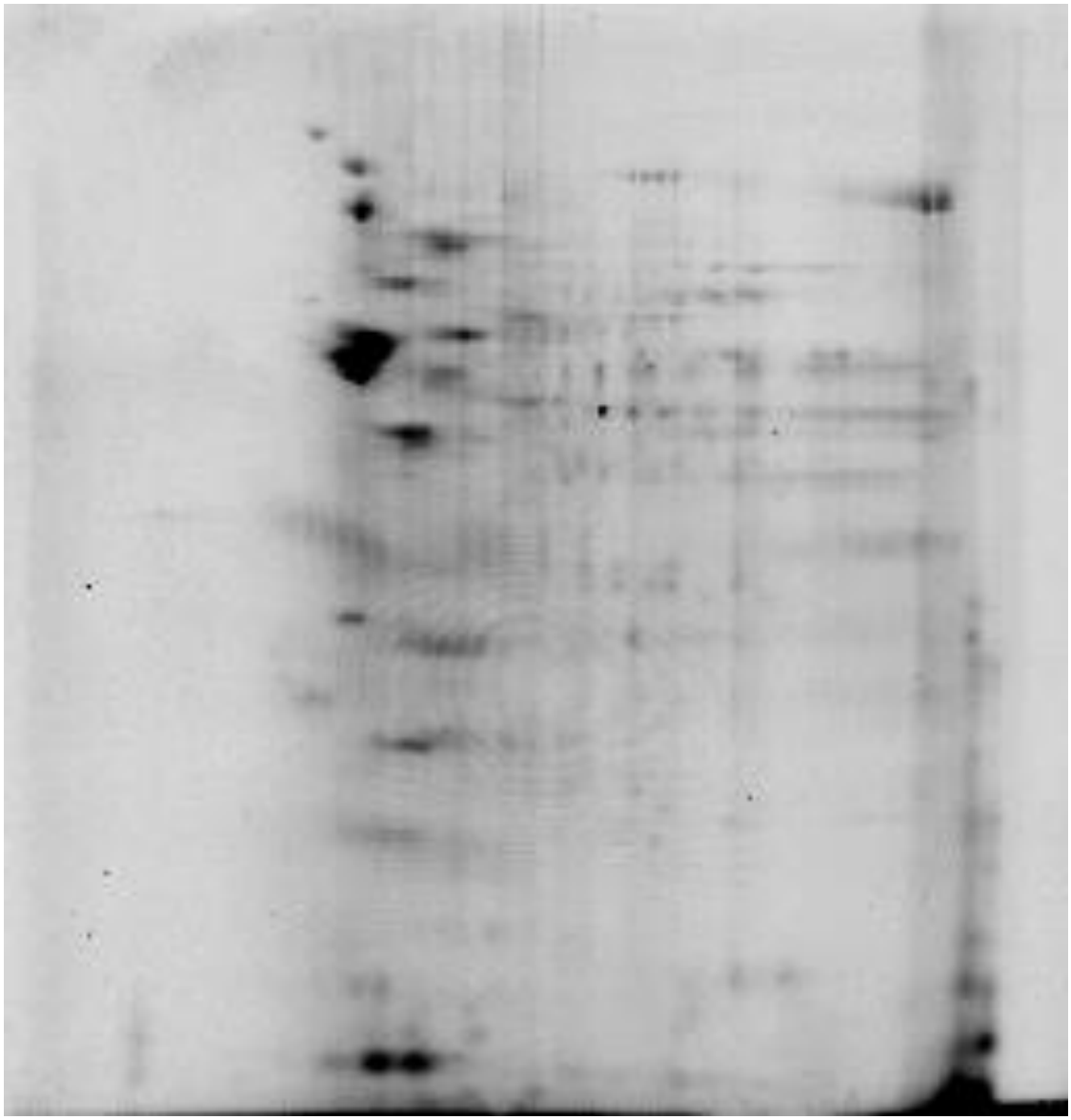
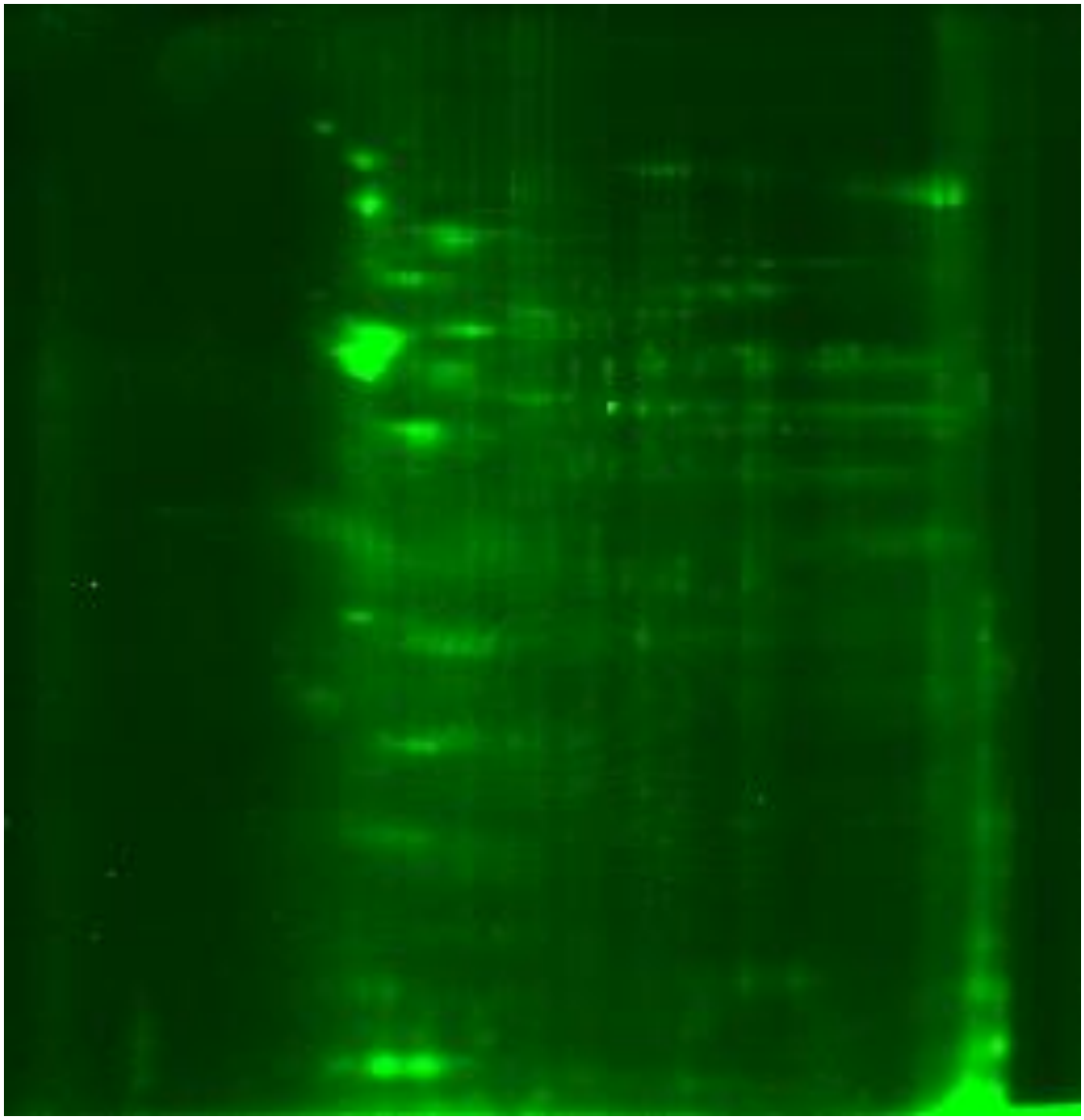
Sample Name - Control (Labelled with Cy-3)

IEF Strip-3-10pH Linear, 17cm strip.



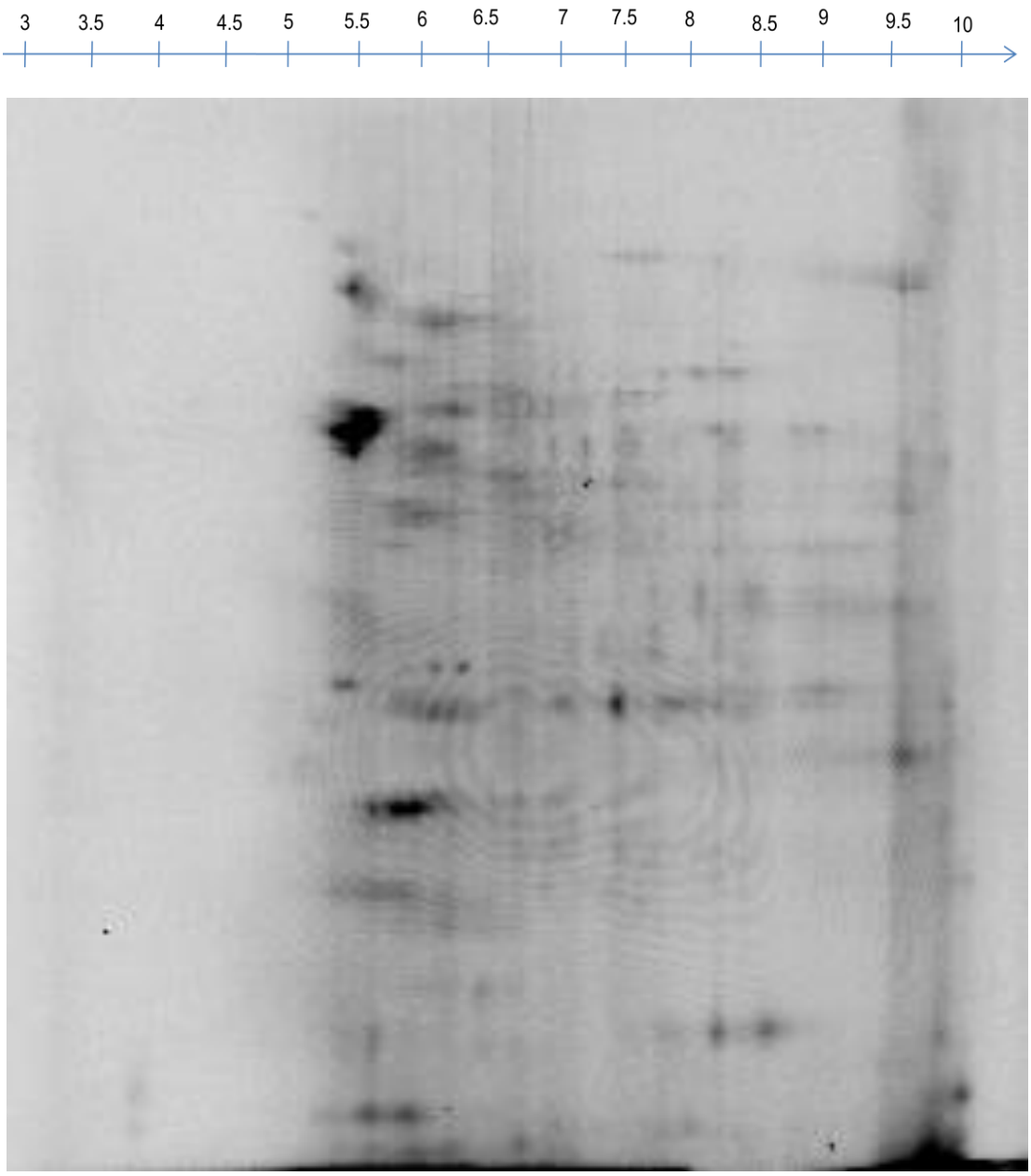
Sample Name - Control (Labelled with Cy-3)

IEF Strip-3-10pH Linear, 17cm strip.



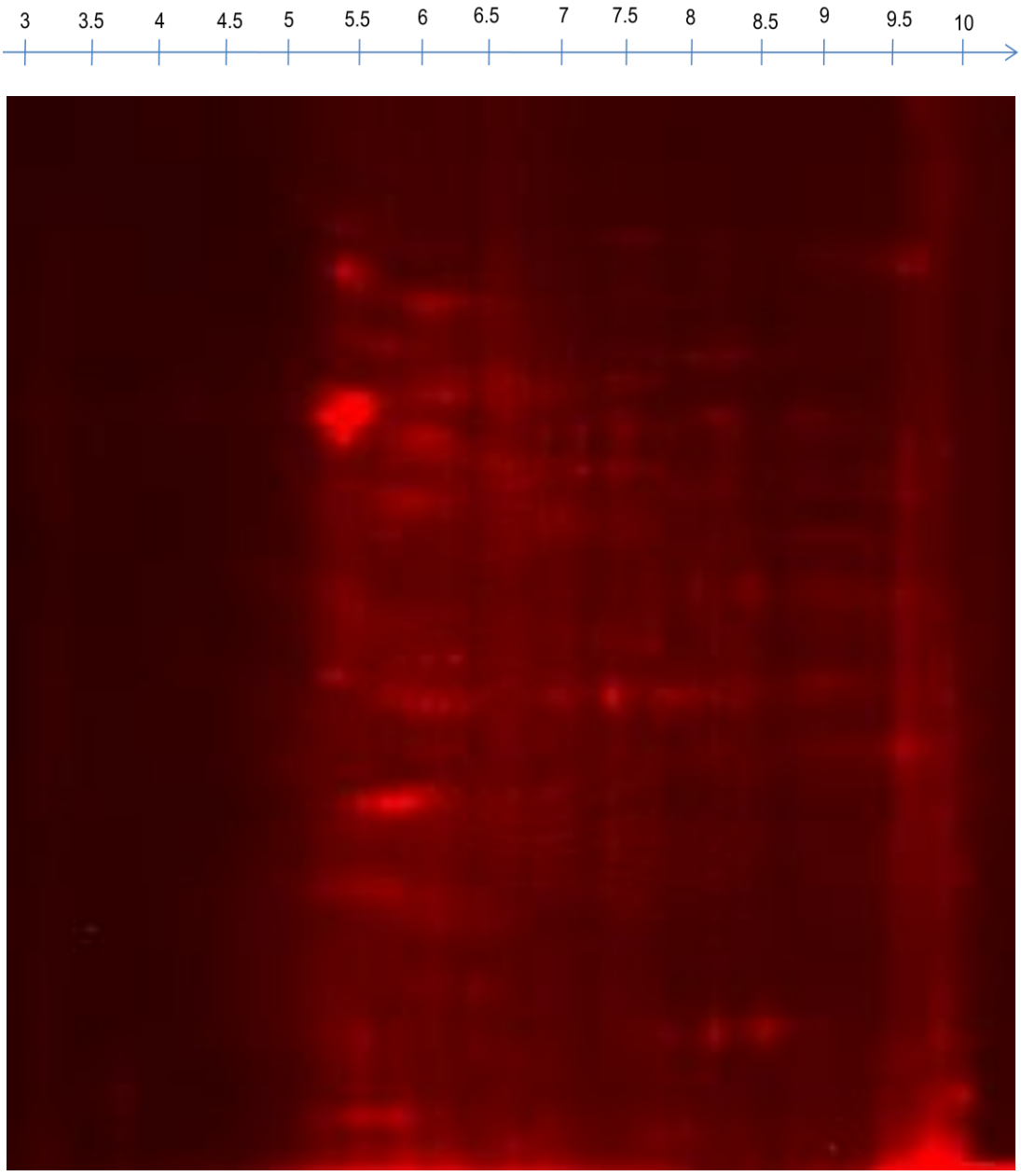
Sample Name – RPL (Labelled with Cy-5)

IEF Strip-3-10pH Linear, 17cm strip.



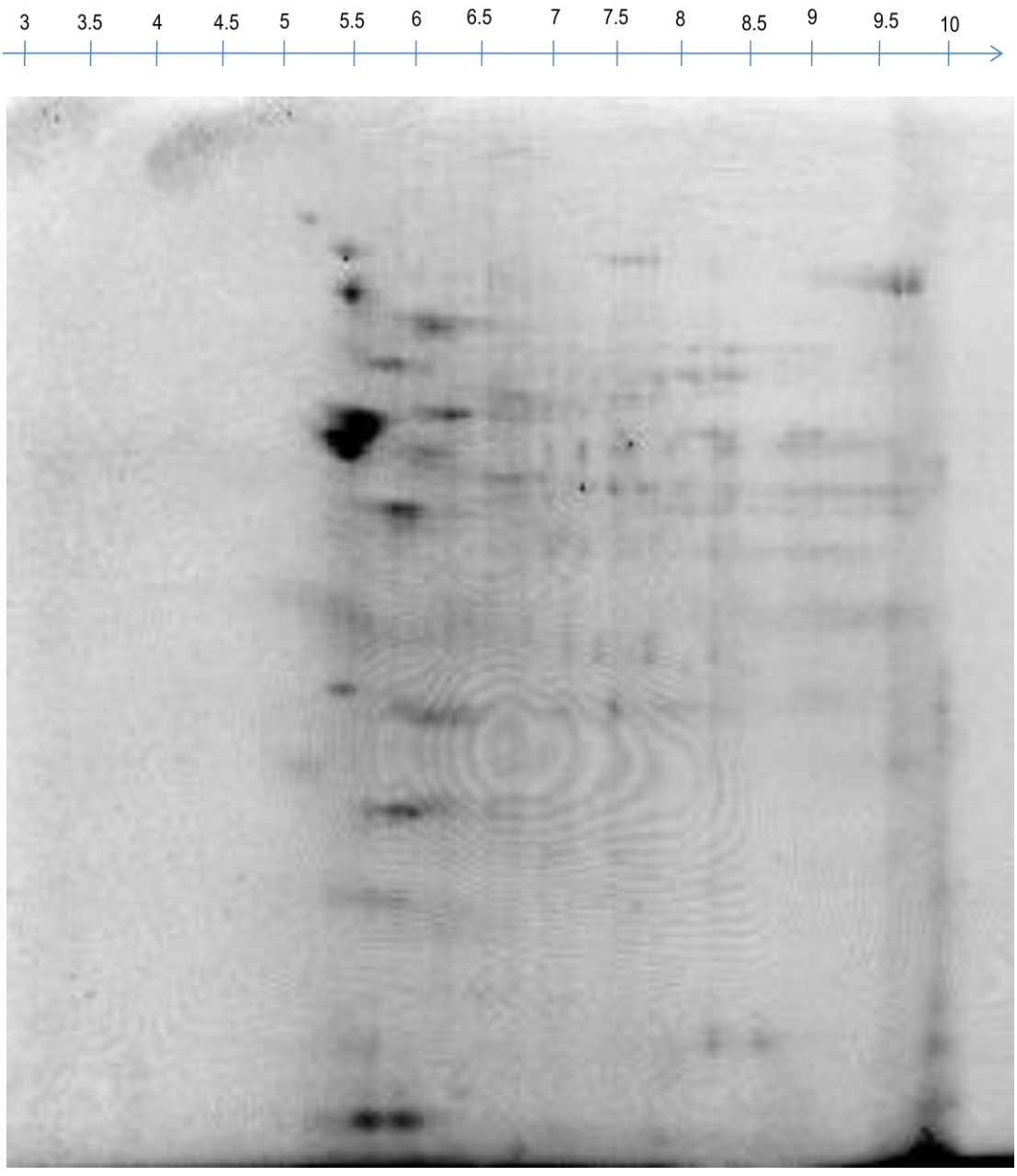
Sample Name - Sample RPL (Labelled with Cy-5)

IEF Strip-3-10pH Linear, 17cm strip.



