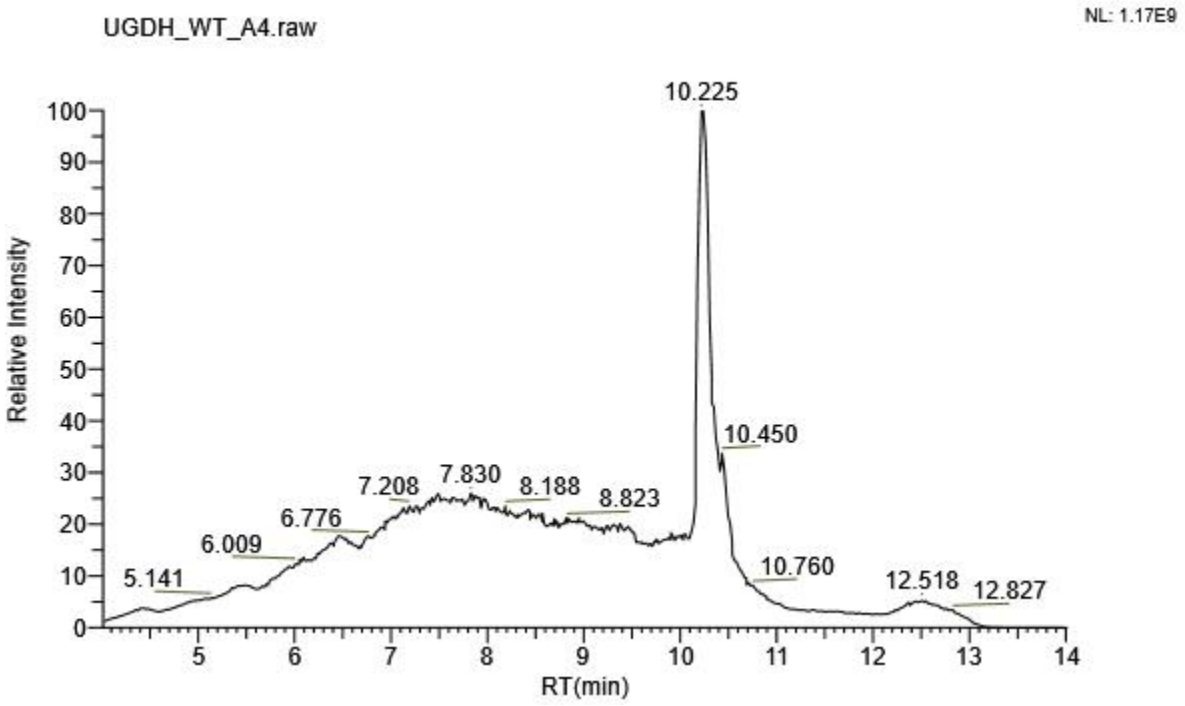
BioPharma Finder Report

Created: 10/15/2025 1:01:04 PM

Sample Information	
Raw File Name	D:\METRIC\Shu\101025_Joe\UGDH_WT_A4_20251010170408.raw
Instrument Method	D:\METRIC\Shu\METHOD\QS_IntactProtein_25min.meth
Vial	Y:D4
Injection Volume (µL)	20
Sample Weight	0
Sample Volume (µL)	0
ISTD Amount	0
Dil Factor	1

Chromatogram Parameters	
Use Restricted Time	True
Time Limits	4.000 - 14.000 minutes
Scan Range	87 - 560
m/z Range	1800 - 4000
Chromatogram Trace Type	TIC
Sensitivity	High
Rel. Intensity Threshold (%)	1

