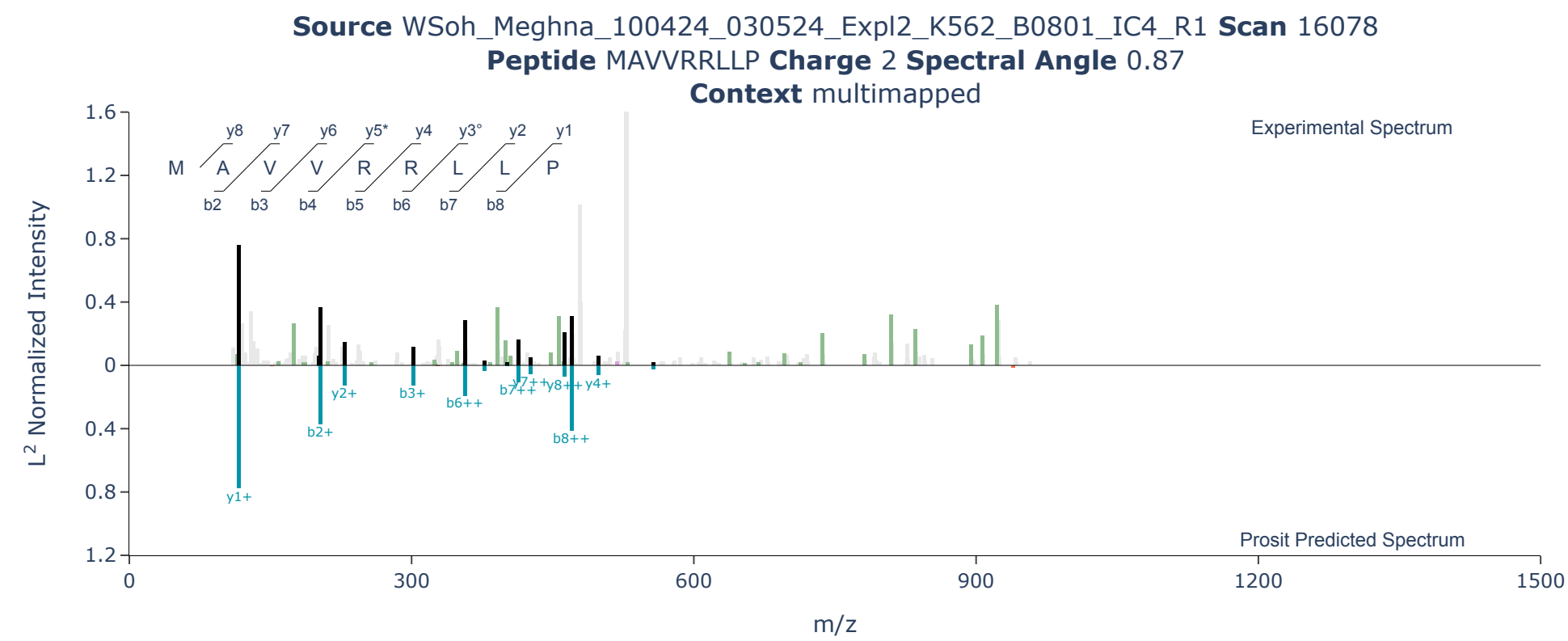
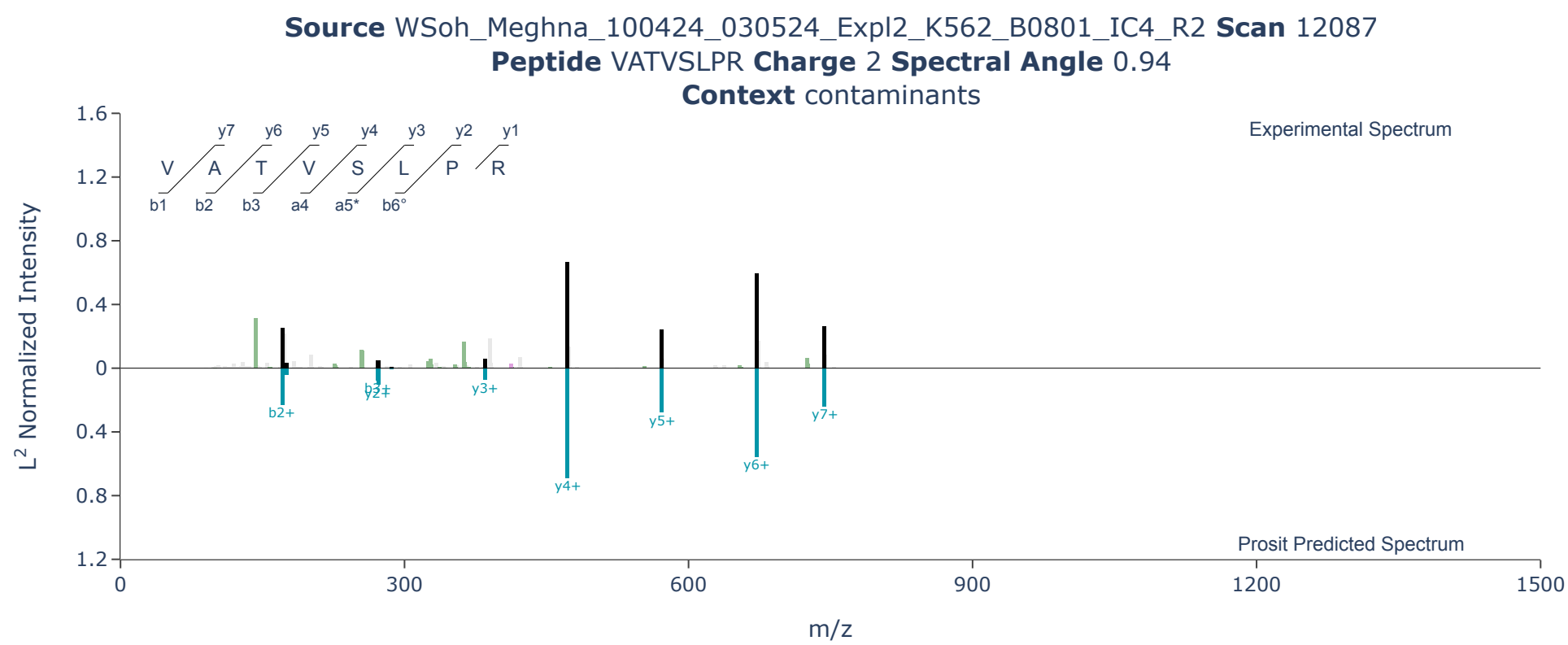
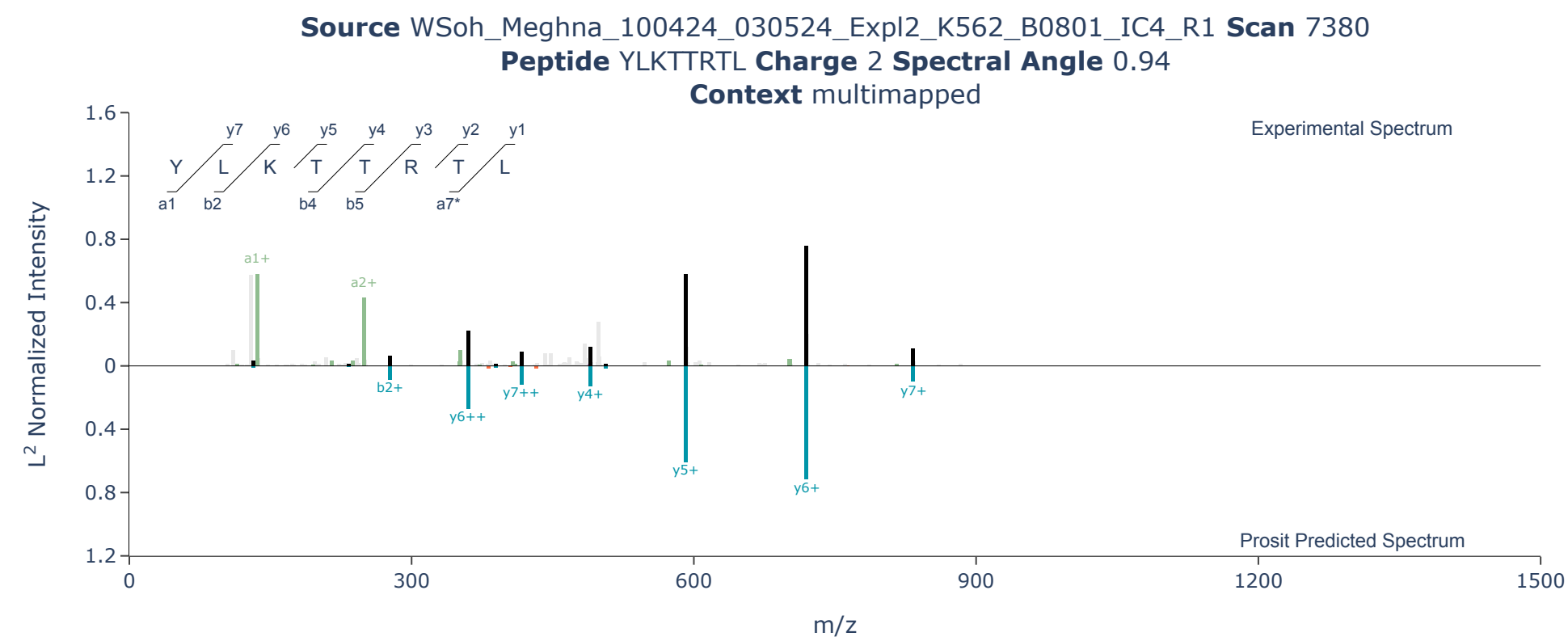
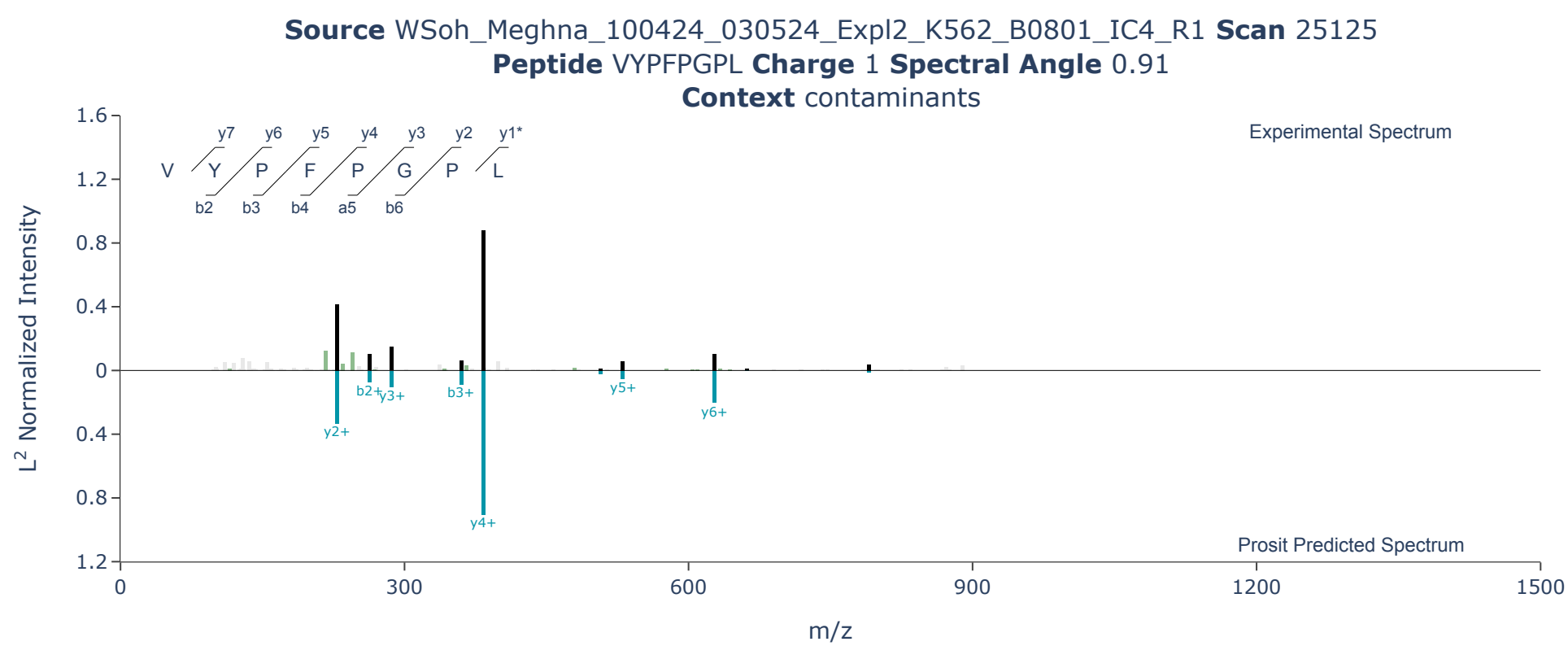
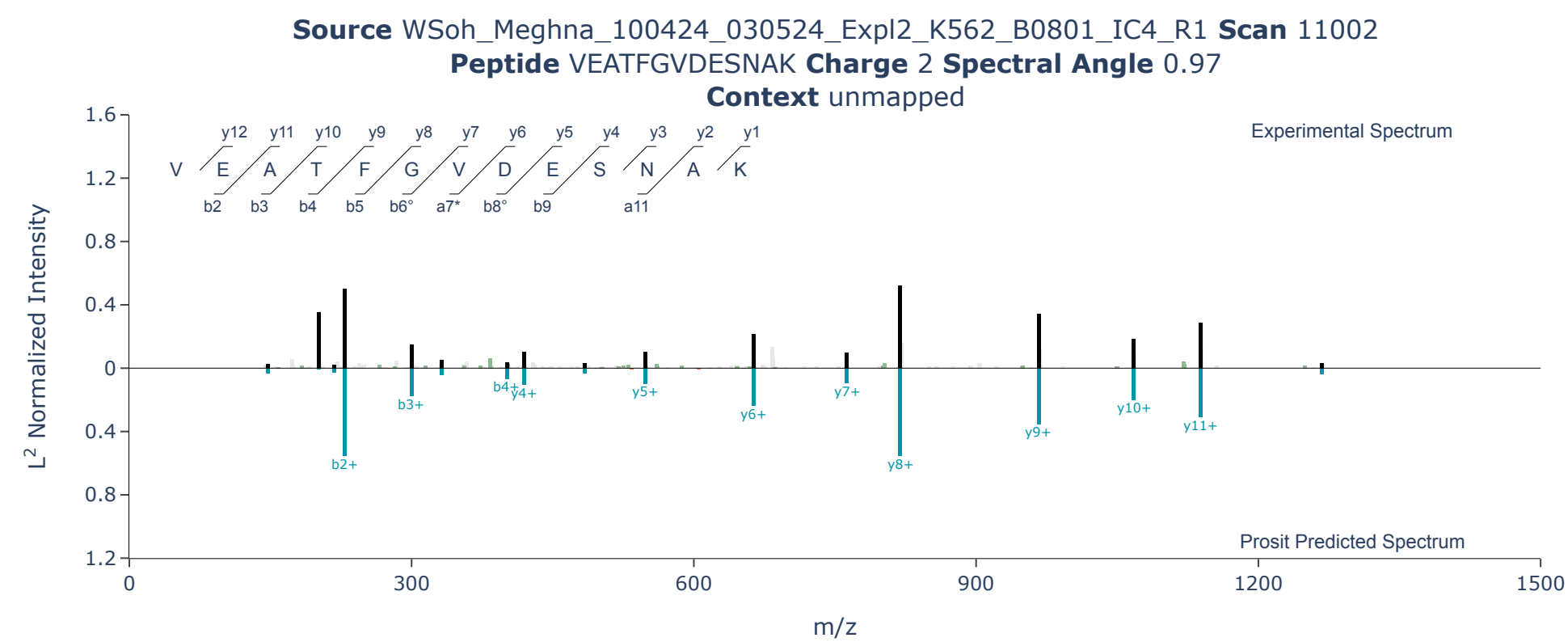