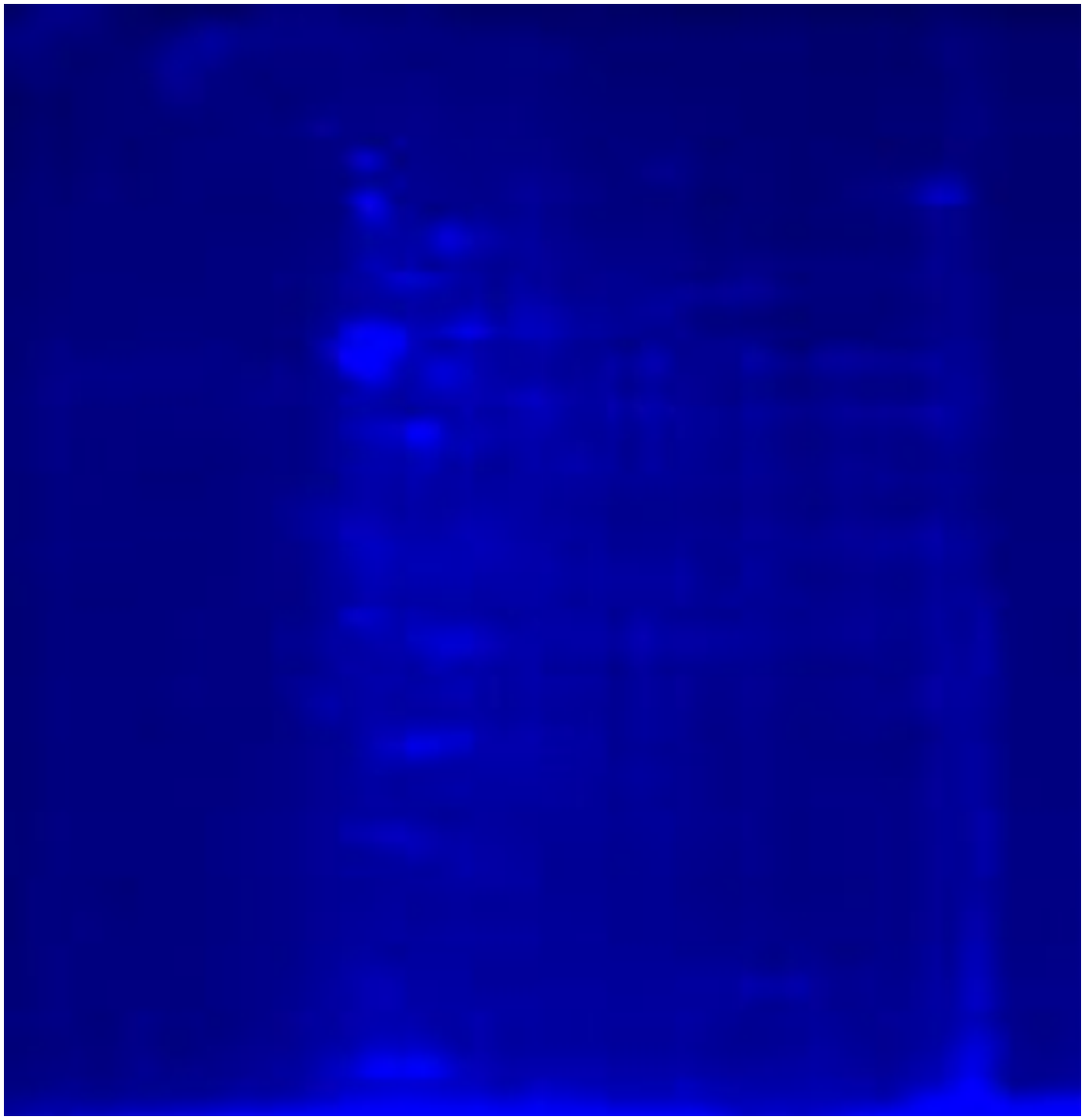
Sample Name- Internal Control (Labelled with Cy-2)

IEF Strip-3-10pH Linear, 17cm strip.



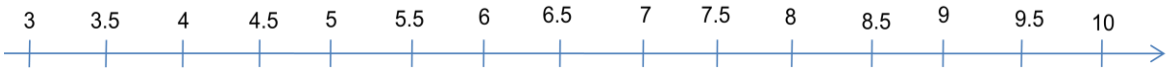
Sample Name – Internal Control (Labelled with Cy-2)

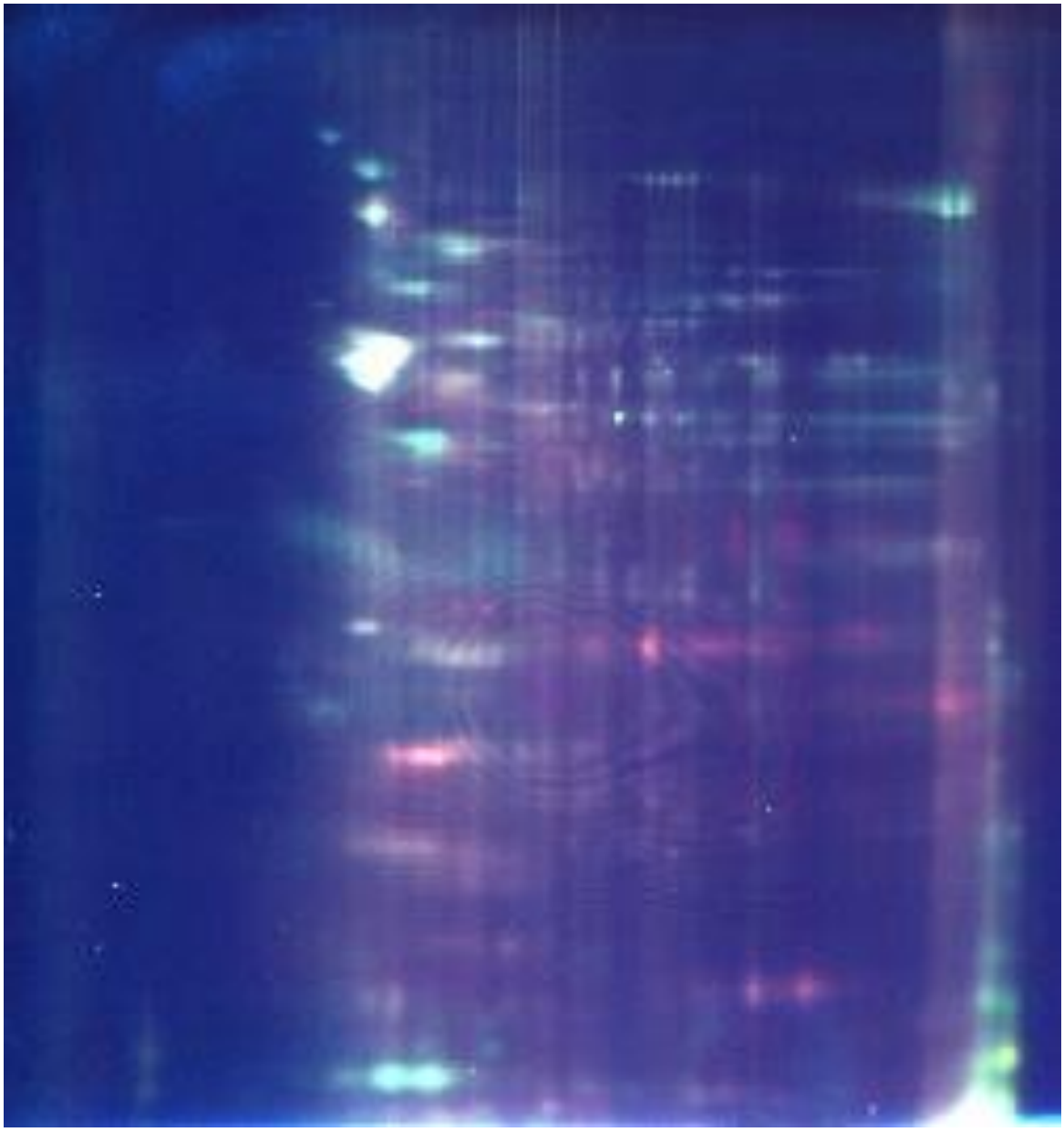
IEF Strip-3-10pH Linear, 17cm strip.



Sample Name: Overlay Image

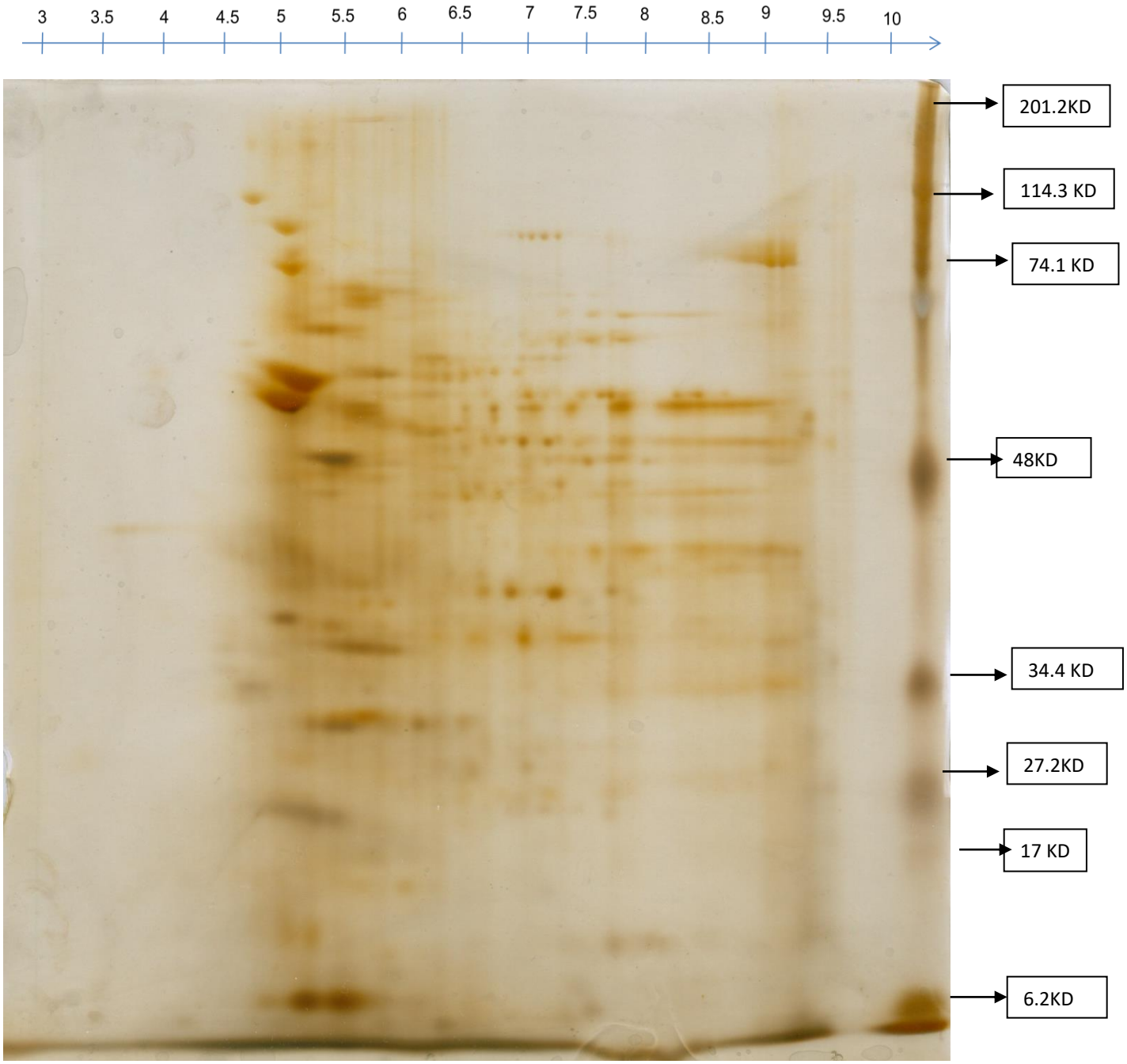
IEF Strip: 3-10pH linear, 17cm strip. 10% Gel