Chromatogram



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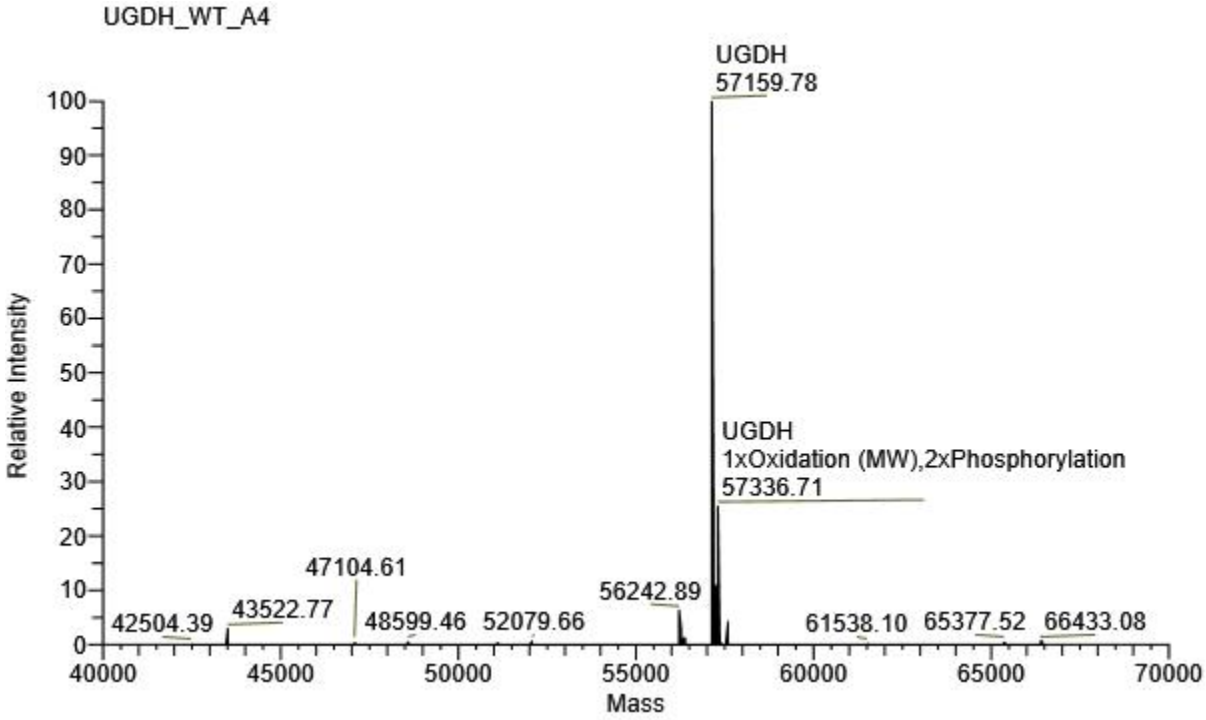
Main Parameters (ReSpect™)	
Deconvolution Results Filter	
Output Mass Range	40000 - 70000
Deconvoluted Spectra Display Mode	Isotopic Profile (new)
Charge State Distribution	
Deconvolution Mass Tolerance	20 ppm
Choice of Peak Model	
Choice of Peak Model	Intact Protein
Resolution at 400 m/z	
Raw File Specific	21213
Generate XIC for Each Component	
Calculate XIC	False
Advanced Parameters (ReSpect™)	
Charge State Distribution	
Model Mass Range	40000 - 70000
Charge State Range	5 - 100
Minimum Adjacent Charges (low & high model mass)	4 - 4
Noise Parameters	
Rel. Abundance Threshold (%)	0
Deconvolution Quality	
Quality Score Threshold	30
Choice of Peak Model	
Target Mass	70000 Da
Peak Model Parameters	
Number of Peak Models	1
Left/Right Peak Shape	2:2
Peak Filter Parameters	
Peak Detection Minimum Significance Measure	1 Standard Deviations
Peak Detection Quality Measure	95%
Specialized Parameters	
Peak Model Width Factor	1
Intensity Threshold Scale	0.01
Deconvolution Parameters	
Noise Compensation	True
Charge Carrier	H
Negative Charge	False
Source Spectra Parameters	
Source Spectra Method	Sliding Windows
Sliding Windows Definition	
RT Range	4.000 - 14.000 minutes
Target Avg Spectrum Width	0.1 minutes
Target Avg Spectrum Offset Scan	1
Sliding Windows Merging Parameters	
Merge Tolerance	30 ppm
Merge Scheme	Legacy Merge Scheme
Max RT Gap	1 minutes
Min. Number of Detected Intervals	3

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Sequences Information	
Sequence Matching Mass Tolerance	20 ppm
Total Number of Sequences	1
Sequence Name	UGDH
Static Modifications	
Max. Number of Modifications	10
Variable Modifications	Oxidation (MW)(SideChain), Phosphorylation(SideChain), Acetylation(SideChain)
Glycosylation	None