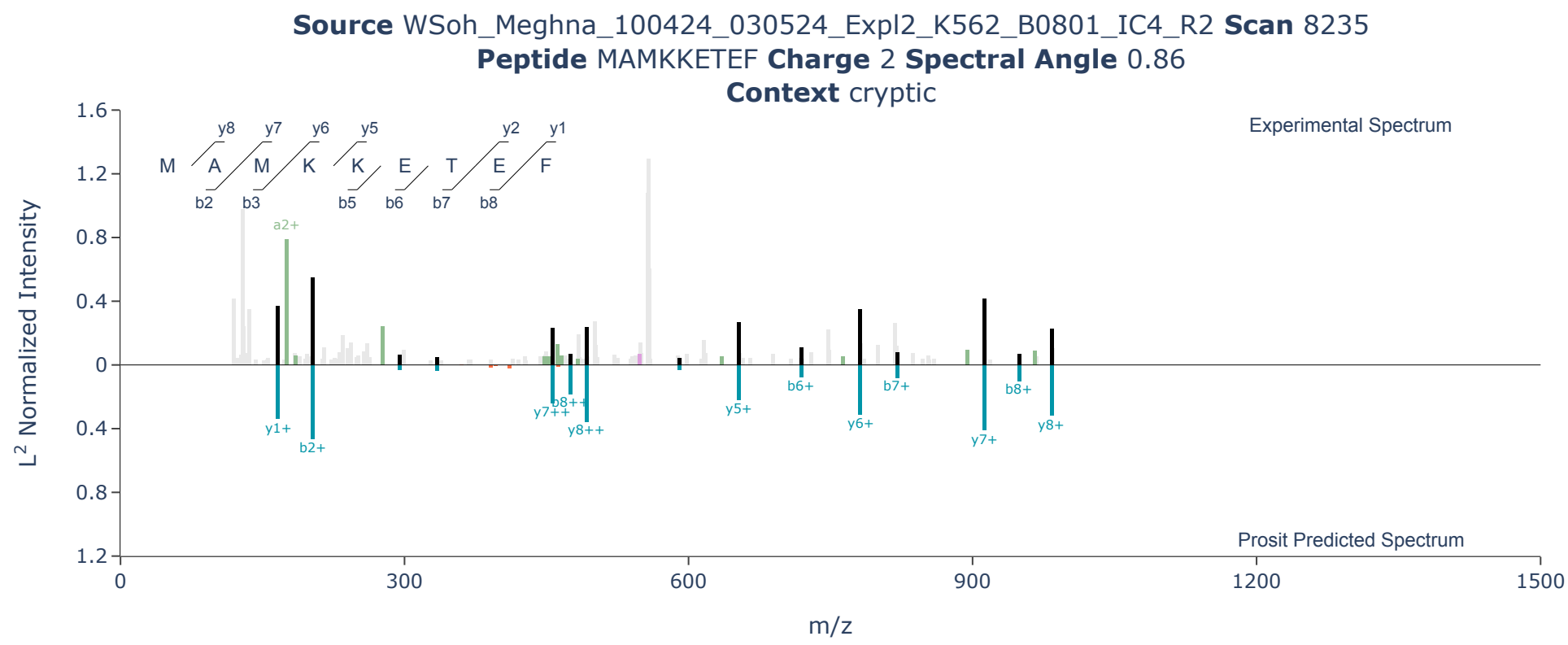
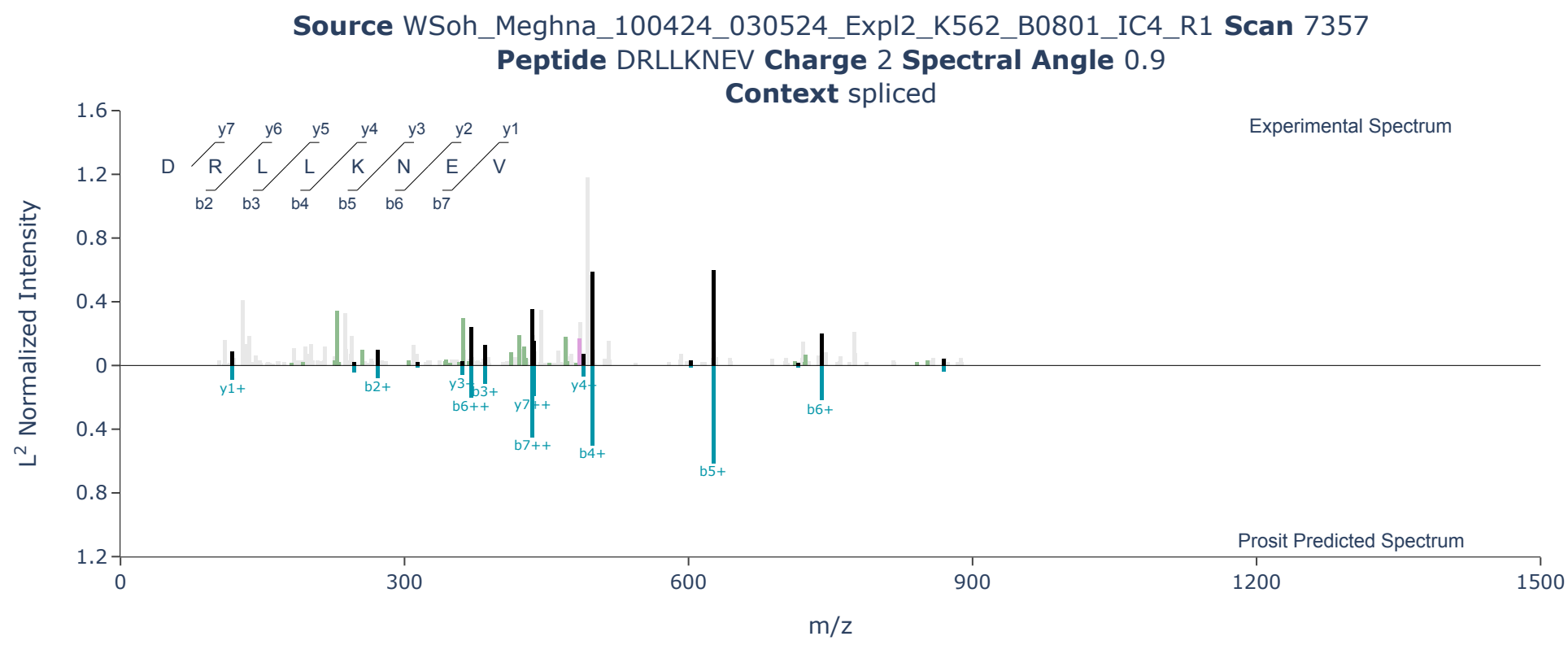
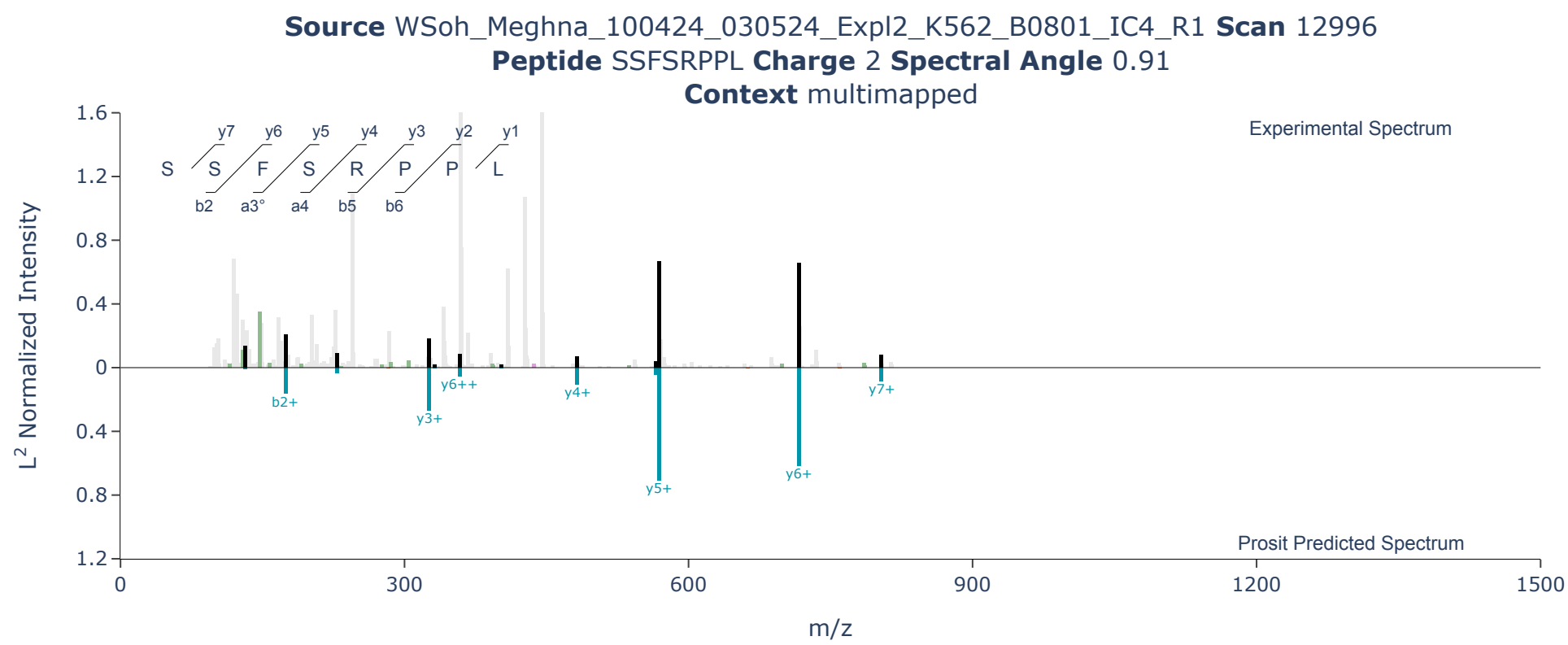
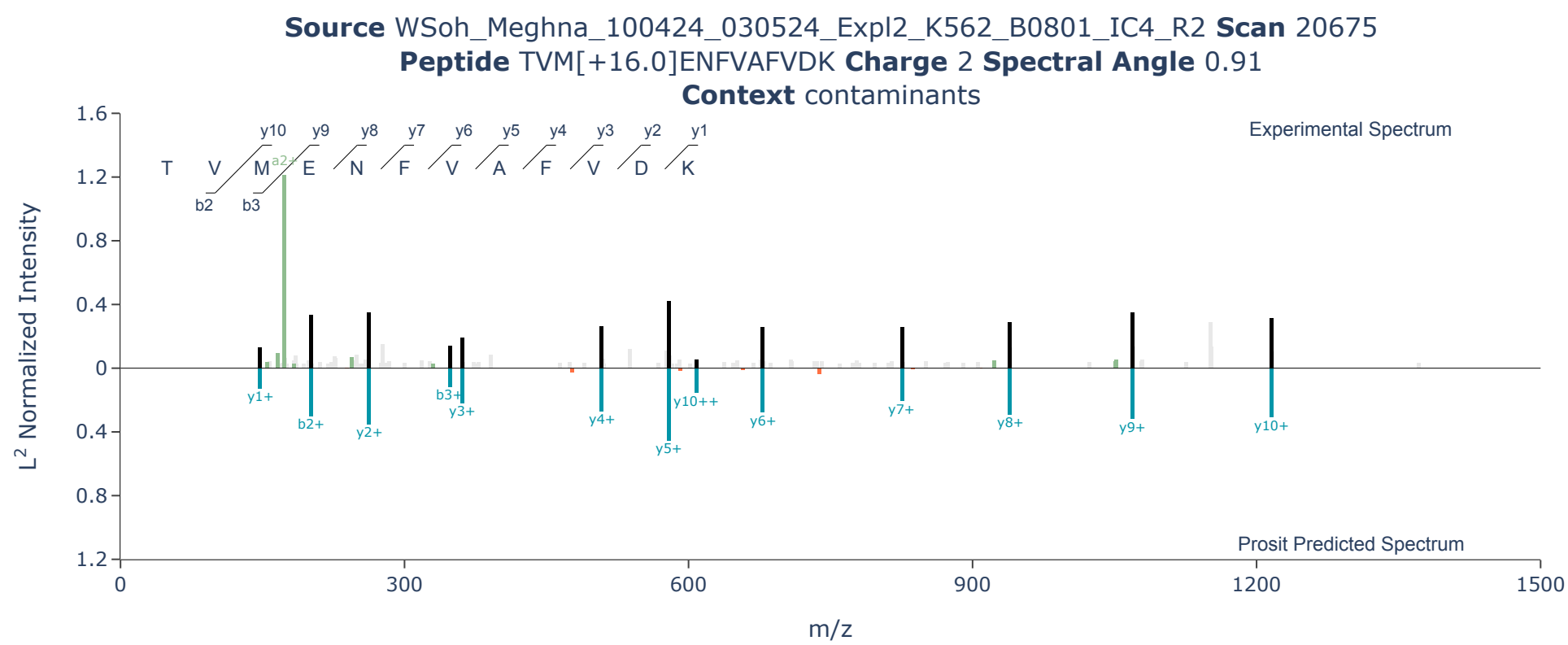
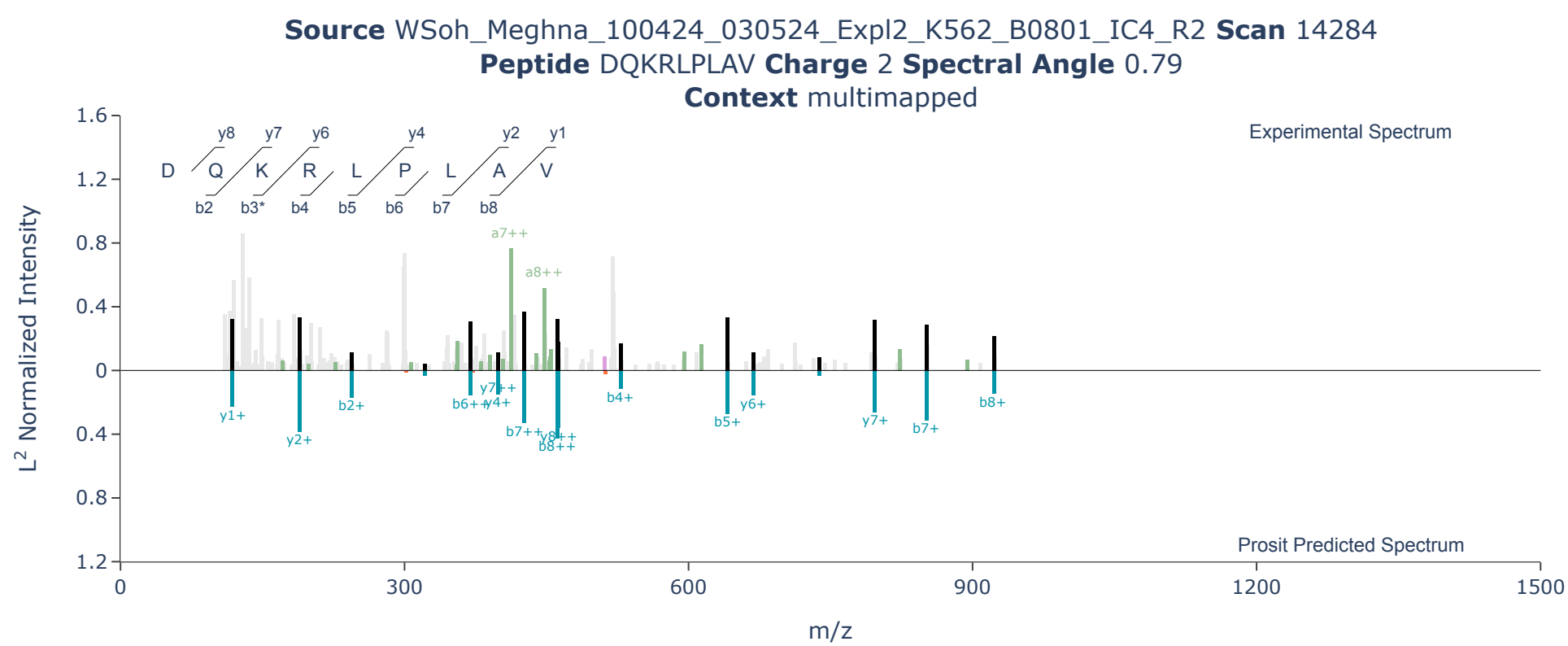