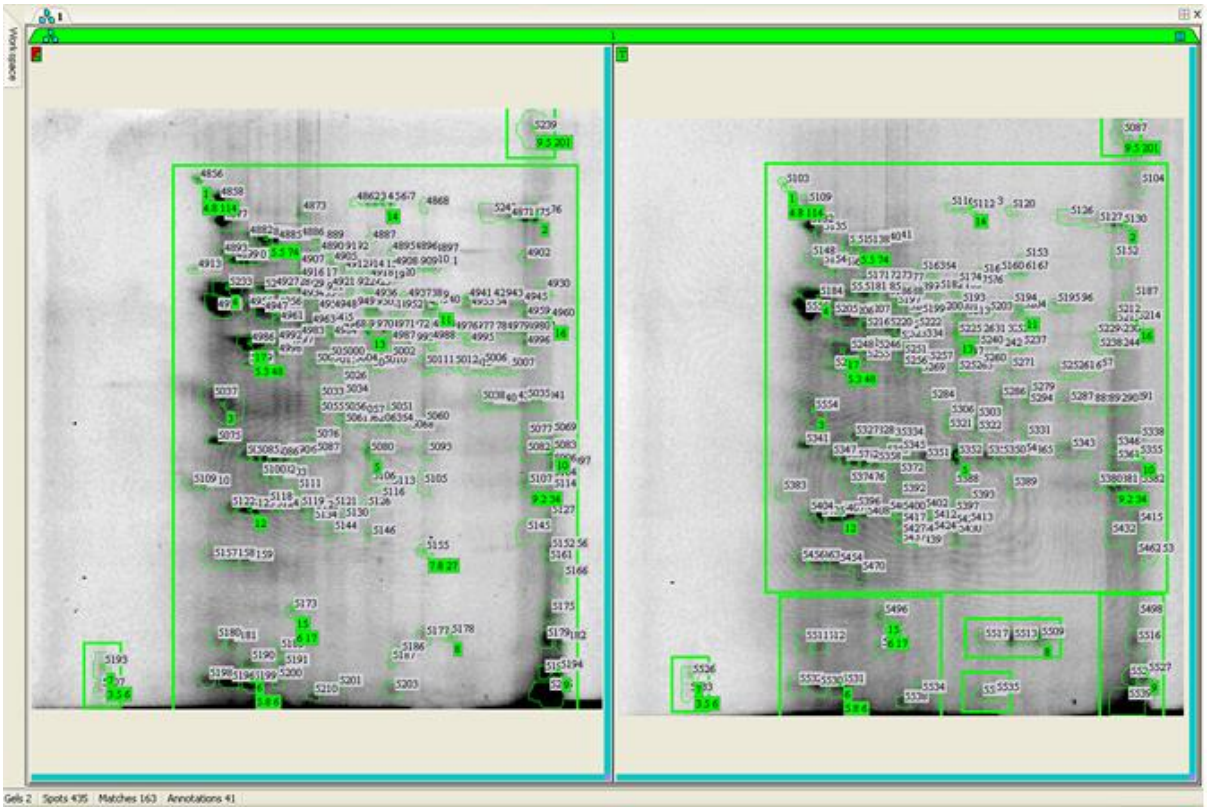


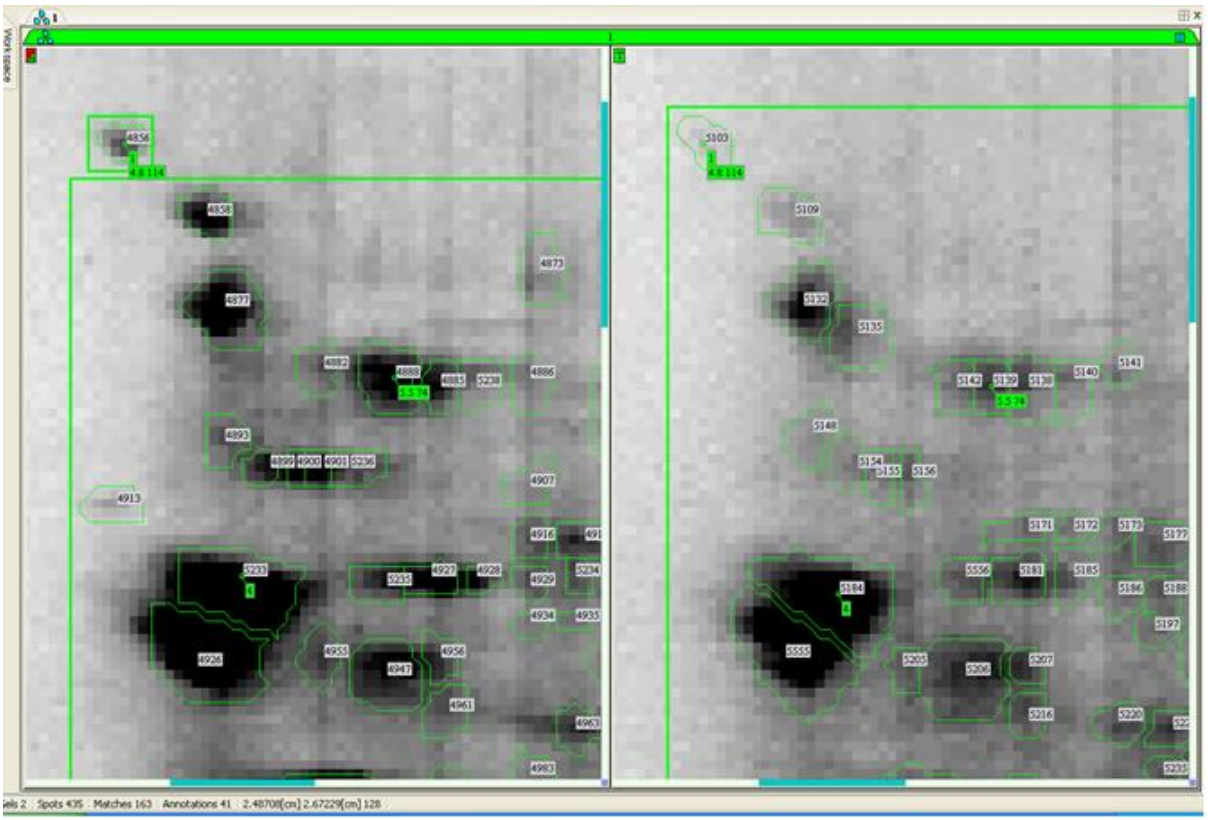


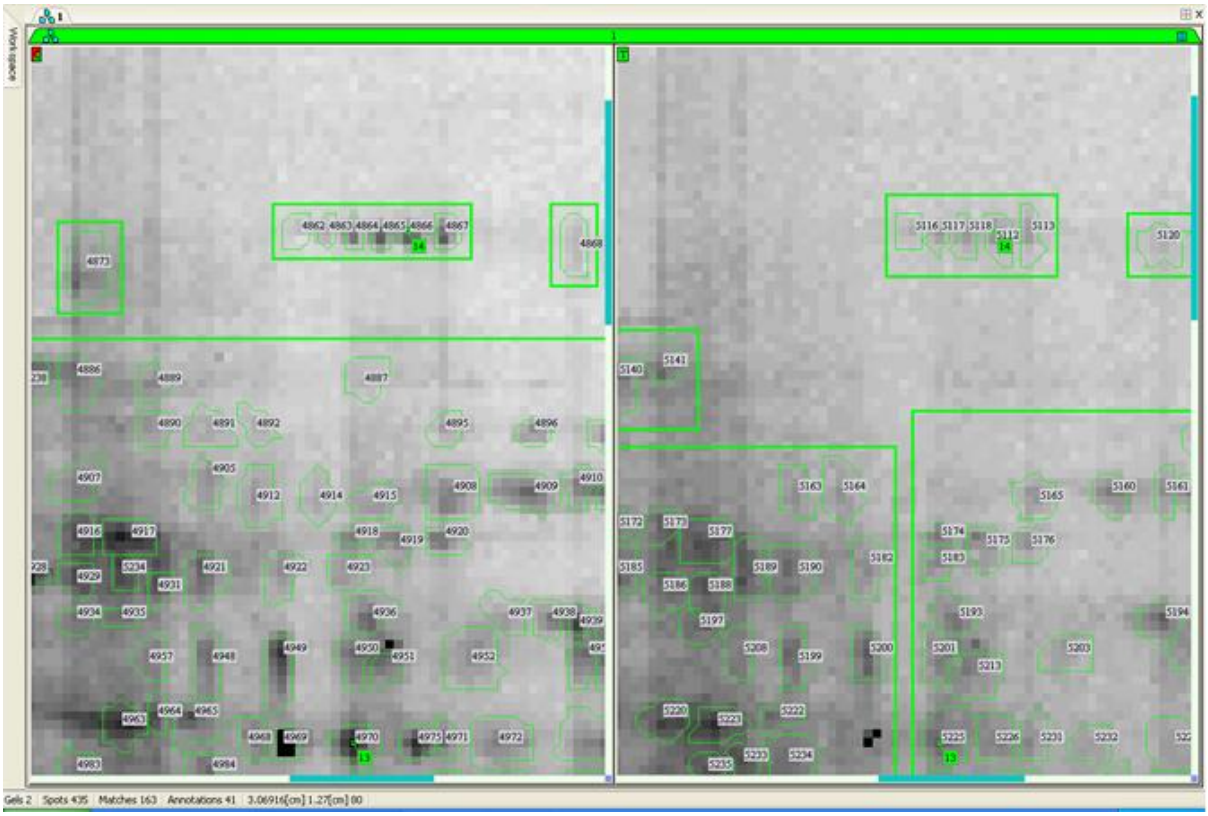
Sample Name: Silver Stained

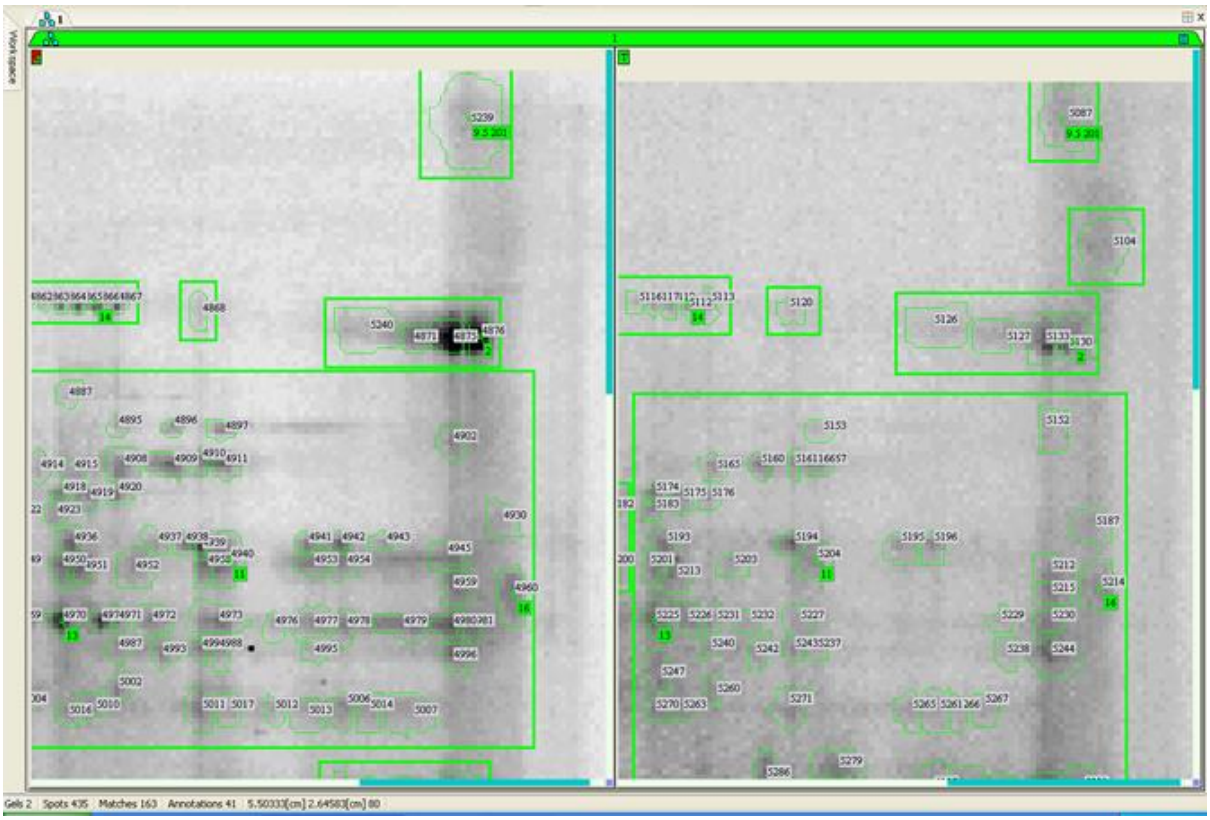
IEF Strip: 3-10pH linear, 17cm strip. 10% Gel

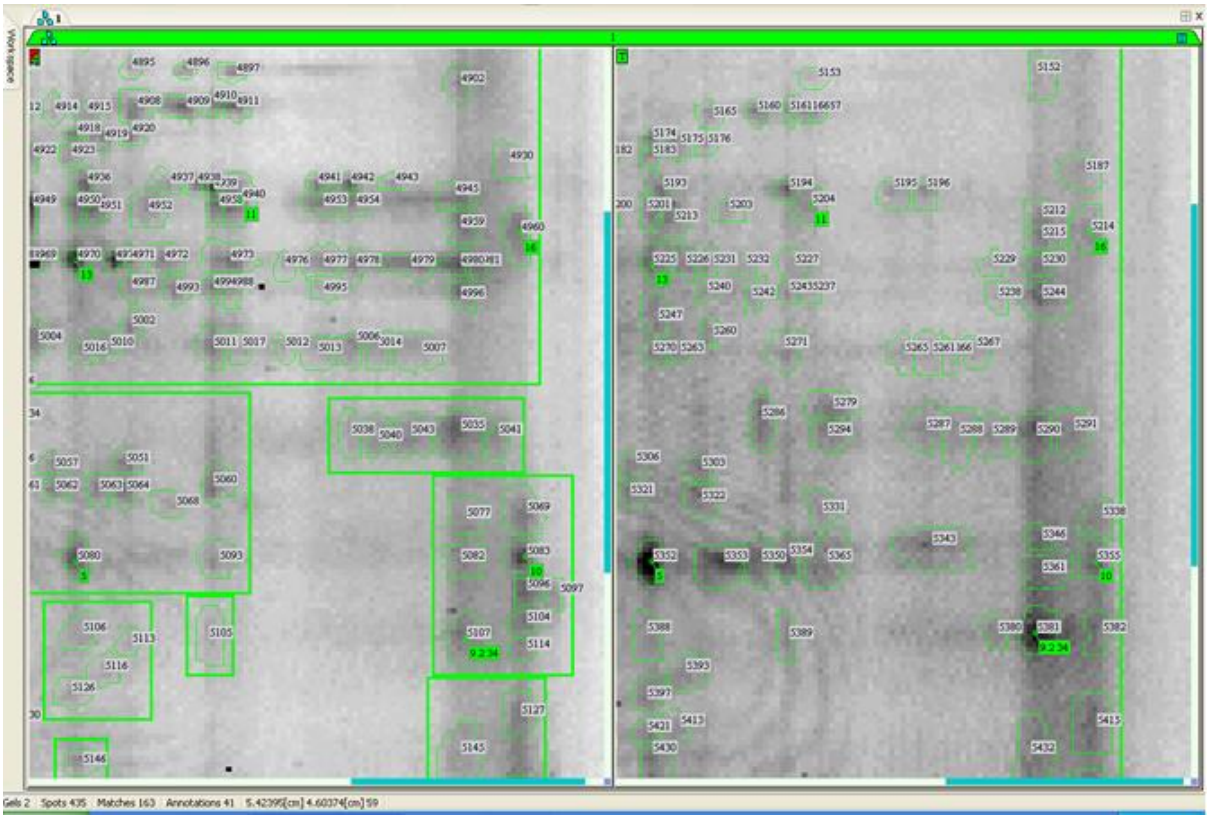


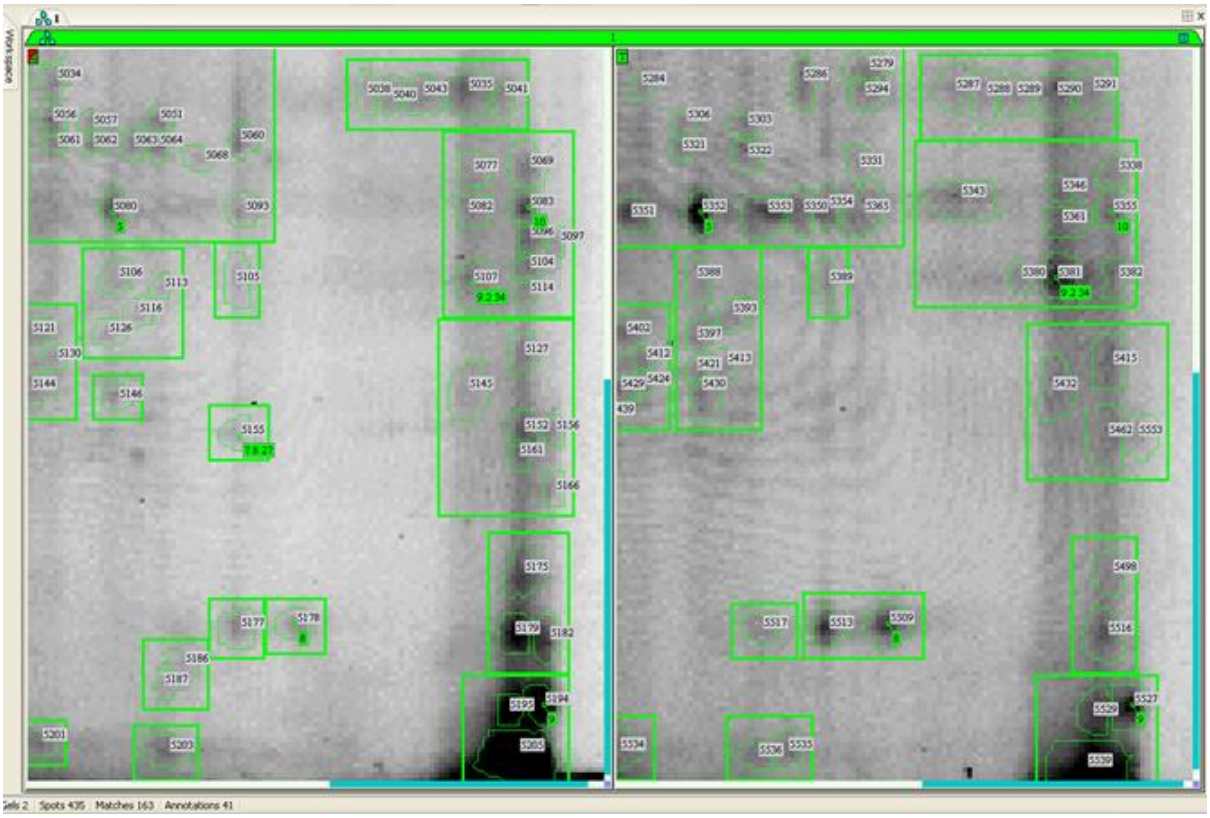

Gels 2 | Spots 435 | Matches 163 | Annotations 41

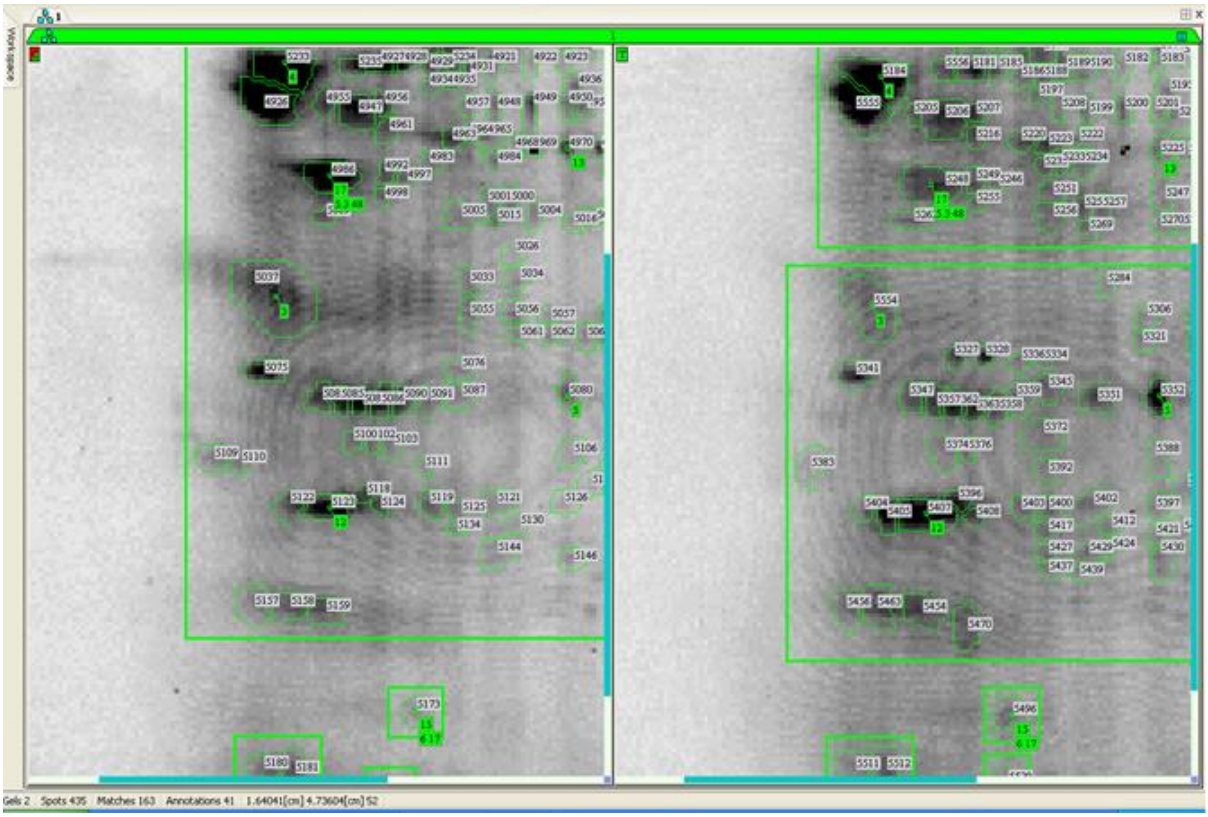

Gels 2 | Spots 435 | Matches 163 | Annotations 41 | 2.48708[cm] 2.67229[cm] 128


Gels 2 | Spots 435 | Matches 163 | Annotations 41 | 3.06916[cm] 1.27[cm] 80


Gels 2 | Spots 435 | Matches 163 | Annotations 41 | 5.50333[cm] 2.64583[cm] 80


Gels 2 | Spots 435 | Matches 163 | Annotations 41 | 5.42395[cm] 4.60374[cm] 59


Gels 2 | Spots 435 | Matches 163 | Annotations 41


Gels 2 Spots 435 Matches 163 Annotations 41 1.64041[cm] 4.73604[cm] 52

Title: Gel Analysis Table [Mean(100%) and M.S.D]

Match ID	Central Tendency	Dispersion	Coef. Variation	C	T
0	0.504457	0.132153	0.26197	0.63661	0.372304
1	1.30276	0.595447	0.457064	1.89821	0.707317
2	0.340966	0.0213522	0.0626228	0.319614	0.362318
3	0.40129	0.0817535	0.203727	0.483043	0.319536
4	5.54663	0.06638	0.0119676	5.61301	5.48025
5	0.391745	0.0735729	0.187808	0.318173	0.465318
6	0.261184	0.00171104	0.0065511	0.262895	0.259473
7	9.42512	0.558375	0.0592433	9.98349	8.86674
8	0.456065	0.12343	0.27064	0.579494	0.332635
9	1.9855	0.666648	0.335758	2.65215	1.31885
10	0.726335	0.044749	0.0616093	0.771084	0.681586
11	1.47278	0.524901	0.356401	1.99768	0.94788
12	0.876196	0.146009	0.16664	1.02221	0.730187
13	1.87262	0.172748	0.0922496	2.04537	1.69987
14	0.532135	0.14571	0.273822	0.677845	0.386425
15	0.244993	0.114061	0.465569	0.130932	0.359054
16	0.228382	0.00929472	0.0406981	0.219087	0.237677
17	0.66655	0.146592	0.219927	0.519958	0.813142
18	0.494825	0.0847633	0.1713	0.410061	0.579588
19	1.06524	0.00632495	0.00593756	1.07157	1.05892
20	0.577498	0.319204	0.552736	0.258294	0.896701
21	0.474089	0.154175	0.325202	0.319914	0.628263
22	0.660346	0.126243	0.191176	0.786589	0.534104
23	0.349754	0.184818	0.528423	0.164936	0.534572
24	0.495595	0.159299	0.32143	0.336296	0.654895
25	0.611902	0.164975	0.269611	0.446927	0.776878
26	0.545859	0.074571	0.136612	0.471288	0.62043
27	0.436367	0.109464	0.250854	0.326903	0.545831
28	0.532321	0.202408	0.380237	0.329913	0.734729
29	0.275033	0.0858475	0.312136	0.189185	0.36088

30	0.711085	0.140212	0.19718	0.570874	0.851297
31	0.215821	0.0941574	0.436275	0.309979	0.121664
32	0.0853665	0.0188454	0.220759	0.0665211	0.104212
33	0.139856	0.0235082	0.168088	0.116348	0.163364
34	0.715656	0.246614	0.344599	0.469042	0.96227
35	0.203619	0.0672117	0.330086	0.136407	0.27083
36	0.188958	0.0460584	0.243749	0.1429	0.235017
37	0.172088	0.0682475	0.396584	0.103841	0.240336
38	2.50156	1.08176	0.432436	1.4198	3.58333
39	0.547304	0.208656	0.381243	0.338648	0.75596
40	0.41131	0.124568	0.302857	0.286742	0.535879
41	0.247429	0.0232366	0.093912	0.270666	0.224193
42	0.400026	0.175768	0.439391	0.224258	0.575793
43	0.228001	0.10945	0.480043	0.118551	0.337452
44	0.0907331	0.0361038	0.397912	0.0546293	0.126837
45	0.190876	0.0547356	0.28676	0.13614	0.245612
46	0.775087	0.359836	0.464252	0.415252	1.13492
47	0.224883	0.0392923	0.174724	0.185591	0.264175
48	0.239996	0.00524697	0.0218627	0.234749	0.245243
49	0.134864	0.0252293	0.187072	0.109634	0.160093
50	0.195946	0.0872711	0.445383	0.108675	0.283217
51	0.372333	0.165994	0.445821	0.206339	0.538327
52	0.258114	0.0595085	0.230552	0.198605	0.317622
53	0.437396	0.0222056	0.0507678	0.41519	0.459602
54	0.460214	0.0401628	0.0872697	0.420051	0.500377
55	0.462501	0.0869706	0.188044	0.37553	0.549471
56	0.260736	0.0423592	0.16246	0.218377	0.303096
57	0.498362	0.0361895	0.0726169	0.534552	0.462172
58	0.442464	0.0202451	0.0457555	0.462709	0.422218
59	0.574181	0.0284044	0.0494695	0.602585	0.545776
60	0.509836	0.11947	0.23433	0.390366	0.629305
61	0.628212	0.320666	0.510442	0.307546	0.948877
62	0.306117	0.0972299	0.317623	0.403347	0.208887

63	0.113009	0.0172735	0.152851	0.130282	0.0957354
64	0.834853	0.0457588	0.0548107	0.880611	0.789094
65	0.479528	0.116346	0.242626	0.595874	0.363182
66	0.267321	0.101019	0.377893	0.166303	0.36834
67	0.15988	0.0116373	0.0727878	0.171517	0.148242
68	0.256494	0.0368573	0.143697	0.293352	0.219637
69	0.148486	0.00111926	0.00753783	0.147367	0.149605
70	0.225663	0.0147394	0.0653159	0.210923	0.240402
71	0.366873	0.0275792	0.0751737	0.394453	0.339294
72	0.373081	0.189464	0.507837	0.183616	0.562545
73	0.306228	0.0929963	0.303683	0.213232	0.399224
74	0.281748	0.120841	0.428897	0.160907	0.402589
75	2.78865	1.43391	0.514194	4.22255	1.35474
76	0.740154	0.0805023	0.108764	0.659652	0.820657
77	0.175991	0.0420649	0.239017	0.218056	0.133926
78	0.13688	0.0149385	0.109136	0.121941	0.151818
79	0.141224	0.0710583	0.503159	0.0701661	0.212283
80	0.210724	0.010905	0.0517501	0.221629	0.199819
81	0.332996	0.0327855	0.0984561	0.30021	0.365781
82	0.142229	0.00798106	0.0561142	0.15021	0.134248
83	0.267477	0.137361	0.513545	0.130116	0.404838
84	0.256524	0.0788306	0.307303	0.177693	0.335355
85	0.266251	0.0187948	0.0705905	0.247456	0.285046
86	0.14177	0.00519077	0.0366141	0.146961	0.136579
87	0.198308	0.0330529	0.166675	0.165255	0.23136
88	0.187343	0.0260519	0.13906	0.161291	0.213395
89	0.118649	0.00302782	0.0255191	0.121677	0.115621
90	0.160629	0.031232	0.194436	0.129397	0.191861
91	0.442124	0.150608	0.340646	0.291516	0.592732
92	0.0902479	0.0073244	0.0811587	0.0829235	0.0975723
93	0.1525	0.044299	0.290486	0.196799	0.108201
94	0.258332	0.0376243	0.145643	0.220707	0.295956
95	0.0739302	0.00136164	0.0184179	0.0725686	0.0752918