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Deconvoluted Spectrum



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Sliding Windows ReSpect Masses Table																		
Row Number	Sequence Name	Modification	Average Mass	Theoretical Mass (Da)	Matched Mass Error (ppm)	Sum Intensity	Relative Abundance	Fractional Abundance	Score	Number of Charge States	Charge State Distribution	Number of Detected Intervals	Mass Std Dev	PPM Std Dev	Delta Mass	Scan Range	Start Time (min)	Stop Time (min)	Apex RT
1	UGDH		57159.78	57160.89	19.4	9834613814.00	100.00	56.12	70.77	15	17 - 31	200	1.40	24.42	0.00	197 - 417	6.426	10.415	8.459
2	UGDH	1xOxidation (MW),2xPhosphorylation	57336.71	57336.85	2.3	2505296173.00	25.47	14.30	50.75	14	18 - 31	149	2.58	44.94	176.94	239 - 414	7.190	10.363	9.397
3			57204.39	0.00	0.0	1838734454.00	18.70	10.49	53.76	12	20 - 31	108	2.65	46.27	44.61	222 - 345	6.885	9.114	7.599
4	UGDH	1xOxidation (MW),1xPhosphorylation	57256.85	57256.87	0.3	1072405843.00	10.90	6.12	49.78	14	18 - 31	69	2.57	44.93	97.07	246 - 337	7.315	8.968	8.081
5			56242.89	0.00	0.0	627234776.00	6.38	3.58	73.16	17	15 - 31	11	2.21	39.25	-916.89	402 - 417	10.139	10.415	10.277
6	UGDH	2xOxidation (MW),4xPhosphorylation,2xAcetylation	57596.93	57596.88	0.9	415337734.69	4.22	2.37	32.58	7	26 - 32	70	2.09	36.35	437.16	87 - 465	4.014	11.376	8.514
7			43522.77	0.00	0.0	293413490.00	2.98	1.67	60.75	12	13 - 24	7	1.60	36.87	-13637.01	408 - 419	10.243	10.450	10.346
8			56284.18	0.00	0.0	285288438.00	2.90	1.63	68.94	16	16 - 31	8	2.14	38.02	-875.60	405 - 417	10.191	10.415	10.294
9			56420.95	0.00	0.0	122430037.00	1.24	0.70	38.52	13	19 - 31	6	1.98	35.12	-738.83	403 - 414	10.157	10.363	10.260
10			56379.49	0.00	0.0	118448383.00	1.20	0.68	54.13	11	21 - 31	5	2.34	41.42	-780.29	404 - 414	10.174	10.363	10.260
11			66433.08	0.00	0.0	68555241.50	0.70	0.39	32.74	6	31 - 36	14	3.20	48.10	9273.30	197 - 340	6.426	9.023	8.777
12			52079.66	0.00	0.0	64960492.50	0.66	0.37	31.21	6	23 - 28	11	3.06	58.82	-5080.12	379 - 397	9.719	10.067	9.875
13			65377.52	0.00	0.0	42714409.50	0.43	0.24	36.27	7	30 - 36	9	3.56	54.46	8217.74	148 - 201	5.459	6.518	6.453
14			48599.46	0.00	0.0	42492883.00	0.43	0.24	30.62	6	22 - 27	8	3.50	71.98	-8560.32	282 - 370	7.955	9.570	9.306
15			47104.61	0.00	0.0	38680713.50	0.39	0.22	38.10	7	18 - 24	3	1.62	34.34	-10055.17	411 - 420	10.294	10.467	10.363
16			51130.70	0.00	0.0	35742932.50	0.36	0.20	36.25	7	13 - 19	3	2.81	54.92	-6029.08	404 - 411	10.174	10.311	10.243
17	UGDH	1xOxidation (MW),3xPhosphorylation,5xAcetylation	57627.32	57627.01	5.3	23476775.25	0.24	0.13	32.25	6	27 - 32	6	3.21	55.76	467.54	181 - 235	6.124	7.137	6.858
18	UGDH	4xOxidation (MW),5xAcetylation	57434.13	57435.07	16.4	20066698.00	0.20	0.11	31.31	6	23 - 28	3	3.90	67.96	274.35	273 - 299	7.795	8.279	7.884
19			65411.70	0.00	0.0	19678946.13	0.20	0.11	31.84	6	31 - 36	7	3.32	50.75	8251.92	111 - 204	4.634	6.573	6.527
20			66466.55	0.00	0.0	16482311.25	0.17	0.09	30.29	5	31 - 35	4	2.45	36.80	9306.78	188 - 217	6.258	6.813	6.767
21			61538.10	0.00	0.0	13669142.00	0.14	0.08	32.33	6	29 - 34	3	4.70	76.33	4378.32	341 - 368	9.023	9.533	9.469
22			48599.08	0.00	0.0	10773954.38	0.11	0.06	31.60	6	22 - 27	5	3.13	64.43	-8560.70	142 - 202	5.335	6.536	6.472
23			42504.39	0.00	0.0	6903865.38	0.07	0.04	33.59	6	18 - 23	4	1.72	40.51	-14655.39	112 - 127	4.659	5.031	4.964
24			62497.78	0.00	0.0	4915980.75	0.05	0.03	32.17	6	28 - 33	3	3.99	63.91	5338.00	112 - 141	4.659	5.335	5.281
25	UGDH	2xOxidation (MW),4xPhosphorylation,2xAcetylation	57596.74	57596.88	2.5	3181362.25	0.03	0.02	34.42	6	27 - 32	3	2.18	37.79	436.96	512 - 518	12.419	12.558	12.489

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