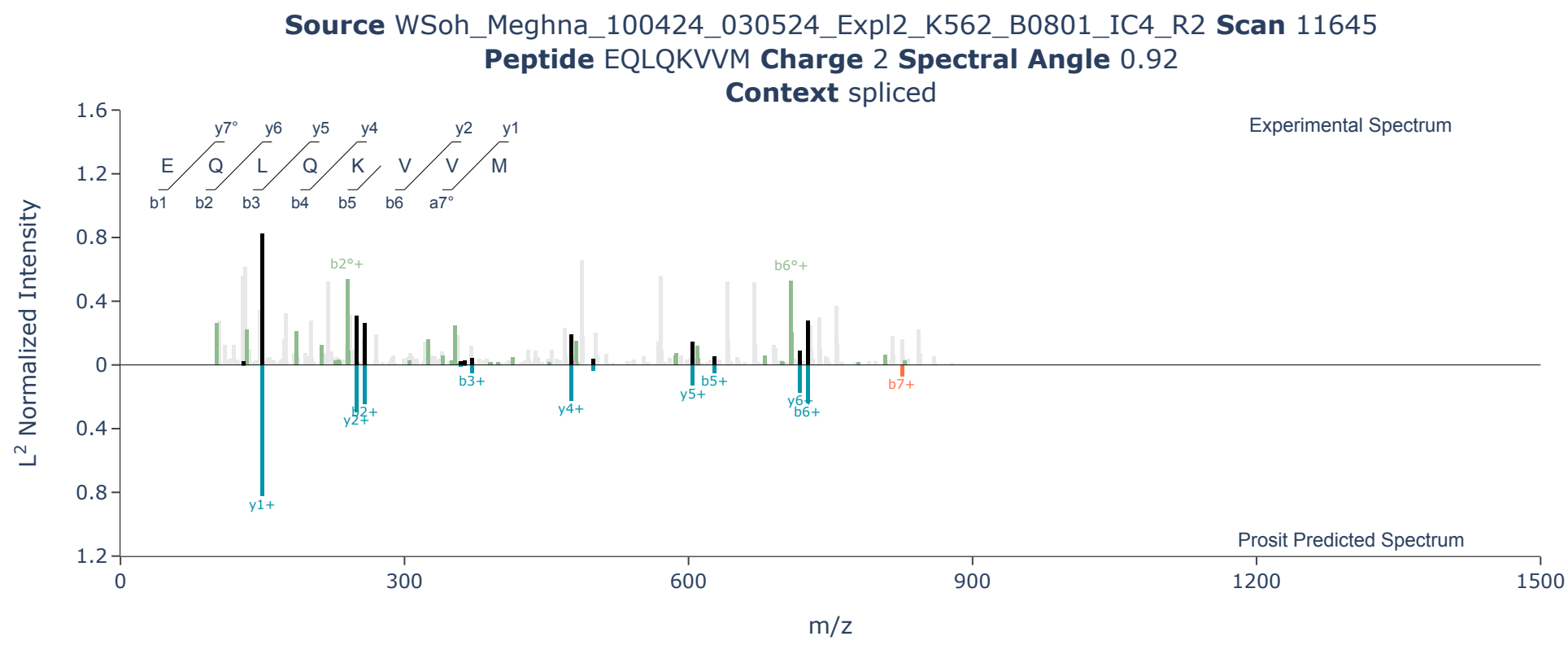
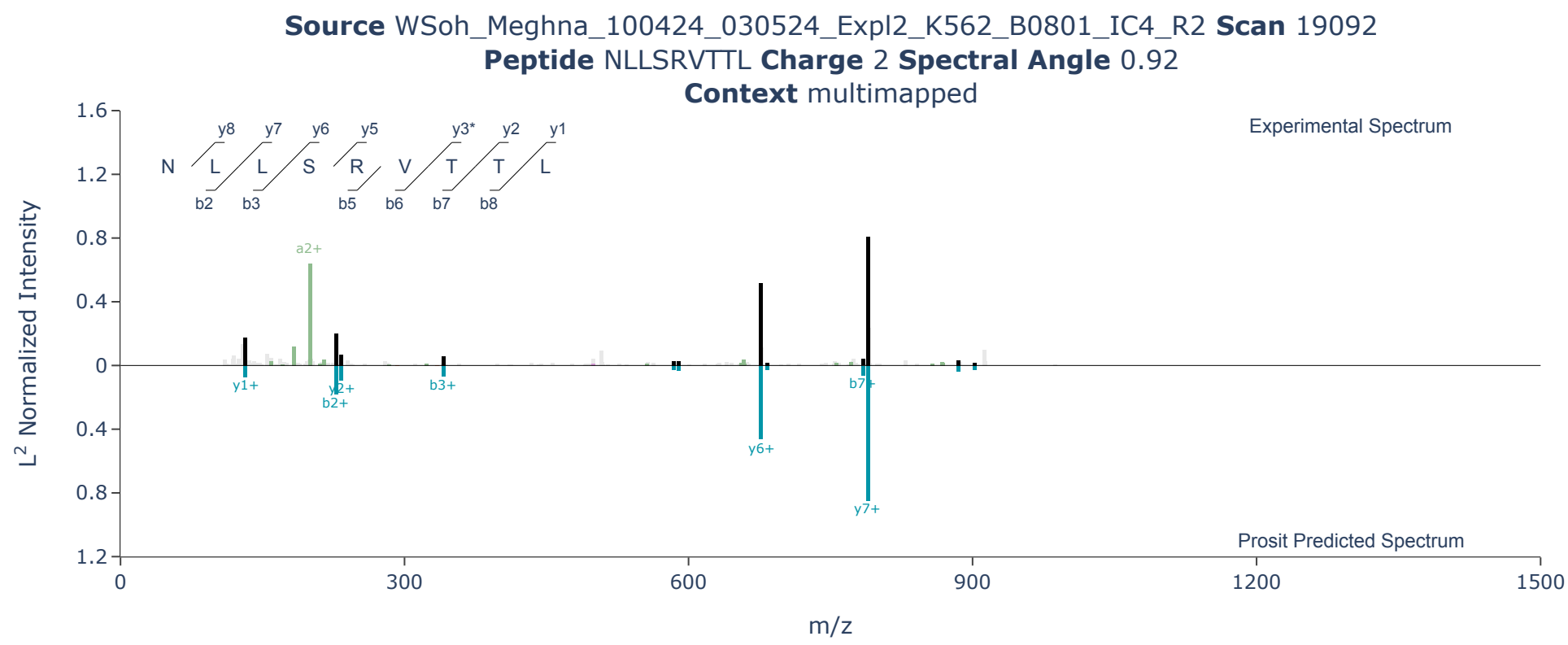
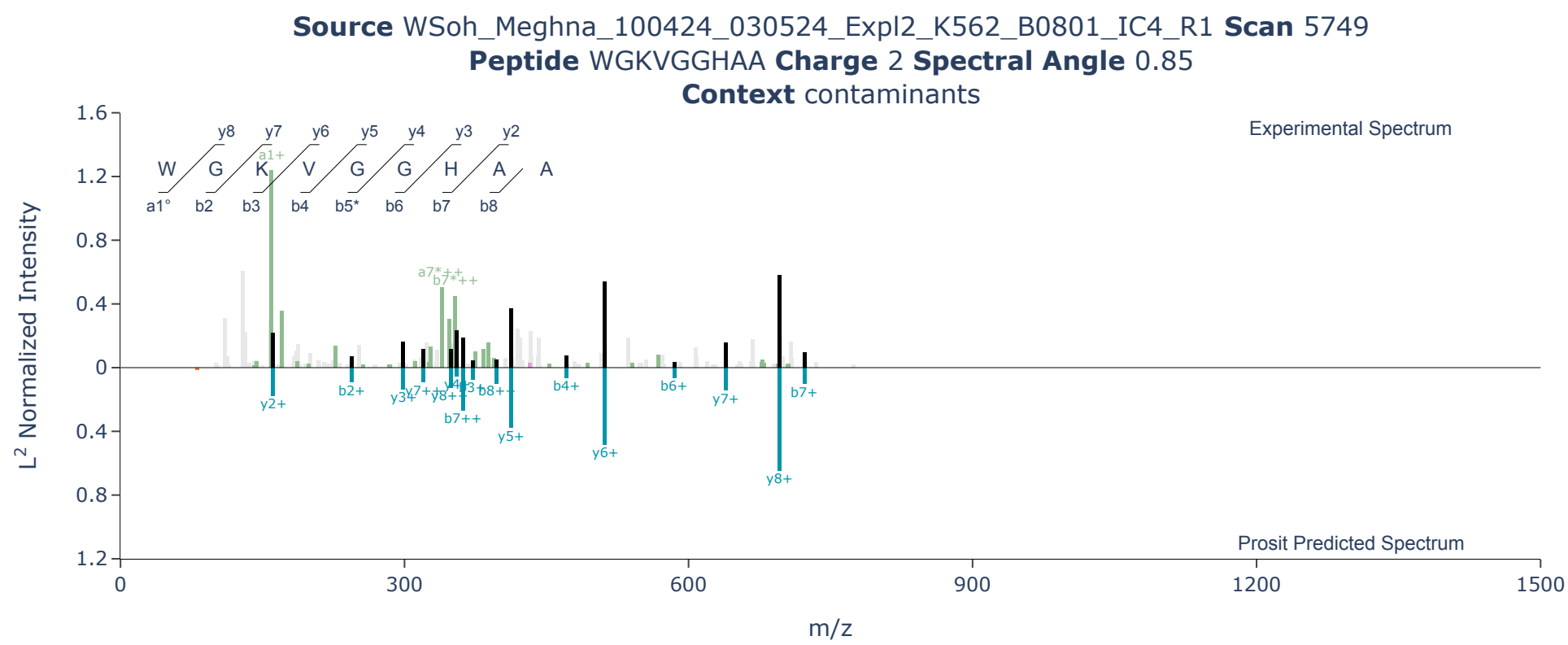
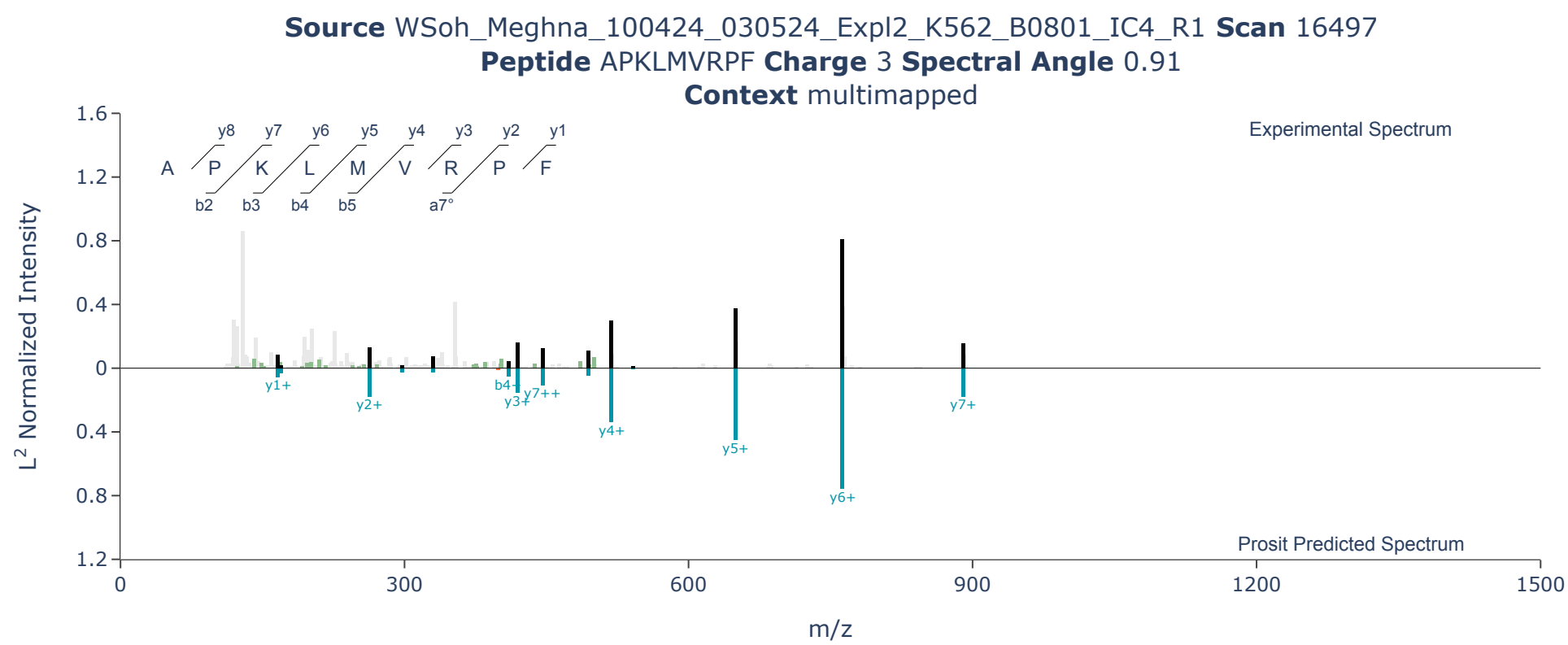
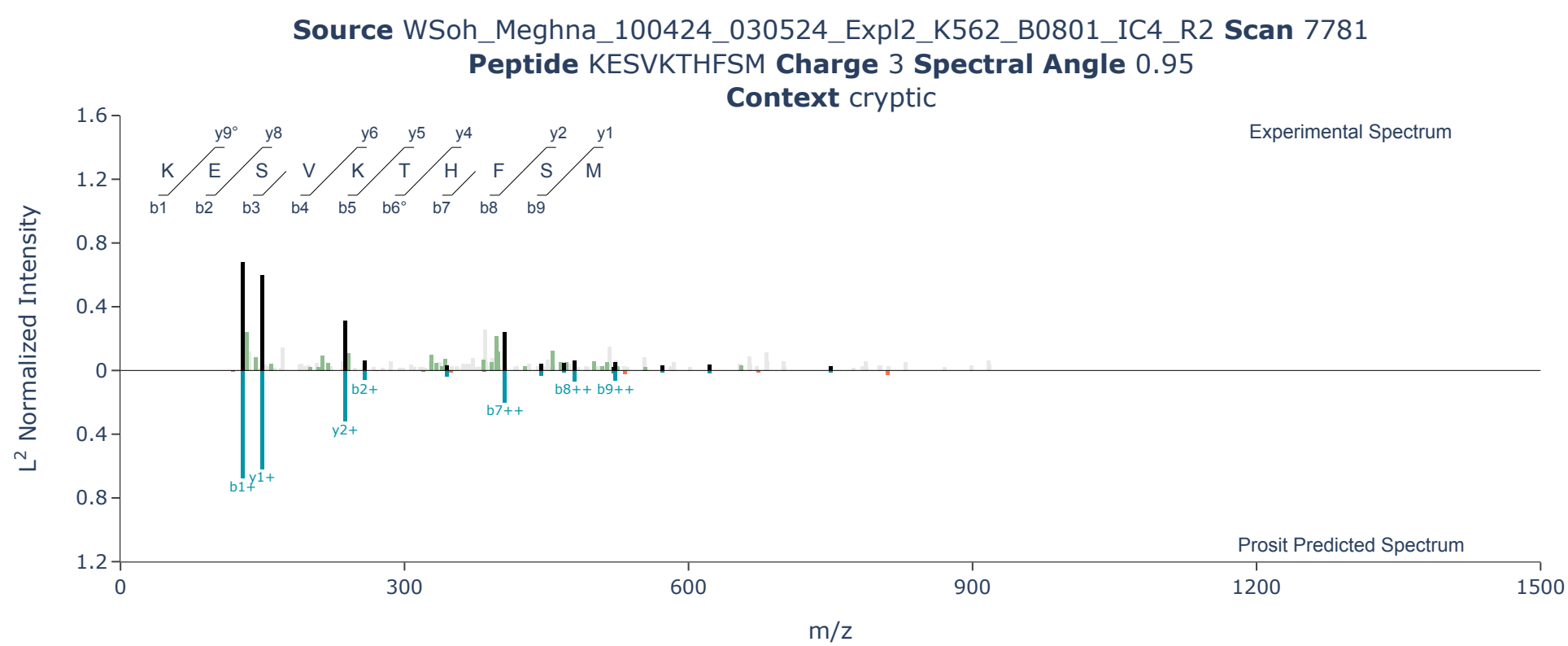