96	2.05235	0.0258232	0.0125823	2.07817	2.02653
97	0.141822	0.0671001	0.473128	0.0747223	0.208922
98	0.265555	0.0997079	0.37547	0.165847	0.365263
99	0.229404	0.0923753	0.402675	0.321779	0.137029
100	0.199543	0.00951986	0.0477083	0.209063	0.190023
101	0.328054	0.0911196	0.277758	0.419174	0.236935
102	0.173824	0.080662	0.464043	0.254486	0.0931625
103	0.12805	0.0237123	0.18518	0.104338	0.151763
104	0.293591	0.0297559	0.101352	0.323347	0.263835
105	0.14901	0.0487312	0.327034	0.197741	0.100278
106	0.306198	0.0444212	0.145074	0.350619	0.261776
107	0.234079	0.0268691	0.114787	0.260948	0.20721
108	0.544761	0.023573	0.0432722	0.521188	0.568334
109	0.328	0.0262368	0.0799901	0.301763	0.354237
110	0.125971	0.0252778	0.200664	0.100693	0.151248
111	0.299323	0.0309337	0.103345	0.330257	0.26839
112	0.204509	0.017703	0.0865637	0.186806	0.222212
113	0.200268	0.0627176	0.313168	0.262986	0.137551
114	0.197538	0.0885463	0.44825	0.108992	0.286084
115	0.227539	0.0361768	0.158992	0.191362	0.263716
116	0.269203	0.00448531	0.0166615	0.264717	0.273688
117	0.195095	0.0176502	0.0904699	0.177445	0.212745
118	1.2507	0.319034	0.255085	0.931664	1.56973
119	0.238107	0.00157359	0.00660875	0.239681	0.236534
120	0.219779	0.045114	0.20527	0.174665	0.264893
121	0.52454	0.134474	0.256365	0.659014	0.390066
122	0.22625	0.0494679	0.218643	0.176782	0.275718
123	0.1823	0.0196421	0.107746	0.162658	0.201942
124	0.209903	0.0850055	0.404974	0.124898	0.294909
125	0.287712	0.0155299	0.0539774	0.272182	0.303242
126	0.178749	0.0457072	0.255706	0.133042	0.224457
127	0.299424	0.0137893	0.0460528	0.313213	0.285634
128	0.636331	0.0568825	0.0893914	0.693213	0.579448

129	5.75341	0.407083	0.0707552	6.16049	5.34632
130	0.114423	0.0291582	0.254829	0.143581	0.0852643
131	0.156217	0.0276975	0.177301	0.12852	0.183915
132	0.244319	8.16E-04	0.00334037	0.243503	0.245135
133	0.145886	0.00876547	0.0600842	0.154652	0.137121
134	0.18976	0.0653748	0.344513	0.124385	0.255135
135	0.092016	0.0131931	0.143379	0.0788229	0.105209
136	0.443934	0.0391453	0.0881781	0.48308	0.404789
137	0.195112	0.059819	0.306589	0.254931	0.135293
138	0.15554	0.0284077	0.182639	0.127132	0.183948
139	0.244805	0.0447113	0.18264	0.289517	0.200094
140	0.139417	0.00362597	0.026008	0.143043	0.135791
141	0.252816	0.0469847	0.185845	0.2998	0.205831
142	0.2581	0.0840632	0.3257	0.342163	0.174037
143	0.117914	0.00674161	0.057174	0.111172	0.124655
144	0.250063	0.043742	0.174924	0.206321	0.293806
145	0.146667	0.0483023	0.329333	0.194969	0.0983646
146	0.331922	0.0761291	0.229358	0.408051	0.255793
147	0.981779	0.541668	0.55172	1.52345	0.440111
148	0.209492	0.0402451	0.192108	0.249737	0.169247
149	0.589296	0.0503908	0.0855101	0.538905	0.639687
150	1.62509	0.258639	0.159154	1.88373	1.36645
151	0.746861	0.235404	0.315192	0.982266	0.511457
152	0.89054	0.143931	0.161622	1.03447	0.74661
153	0.371394	0.0288327	0.0776336	0.342562	0.400227
154	0.111342	0.00663182	0.0595624	0.117974	0.104711
155	0.144928	0.0256576	0.177037	0.170586	0.11927
156	0.12524	0.0090557	0.0723069	0.116184	0.134295
157	0.0730122	0.0281362	0.385363	0.101148	0.044876
158	0.0744659	0.0252585	0.339196	0.0492074	0.0997244
159	0.617836	0.195567	0.316535	0.813402	0.422269
160	0.229251	0.069493	0.30313	0.298744	0.159758
161	0.307982	0.0601447	0.195287	0.247837	0.368126

162	0.330635	0.0175504	0.053081	0.348185	0.313085

Spot Table

SpotID	Match ID	Pixel X	Pixel Y	pI	MW	Intensity	Area	Vol	%Vol	Saliency	Ac	Bookmark	Comment	Landmark	pI_MW
5240	0	206	46	8.71304	89	37	6.93041	97.8117	0.63661	0					
5239	1	224	8	9.5	201	37	14.0708	291.65	1.89821	0					9.5 201
5238	2	114	57	5.875	74	46	2.52015	49.1069	0.319614	0					
5236		100	67	5.75	67	78	2.24013	71.8285	0.467497	0					
5235	3	104	80	5.55	60	78	2.38014	74.217	0.483043	0					
5234		125	79	6.24407	60	30	1.33008	20.6162	0.134181	0					
5233	4	88	79	5.08261	60	159	8.05048	862.409	5.61301	0				4	
5210	5	126	261	6.27458	5	41	2.31014	48.8855	0.318173	0					
5207	6	31	258	3.47273	6	28	4.20025	40.3924	0.262895	6.44855					
5205	7	231	259	9.74792	5	155	12.6007	1533.91	9.98349	0					
5203	8	162	259	7.37288	5	37	4.48027	89.0362	0.579494	0					
5201	161	137	257	6.61017	6	24	2.94018	38.0788	0.247837	0					
5200		110	254	5.70833	6	61	3.01018	45.7724	0.297911	0					
5199	9	99	255	5.8	6	136	6.58039	407.489	2.65215	0				6	5.8 6
5198	10	79	254	4.88696	6	52	4.13025	118.473	0.771084	0					
5196	11	89	255	5.10435	6	118	5.18031	306.933	1.99768	0					
5195	12	229	251	9.67708	6	87	2.73016	157.056	1.02221	0					
5194	13	236	250	9.925	6	157	3.92023	314.26	2.04537	0				9	
5193	14	32	248	3.5	6	32	7.07042	104.147	0.677845	0				7	3.5 6
5191		113	248	5.83333	6	31	3.2902	44.6736	0.290759	0					
5190		98	246	5.3	7	35	3.3602	57.9098	0.376907	0					
5187		161	246	7.34237	7	13	2.24013	17.1743	0.11178	0					
5186	15	165	242	7.46441	8	15	2.73016	20.117	0.130932	0					
5185	16	111	241	5.75	8	22	3.50021	33.6616	0.219087	0					
5182		237	237	9.96042	9	79	3.78022	155.703	1.01339	0					
5181	17	90	237	5.12609	9	37	4.69028	79.8887	0.519958	0					
5180	18	83	236	4.97391	10	35	4.20025	63.0037	0.410061	0					
5179	19	230	236	9.7125	10	72	4.34026	164.641	1.07157	0					
5178	20	187	234	8.13478	11	28	3.64022	39.6855	0.258294	0				8	

5177	21	176	235	7.8	10	33	4.41026	49.1531	0.319914	0					
5175	22	232	224	9.78333	16	47	5.46032	120.855	0.786589	0					
5173	23	117	223	6	17	21	3.78022	25.3415	0.164936	10.116				15	6 17
5166		238	208	9.99583	22	39	2.80017	56.0752	0.364966	0					
5161		231	201	9.74792	25	33	2.03012	36.7677	0.239304	0					
5159	24	97	201	5.27826	25	34	3.85023	51.6701	0.336296	0					
5158	25	89	200	5.10435	26	35	4.06024	68.6679	0.446927	0					
5157	26	81	200	4.93043	26	28	5.25031	72.4109	0.471288	0					
5156	27	238	196	9.99583	27	39	2.31014	50.2269	0.326903	0					
5155		176	197	7.8	27	19	3.4302	24.346	0.158457	0					7.8 27
5152	28	232	196	9.78333	27	37	3.15019	50.6894	0.329913	0					
5146	29	152	189	7.0678	29	30	2.59015	29.0673	0.189185	0					
5145	30	221	188	9.16957	29	22	6.51039	87.7117	0.570874	0					
5144	31	135	188	6.54915	29	22	4.20025	47.6266	0.309979	0					
5134	32	126	183	6.27458	30	18	1.26007	10.2206	0.066521	2.1166					
5130	33	140	182	6.70169	30	18	1.96012	17.8763	0.116348	0					
5127	34	232	181	9.78333	31	33	4.13025	72.0658	0.469042	0					
5126	35	150	177	7.00678	31	19	2.94018	20.9582	0.136407	0					
5125	36	127	179	6.30508	31	22	1.7501	21.9558	0.1429	0					
5124	37	109	178	5.66667	31	26	1.6101	15.9546	0.103841	0					
5123	38	98	178	5.3	31	94	4.83029	218.144	1.4198	0				12	
5122	39	89	177	5.10435	31	43	3.22019	52.0315	0.338648	0					
5121	40	135	177	6.54915	31	21	3.57021	44.0564	0.286742	0					
5119	41	120	177	6.09153	31	32	2.59015	41.5864	0.270666	0					
5118	42	106	175	5.54167	32	39	1.6101	34.456	0.224258	0					
5116	43	156	173	7.18983	32	15	2.94018	18.2147	0.118551	0					
5114		233	169	9.81875	33	24	1.89011	26.3162	0.171279	0					
5113		161	168	7.34237	34	13	1.89011	8.7963	0.057251	0					
5111	44	119	169	6.06102	33	11	1.54009	8.3935	0.054629	0					
5110	45	78	168	4.86522	34	22	1.6801	20.9172	0.13614	0					
5109		72	167	4.7093	34	44	3.4302	67.4607	0.43907	0					
5107	46	222	167	9.2	34	30	5.60033	63.8012	0.415252	0					9.2 34

5106	47	152	166	7.0678	34	15	3.2902	28.515	0.185591	0					
5105	48	175	167	7.76949	34	19	4.62028	36.068	0.234749	0					
5104		233	164	9.81875	35	26	1.96012	28.3128	0.184274	0					
5103		112	164	5.79167	35	21	1.89011	16.4062	0.10678	0					
5102	49	107	163	5.58333	35	20	1.7501	16.8448	0.109634	0					
5100	50	103	163	5.6	35	18	1.96012	16.6973	0.108675	0					
5097		239	159	10.0313	36	26	2.03012	30.9203	0.201245	0					
5096		233	158	9.81875	36	22	2.17013	20.4412	0.133042	6.2211					
5093	51	177	153	7.83043	37	24	3.85023	31.7029	0.206339	0					
5091	52	120	154	6.09153	37	22	2.80017	30.5146	0.198605	0					
5090	53	114	154	5.875	37	50	2.59015	63.7918	0.41519	0					
5089	54	105	155	5.5	36	63	1.96012	64.5387	0.420051	0					
5088	55	96	154	5.25652	37	41	2.80017	57.6982	0.37553	0					
5087	56	127	153	6.30508	37	22	3.01018	33.5525	0.218377	0					
5086	57	109	155	5.66667	36	59	2.87017	82.131	0.534552	0					
5085	58	100	154	5.75	37	51	2.31014	71.0927	0.462709	0					
5083	59	233	152	9.81875	37	63	3.3602	92.584	0.602585	0				10	
5082	60	221	153	9.16957	37	28	4.06024	59.9776	0.390366	0					
5080	61	151	153	7.03729	37	46	3.15019	47.2528	0.307546	0				5	
5077	62	222	145	9.2	38	26	4.06024	61.9721	0.403347	0					
5076	63	127	147	6.30508	38	18	2.52015	20.0172	0.130282	0					
5075	64	83	148	4.97391	38	92	4.13025	135.301	0.880611	0					
5069	65	233	144	9.81875	39	37	4.83029	91.5528	0.595874	0					
5068		169	143	7.58644	39	17	2.59015	15.6809	0.10206	5.6822					
5064	66	160	140	7.31186	39	35	2.03012	25.5515	0.166303	14.9411					
5063		155	140	7.15932	39	24	2.31014	26.8274	0.174607	0					
5062	67	147	140	6.91525	39	29	1.96012	26.3526	0.171517	0					
5061		140	140	6.70169	39	18	1.6801	13.4408	0.08748	0					
5060	68	176	139	7.8	40	35	3.15019	45.0719	0.293352	0					
5057	69	147	136	6.91525	40	22	1.82011	22.6421	0.147367	0					
5056		139	135	6.67119	41	39	2.52015	36.0741	0.234789	0					
5055		129	135	6.3661	41	29	2.73016	38.0706	0.247783	0					

5051	70	160	135	7.31186	41	29	2.24013	32.4072	0.210923	0					
5043	71	212	130	8.89565	42	24	4.41026	60.6055	0.394453	0					
5041	72	228	130	9.64167	42	24	2.59015	28.2117	0.183616	5.00073					
5040	73	206	131	8.71304	41	22	2.66016	32.7619	0.213232	4.0171					
5038	74	201	130	8.56087	42	15	3.08018	24.7225	0.160907	0					
5037	75	86	131	5.03913	41	70	19.8812	648.773	4.22255	0				3	
5035	76	221	129	9.16957	42	39	6.23037	101.352	0.659652	0					
5034	77	140	127	6.70169	42	29	2.52015	33.5032	0.218056	0					
5033		129	128	6.3661	42	22	2.73016	29.8162	0.19406	0					
5026		139	121	6.67119	44	13	1.96012	11.1307	0.072444	2.46763					
5017		181	114	7.95217	45	19	2.31014	22.7404	0.148007	0					
5016	78	152	115	7.0678	45	22	1.6101	18.7356	0.121941	0					
5015	79	135	114	6.54915	45	24	1.05006	10.7806	0.070166	7.67126					
5014		206	114	8.71304	45	30	2.59015	31.2977	0.203702	0					
5013	80	195	115	8.37826	45	21	3.15019	34.0521	0.221629	0					
5012		189	114	8.19565	45	21	1.6101	12.7408	0.082924	3.25271					
5011	81	176	114	7.8	45	35	3.08018	46.1257	0.30021	0					
5010	82	157	114	7.22034	45	24	1.82011	23.079	0.15021	0					
5009	83	97	113	5.27826	46	30	1.89011	19.9916	0.130116	0					
5007		213	114	8.92609	45	22	4.90029	53.0255	0.345118	0					
5006	84	202	113	8.5913	46	26	2.52015	27.3016	0.177693	6.21846					
5005	85	127	113	6.30508	46	20	3.78022	38.0203	0.247456	0					
5004		144	113	6.82373	46	29	2.45015	35.8612	0.233404	0					
5002	86	161	110	7.34237	46	27	2.31014	22.5797	0.146961	0					
5001	87	133	110	6.48814	46	22	2.17013	25.3905	0.165255	0					
5000	88	138	110	6.64068	46	22	2.66016	24.7815	0.161291	5.98443					
4998	89	110	109	5.70833	47	28	1.33008	18.695	0.121677	0					
4997	90	115	105	5.91667	48	28	1.54009	19.8812	0.129397	4.15506					
4996	91	221	105	9.16957	48	39	2.38014	44.7899	0.291516	0					
4995		196	104	8.4087	48	11	1.54009	7.70046	0.050119	0					
4994	92	176	103	7.8	48	30	1.47009	12.7408	0.082924	4.58234					
4993	93	169	104	7.58644	48	31	2.17013	30.2371	0.196799	0					

4992	94	110	103	5.70833	48	35	2.03012	33.9105	0.220707	0					
4988		179	103	7.8913	48	28	2.24013	28.3517	0.184528	4.49616					
4987	95	161	103	7.34237	48	17	1.6801	11.1498	0.072569	0					
4986	96	98	104	5.3	48	129	6.44038	319.3	2.07817	0				17	5.3 48
4984	97	135	101	6.54915	49	27	1.47009	11.4807	0.074722	6.23323					
4983		120	101	6.09153	49	19	2.17013	25.5765	0.166465	0					
4981		224	99	9.5	50	22	1.33008	12.5527	0.081699	0					
4980	98	221	99	9.16957	50	33	2.03012	25.4815	0.165847	6.78021					
4979	99	212	99	8.89565	50	35	3.4302	49.4397	0.321779	0					
4978		202	99	8.5913	50	29	2.38014	32.2401	0.209835	0					
4977		196	99	8.4087	50	28	3.50021	41.8625	0.272463	4.18656					
4976		189	99	8.19565	50	22	1.7501	17.7198	0.11533	0					
4975	100	158	98	7.25085	51	61	1.47009	32.1214	0.209063	0					
4973	101	179	98	7.8913	51	43	4.48027	64.4038	0.419174	14.8532					
4972	102	167	98	7.52542	51	31	3.3602	39.1005	0.254486	0					
4971	103	161	98	7.34237	51	37	1.26007	16.031	0.104338	4.01112					
4970	104	151	98	7.03729	51	75	2.17013	49.6805	0.323347	0				13	
4969		143	98	6.79322	51	177	1.26007	73.6031	0.479047	0					
4968		139	98	6.67119	51	24	1.54009	17.6705	0.115009	0					
4965	105	133	95	6.48814	52	48	2.24013	30.3818	0.197741	8.74106					
4964		129	95	6.3661	52	39	1.05006	19.8762	0.129365	0					
4963	106	125	96	6.24407	52	56	2.03012	53.8707	0.350619	0					
4961	107	111	94	5.75	53	32	2.45015	40.0933	0.260948	0					
4960	108	232	93	9.78333	53	37	4.34026	80.0778	0.521188	0				16	
4959	109	221	92	9.16957	54	28	2.94018	46.3643	0.301763	0					
4958		176	89	7.8	55	42	1.54009	32.804	0.213505	0					
4957	110	128	89	6.33559	55	18	1.6801	15.4709	0.100693	2.06732					
4956	111	110	88	5.70833	56	54	1.89011	50.7422	0.330257	0					
4955	112	97	88	5.27826	56	30	2.31014	28.7017	0.186806	4.85196					
4954		202	88	8.5913	56	29	1.96012	27.6678	0.180077	0					
4953		196	88	8.4087	56	24	2.45015	27.2316	0.177238	5.65485					
4952	113	164	89	7.4339	55	24	3.78022	40.4064	0.262986	0					

