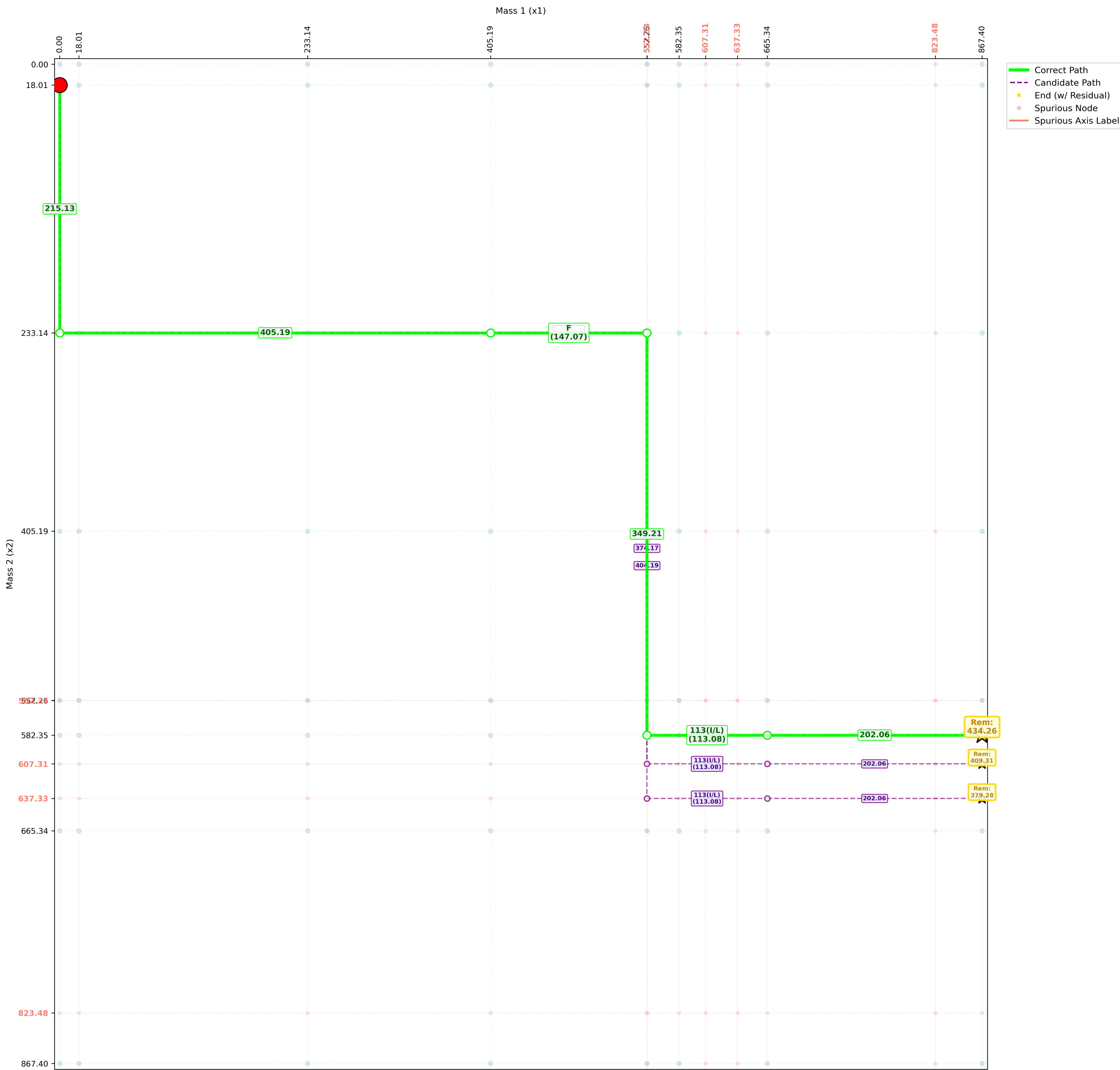


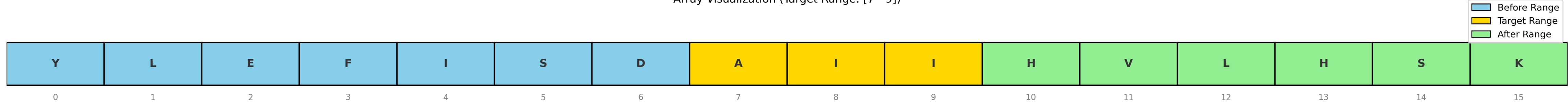
Peptide Fragmentation Analysis: MS/MS Spectrum Interpretation																
Legend: Ion Type (b-ion: Blue, y-ion: Green, Spurious: Red)																
Peptide Sequence: YLEFSDAIIHVLHSK																
Ground Truth	233.138	405.190	552.258	552.338	582.349	607.305	637.332	665.342	823.479	867.401	1016.613	1218.672	1301.666	1331.756	1478.824	1650.877
Peptide 1		405.190	552.258			607.305		665.342		867.401						1650.877
Peptide 2		405.190	552.258					665.342		867.401						1650.877
Peptide 3		405.190	552.258					665.342		867.401			1301.666			1650.877

test1_3+: [YLEFISDAIIHVLHSK+3H]3+



	b1y15(Y)	b2y14(L)	b3y13(E)	b4y12(F)	b5y11(I)	b6y10(S)	b7y9(D)	b8y8(A)	b9y7(I)	b10y6(I)	b11y5(H)	b12y4(V)	b13y3(L)	b14y2(H)	b15y1(S)	Row_Count	Unexplained Count	Abs Average Mass Difference	Unexplained Pairs
Parent	--	--	(b3,y13) (1+ , 2+) (0.0, 0.0) 15	(b4,y12) (1+ , 2+) (0.0, 0.0) 41	(b5,y11) (1+ , 2+) (0.0, 0.0) 39	--	(b7,y9) (1+ , 2+) (0.5, 0.0) 20	--	--	--	(b11,y5) (2+ , 1+) (0.0, 0.0) 25	--	--	(b14,y2) (2+ , 1+) (0.0, 0.5) 2	--	6	0	0.23	
Col_Count	0	0	1	2	2	0	1	0	0	0	1	0	0	1	0	8	0	0.05	nan
Ion Mass	(164.07, 1721.96)	(277.15, 1608.87)	(406.2, 1479.83)	(553.27, 1332.76)	(666.35, 1219.68)	(753.38, 1132.65)	(868.41, 1017.62)	(939.45, 946.58)	(1052.53, 833.5)	(1165.61, 720.42)	(1302.67, 583.36)	(1401.74, 484.29)	(1514.83, 371.2)	(1651.88, 234.14)	(1738.92, 147.11)	0	0	0.0	0

Array Visualization (Target Range: [7 - 9])



■ b-ion ■ y-ion ■ Middle Point

233.138

405.19

552.258

582.349

665.342

867.401

867.401

582.349