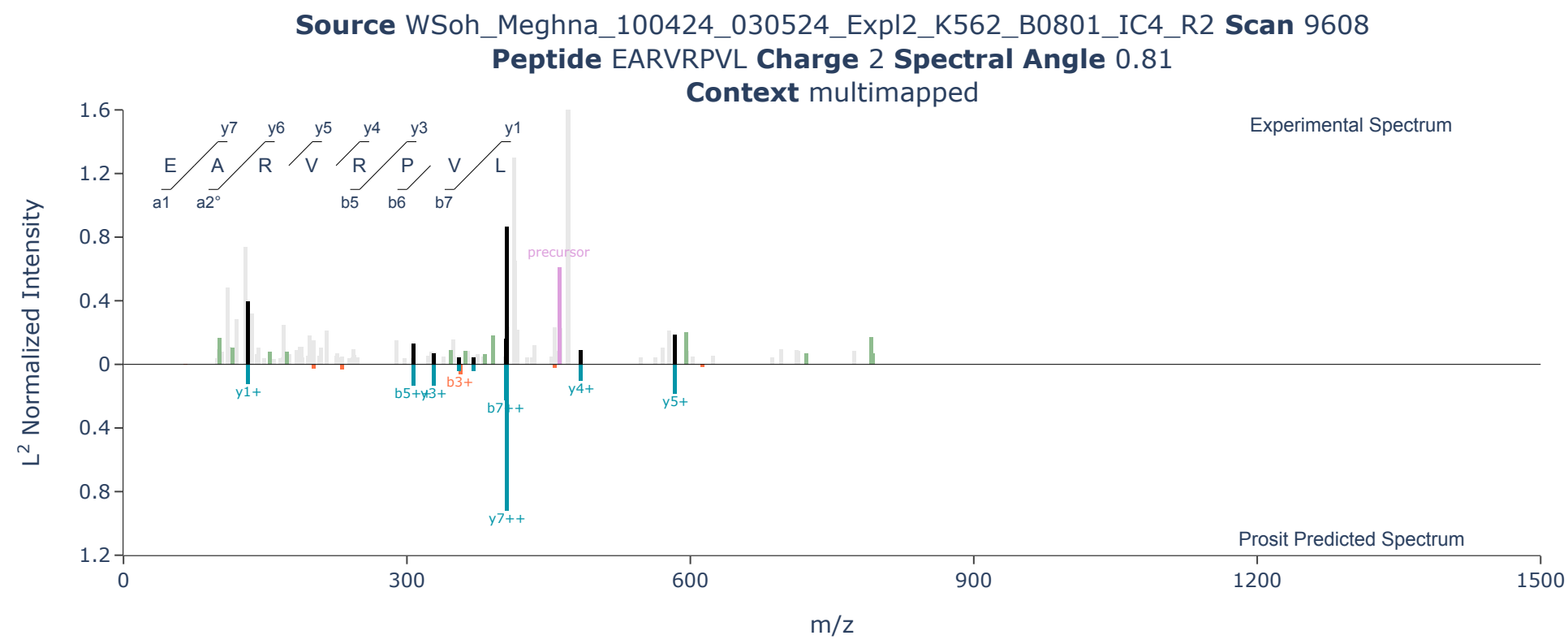
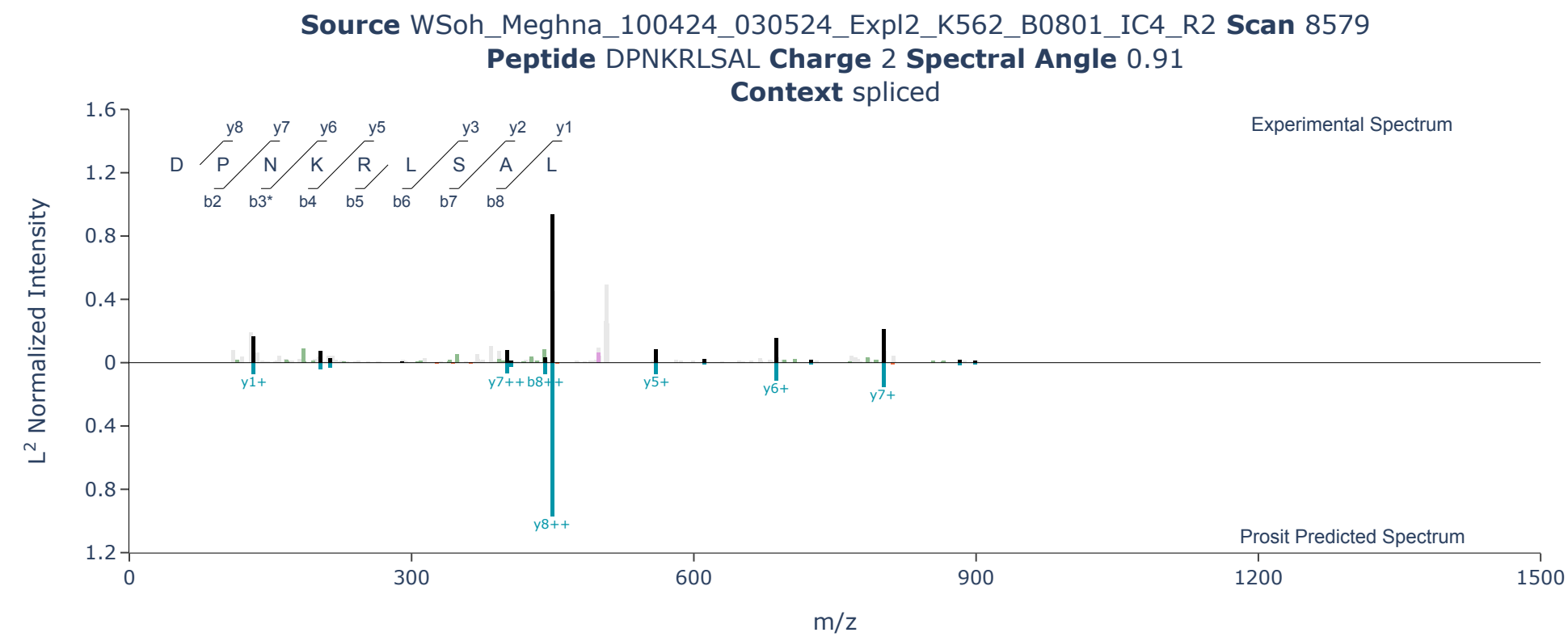
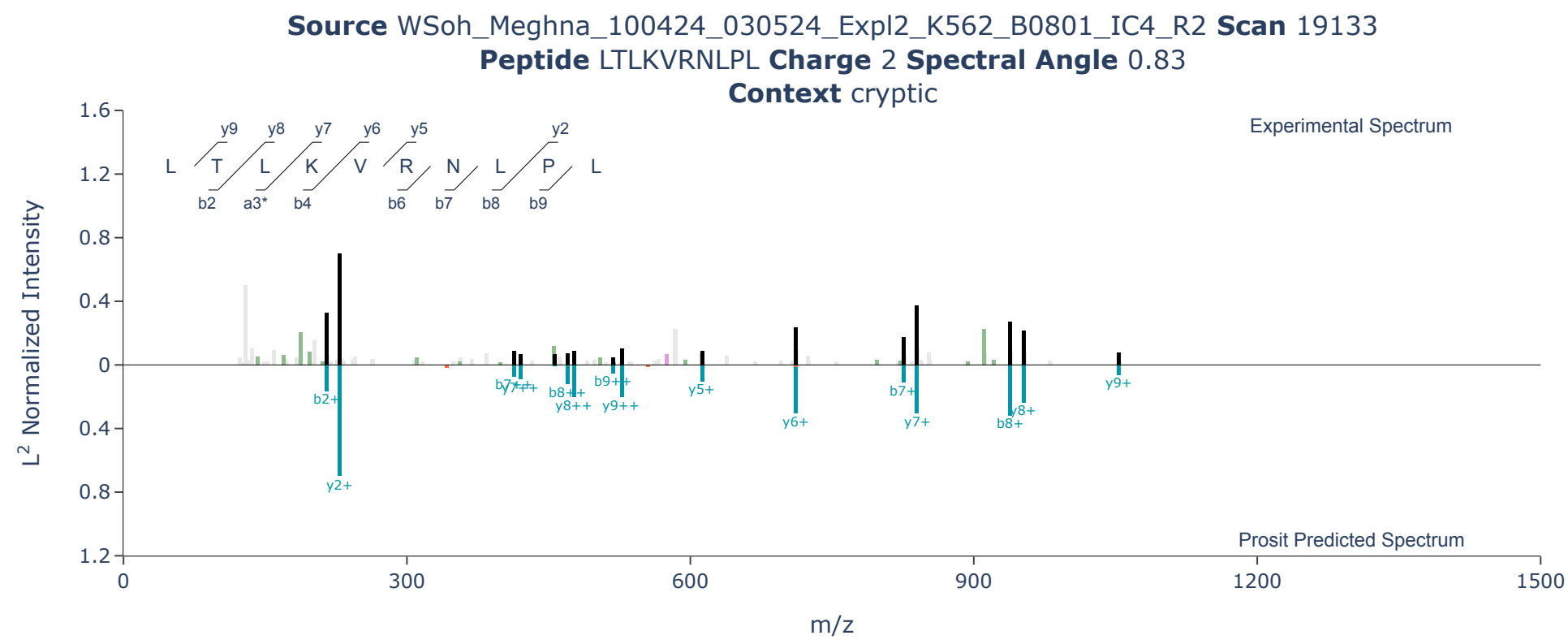