4951	114	155	89	7.15932	55	30	1.19007	16.746	0.108992	0					
4950	115	151	88	7.03729	56	35	1.82011	29.4018	0.191362	2.46983					
4949	116	143	88	6.79322	56	61	2.45015	40.6724	0.264717	15.1099					
4948	117	135	89	6.54915	55	30	2.38014	27.2635	0.177445	0					
4947	118	104	90	5.55	55	56	4.83029	143.145	0.931664	0					
4945	162	220	86	9.13913	57	35	2.94018	53.4968	0.348185	0					
4943		209	84	8.80435	58	29	1.7501	21.1413	0.137598	2.39844					
4942	119	201	84	8.56087	58	56	1.47009	36.8257	0.239681	0					
4941	120	195	84	8.37826	58	42	1.33008	26.8363	0.174665	0					
4940	121	181	87	7.95217	56	47	4.48027	101.254	0.659014	0				11	
4939	122	176	85	7.8	57	63	1.05006	27.1616	0.176782	12.6713					
4938		173	84	7.70847	58	43	1.54009	22.4013	0.1458	2.3478					
4937		168	84	7.55593	58	23	1.7501	18.2011	0.118462	4.27274					
4936	123	153	84	7.09831	58	39	2.10012	24.9915	0.162658	12.9343					
4935		125	84	6.24407	58	18	1.05006	8.17551	0.053211	0					
4934		120	84	6.09153	58	19	1.19007	13.0115	0.084685	0					
4931	124	129	81	6.3661	59	35	1.19007	19.1899	0.124898	0					
4930	125	230	80	9.7125	60	24	3.4302	41.8193	0.272182	0					
4929	126	120	80	6.09153	60	30	1.47009	20.4412	0.133042	7.45876					
4928	127	114	79	5.875	60	91	1.19007	48.1235	0.313213	0					
4927	128	109	79	5.66667	60	122	2.03012	106.509	0.693213	0					
4926	129	83	89	4.97391	55	159	8.68052	946.526	6.16049	0					
4923	130	150	79	7.00678	60	26	1.6801	22.0604	0.143581	0					
4922	131	143	79	6.79322	60	24	1.96012	19.7464	0.12852	0					
4921	132	134	79	6.51864	60	39	2.38014	37.4129	0.243503	0					
4920	133	161	75	7.34237	63	39	1.54009	23.7614	0.154652	0					
4919	134	156	76	7.18983	62	31	1.6801	19.1111	0.124385	5.30233					
4918	135	151	75	7.03729	63	31	0.84005	12.1107	0.078823	7.72377					
4917	136	126	75	6.27458	63	63	2.31014	74.2226	0.48308	0					
4916	137	120	75	6.09153	63	39	1.82011	39.1687	0.254931	0					
4915		153	71	7.09831	65	15	1.7501	14.0008	0.091125	0					
4914		147	71	6.91525	65	17	1.89011	14.612	0.095103	0					

4913		74	71	4.76977	65	35	2.38014	27.8404	0.1812	0					
4912	138	140	71	6.70169	65	24	2.66016	19.5332	0.127132	0					
4911	139	180	70	7.92174	66	52	2.24013	44.4827	0.289517	0					
4910	140	176	69	7.8	66	35	1.47009	21.9778	0.143043	0					
4909	141	171	70	7.64746	66	48	2.80017	46.0627	0.2998	13.6991					
4908	142	162	70	7.37288	66	37	3.2902	52.5716	0.342163	0					
4907		120	69	6.09153	66	22	2.31014	24.5715	0.159924	4.18212					
4905	143	135	68	6.54915	67	22	1.96012	17.081	0.111172	6.26439					
4902	144	221	66	9.16957	68	27	2.66016	31.7002	0.206321	0					
4901		97	67	5.27826	67	105	1.40008	76.3416	0.496871	0					
4900		94	67	5.21304	67	89	1.05006	48.6029	0.316333	0					
4899		91	67	5.14783	67	55	1.40008	40.6724	0.264717	4.27171					
4897	145	180	64	7.92174	69	43	1.82011	29.956	0.194969	0					
4896		171	63	7.64746	70	35	1.19007	18.3611	0.119504	0					
4895		161	63	7.34237	70	26	1.40008	14.6641	0.095441	0					
4893	146	86	64	5.03913	69	44	2.45015	62.6949	0.408051	0					
4892		140	63	6.70169	70	16	1.54009	11.4807	0.074722	6.74198					
4891		135	63	6.54915	70	17	2.10012	18.9735	0.12349	0					
4890		129	63	6.3661	70	20	1.54009	16.1343	0.10501	0					
4889		129	58	6.3661	73	24	1.40008	14.9342	0.0972	0					
4888	147	105	57	5.5	74	122	4.06024	234.069	1.52345	0					5.5 74
4887		152	58	7.0678	73	15	2.03012	16.3135	0.106177	0					
4886	148	120	57	6.09153	74	35	2.38014	38.3708	0.249737	0					
4885	149	110	58	5.70833	73	92	2.03012	82.7999	0.538905	0					
4882		97	56	5.27826	75	46	2.31014	49.2348	0.320446	0					
4877	150	86	49	5.03913	85	159	5.39032	289.425	1.88373	0					
4876	151	226	47	9.56542	87	118	3.2902	150.92	0.982266	0				2	
4875	152	221	48	9.16957	86	122	3.15019	158.941	1.03447	0					
4873		121	45	6.12203	90	46	3.08018	50.3574	0.327753	0					
4871	153	214	48	8.95652	86	48	2.03012	52.6328	0.342562	0					
4868	154	176	43	7.8	93	19	2.03012	18.1261	0.117974	0					
4867	155	161	41	7.34237	97	61	1.26007	26.2096	0.170586	0					

4866	156	157	41	7.22034	97	46	0.980058	17.8511	0.116184	26.058				14	
4865		154	41	7.12881	97	56	0.84005	18.6211	0.121196	17.6438					
4864	157	151	41	7.03729	97	46	0.910054	15.5409	0.101148	13.9052					
4863	158	148	41	6.94576	97	20	0.84005	7.56045	0.049207	2.9542					
4862		145	41	6.85424	97	15	1.26007	9.29305	0.060484	0					
4858	159	84	39	4.99565	100	109	2.59015	124.975	0.813402	0					
4856	160	75	31	4.8	114	63	1.7501	45.9005	0.298744	0				1	4.8 114
5556	3	103	77	5.4	61	37	2.31014	44.8614	0.319536	0					
5555	129	83	86	5.16	56	162	9.24055	750.599	5.34632	0					
5554	75	87	130	5.32	41	37	10.5706	190.199	1.35474	0				3	
5553	27	237	194	9.92924	23	39	4.55027	76.6322	0.545831	0					
5539	7	227	259	9.59906	5	133	14.9109	1244.85	8.86674	0					
5538	5	127	260	6.27961	5	41	3.08018	65.3285	0.465318	0					
5536		162	257	7.36699	5	15	3.08018	24.8912	0.177294	0					
5535	8	168	256	7.5534	6	28	3.71022	46.7004	0.332635	0					
5534	161	135	256	6.52816	6	28	4.69028	51.6832	0.368126	0					
5533	6	31	256	3.46567	6	17	4.13025	36.4288	0.259473	0					
5532	10	80	252	5.04	6	33	5.32032	95.6915	0.681586	0					
5531	9	99	252	5.8	6	74	7.56045	185.161	1.31885	22.3206				6	5.8 6
5530	11	89	253	5.4	6	65	5.46032	133.078	0.94788	23.6747					
5529	12	228	249	9.63208	6	50	4.48027	102.515	0.730187	0					
5527	13	236	247	9.89623	6	98	5.18031	238.654	1.69987	0				9	
5526	14	32	248	3.5	6	24	5.32032	54.2522	0.386425	0				7	3.5 6
5520	16	117	236	5.95833	10	20	3.50021	33.3687	0.237677	0					
5517	15	163	232	7.39806	11	24	3.85023	50.4095	0.359054	0					
5516	19	231	233	9.73113	11	50	6.02036	148.667	1.05892	0					
5513	21	176	232	7.80194	11	70	3.71022	88.2052	0.628263	23.8451					
5512	17	90	233	5.44	11	42	5.74034	114.161	0.813142	0					
5511	18	83	233	5.16	11	24	5.95035	81.3714	0.579588	0					
5509	20	188	231	8.17476	12	65	5.60033	125.893	0.896701	0				8	
5498	22	232	221	9.76415	17	29	4.13025	74.9857	0.534104	0					
5496	23	118	221	6	17	37	4.9703	75.0515	0.534572	0				15	6 17

5470		108	202	5.58333	21	31	4.90029	91.9694	0.655074	0					
5463	25	88	197	5.36	23	48	5.18031	109.07	0.776878	0					
5462	28	231	194	9.73113	23	28	7.28043	103.153	0.734729	0					
5456	26	81	197	5.08	23	41	4.69028	87.1055	0.62043	0					
5454	24	98	198	5.76	22	37	5.32032	91.9442	0.654895	0					
5439		133	190	6.46602	25	24	1.47009	15.8034	0.112564	0					
5437		126	189	6.24854	25	19	1.33008	13.6078	0.096925	0					
5432	30	220	185	9.16893	26	32	6.58039	119.518	0.851297	0					
5430	29	151	188	7.02524	25	32	3.64022	50.6659	0.36088	0					
5429	31	135	185	6.52816	26	24	2.45015	17.081	0.121664	4.09862					
5427		126	185	6.24854	26	24	1.7501	17.7293	0.126281	0					
5424		140	184	6.6835	26	20	1.7501	15.8909	0.113187	5.22608					
5421		150	181	6.99417	27	24	1.6101	18.9378	0.134889	0					
5417	32	126	180	6.24854	28	20	1.6801	14.6309	0.104212	7.66405					
5415	34	232	180	9.76415	28	41	6.44038	135.098	0.96227	0					
5413		156	180	7.18058	28	26	2.52015	46.3708	0.330287	0					
5412	33	140	179	6.6835	28	20	1.7501	22.9356	0.163364	0					
5408	37	110	177	5.66667	29	50	1.54009	33.742	0.240336	2.47061					
5407	38	99	176	5.8	29	142	7.14042	503.082	3.58333	0				12	
5405	39	90	177	5.44	29	87	2.94018	106.133	0.75596	0					
5404		85	175	5.24	29	42	2.31014	39.4263	0.280824	0					
5403	41	120	175	6.06214	29	28	2.31014	31.4756	0.224193	0					
5402	40	136	174	6.55922	30	33	5.1103	75.2349	0.535879	0					
5400	36	126	175	6.24854	29	37	2.45015	32.9953	0.235017	0					
5397	35	150	175	6.99417	29	24	3.01018	38.0233	0.27083	0					
5396	42	106	173	5.5	30	70	1.89011	80.8387	0.575793	0					
5393	43	157	170	7.21165	31	22	3.71022	47.3766	0.337452	0					
5392	44	126	167	6.24854	32	15	2.59015	17.8073	0.126837	0					
5389	48	176	164	7.80194	34	24	2.94018	34.431	0.245243	0					
5388	47	150	163	6.99417	34	19	3.78022	37.089	0.264175	0					
5383	45	73	166	4.76905	33	13	4.13025	34.4827	0.245612	0					
5382		233	163	9.79717	34	33	3.15019	52.5031	0.373966	0					

5381	46	221	163	9.2	34	70	4.9703	159.338	1.13492	0					9.2 34
5380		214	163	8.98252	34	19	2.31014	25.6425	0.182645	0					
5376	49	108	162	5.58333	34	24	2.03012	22.4763	0.160093	0					
5374	50	103	162	5.4	34	20	3.85023	39.7624	0.283217	2.7616					
5372		125	158	6.21748	35	24	5.1103	53.5852	0.381673	0					
5365		183	150	8.01942	37	32	5.46032	83.0424	0.59149	0					
5363	57	110	153	5.66667	36	59	2.17013	64.8869	0.462172	0					
5362	54	105	152	5.46667	36	57	2.38014	70.2506	0.500377	0					
5361	60	222	152	9.3	36	37	4.90029	88.3516	0.629305	0					
5359	52	119	150	6.03107	37	32	3.2902	44.5927	0.317622	4.87198					
5358	53	115	153	5.875	36	37	3.08018	64.5259	0.459602	0					
5357	58	101	152	5.33333	36	41	2.59015	59.2775	0.422218	0					
5355	59	232	150	9.76415	37	41	3.50021	76.6245	0.545776	0				10	
5354	51	176	149	7.80194	37	45	3.85023	75.5786	0.538327	0					
5353		164	150	7.42913	37	61	5.60033	142.844	1.01744	0					
5352	61	151	150	7.02524	37	111	3.57021	133.218	0.948877	50.5884				5	
5351		137	151	6.59029	36	48	4.34026	72.2905	0.514907	0					
5350		171	150	7.6466	37	45	3.85023	83.4702	0.594537	0					
5347	55	95	150	5.64	37	37	3.4302	77.1432	0.549471	0					
5346	62	222	146	9.3	37	24	2.10012	29.3268	0.208887	0					
5345	56	126	148	6.24854	37	31	3.2902	42.5532	0.303096	0					
5343		202	147	8.60971	37	50	8.19049	133.921	0.953888	0					
5341	64	83	145	5.16	38	81	3.85023	110.785	0.789094	0					
5338	65	233	142	9.79717	38	29	3.15019	50.9891	0.363182	0					
5336		120	142	6.06214	38	19	1.7501	12.8108	0.091248	3.55552					
5334	63	125	142	6.21748	38	15	1.6801	13.4408	0.095735	0					
5331	68	182	141	7.98835	39	22	3.01018	30.836	0.219637	0					
5328		112	141	5.75	39	70	1.7501	45.0652	0.320988	0					
5327		105	141	5.46667	39	50	1.82011	32.5344	0.231734	0					
5322	66	160	139	7.30485	39	41	3.2902	51.7133	0.36834	0					
5321	67	147	138	6.90097	39	24	1.82011	20.8125	0.148242	0					
5306	69	148	132	6.93204	41	19	2.03012	21.0039	0.149605	0					

5303	70	160	133	7.30485	40	32	2.24013	33.7513	0.240402	0					
5294		183	127	8.01942	42	28	3.08018	42.1459	0.300195	0					
5291	72	228	126	9.63208	42	33	4.34026	78.9787	0.562545	0					
5290	76	221	127	9.2	42	54	4.83029	115.216	0.820657	0					
5289	71	213	127	8.95146	42	22	4.06024	47.6353	0.339294	0					
5288	73	207	127	8.76505	42	22	5.18031	56.0493	0.399224	0					
5287	74	201	126	8.57864	42	24	4.83029	56.5216	0.402589	0					
5286		171	124	7.6466	43	37	4.06024	59.1077	0.421009	0					
5284	77	139	125	6.65243	42	28	1.96012	18.8026	0.133926	0					
5279		184	122	8.05049	43	37	4.06024	70.112	0.49939	0					
5271	81	175	111	7.77087	46	30	3.78022	51.354	0.365781	0					
5270	78	151	112	7.02524	46	24	1.6101	21.3146	0.151818	0					
5269	79	135	113	6.52816	45	29	1.6801	29.8035	0.212283	0					
5267		210	111	8.85825	46	22	2.66016	35.8741	0.255522	0					
5266		205	112	8.70291	46	26	1.96012	27.369	0.194943	0					
5265	80	197	112	8.45437	46	21	2.87017	28.0536	0.199819	0					
5263	82	156	112	7.18058	46	19	1.54009	18.8478	0.134248	0					
5262	83	96	111	5.68	46	46	3.3602	56.8374	0.404838	0					
5261	84	202	112	8.60971	46	26	3.57021	47.0822	0.335355	0					
5260	86	162	109	7.36699	46	22	1.7501	19.1751	0.136579	0					
5259	87	134	108	6.49709	47	39	2.03012	32.4819	0.23136	0					
5257	88	138	108	6.62136	47	28	2.31014	29.9596	0.213395	0					
5256	85	127	110	6.27961	46	18	3.4302	40.0191	0.285046	0					
5255	89	110	107	5.66667	47	33	1.26007	16.2327	0.115621	0					
5251		127	105	6.27961	47	26	2.59015	36.3341	0.258799	0					
5249	94	110	102	5.66667	48	42	2.24013	41.5508	0.295956	0					
5248	96	100	103	5.3	48	65	8.82053	284.515	2.02653	0				17	5.3 48
5247		152	106	7.05631	47	33	3.2902	54.7174	0.389738	0					
5246	90	115	103	5.875	48	29	1.7501	26.9364	0.191861	0					
5244	91	222	102	9.3	48	42	4.41026	83.2168	0.592732	0					
5243	92	176	101	7.80194	49	22	1.54009	13.6987	0.097572	0					
5242	93	169	102	7.58447	48	17	2.10012	15.1909	0.108201	5.57665					

5240	95	161	101	7.33592	49	18	1.33008	10.5706	0.075292	3.16436					
5238		214	102	8.98252	48	13	2.38014	17.3018	0.123236	0					
5237		180	101	7.92621	49	17	1.6101	14.9381	0.1064	0					
5235		125	99	6.21748	50	18	1.33008	14.2614	0.10158	0					
5234	97	134	98	6.49709	50	19	2.94018	29.3317	0.208922	6.0794					
5233		129	98	6.34175	50	26	1.33008	17.6235	0.125528	0					
5232	102	168	96	7.5534	51	13	1.89011	13.0796	0.093163	0					
5231	103	162	96	7.36699	51	28	1.6801	21.3067	0.151763	0					
5230	98	222	96	9.3	51	33	2.38014	51.2812	0.365263	0					
5229	99	213	96	8.95146	51	18	1.96012	19.2382	0.137029	0					
5227	101	177	96	7.83301	51	17	2.87017	33.2645	0.236935	0					
5226	100	157	96	7.21165	51	24	2.31014	26.6784	0.190023	0					
5225	104	151	96	7.02524	51	37	3.08018	37.0412	0.263835	0				13	
5223	106	126	94	6.24854	52	42	2.10012	36.7522	0.261776	0					
5222	105	133	93	6.46602	53	24	1.40008	14.0786	0.100278	0					
5220		120	93	6.06214	53	37	2.10012	36.4799	0.259837	0					
5216	107	110	93	5.66667	53	29	1.89011	29.0913	0.20721	0					
5215	109	222	91	9.3	54	33	2.73016	49.7332	0.354237	0					
5214	108	231	90	9.73113	54	32	4.76028	79.7915	0.568334	0				16	
5213	114	155	88	7.14951	55	33	2.52015	40.1649	0.286084	0					
5212	162	222	87	9.3	56	28	3.22019	43.9556	0.313085	0					
5208	110	129	86	6.34175	56	20	1.82011	21.2346	0.151248	0					
5207	111	110	87	5.66667	56	46	1.47009	37.6807	0.26839	0					
5206	118	103	88	5.4	55	63	6.6504	220.383	1.56973	0					
5205	112	96	87	5.68	56	37	1.7501	31.1975	0.222212	0					
5204	121	180	85	7.92621	57	30	3.2902	54.7635	0.390066	0				11	
5203	113	165	86	7.46019	56	21	2.24013	19.3115	0.137551	0					
5201	115	150	86	6.99417	56	37	1.96012	37.0244	0.263716	0					
5200	116	143	86	6.7767	56	45	2.10012	38.4245	0.273688	0					
5199	117	135	87	6.52816	56	33	2.24013	29.8685	0.212745	0					
5197		124	83	6.18641	58	28	1.54009	18.9211	0.13477	0					
5196	119	201	82	8.57864	58	35	2.31014	33.2082	0.236534	0					

5195	120	195	82	8.39223	58	26	2.80017	37.1897	0.264893	0					
5194	122	176	82	7.80194	58	54	1.89011	38.7095	0.275718	0					
5193	123	153	82	7.08738	58	33	1.89011	28.3517	0.201942	0					
5190	132	135	77	6.52816	61	29	2.66016	34.4158	0.245135	0					
5189	124	130	77	6.37282	61	41	2.24013	41.4038	0.294909	0					
5188		125	79	6.21748	60	31	1.82011	30.7234	0.218835	0					
5187	125	230	79	9.69811	60	21	3.92023	42.5737	0.303242	0					
5186	126	120	79	6.06214	60	32	1.96012	31.5127	0.224457	0					
5185	127	115	77	5.875	61	43	2.38014	40.1017	0.285634	0					
5184	4	89	79	5.4	60	153	9.45056	769.402	5.48025	0				4	
5183	130	151	76	7.02524	62	24	1.33008	11.9707	0.085264	3.03279					
5182	131	143	76	6.7767	62	22	2.45015	25.8208	0.183915	0					
5181	128	109	77	5.625	61	65	3.01018	81.3518	0.579448	0					
5177	136	125	73	6.21748	63	37	2.73016	56.8305	0.404789	0					
5176	133	161	74	7.33592	63	31	1.54009	19.2511	0.137121	0					
5175	134	156	74	7.18058	63	46	1.82011	35.8197	0.255135	0					
5174	135	151	73	7.02524	63	37	0.980058	14.7709	0.105209	6.53666					
5173	137	120	72	6.06214	64	28	1.54009	18.9944	0.135293	0					
5172		115	72	5.875	64	19	1.12007	8.96053	0.063824	4.74067					
5171		110	61	5.66667	64	28	2.17013	23.1714	0.165044	7.91181					
5167		181	68	7.95728	66	37	1.12007	16.961	0.120809	0					
5166	139	179	68	7.89515	66	48	1.26007	28.0923	0.200094	0					
5165	142	162	69	7.36699	66	28	2.03012	24.434	0.174037	0					
5164	138	140	68	6.6835	66	26	2.59015	25.8254	0.183948	0					
5163	143	135	68	6.52816	66	18	2.10012	17.501	0.124655	0					
5161	140	176	68	7.80194	66	31	1.33008	19.0644	0.135791	0					
5160	141	170	68	7.61553	66	37	1.6801	28.8977	0.205831	0					
5156		97	66	5.72	67	42	1.82011	34.1684	0.243373	0					
5155		93	66	5.56	67	37	1.89011	31.6957	0.22576	0					
5154		91	65	5.48	68	28	2.03012	24.2214	0.172523	4.39224					
5153	145	181	62	7.95728	70	15	1.96012	13.8099	0.098365	0					
5152	144	222	62	9.3	70	22	3.71022	41.2489	0.293806	0					

