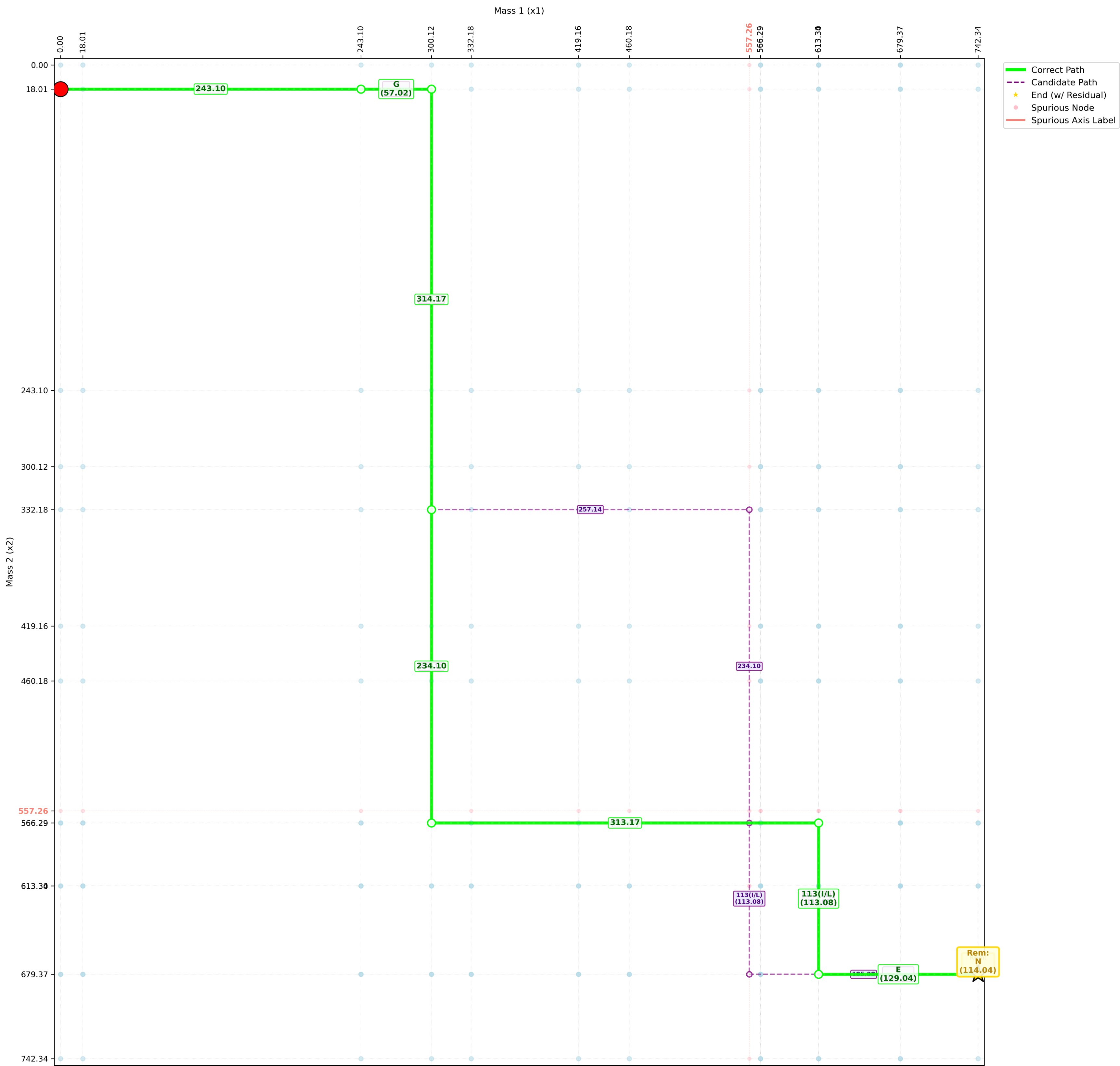


	Peptide Fragmentation Patterns and Masses																					
	Peptide 1: R(ME2)G									Peptide 2: R(ME2)G												
	Fragmentation Pattern (b-ion, y-ion, Spurious)									Fragmentation Pattern (b-ion, y-ion, Spurious)												
	Masses (Da)									Masses (Da)												
	Ground Truth									Ground Truth												
	GW	G		R(Me2)						E				N		L	FS	WK				
Ground Truth	243.101	300.122	332.185	419.159	460.179	557.257				566.285	613.297	613.338	679.369	742.340	793.412	856.383	922.455	969.467	1203.567	1235.630	1292.651	1499.731
Peptide 1	243.101	300.122									613.297			742.340		856.383		969.467	1203.567			
Peptide 2	243.101	300.122				557.257								742.340		856.383		969.467	1203.567			

ME9_3+: [GWGR(Me2)EENLFSWK+3H]3+



	b1y11(G)	b2y10(W)	b3y9(G)	b4y8(R(Me2))	b5y7(E)	b6y6(E)	b7y5(N)	b8y4(L)	b9y3(F)	b10y2(S)	b11y1(W)	Row_Count	Unexplained Count	Abs Average Mass Difference	Unexplained Pairs
Parent	--	(b2,y10) (1+ , 2+) (-0.33, 0.31) 8	(b3,y9) (1+ , 2+) (-0.11, 0.24) 25	--	(b5,y7) (2+ , 1+) (-0.13, 0.4) 24	(b6,y6) (1+ , 2+) (0.03, 0.05) 4	(b7,y5) (1+ , 2+) (0.04, 0.04) 7	(b8,y4) (1+ , 2+) (-0.07, 0.23) 22	--	(b10,y2) (2+ , 1+) (-0.2, 0.21) 33	--	7	0	0.27	
Col_Count	0	3	1	0	3	3	3	3	1	2	0	19	0	0.23	nan
Ion Mass	(58.03, 1479.74)	(244.11, 1293.66)	(301.13, 1236.64)	(485.26, 1052.5)	(614.3, 923.46)	(743.35, 794.42)	(857.39, 680.38)	(970.47, 567.29)	(1117.54, 420.22)	(1204.57, 333.19)	(1390.65, 147.11)	0	0	0.0	0

Array Visualization (Target Index: 6)

- Before Index
- At Index
- After Index



■ b-ion ■ y-ion ■ Middle Point

243.101

300.122

332.185

566.285

613.297

679.369

742.34

742.34

679.369