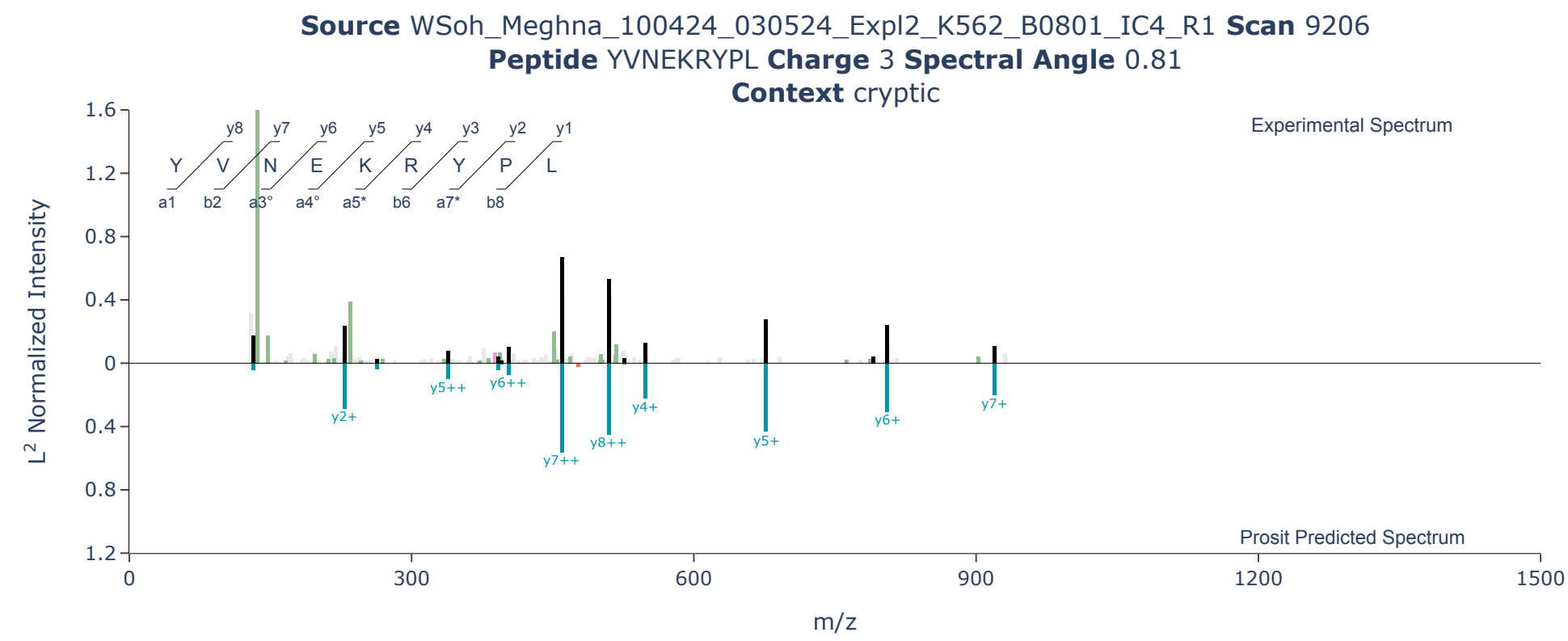
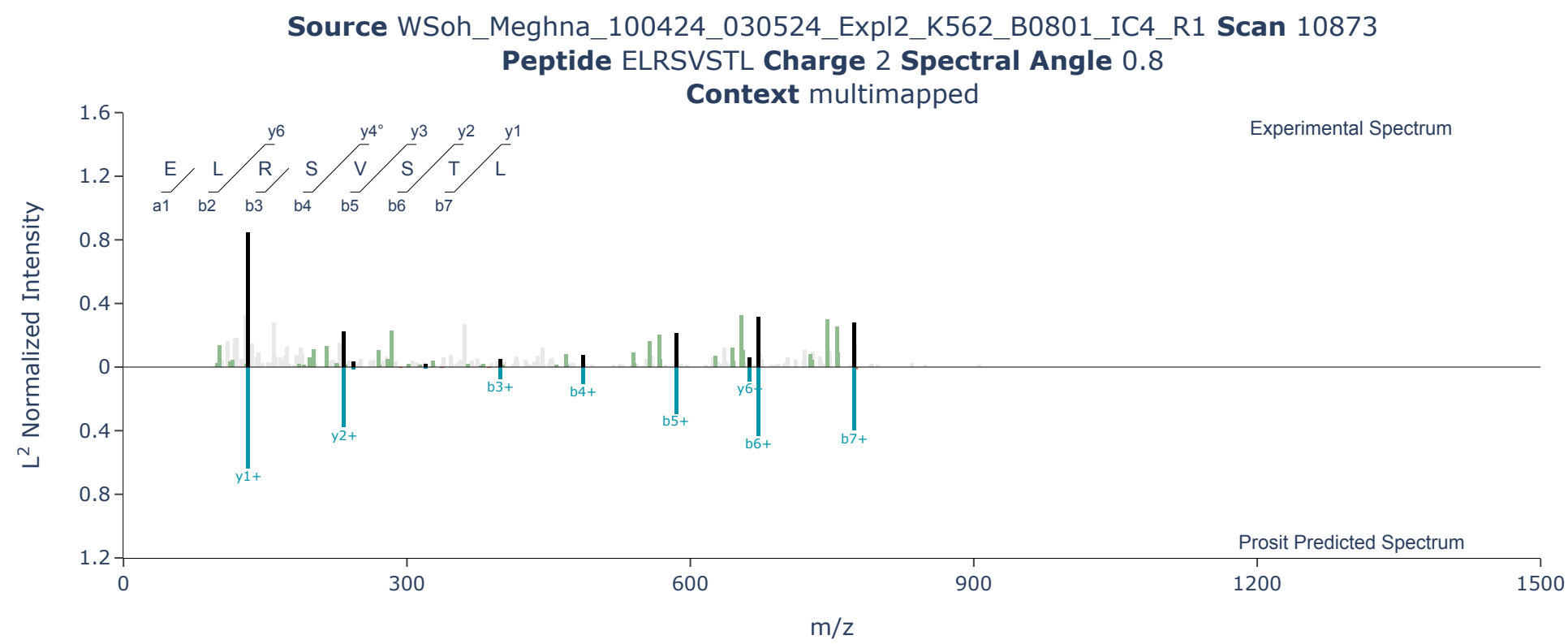
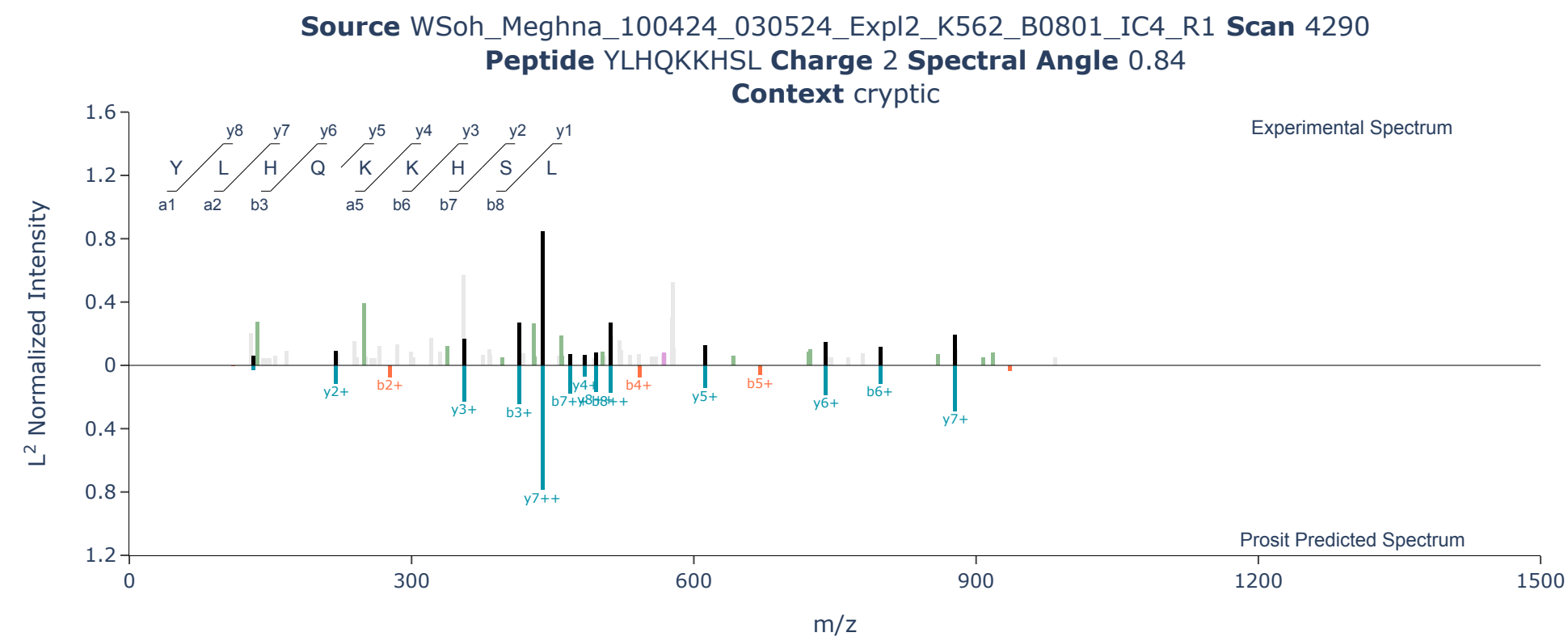
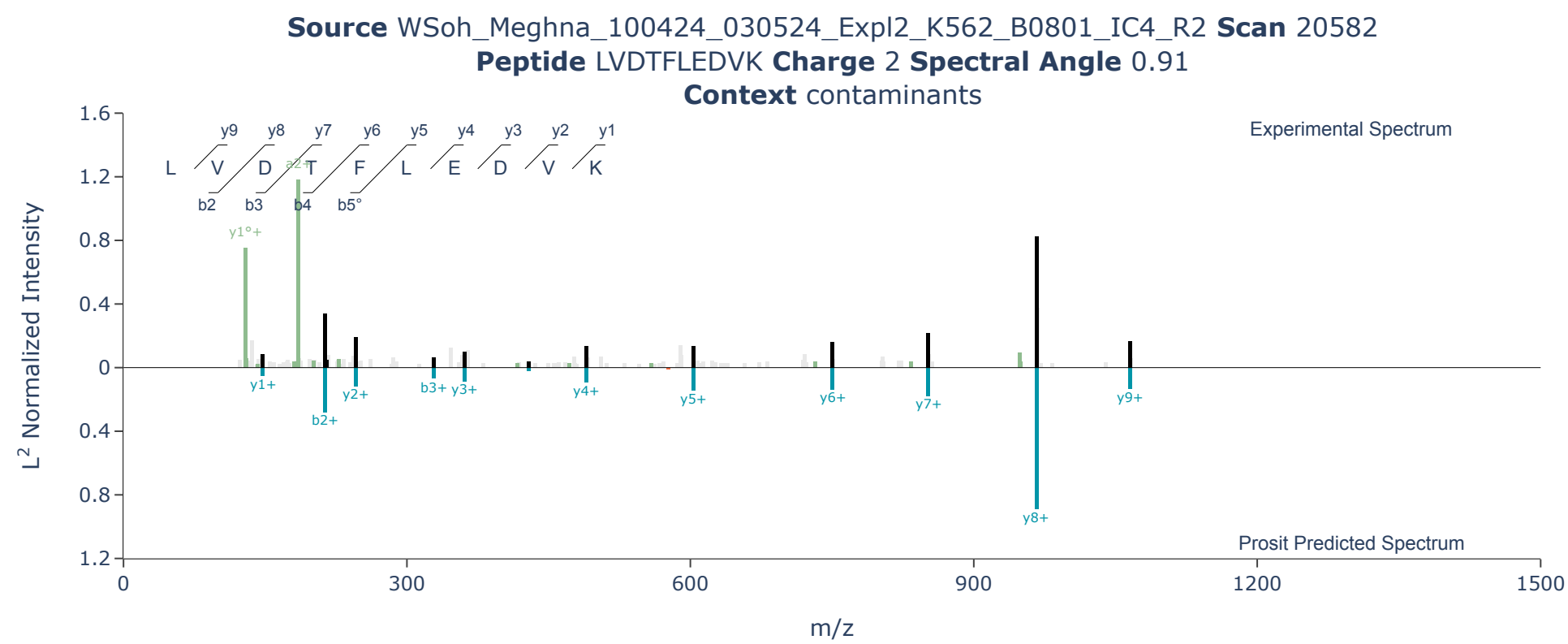