5148	146	86	61	5.28	71	24	2.66016	35.9121	0.255793	0					
5142		102	56	5.36667	74	54	2.38014	63.6869	0.453625	0					
5141	148	120	54	6.06214	76	37	1.6801	23.7614	0.169247	0					
5140	2	115	55	5.875	75	46	2.59015	50.8678	0.362318	0					
5139	147	106	56	5.5	74	55	2.45015	61.7896	0.440111	0					5.5 74
5138	149	110	56	5.66667	74	61	3.3602	89.809	0.639687	0					
5135		91	50	5.48	81	61	3.85023	109.041	0.776673	0					
5133	152	221	46	9.2	87	74	3.85023	104.821	0.74661	0					
5132	150	85	47	5.24	85	131	4.13025	191.843	1.36645	0					
5130	151	226	46	9.56604	87	51	4.06024	71.8061	0.511457	0				2	
5127	153	212	45	8.92039	88	28	3.92023	56.19	0.400227	0					
5126	0	202	44	8.60971	90	19	6.86041	52.2698	0.372304	0					
5120	154	176	40	7.80194	96	19	2.10012	14.7009	0.104711	0					
5118		154	39	7.11845	97	28	1.26007	12.9945	0.092557	0					
5117	157	151	39	7.02524	97	26	0.910054	6.30038	0.044876	5.46733					
5116	158	148	39	6.93204	97	24	1.40008	14.0008	0.099724	0					
5113	155	161	39	7.33592	97	28	1.6101	16.745	0.11927	0					
5112	156	157	39	7.21165	97	28	1.6801	18.8545	0.134295	0				14	
5109	159	84	37	5.2	100	37	3.22019	59.2846	0.422269	0					
5104		232	29	9.76415	114	31	6.44038	96.5326	0.687577	0					
5103	160	74	29	4.8	114	24	2.52015	22.4293	0.159758	0				1	4.8 114
5087	1	224	6	9.5	201	24	7.49045	99.304	0.707317	0					9.5 201

MATRIX SCIENCE Mascot Search Results

```
User            : JOY
Email           : joyprashant88@gmail.com
Search title    :
Database        : SwissProt 2015_08 (549008 sequences; 195692017 residues)
Taxonomy        : Homo sapiens (human) (20204 sequences)
Timestamp       : 31 Jul 2015 at 05:17:49 GMT
Top Score       : 58 for GPX4_HUMAN, Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE
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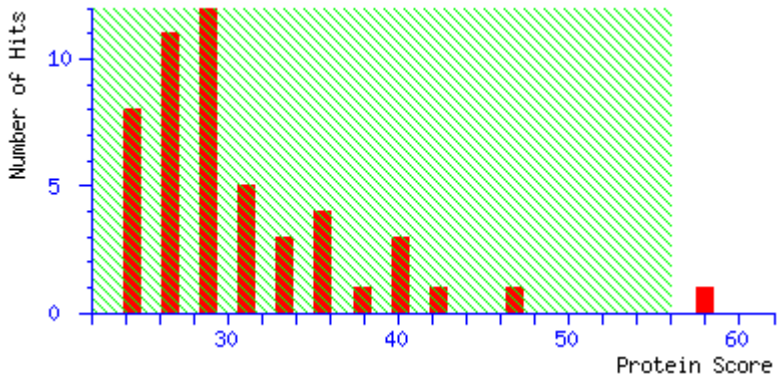
Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant (p<0.05).



Protein Summary Report

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Significance threshold p< [0.05] Max. number of hits [20]

Preferred taxonomy [All entries]

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Index

	Accession	Mass	Score	Description
1.	GPX4_HUMAN	22674	58	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV
2.	ACAD8_HUMAN	45896	47	Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 PE=1 SV=1
3.	T23O_HUMAN	48012	43	Tryptophan 2,3-dioxygenase OS=Homo sapiens GN=TDO2 PE=1 SV=1
4.	OLIG3_HUMAN	29567	40	Oligodendrocyte transcription factor 3 OS=Homo sapiens GN=OLIG3 PE=1 SV=2
5.	Z658B_HUMAN	97349	40	Zinc finger protein 658B OS=Homo sapiens GN=ZNF658B PE=2 SV=1
6.	PAL4A_HUMAN	18398	39	Peptidyl-prolyl cis-trans isomerase A-like 4A/B/C OS=Homo sapiens GN=PPIAL4A PE=2 SV=1
7.	MPP2_HUMAN	64882	39	MAGUK p55 subfamily member 2 OS=Homo sapiens GN=MPP2 PE=1 SV=3
8.	JIP4_HUMAN	146913	37	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4
9.	LMO7_HUMAN	194002	36	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3
10.	PRVA_HUMAN	12051	36	Parvalbumin alpha OS=Homo sapiens GN=PVALB PE=1 SV=2
11.	CDY2_HUMAN	61113	35	Testis-specific chromodomain protein Y 2 OS=Homo sapiens GN=CDY2A PE=1 SV=1
12.	ZN658_HUMAN	125674	34	Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2
13.	K22E_HUMAN	65678	33	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
14.	TEPP_HUMAN	31268	33	Testis, prostate and placenta-expressed protein OS=Homo sapiens GN=TEPP PE=2 SV=3
15.	AP4AT_HUMAN	55844	32	AP-4 complex accessory subunit tepsin OS=Homo sapiens GN=ENTHD2 PE=1 SV=1
16.	KI18B_HUMAN	95020	31	Kinesin-like protein KIF18B OS=Homo sapiens GN=KIF18B PE=1 SV=3
17.	F214A_HUMAN	123076	31	Protein FAM214A OS=Homo sapiens GN=FAM214A PE=1 SV=2
18.	KTNA1_HUMAN	56214	31	Katanin p60 ATPase-containing subunit A1 OS=Homo sapiens GN=KATNA1 PE=1 SV=1
19.	SGTA_HUMAN	34270	31	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA P
20.	ZN248_HUMAN	68868	30	Zinc finger protein 248 OS=Homo sapiens GN=ZNF248 PE=2 SV=1

Results List

1. GPX4_HUMAN **Mass:** 22674 **Score:** 58 **Expect:** 0.032 **Matches:** 6

Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.4190	867.4118	867.3909	24.1	90 -	96	0	R.YAECGLR.I
1294.7460	1293.7387	1293.6540	65.5	97 -	107	0	R.ILAFPCNQFGK.Q
1524.8067	1523.7994	1523.7191	52.7	133 -	145	0	K.ICVNGDDAHPLWK.W
1575.8464	1574.8391	1574.7511	55.9	48 -	60	1	K.DIDGHMVNLDKYR.G
1658.9339	1657.9267	1657.8424	50.8	76 -	89	0	K.TEVNYTQLVDLHAR.Y
2110.0693	2109.0620	2109.0014	28.7	108 -	126	1	K.QEPGSNEEIKEFAAGYNVK.F

No match to: 807.3866, 842.5181, 856.5321, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1527.8390, 1598.8407, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2399.0571, 2501.2326, 2584.2114, 2717.1020

2. ACAD8_HUMAN **Mass:** 45896 **Score:** 47 **Expect:** 0.41 **Matches:** 7

Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1527.8390	1526.8318	1526.7511	52.8	393 -	405	0	R.VHQILEGSNEVMR.I + Oxidation (M)
1598.8407	1597.8334	1597.8498	-10.24	207 -	222	1	R.TGGPGPKGISCIVVEK.G
2094.1288	2093.1215	2093.1415	-9.57	393 -	410	1	R.VHQILEGSNEVMRILISR.S

2110.0693	2109.0620	2109.1364	-35.29	393 - 410	1	R.VHQILEGSNEVMRILISR.S + Oxidation (M)
2343.0395	2342.0322	2342.0460	-5.87	51 - 70	1	K.VAFDFAAREMAPNMAEWDQK.E + Oxidation (M)
2501.2326	2500.2253	2500.2056	7.87	304 - 325	0	K.QFGEPLASNQYLQFTLADMATR.L
2584.2114	2583.2042	2583.1444	23.1	59 - 79	1	R.EMAPNMAEWDQKELFPVDVMR.K + 3 Oxidation (M)

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1575.8464, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2717.1020

3. T23O_HUMAN **Mass:** 48012 **Score:** 43 **Expect:** 0.97 **Matches:** 6

Tryptophan 2,3-dioxygenase OS=Homo sapiens GN=TDO2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1527.8390	1526.8318	1526.8602	-18.66	160 - 172		1	R.LLENKIGVLQNMR.V
1575.8464	1574.8391	1574.8351	2.55	165 - 177		1	K.IGVLQNMRVPYNR.R + Oxidation (M)
1658.9339	1657.9267	1657.8635	38.1	51 - 65		1	K.VLNAQELQSETKGNK.I
1839.0040	1837.9967	1837.8217	95.2	245 - 259		1	K.EESEEKEEQVAEFQK.Q
2343.0395	2342.0322	2342.1902	-67.45	304 - 323		0	R.FQVPFQLLTSLMDIDSLMTK.W + Oxidation (M)
2501.2326	2500.2253	2500.2672	-16.75	124 - 144		0	K.LLVQQFSILETMTALDFNDFR.E

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1598.8407, 1803.9932, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2584.2114, 2717.1020

4. OLIG3_HUMAN **Mass:** 29567 **Score:** 40 **Expect:** 1.9 **Matches:** 5

Oligodendrocyte transcription factor 3 OS=Homo sapiens GN=OLIG3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5512	869.5440	869.5698	-29.73	124 - 131		0	K.IATLLLAR.N
1598.8407	1597.8334	1597.8787	-28.35	75 - 87		1	K.QLSEQDLQQLRLK.I
2097.0388	2096.0315	2095.8952	65.0	12 - 28		1	R.ASSPDMDEMYLRDHHHR.H
2399.0571	2398.0498	2398.0927	-17.88	37 - 58		1	R.LNSVSSTQGDMMQKMPGESLSR.A + Oxidation (M)
2584.2114	2583.2042	2583.0523	58.8	1 - 23		1	-.MNSDSSSVSSRASSPDMDEMYLR.D + 2 Oxidation (M)

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2501.2326, 2717.1020

5. Z658B_HUMAN **Mass:** 97349 **Score:** 40 **Expect:** 2.3 **Matches:** 7

Zinc finger protein 658B OS=Homo sapiens GN=ZNF658B PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5512	869.5440	869.4831	70.0	515 - 521		1	K.TRLSTHR.R
1001.5423	1000.5351	1000.5706	-35.47	398 - 406		0	R.SFAHISVLK.A
1493.8218	1492.8145	1492.8263	-7.89	398 - 410		1	R.SFAHISVLKAHQR.I

1527.8390	1526.8318	1526.8066	16.5	762 - 774	1	K.AFAQNSTLRVHQR.I
2343.0395	2342.0322	2342.0532	-8.96	771 - 789	1	R.VHQRIHTGEKPYECDECGK.T
2501.2326	2500.2253	2500.1401	34.1	86 - 107	1	K.CEENFSQSSAHIVHQKTQAGDK.F
2584.2114	2583.2042	2583.1304	28.5	38 - 58	1	K.TTAVEYNKVHMAMTHYECNER.G

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1524.8067, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2717.1020

6. PAL4A_HUMAN **Mass:** 18398 **Score:** 39 **Expect:** 2.5 **Matches:** 5

Peptidyl-prolyl cis-trans isomerase A-like 4A/B/C OS=Homo sapiens GN=PPIAL4A PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1487.8391	1486.8318	1486.7569	50.4	119 - 131		1	K.TEWLDGKHVAFGK.V
1598.8407	1597.8334	1597.7381	59.6	56 - 69		0	R.IIPGFMCQGGDFTR.H
2094.1288	2093.1215	2093.0980	11.2	1 - 19		0	-.MVNSVVFFDITVDGKPLGR.I
2110.0693	2109.0620	2109.0929	-14.65	1 - 19		0	-.MVNSVVFFDITVDGKPLGR.I + Oxidation (M)
2343.0395	2342.0322	2342.0507	-7.91	50 - 69		1	K.GSCFHRIIPGFMCQGGDFTR.H

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2501.2326, 2584.2114, 2717.1020

7. MPP2_HUMAN **Mass:** 64882 **Score:** 39 **Expect:** 2.8 **Matches:** 8

MAGUK p55 subfamily member 2 OS=Homo sapiens GN=MPP2 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
807.3866	806.3793	806.3770	2.89	525 - 531		0	R.TVEESSR.I
842.5181	841.5108	841.5021	10.4	223 - 229		0	R.ALQELLR.N
1001.5423	1000.5351	1000.5375	-2.47	38 - 46		0	R.GIMESPIVR.S
1061.5614	1060.5542	1060.5012	50.0	394 - 401		0	K.LIMWDPDR.Y + Oxidation (M)
1234.7356	1233.7283	1233.6387	72.6	555 - 564		1	R.ELQTAMEKLR.T + Oxidation (M)
2110.0693	2109.0620	2109.0978	-16.96	51 - 67		0	K.VIMVLWFMQQNVFVPMK.Y
2211.1438	2210.1365	2210.1808	-20.03	170 - 190		1	K.TAGEHLGVTFRVEGGELVIAR.I
2343.0395	2342.0322	2342.1835	-64.57	482 - 501		0	R.TAEFVPYVVFIEAPDFETLR.A

No match to: 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1077.2501, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2129.1086, 2225.1687, 2399.0571, 2501.2326, 2584.2114, 2717.1020

8. JIP4_HUMAN **Mass:** 146913 **Score:** 37 **Expect:** 4.3 **Matches:** 8

C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6657	1319.6584	1319.7085	-37.97	38 - 48		1	R.LIGRYDEEVVK.E
1365.7172	1364.7100	1364.6684	30.4	654 - 665		1	K.YKQVTNGQGENK.M

1493.8218	1492.8145	1492.7270	58.6	137 - 148	1	K.NYADQISRLEER.E
1527.8390	1526.8318	1526.8304	0.89	446 - 459	1	K.DVLQGELEAVKQAK.L
1575.8464	1574.8391	1574.7551	53.3	1309 - 1321	0	R.SHLIVWQVMYGNE.-
2211.1438	2210.1365	2210.1179	8.43	946 - 964	1	K.DQISVLPNEQDLVREEAQK.M
2501.2326	2500.2253	2500.0734	60.8	1 - 23	0	-.MELEDGVVYQEEPGGSGAVMSER.V + 2 Oxidation (M)
2584.2114	2583.2042	2583.2262	-8.51	339 - 361	1	K.SEVQAIIESTPELDMDKDLSGYK.G + Oxidation (M)

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1356.8051, 1487.8391, 1524.8067, 1598.8407, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2225.1687, 2343.0395, 2399.0571, 2717.1020

9. LMO7_HUMAN **Mass:** 194002 **Score:** 36 **Expect:** 4.8 **Matches:** 10

LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
807.3866	806.3793	806.3592	24.9	783 -	788	0	K.EMLQDR.E + Oxidation (M)
842.5181	841.5108	841.4294	96.8	475 -	482	0	K.IDPTSGPR.L
1061.5614	1060.5542	1060.5335	19.5	1468 -	1475	0	R.QQILQEMR.K + Oxidation (M)
1365.7172	1364.7100	1364.6208	65.3	1406 -	1418	0	K.TEEASSGFLPGDR.N
1527.8390	1526.8318	1526.7624	45.5	1111 -	1123	1	K.AQETGHLVMDVRR.Y + Oxidation (M)
1658.9339	1657.9267	1657.8709	33.7	89 -	103	0	R.ASLENGVLLCDLINK.L
1839.0040	1837.9967	1837.8628	72.8	815 -	830	0	K.RPPTMTVSEASYQSER.V
2110.0693	2109.0620	2108.9797	39.0	539 -	555	1	K.FSEQDDSVERDIILQCR.E
2343.0395	2342.0322	2342.1940	-69.10	650 -	671	1	K.LGTTVPPISFTPGPCSEADLKR.W
2399.0571	2398.0498	2398.1070	-23.88	696 -	717	1	K.IYGENGSKSMSDVSAEDVQNLR.Q

No match to: 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1487.8391, 1493.8218, 1524.8067, 1575.8464, 1598.8407, 1803.9932, 2083.0739, 2094.1288, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2501.2326, 2584.2114, 2717.1020

10. PRVA_HUMAN **Mass:** 12051 **Score:** 36 **Expect:** 5 **Matches:** 4

Parvalbumin alpha OS=Homo sapiens GN=PVALB PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.4190	867.4118	867.3830	33.2	85 -	92	0	K.MLMAAGDK.D + 2 Oxidation (M)
1365.7172	1364.7100	1364.6493	44.4	2 -	13	0	M.SMTDLLNAEDIK.K + Oxidation (M)
1493.8218	1492.8145	1492.7443	47.0	2 -	14	1	M.SMTDLLNAEDIKK.A + Oxidation (M)
1839.0040	1837.9967	1837.8582	75.4	93 -	110	1	K.DGDGKIGVDEFSTLVAES.-

No match to: 807.3866, 842.5181, 856.5321, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1487.8391, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2399.0571, 2501.2326, 2584.2114, 2717.1020

11. CDY2_HUMAN **Mass:** 61113 **Score:** 35 **Expect:** 6.1 **Matches:** 6

Testis-specific chromodomain protein Y 2 OS=Homo sapiens GN=CDY2A PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide

1001.5423	1000.5351	1000.5553	-20.21	308 - 316	0	K.NALNTEVIK.E
1365.7172	1364.7100	1364.6936	12.0	292 - 303	0	K.EDGFTQIVLSTR.S
1493.8218	1492.8145	1492.7886	17.4	291 - 303	1	K.KEDGFTQIVLSTR.S
1839.0040	1837.9967	1837.9509	24.9	271 - 285	1	K.MHFTIRLTESAITYR.D
2083.0739	2082.0667	2082.0455	10.1	520 - 537	1	K.IWSSAQGIESMLKYVENK.I
2584.2114	2583.2042	2583.1550	19.0	202 - 226	0	K.TQMHPLMSQMSGSVTASMATGSATR.K + Oxidation (M)

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1487.8391, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2399.0571, 2501.2326, 2717.1020

12. ZN658_HUMAN **Mass:** 125674 **Score:** 34 **Expect:** 8.2 **Matches:** 7

Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5512	869.5440	869.4831	70.0	755 -	761	1	K.TRLSTHR.R
1001.5423	1000.5351	1000.5706	-35.47	638 -	646	0	R.SFAHISVLK.A
1493.8218	1492.8145	1492.8263	-7.89	638 -	650	1	R.SFAHISVLKAHQR.I
1527.8390	1526.8318	1526.8066	16.5	1002 -	1014	1	K.AFAQNSTLRVHQR.I
2343.0395	2342.0322	2342.0532	-8.96	1011 -	1029	1	R.VHQRIHTGEKPYECDECGK.T
2501.2326	2500.2253	2500.1401	34.1	330 -	351	1	K.CEENFSQSSAHIVHQKTQAGDK.F
2584.2114	2583.2042	2583.1304	28.5	282 -	302	1	K.TTAVEYNKVHMAMTHYECNER.G

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1524.8067, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2717.1020

13. K22E_HUMAN **Mass:** 65678 **Score:** 33 **Expect:** 9.7 **Matches:** 5

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1001.5423	1000.5351	1000.5301	4.94	176 -	183	1	K.AQEREQIK.T
1320.6657	1319.6584	1319.5756	62.7	46 -	61	0	R.HGGGGGGFGGGGFGSR.S
1839.0040	1837.9967	1837.9072	48.7	71 -	92	0	K.SISISVAGGGGGFGAAGGFGGR.G
2399.0571	2398.0498	2398.0113	16.1	93 -	122	0	R.GGGFGGGSSFGGGSGFSGGGFGGGGFGGGR.F
2501.2326	2500.2253	2500.0600	66.1	516 -	544	1	K.AAFGGSGGRGSSSGGGYSSGSSSYGSGGR.Q

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2584.2114, 2717.1020

14. TEPP_HUMAN **Mass:** 31268 **Score:** 33 **Expect:** 11 **Matches:** 5

Testis, prostate and placenta-expressed protein OS=Homo sapiens GN=TEPP PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide

1001.5423	1000.5351	1000.4760	59.0	106 - 113	1	R.HMDRDTVK.A
1839.0040	1837.9967	1837.9574	21.4	34 - 50	0	R.TESPYKPVHLGLGPTDK.V
2083.0739	2082.0667	2082.0833	-8.00	168 - 185	1	K.LAPIAPGINRVDWPCFTR.A
2094.1288	2093.1215	2093.1199	0.74	1 - 18	0	-.MGIVCAQCSFILLLSIIR.A
2110.0693	2109.0620	2109.1149	-25.06	1 - 18	0	-.MGIVCAQCSFILLLSIIR.A + Oxidation (M)

No match to: 807.3866, 842.5181, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2399.0571, 2501.2326, 2584.2114, 2717.1020

15. AP4AT_HUMAN **Mass:** 55844 **Score:** 32 **Expect:** 14 **Matches:** 5

AP-4 complex accessory subunit tepsin OS=Homo sapiens GN=ENTHD2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.5181	841.5108	841.4480	74.7	1 -	8	0	-.MAAAPPLR.D + Oxidation (M)
1001.5423	1000.5351	1000.4978	37.3	264 -	271	0	R.EEAQHFIK.A
1575.8464	1574.8391	1574.8205	11.8	259 -	271	1	R.AFLSREEAQHFIK.A
1598.8407	1597.8334	1597.7518	51.1	482 -	498	0	R.LVGAGAAAGESCPDAPR.A
2584.2114	2583.2042	2583.1182	33.3	209 -	234	1	R.VSDSGSHSGSDSHSGASREPGDLAER.V

No match to: 807.3866, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2399.0571, 2501.2326, 2717.1020

16. KI18B_HUMAN **Mass:** 95020 **Score:** 31 **Expect:** 15 **Matches:** 6

Kinesin-like protein KIF18B OS=Homo sapiens GN=KIF18B PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.5181	841.5108	841.4657	53.6	757 -	763	0	K.IPQELSR.L
1001.5423	1000.5351	1000.5301	4.94	149 -	156	1	R.LEARQQEK.H
1487.8391	1486.8318	1486.7450	58.4	781 -	795	0	K.GPKPTSSLPGTSACK.K
2110.0693	2109.0620	2109.0711	-4.31	711 -	730	0	R.VPLGPSAMQNCSTPLALPTR.D
2225.1687	2224.1615	2224.1522	4.16	2 -	22	0	M.SHPGVTTVMAVEDSTLQVVVR.V
2399.0571	2398.0498	2398.2890	-99.74	247 -	269	1	R.VPGLTQAVQVAKMSLIDLAGSER.A + Oxidation (M)

No match to: 807.3866, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2129.1086, 2211.1438, 2343.0395, 2501.2326, 2584.2114, 2717.1020

17. F214A_HUMAN **Mass:** 123076 **Score:** 31 **Expect:** 16 **Matches:** 7

Protein FAM214A OS=Homo sapiens GN=FAM214A PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.4190	867.4118	867.4450	-38.34	1027 -	1034	1	R.FQSSKSGK.I
1061.5614	1060.5542	1060.5149	37.0	619 -	627	0	K.ENNLDLTSR.F

1524.8067	1523.7994	1523.6674	86.6	506 - 519	0	R.QSFNMHDSSSVASK.V
1527.8390	1526.8318	1526.7286	67.6	1048 - 1061	1	R.KSMEVDSGAAYELK.S
1598.8407	1597.8334	1597.7923	25.8	271 - 284	0	K.QTWTMAPESVLHAK.S
2110.0693	2109.0620	2108.9296	62.8	41 - 58	0	R.TESFHCPPAQSCYPVTTK.H
2343.0395	2342.0322	2342.1179	-36.57	660 - 679	1	K.IINENYNPKFFGNLQSDDSK.K

No match to: 807.3866, 842.5181, 856.5321, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1575.8464, 1658.9339, 1803.9932, 1839.0040, 2083.0739, 2094.1288, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2501.2326, 2584.2114, 2717.1020

18. KTNA1_HUMAN **Mass:** 56214 **Score:** 31 **Expect:** 16 **Matches:** 7

Katanin p60 ATPase-containing subunit A1 OS=Homo sapiens GN=KATNA1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.4190	867.4118	867.4086	3.64	282 - 288		1	K.YRGESEK.L
870.5512	869.5440	869.4793	74.4	65 - 71		1	K.HVKDIMK.T
1001.5423	1000.5351	1000.5957	-60.59	377 - 385		0	R.IYIPLPSAK.G
1598.8407	1597.8334	1597.8675	-21.32	437 - 450		1	R.IEGLTPEEIRNLSK.E
1839.0040	1837.9967	1837.9210	41.2	268 - 283		1	K.TTFFNVSSSTLTSKYR.G
2094.1288	2093.1215	2093.1093	5.80	220 - 236		1	K.LLKEAVVLPMWMPEFFK.G + Oxidation (M)
2110.0693	2109.0620	2109.1043	-20.04	220 - 236		1	K.LLKEAVVLPMWMPEFFK.G + 2 Oxidation (M)

No match to: 807.3866, 842.5181, 856.5321, 881.2690, 886.1635, 901.6230, 917.3032, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1658.9339, 1803.9932, 2083.0739, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2343.0395, 2399.0571, 2501.2326, 2584.2114, 2717.1020

19. SGTA_HUMAN **Mass:** 34270 **Score:** 31 **Expect:** 17 **Matches:** 5

Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.5181	841.5108	841.5385	-32.87	201 - 207		1	K.IAELKLR.E
1658.9339	1657.9267	1657.7795	88.8	81 - 95		1	R.TPPSEEDSAEAERLK.T
2094.1288	2093.1215	2093.0979	11.3	165 - 183		1	R.MGLALSSLNKHVEAVAYYK.K
2110.0693	2109.0620	2109.0928	-14.62	165 - 183		1	R.MGLALSSLNKHVEAVAYYK.K + Oxidation (M)
2343.0395	2342.0322	2342.1477	-49.30	117 - 137		1	K.AIELNPANAVYFCNRAAAYSK.L

No match to: 807.3866, 856.5321, 868.4190, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1598.8407, 1803.9932, 1839.0040, 2083.0739, 2097.0388, 2129.1086, 2211.1438, 2225.1687, 2399.0571, 2501.2326, 2584.2114, 2717.1020

20. ZN248_HUMAN **Mass:** 68868 **Score:** 30 **Expect:** 21 **Matches:** 6

Zinc finger protein 248 OS=Homo sapiens GN=ZNF248 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.4190	867.4118	867.4338	-25.37	326 - 332		1	R.EYKVSDK.T

1598.8407	1597.8334	1597.7896	27.4	472 - 484	1	K.SFCHRSALTVHQR.T
1839.0040	1837.9967	1837.8496	80.0	219 - 234	1	K.NGQGFHDEAAFFTNKR.S
2211.1438	2210.1365	2210.0745	28.1	139 - 157	1	K.ICDSCEMNLKNISGLIISK.K + Oxidation (M)
2399.0571	2398.0498	2398.0868	-15.45	485 - 504	1	R.THTGEKPFICNECGKSFCVK.S
2717.1020	2716.0947	2716.2082	-41.77	449 - 471	1	K.SNLTEHQRTHTGEKPYECNACGK.S

No match to: 807.3866, 842.5181, 856.5321, 870.5512, 881.2690, 886.1635, 901.6230, 917.3032, 1001.5423, 1017.2206, 1046.0431, 1061.5614, 1077.2501, 1234.7356, 1294.7460, 1320.6657, 1356.8051, 1365.7172, 1487.8391, 1493.8218, 1524.8067, 1527.8390, 1575.8464, 1658.9339, 1803.9932, 2083.0739, 2094.1288, 2097.0388, 2110.0693, 2129.1086, 2225.1687, 2343.0395, 2501.2326, 2584.2114

Search Parameters

Type of search : **Peptide Mass Fingerprint**
Enzyme : **Trypsin**
Fixed modifications : **Carbamidomethyl (C)**
Variable modifications : **Oxidation (M)**
Mass values : **Monoisotopic**
Protein Mass : **Unrestricted**
Peptide Mass Tolerance : **± 100 ppm**
Peptide Charge State : **1+**
Max Missed Cleavages : **1**
Number of queries : **40**
Selected for scoring : **32**

MATRIX SCIENCE Mascot Search Results