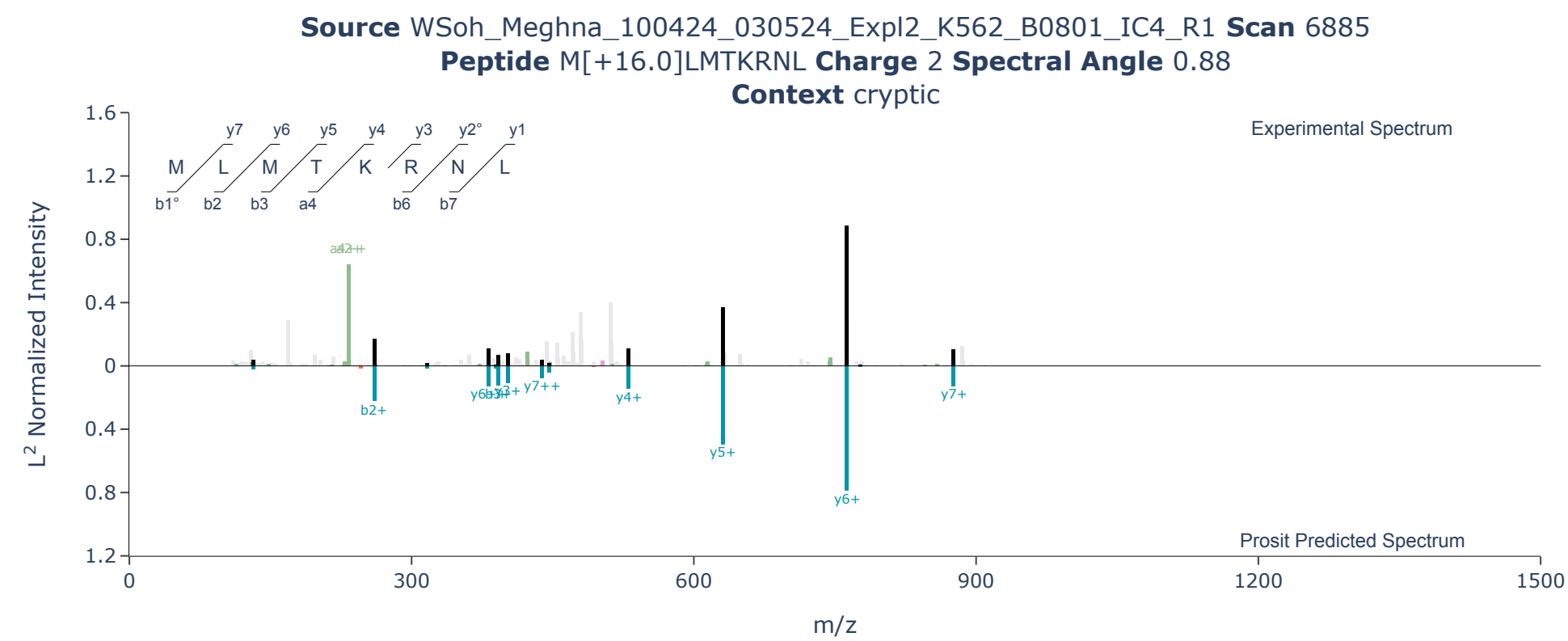
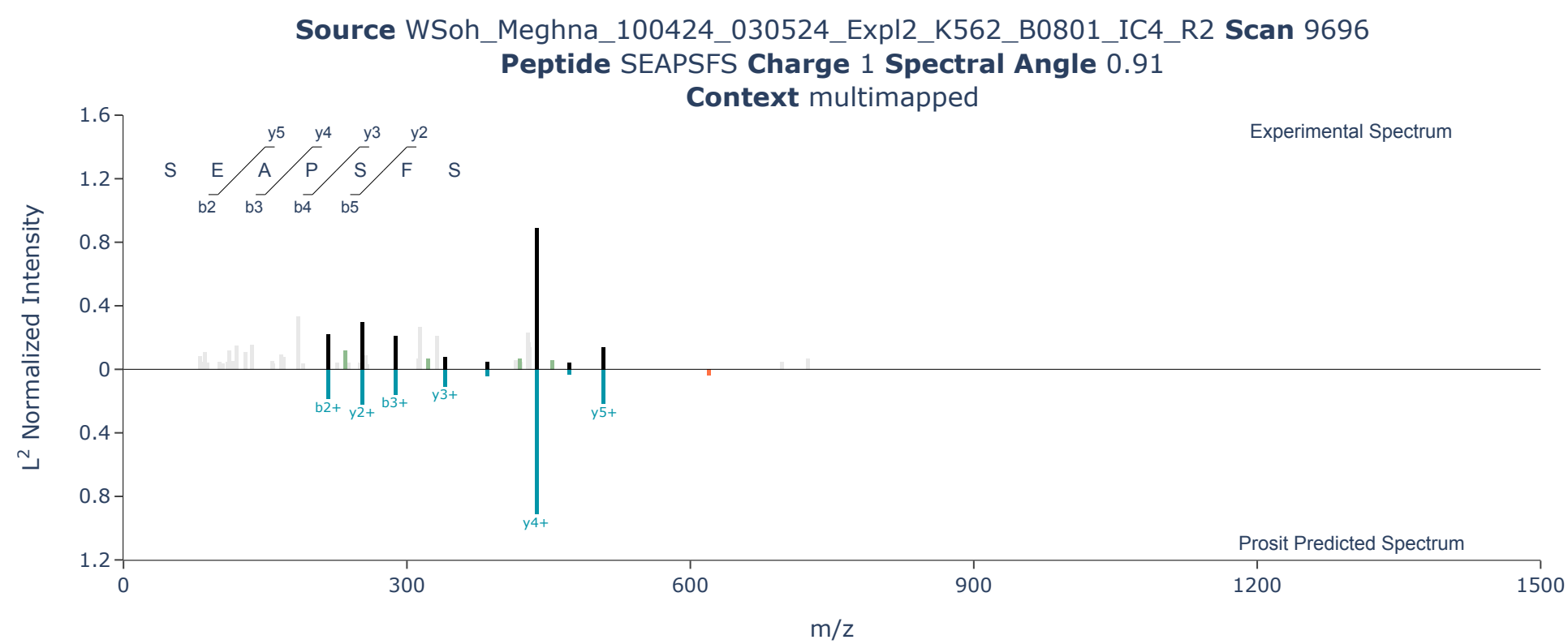
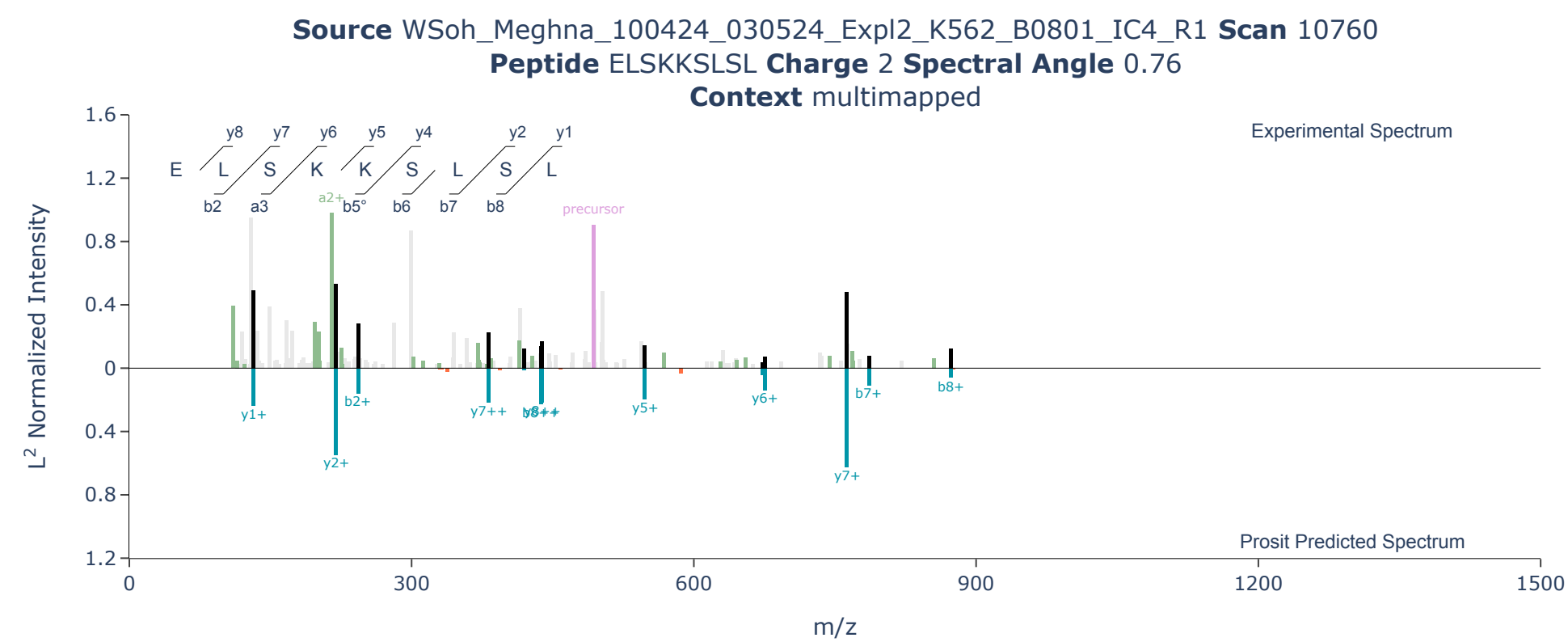