```
User            : joy
Email           : joyprashant88@gmail.com
Search title    :
Database        : SwissProt 2015_08 (549008 sequences; 195692017 residues)
Taxonomy        : Homo sapiens (human) (20204 sequences)
Timestamp       : 31 Jul 2015 at 05:26:55 GMT
Top Score       : 59 for JIP4_HUMAN, C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4
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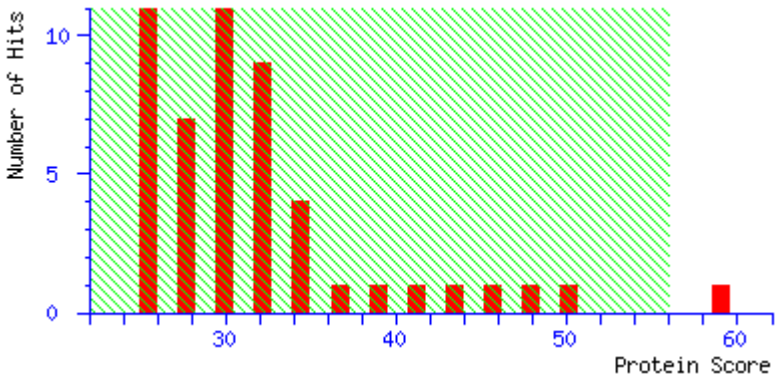
Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant (p<0.05).



Protein Summary Report

Format As | Protein Summary | Help

Significance threshold p< 0.05 Max. number of hits 20

Preferred taxonomy All entries

Overview Table

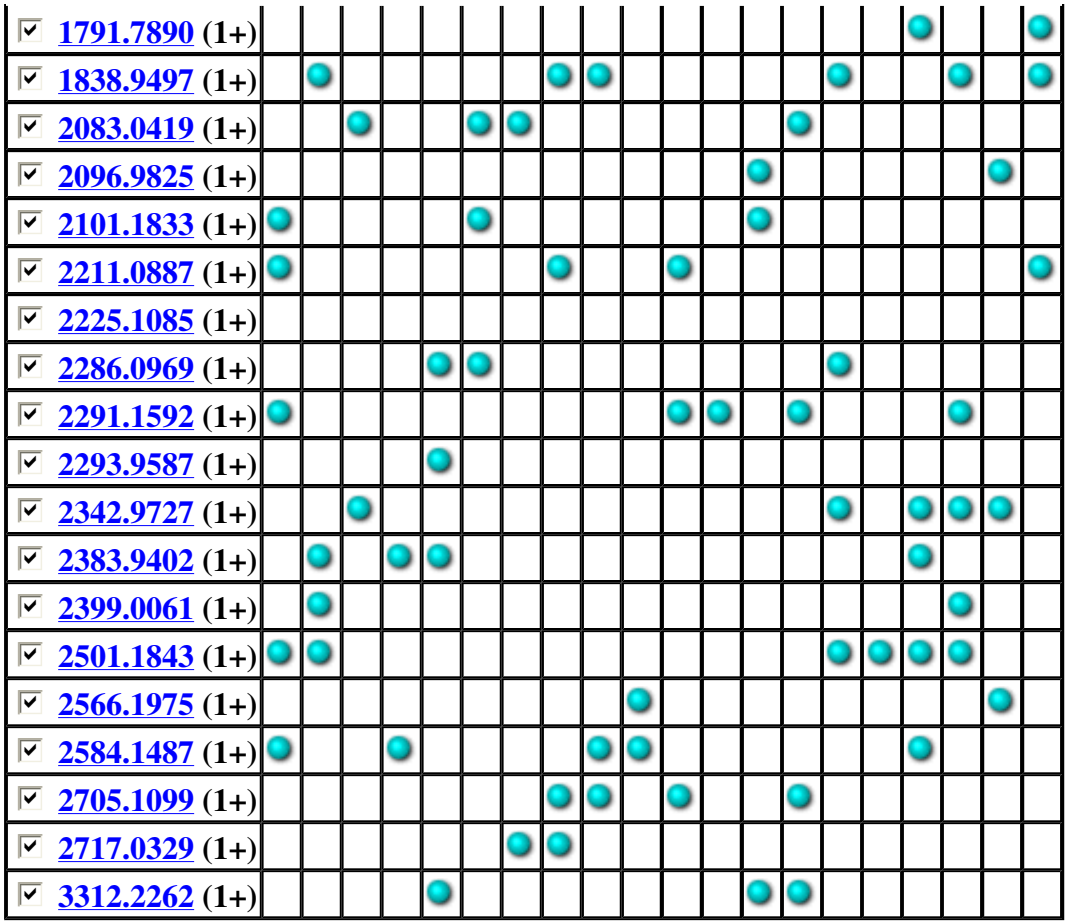
Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.

Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
842.4951 (1+)							●			●	●		●			●				
856.5073 (1+)															●	●				
870.5331 (1+)							●										●			
881.3265 (1+)	●								●											
886.1516 (1+)																				
901.6158 (1+)							●				●	●								
917.3060 (1+)																				
1107.5881 (1+)		●						●	●					●	●					
1165.6325 (1+)	●		●							●				●		●				
1179.6458 (1+)					●	●				●										●
1193.6580 (1+)		●											●						●	●
1234.7160 (1+)			●			●	●			●			●						●	
1320.6409 (1+)	●	●				●					●	●						●	●	
1350.7517 (1+)								●												
1365.6962 (1+)	●		●	●						●	●	●								
1434.8149 (1+)			●								●							●		
1475.8162 (1+)	●	●			●			●											●	
1487.7911 (1+)																			●	
1493.7857 (1+)	●		●			●		●	●			●					●			
1657.8508 (1+)	●			●	●						●									
1673.8901 (1+)							●											●		●
1687.9314 (1+)					●															
1707.8239 (1+)			●	●				●			●		●							
1765.7810 (1+)	●				●							●					●			



Select All | Select None | Search Selected

Index

	Accession	Mass	Score	Description
1.	JIP4_HUMAN	146913	59	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4
2.	K22E_HUMAN	65678	49	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
3.	K1C10_HUMAN	59020	48	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
4.	PARK7_HUMAN	20050	44	Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2
5.	K2C1_HUMAN	66170	43	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
6.	ZSC25_HUMAN	62576	40	Zinc finger and SCAN domain-containing protein 25 OS=Homo sapiens GN=ZSCAN25 PE=2 SV=3
7.	CFA99_HUMAN	52489	38	Cilia- and flagella-associated protein 99 OS=Homo sapiens GN=CFAP99 PE=3 SV=1
8.	ZN624_HUMAN	102544	36	Zinc finger protein 624 OS=Homo sapiens GN=ZNF624 PE=1 SV=3
9.	SEP14_HUMAN	50449	35	Septin-14 OS=Homo sapiens GN=SEPT14 PE=1 SV=2

10.	PTH1R_HUMAN	67173	34	Parathyroid hormone/parathyroid hormone-related peptide receptor OS=Homo sapiens GN=PTH1R PE=1 S
11.	AXDN1_HUMAN	118637	34	Axonemal dynein light chain domain-containing protein 1 OS=Homo sapiens GN=AXDND1 PE=2 SV=1
12.	UMPS_HUMAN	52645	34	Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1
13.	ERCC2_HUMAN	87652	33	TFIIH basal transcription factor complex helicase XPD subunit OS=Homo sapiens GN=ERCC2 PE=1 SV=1
14.	GBRB2_HUMAN	59341	33	Gamma-aminobutyric acid receptor subunit beta-2 OS=Homo sapiens GN=GABRB2 PE=1 SV=2
15.	T23O_HUMAN	48012	33	Tryptophan 2,3-dioxygenase OS=Homo sapiens GN=TDO2 PE=1 SV=1
16.	PAEP_HUMAN	20953	32	Glycodelin OS=Homo sapiens GN=PAEP PE=1 SV=2
17.	ZN658_HUMAN	125674	32	Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2
18.	RHG39_HUMAN	122236	32	Rho GTPase-activating protein 39 OS=Homo sapiens GN=ARHGAP39 PE=1 SV=2
19.	ZN836_HUMAN	111011	32	Zinc finger protein 836 OS=Homo sapiens GN=ZNF836 PE=2 SV=2
20.	GDIA_HUMAN	51177	32	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2

Results List

1. JIP4_HUMAN **Mass:** 146913 **Score:** 59 **Expect:** 0.025 **Matches:** 13

C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
881.3265	880.3192	880.4178	-112.02	42 -	48	0	R.YDEEVVK.E
1165.6325	1164.6252	1164.5887	31.4	135 -	144	1	K.AKNYADQISR.L
1320.6409	1319.6336	1319.7085	-56.73	38 -	48	1	R.LIGRYDEEVVK.E
1365.6962	1364.6889	1364.6684	15.0	654 -	665	1	K.YKQVTNGQGENK.M
1475.8162	1474.8090	1474.6536	105	489 -	501	1	K.DDDDSDIPTAQRK.R
1493.7857	1492.7785	1492.7270	34.5	137 -	148	1	K.NYADQISRLEER.E
1657.8508	1656.8436	1656.8584	-8.93	234 -	247	1	K.FQELSQPRSHTSLK.V
1765.7810	1764.7737	1765.0250	-142.41	1011 -	1027	0	K.GIVLVALADGTLAIFHR.G
2101.1833	2100.1760	2099.9517	107	163 -	178	1	R.HTEMIHNYMEHLERTK.L + 2 Oxidation (M)
2211.0887	2210.0814	2210.1179	-16.49	946 -	964	1	K.DQISVLPNEQDLVREEAQK.M
2291.1592	2290.1520	2290.0900	27.1	750 -	769	0	K.NQEELSSLVWICTSTHSATK.V
2501.1843	2500.1770	2500.0734	41.5	1 -	23	0	-.MELEDGVVYQEEPGGSGAVMSER.V + 2 Oxidation (M)
2584.1487	2583.1415	2583.2262	-32.78	339 -	361	1	K.SEVQAIIESTPELDMDKDLSGYK.G + Oxidation (M)

No match to: 842.4951, 856.5073, 870.5331, 886.1516, 901.6158, 917.3060, 1107.5881, 1179.6458, 1193.6580, 1234.7160, 1350.7517, 1434.8149, 1487.7911, 1673.8901, 1687.9314, 1707.8239, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2225.1085, 2286.0969, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2566.1975, 2705.1099, 2717.0329, 3312.2262

2. K22E_HUMAN **Mass:** 65678 **Score:** 49 **Expect:** 0.25 **Matches:** 8

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1107.5881	1106.5808	1106.5356	40.8	354 -	362	0	K.AQYEEIAQR.S
1193.6580	1192.6507	1192.6200	25.7	238 -	247	1	K.RYLDGLTAER.T
1320.6409	1319.6336	1319.5756	44.0	46 -	61	0	R.HGGGGGGFGGGGFGSR.S
1475.8162	1474.8090	1474.7780	21.0	198 -	209	0	R.FLEQQNQVLQTK.W
1838.9497	1837.9425	1837.9072	19.2	71 -	92	0	K.SISISVAGGGGGFGAAGGFGGR.G