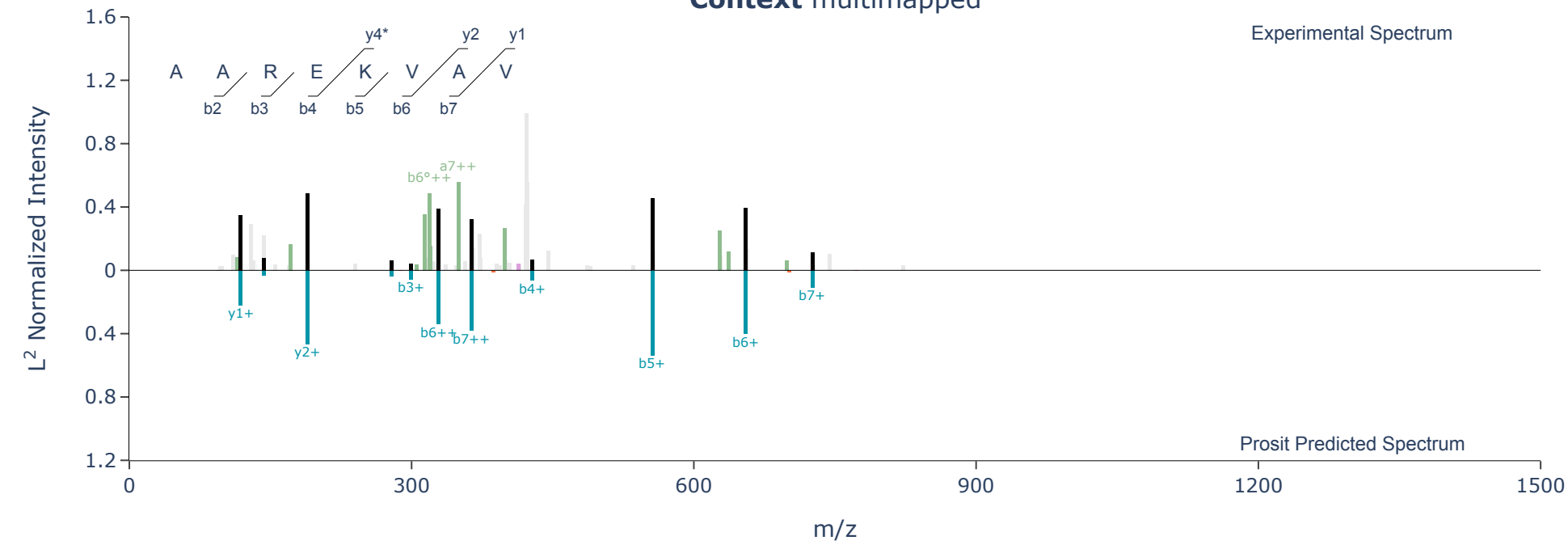






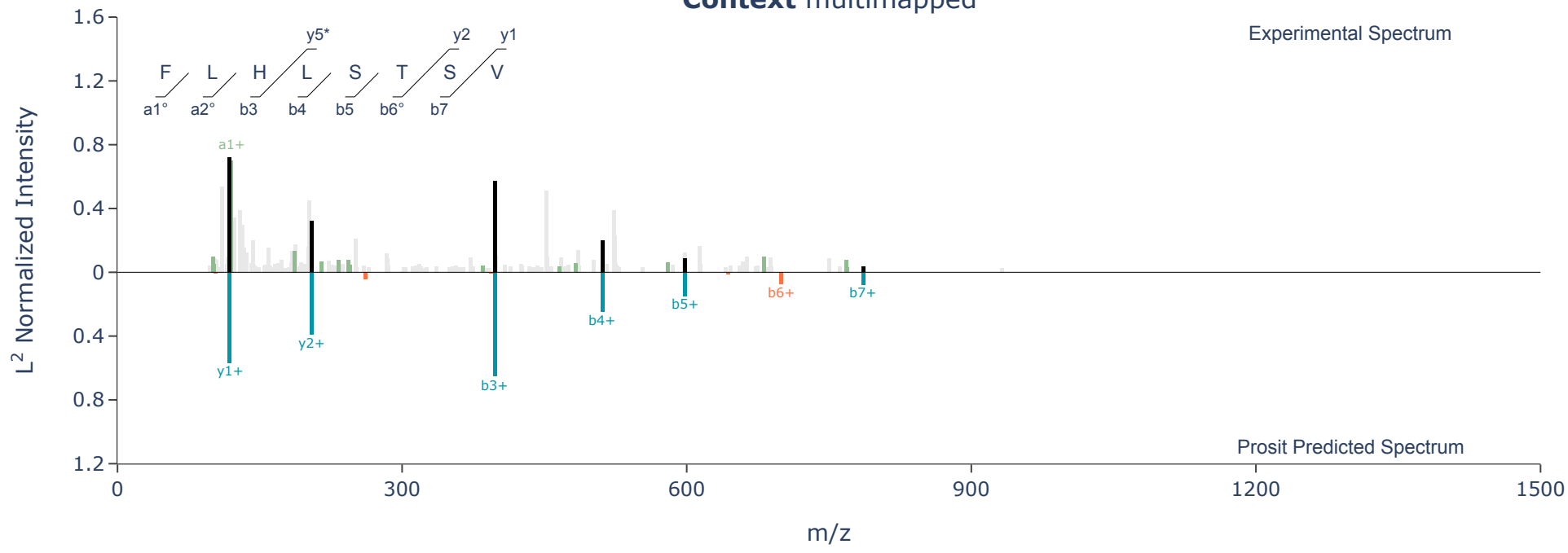
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R2 Scan 5594
Peptide AAREKVAV Charge 2 Spectral Angle 0.88

Context multimapped



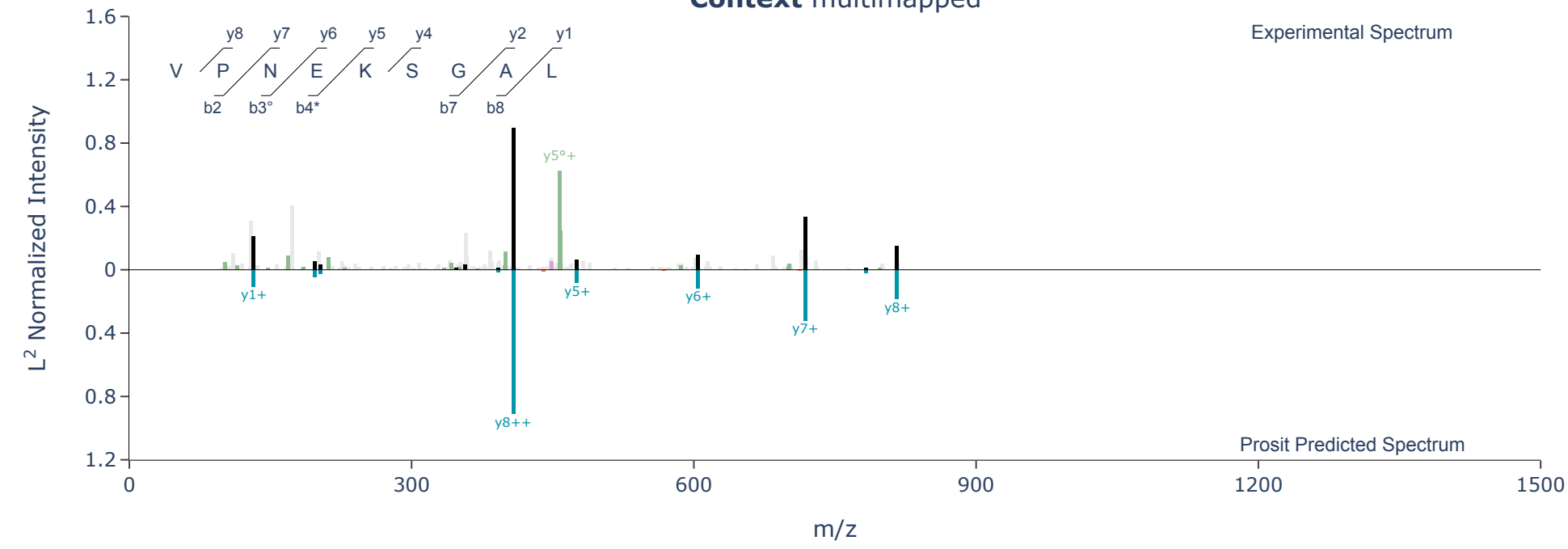
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Peptide FLHLSTSV Charge 2 Spectral Angle 0.86

Context multimapped



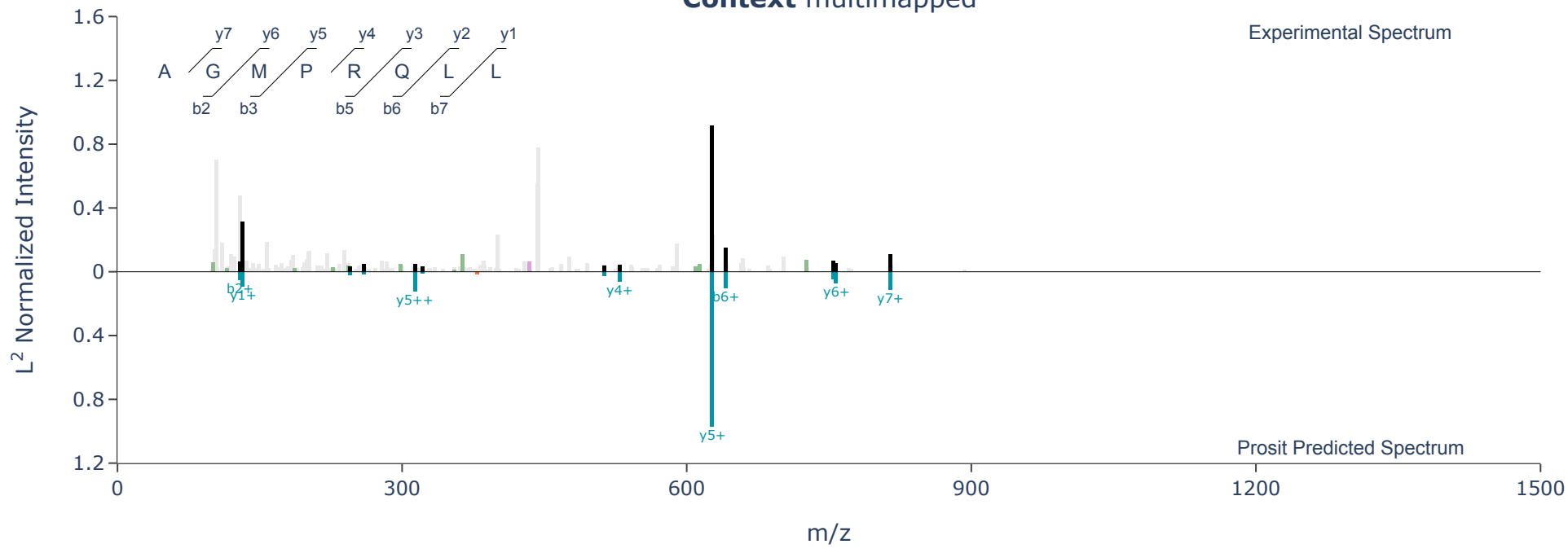
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Peptide VPNEKSGAL Charge 2 Spectral Angle 0.93

Context multimapped



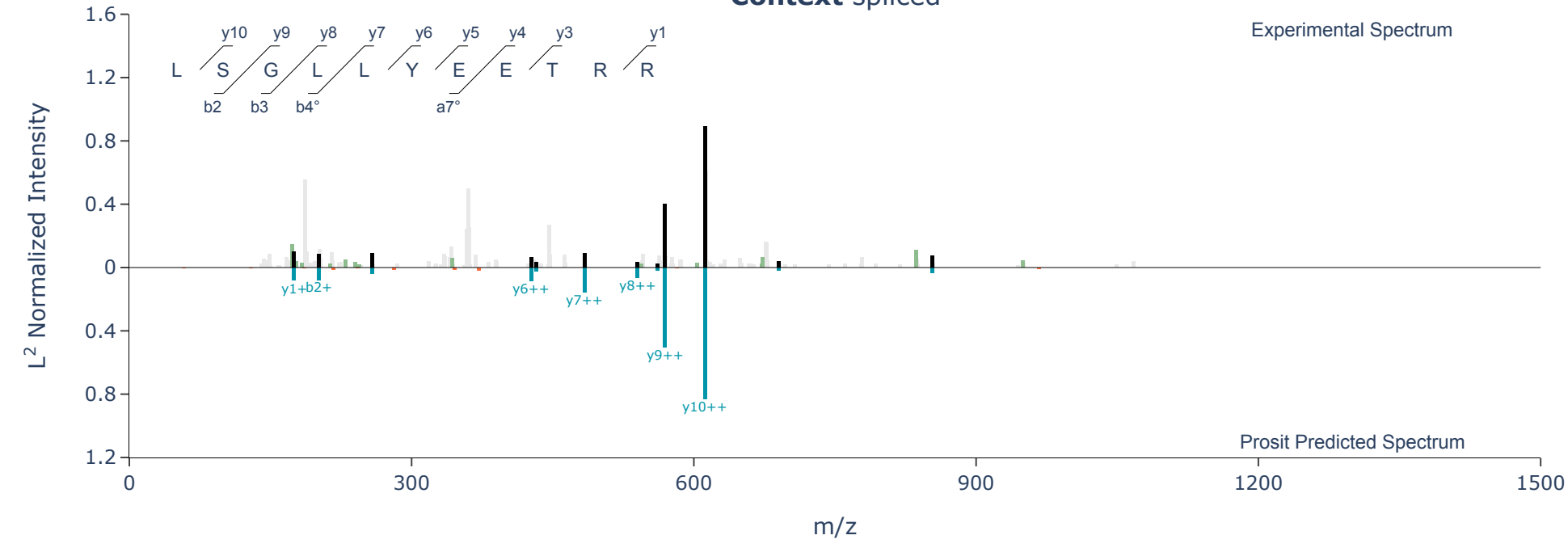
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R1 Scan 14421
Peptide AGMPRQLL Charge 2 Spectral Angle 0.84

Context multimapped



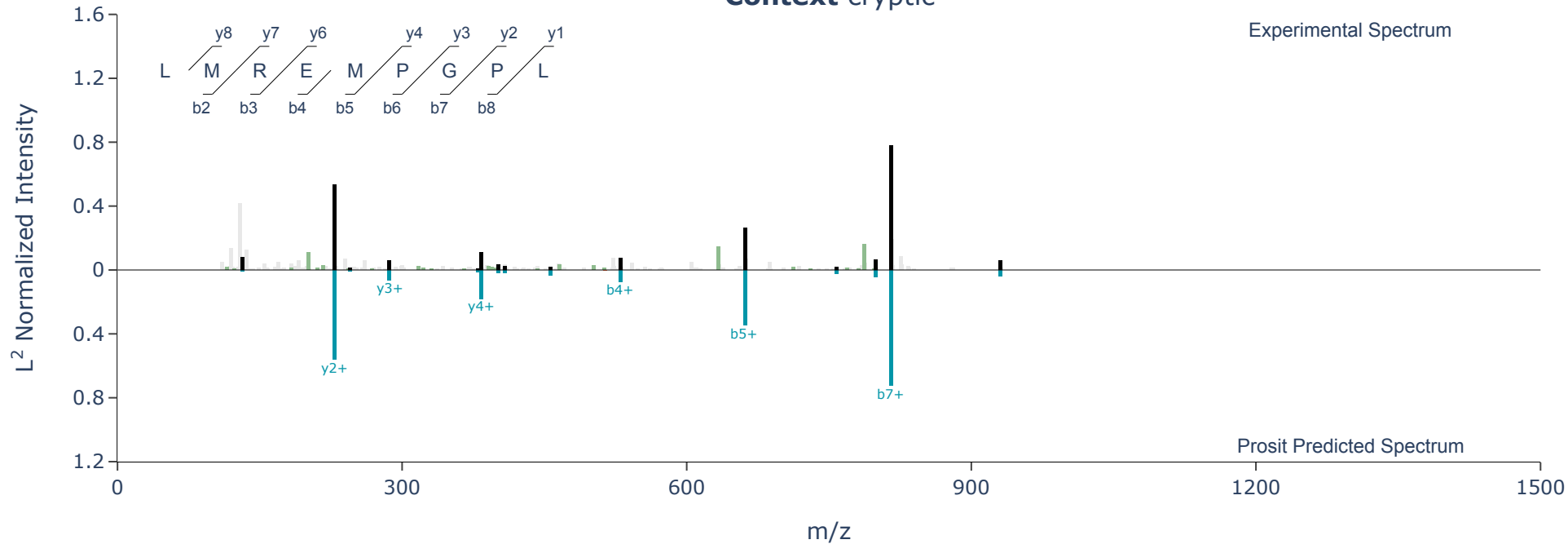
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Peptide LSGLYEETRR Charge 3 Spectral Angle 0.9

Context spliced



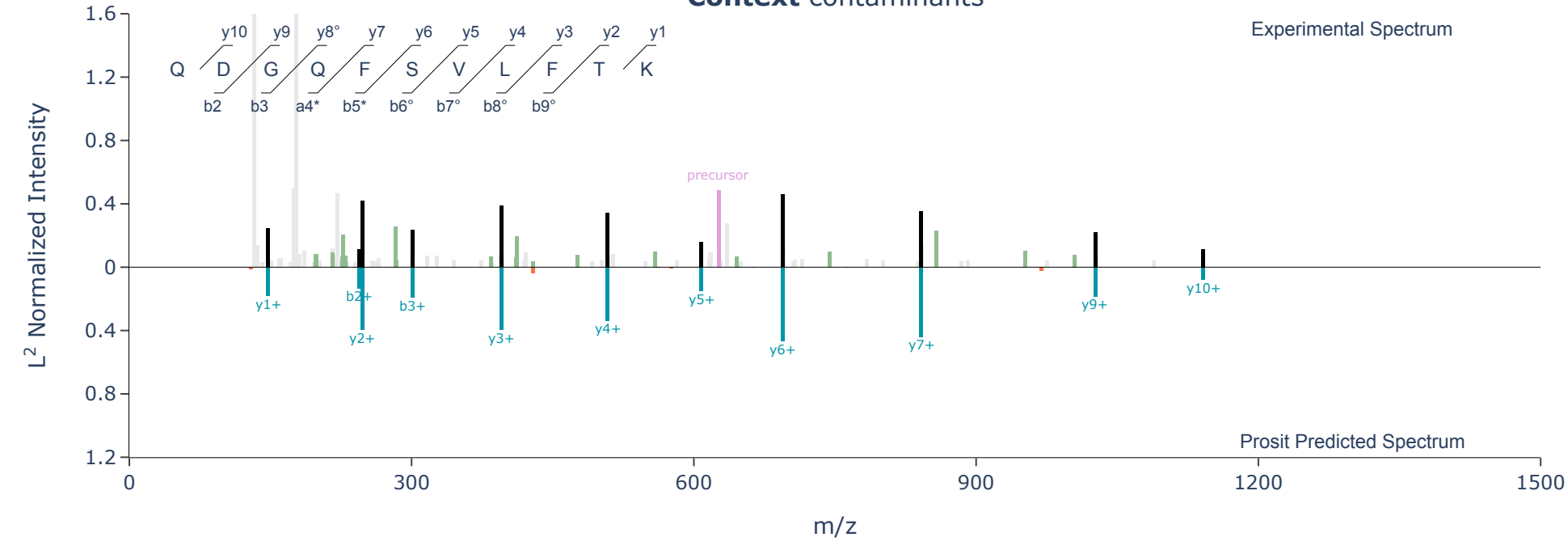
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R2 Scan 17067
Peptide LMREMPGPL Charge 2 Spectral Angle 0.92

Context cryptic



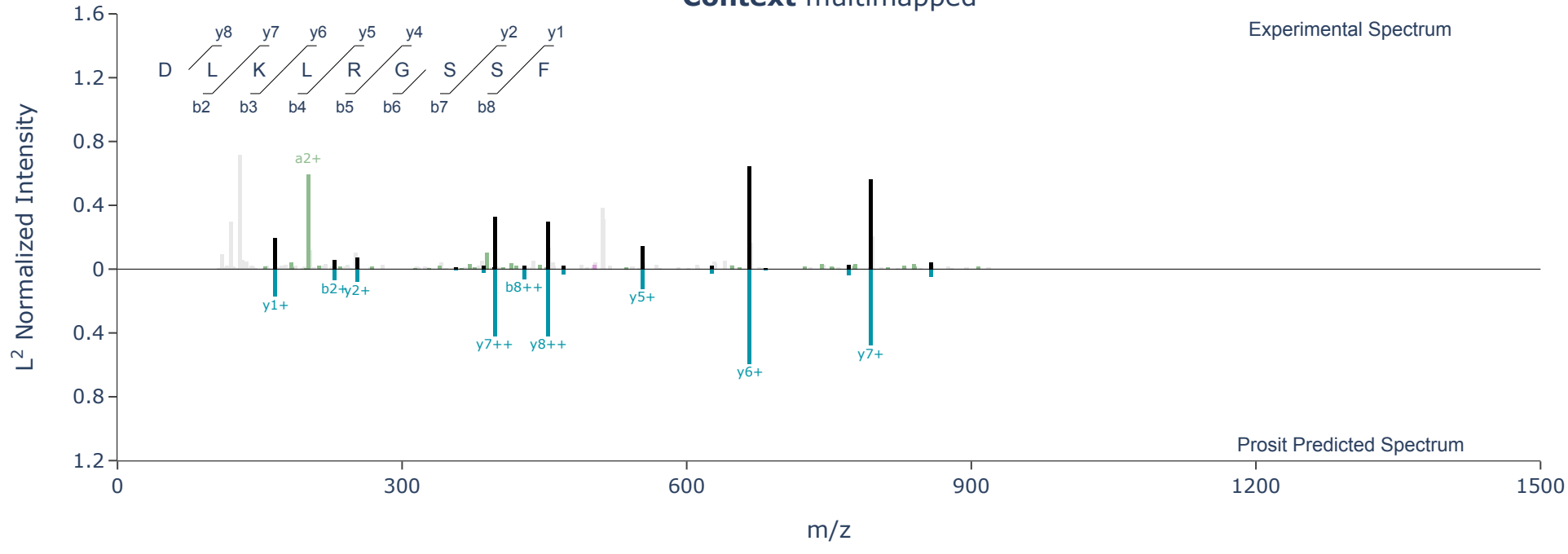
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R1 Scan 20188
Peptide QDGQFSLVFTK Charge 2 Spectral Angle 0.91

Context contaminants



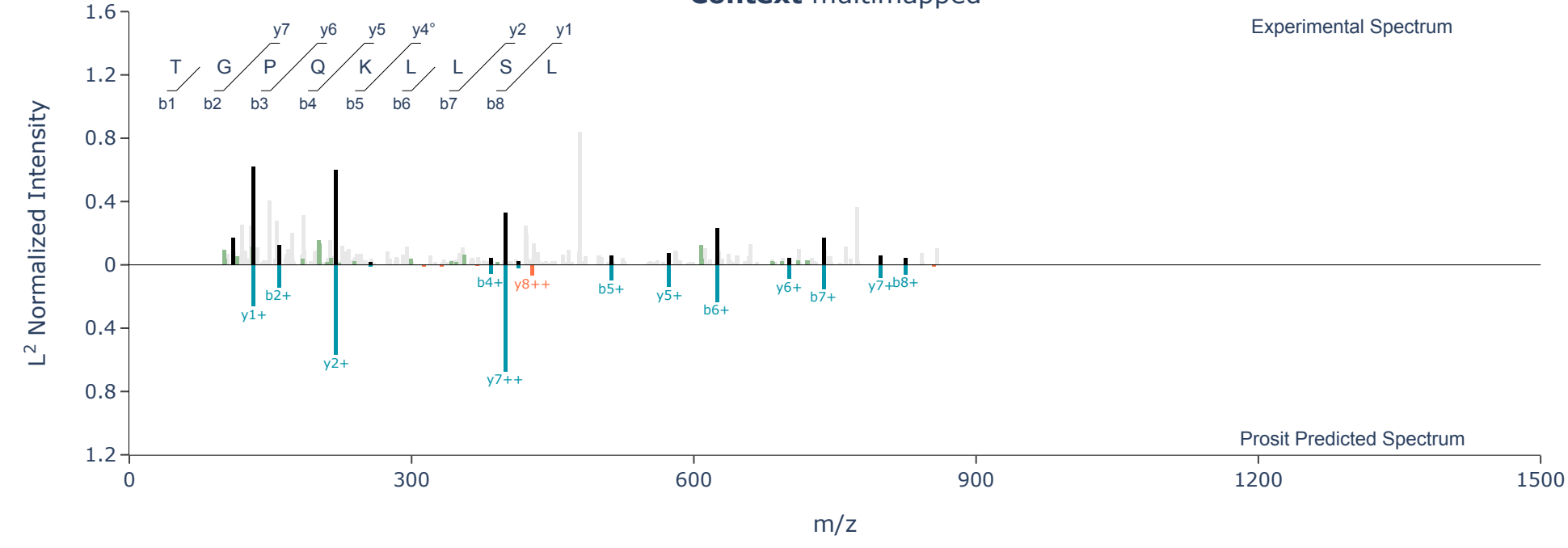
Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R2 Scan 12735
Peptide DLKLRGSSF Charge 2 Spectral Angle 0.88

Context multimapped



Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R2 Scan 17325
Peptide TGPQKLLSL Charge 2 Spectral Angle 0.67

Context multimapped



Source WSoh_Meghna_100424_030524_Expl2_K562_B0801_IC4_R1 Scan 5642
Peptide NTMKKTSF Charge 2 Spectral Angle 0.8

Context multimapped