2383.9402	2382.9330	2383.2093	-115.95	462 - 481	1	R.DYQELMNVKLALDVEIATYR.K
2399.0061	2397.9988	2398.0113	-5.19	93 - 122	0	R.GGGFGGGSSFGGGSGFSGGGFGGGGFGGGR.F
2501.1843	2500.1770	2500.0600	46.8	516 - 544	1	K.AAFGGSGGRGSSSGGGYSSGSSSYGSGGR.Q

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1165.6325, 1179.6458, 1234.7160, 1350.7517, 1365.6962, 1434.8149, 1487.7911, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

3. K1C10_HUMAN **Mass:** 59020 **Score:** 48 **Expect:** 0.32 **Matches:** 8

Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1165.6325	1164.6252	1164.5775	41.0	442 -	450	0	R.LENEIQTYR.S
1234.7160	1233.7087	1233.6717	30.0	236 -	245	1	R.LKYENEVALR.Q
1365.6962	1364.6889	1364.6320	41.7	323 -	333	0	R.SQYEQLAEQNR.K
1434.8149	1433.8076	1433.7626	31.4	440 -	450	1	K.IRLENEIQTYR.S
1493.7857	1492.7785	1492.7270	34.5	323 -	334	1	R.SQYEQLAEQNRK.D
1707.8239	1706.8167	1706.7649	30.3	41 -	59	0	K.GSLGGGFSSGGFSGGSFSR.G
2083.0419	2082.0346	2081.9575	37.0	423 -	439	0	R.AETECQNTEYQQLLDIK.I
2342.9727	2341.9654	2341.9771	-5.01	60 -	86	0	R.GSSGGGCFGGSSGGYGGLGGFGGGSFR.G

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1179.6458, 1193.6580, 1320.6409, 1350.7517, 1475.8162, 1487.7911, 1657.8508, 1673.8901, 1687.9314, 1765.7810, 1791.7890, 1838.9497, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

4. PARK7_HUMAN **Mass:** 20050 **Score:** 44 **Expect:** 0.72 **Matches:** 5

Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1365.6962	1364.6889	1364.8391	-110.04	176 -	188	1	K.EVAAQVKAPLVLK.D
1657.8508	1656.8436	1656.8618	-10.98	33 -	48	1	K.VTVAGLAGKDPVQCSR.D
1707.8239	1706.8167	1706.7855	18.2	13 -	27	0	K.GAEEMETVIPVDVMR.R + 2 Oxidation (M)
2383.9402	2382.9330	2383.2855	-147.90	6 -	27	1	R.ALVILAKGAEEMETVIPVDVMR.R
2584.1487	2583.1415	2583.3180	-68.35	64 -	89	0	K.EGPYDVVVLPGGNLGAQNLSESAAVK.E

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1673.8901, 1687.9314, 1765.7810, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2399.0061, 2501.1843, 2566.1975, 2705.1099, 2717.0329, 3312.2262

5. K2C1_HUMAN **Mass:** 66170 **Score:** 43 **Expect:** 1.1 **Matches:** 9

Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1179.6458	1178.6386	1178.5931	38.6	377 -	386	0	K.YEELQITAGR.H
1475.8162	1474.8090	1474.7780	21.0	200 -	211	0	R.FLEQQNQVLQTK.W

1657.8508	1656.8436	1656.7856	35.0	13 - 29	0	R.SGGGFSSGSAGIINYQR.R
1687.9314	1686.9242	1686.9628	-22.92	66 - 82	1	R.SLVNLGGSKSISISVAR.G
1765.7810	1764.7737	1764.7275	26.2	46 - 65	0	R.FSSCGGGGGSFGAGGGFGSR.S
2286.0969	2285.0896	2285.1175	-12.21	367 - 386	1	K.AEAESLYQSKYEELQITAGR.H
2293.9587	2292.9515	2292.9680	-7.20	39 - 65	1	R.SGGGGGRFSSCGGGGGSFGAGGGFGSR.S
2383.9402	2382.9330	2382.9447	-4.90	519 - 549	0	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G
3312.2262	3311.2189	3311.3009	-24.77	550 - 588	0	R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1487.7911, 1493.7857, 1673.8901, 1707.8239, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2291.1592, 2342.9727, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 2717.0329

6. ZSC25_HUMAN **Mass:** 62576 **Score:** 40 **Expect:** 1.8 **Matches:** 7

Zinc finger and SCAN domain-containing protein 25 OS=Homo sapiens GN=ZSCAN25 PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1179.6458	1178.6386	1178.6560	-14.80	70 -	78	0	R.WLRPELHTK.E
1234.7160	1233.7087	1233.6578	41.3	522 -	531	1	R.SFNQRSILNR.H
1320.6409	1319.6336	1319.5776	42.5	135 -	145	0	R.QGEQEETALCR.G
1493.7857	1492.7785	1492.6656	75.6	234 -	245	0	K.DMALAFPEEEWR.H
2083.0419	2082.0346	2082.0507	-7.75	416 -	432	1	R.HHLEVHQRSHTGEKPYK.C
2101.1833	2100.1760	2100.0674	51.8	4 -	22	0	K.EHPEMAEAPQQQLGIPVVK.L
2286.0969	2285.0896	2285.2128	-53.91	286 -	308	1	K.GALVALTSERFGEASLQGPGLGR.V

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1193.6580, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 1838.9497, 2096.9825, 2211.0887, 2225.1085, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

7. CFA99_HUMAN **Mass:** 52489 **Score:** 38 **Expect:** 2.9 **Matches:** 7

Cilia- and flagella-associated protein 99 OS=Homo sapiens GN=CFAP99 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4951	841.4878	841.5385	-60.23	247 -	253	1	R.ERLALLK.E
870.5331	869.5258	869.4832	49.1	377 -	385	1	R.RAGTGVPGR.G
901.6158	900.6085	900.5392	76.9	42 -	49	0	K.LNTTAILR.E
1234.7160	1233.7087	1233.6023	86.2	126 -	135	1	R.VEQQKEQMAK.L + Oxidation (M)
1673.8901	1672.8828	1672.8394	26.0	394 -	413	1	R.SAAGRYAAAGAGGGGGVPAR.A
2083.0419	2082.0346	2082.0527	-8.71	106 -	123	1	K.LSHEEAVLARQSLMQENK.Q
2717.0329	2716.0256	2716.4105	-141.70	225 -	248	1	K.LVDLTQIPGYGLEGEMSIVELRER.L

No match to: 856.5073, 881.3265, 886.1516, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1193.6580, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 1838.9497, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 3312.2262

8. ZN624_HUMAN **Mass:** 102544 **Score:** 36 **Expect:** 5.6 **Matches:** 9

Zinc finger protein 624 OS=Homo sapiens GN=ZNF624 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1107.5881	1106.5808	1106.5720	7.97	269 -	277	1	K.SNNKEKPYK.C
1350.7517	1349.7444	1349.6186	93.2	165 -	174	1	R.MEGLWKWNDR.I + Oxidation (M)
1475.8162	1474.8090	1474.7641	30.4	844 -	856	1	K.AFRSSSSLTVHQR.I
1493.7857	1492.7785	1492.7198	39.3	58 -	69	0	K.DVAIDFTLEEWR.L
1707.8239	1706.8167	1706.7505	38.8	690 -	703	1	R.HTGEKPYKCNECGK.V
1838.9497	1837.9425	1837.7909	82.5	829 -	843	1	R.MHTGEKPYKCNECGK.A
2211.0887	2210.0814	2210.0031	35.5	334 -	352	1	K.CNECGKAFIASSSLMVHQR.I + Oxidation (M)
2705.1099	2704.1026	2704.3002	-73.08	536 -	557	1	K.AFINYSCLTVHHRMHTGEKPYK.C + Oxidation (M)
2717.0329	2716.0256	2716.3555	-121.44	141 -	164	1	K.AISEDLSQEAILEKLTENGLWDSR.M

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1365.6962, 1434.8149, 1487.7911, 1657.8508, 1673.8901, 1687.9314, 1765.7810, 1791.7890, 2083.0419, 2096.9825, 2101.1833, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 3312.2262

9. SEP14_HUMAN **Mass:** 50449 **Score:** 35 **Expect:** 6.2 **Matches:** 6

Septin-14 OS=Homo sapiens GN=SEPT14 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
881.3265	880.3192	880.4337	-130.13	354 -	359	1	K.QRFMQR.V + Oxidation (M)
1107.5881	1106.5808	1106.5720	7.94	202 -	210	1	K.NDLQTFKNK.I
1493.7857	1492.7785	1492.7807	-1.48	174 -	186	1	K.SLDLLTMKNLDSK.V + Oxidation (M)
1838.9497	1837.9425	1837.9091	18.1	409 -	425	1	K.MKAASEALQTQLSTDTK.K + Oxidation (M)
2584.1487	2583.1415	2583.2077	-25.65	263 -	283	1	R.GRHYPWGVLQVENENHCDFVK.L
2705.1099	2704.1026	2704.3578	-94.35	26 -	48	1	R.CLTTIGHFGFECLPNQLVSRSIR.Q

No match to: 842.4951, 856.5073, 870.5331, 886.1516, 901.6158, 917.3060, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2717.0329, 3312.2262

10. PTH1R_HUMAN **Mass:** 67173 **Score:** 34 **Expect:** 7.3 **Matches:** 7

Parathyroid hormone/parathyroid hormone-related peptide receptor OS=Homo sapiens GN=PTH1R PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4951	841.4878	841.4341	63.9	214 -	219	1	R.RLHCTR.N
1165.6325	1164.6252	1164.5887	31.4	173 -	181	1	K.FLTNETRER.E
1179.6458	1178.6386	1178.5098	109	391 -	400	1	R.ETNAGRCDTR.Q
1234.7160	1233.7087	1233.6102	79.8	68 -	79	0	K.GWTSASTSGKPR.K
1365.6962	1364.6889	1364.6585	22.3	151 -	162	0	R.NGSWELVPGHNR.T
2566.1975	2565.1903	2565.3752	-72.10	220 -	240	1	R.NYIHMHLFLSFMLRAVSIFVK.D
2584.1487	2583.1415	2583.2136	-27.93	487 -	511	1	K.ARSGSSSYSYGPMVSHTSVTNVGPR.V

No match to: 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1193.6580, 1320.6409, 1350.7517, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2705.1099, 2717.0329, 3312.2262

11. AXDN1_HUMAN **Mass:** 118637 **Score:** 34 **Expect:** 7.7 **Matches:** 10

Axonemal dynein light chain domain-containing protein 1 OS=Homo sapiens GN=AXDND1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4951	841.4878	841.4294	69.5	350 -	356	1	K.ETEKAHK.D
901.6158	900.6085	900.5392	76.9	281 -	288	1	R.GELLSKVR.E
1320.6409	1319.6336	1319.6755	-31.71	962 -	972	1	K.DLEELVMTSRK.E
1365.6962	1364.6889	1364.7187	-21.85	527 -	538	1	K.KEEFTGDVLLSK.Y
1434.8149	1433.8076	1433.7184	62.2	960 -	971	1	K.NKDLEELVMTSR.K
1657.8508	1656.8436	1656.7743	41.8	590 -	603	1	K.EYEIRINGDNGYSK.I
1707.8239	1706.8167	1706.8007	9.33	918 -	931	0	K.YLEAMAVIEHMQEK.L + Oxidation (M)
2211.0887	2210.0814	2210.2310	-67.69	436 -	454	1	K.HFIILLSNKDTEDLALLQK.L
2291.1592	2290.1520	2290.2307	-34.39	818 -	836	1	K.ITLLTYEEIERLLEEEAVK.E
2705.1099	2704.1026	2704.3133	-77.90	884 -	906	0	R.FIGEDENVHSKPLFETDVLSSWR.E

No match to: 856.5073, 870.5331, 881.3265, 886.1516, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1350.7517, 1475.8162, 1487.7911, 1493.7857, 1673.8901, 1687.9314, 1765.7810, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2225.1085, 2286.0969, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2717.0329, 3312.2262

12. UMPS_HUMAN **Mass:** 52645 **Score:** 34 **Expect:** 8 **Matches:** 6

Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
901.6158	900.6085	900.5579	56.2	243 -	249	1	K.LLRLMQK.K
1320.6409	1319.6336	1319.7085	-56.73	30 -	41	0	K.SGLSSPIYIDLR.G
1365.6962	1364.6889	1364.6183	51.7	304 -	313	0	K.CHEFLIFEDR.K
1493.7857	1492.7785	1492.7133	43.7	304 -	314	1	K.CHEFLIFEDRK.F
1765.7810	1764.7737	1764.8828	-61.84	452 -	467	1	R.GIISAADRLEAAEMYR.K
2291.1592	2290.1520	2290.2507	-43.13	1 -	22	1	-.MAVARAALGPLVTGLYDVQAFK.F

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1350.7517, 1434.8149, 1475.8162, 1487.7911, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

13. ERCC2_HUMAN **Mass:** 87652 **Score:** 33 **Expect:** 10 **Matches:** 7

TFIIH basal transcription factor complex helicase XPD subunit OS=Homo sapiens GN=ERCC2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4951	841.4878	841.5134	-30.37	287 -	293	1	R.RLVEGLR.E
1193.6580	1192.6507	1192.5659	71.1	134 -	143	0	K.CHSLTASYVR.A

1234.7160	1233.7087	1233.6032	85.5	488 - 497	0	R.VCLCPMIIGR.G + Oxidation (M)
1707.8239	1706.8167	1706.8046	7.05	129 - 143	1	K.DVDGKCHSLTASYVR.A
2096.9825	2095.9752	2096.0435	-32.56	470 - 487	0	K.ILDFHPVTMATFTMTLAR.V + 2 Oxidation (M)
2101.1833	2100.1760	2100.1442	15.2	617 - 634	1	R.AVIMFGVPYVYTQSRILK.A + Oxidation (M)
3312.2262	3311.2189	3311.6361	-126.00	470 - 497	1	K.ILDFHPVTMATFTMTLARVCLCPMIIGR.G + 3 Oxidation (M)

No match to: 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1765.7810, 1791.7890, 1838.9497, 2083.0419, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 2717.0329

14. GBRB2_HUMAN **Mass:** 59341 **Score:** 33 **Expect:** 11 **Matches:** 6

Gamma-aminobutyric acid receptor subunit beta-2 OS=Homo sapiens GN=GABRB2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1107.5881	1106.5808	1106.5138	60.5	345 - 354		1	K.AASANNEKMR.L + Oxidation (M)
1165.6325	1164.6252	1164.6363	-9.52	454 - 463		1	R.NALERHVAQK.K
2083.0419	2082.0346	2082.1321	-46.81	471 - 489		1	R.ASQLKITIPDLTDVNAIDR.W
2291.1592	2290.1520	2290.1091	18.7	367 - 386		1	K.QNGTQYRSLWDPTGNLSPTR.R
2705.1099	2704.1026	2704.3499	-91.44	142 - 165		1	R.LHPDGTVLYGLRITTTAACMMDLR.R
3312.2262	3311.2189	3311.4744	-77.16	413 - 442		1	K.NEMATSEAVMGLGDPRSTMLAYDASSIQYR.K + 3 Oxidation (M)

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 1838.9497, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2717.0329

15. T23O_HUMAN **Mass:** 48012 **Score:** 33 **Expect:** 11 **Matches:** 6

Tryptophan 2,3-dioxygenase OS=Homo sapiens GN=TDO2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5073	855.5000	855.4273	85.1	381 - 387		0	K.MNPTIHK.F + Oxidation (M)
1107.5881	1106.5808	1106.5244	51.0	251 - 259		0	K.EEQVAEFQK.Q
1838.9497	1837.9425	1837.8217	65.7	245 - 259		1	K.EESEEKEEQVAEFQK.Q
2286.0969	2285.0896	2284.8630	99.2	388 - 406		0	K.FLYTAEYCDSSYFSSDESD.-
2342.9727	2341.9654	2342.1902	-95.98	304 - 323		0	R.FQVPFQLLTSLMDIDSLMTK.W + Oxidation (M)
2501.1843	2500.1770	2500.2672	-36.06	124 - 144		0	K.LLVQQFSILETMTALDFNDFR.E

No match to: 842.4951, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2291.1592, 2293.9587, 2383.9402, 2399.0061, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

16. PAEP_HUMAN **Mass:** 20953 **Score:** 32 **Expect:** 12 **Matches:** 4

Glycodelin OS=Homo sapiens GN=PAEP PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4951	841.4878	841.4545	39.6	26 - 32		0	K.QDLELPK.L

856.5073	855.5000	855.5079	-9.17	157 - 163	0	R.AFRPLPR.H
1165.6325	1164.6252	1164.4870	119	79 - 87	0	R.WENNSCVEK.K
2501.1843	2500.1770	2500.3260	-59.59	143 - 163	1	R.VLVEDDEIMQGFIRAFRPLPR.H

No match to: 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

17. ZN658_HUMAN **Mass:** 125674 **Score:** 32 **Expect:** 13 **Matches:** 8

Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5331	869.5258	869.4831	49.1	755 -	761	1	K.TRLSTHR.R
1493.7857	1492.7785	1492.8263	-32.02	638 -	650	1	R.SFAHISVLKAHQR.I
1765.7810	1764.7737	1764.9496	-99.65	396 -	410	1	R.KAHLIQHQRPHSGEK.T
1791.7890	1790.7817	1790.8080	-14.66	791 -	805	0	R.IHTGEKPYECNVCGK.T
2342.9727	2341.9654	2342.0532	-37.48	1011 -	1029	1	R.VHQRIHTGEKPYECDECGK.T
2383.9402	2382.9330	2383.0256	-38.87	290 -	308	1	K.VHMAMTHYECNERGINFSR.K + 2 Oxidation (M)
2501.1843	2500.1770	2500.1401	14.8	330 -	351	1	K.CEENFSQSSAHIVHQKTQAGDK.F
2584.1487	2583.1415	2583.1304	4.27	282 -	302	1	K.TTAVEYNKVHMAMTHYECNER.G

No match to: 842.4951, 856.5073, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1838.9497, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2399.0061, 2566.1975, 2705.1099, 2717.0329, 3312.2262

18. RHG39_HUMAN **Mass:** 122236 **Score:** 32 **Expect:** 13 **Matches:** 8

Rho GTPase-activating protein 39 OS=Homo sapiens GN=ARHGAP39 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6409	1319.6336	1319.7309	-73.74	869 -	879	1	K.KPNVEEIRHAK.N
1434.8149	1433.8076	1433.6859	84.9	118 -	132	1	R.ASAESSPGRGSSVSR.E
1673.8901	1672.8828	1672.7765	63.6	111 -	126	1	K.QNTESPRASAESSPGR.G
1838.9497	1837.9425	1837.8880	29.6	441 -	457	1	R.LGVKSGDYSTMEGPELR.H
2291.1592	2290.1520	2290.2474	-41.66	952 -	971	1	K.VPTGLEDPHVPASLLKLWYR.E
2342.9727	2341.9654	2342.1404	-74.69	221 -	243	1	R.EPSFLAAQGNGYAPDGPPGVRSR.R
2399.0061	2397.9988	2398.1852	-77.71	416 -	437	1	R.HKYAPNPGGGSYSLQPSPCLLR.D
2501.1843	2500.1770	2500.1481	11.6	821 -	840	1	K.FHSYLEGYIYRHMDPVNDTK.G + Oxidation (M)

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1193.6580, 1234.7160, 1350.7517, 1365.6962, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 2083.0419, 2096.9825, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2293.9587, 2383.9402, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

19. ZN836_HUMAN **Mass:** 111011 **Score:** 32 **Expect:** 13 **Matches:** 8

Zinc finger protein 836 OS=Homo sapiens GN=ZNF836 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1193.6580	1192.6507	1192.7040	-44.70	817	826	1	R.VRSILVNHQK.M
1234.7160	1233.7087	1233.6540	44.3	1	11	0	-.MALTQGPLTFR.D
1320.6409	1319.6336	1319.6510	-13.15	94	103	0	K.NLQDLEFQWK.D
1475.8162	1474.8090	1474.7238	57.7	491	502	1	R.IHTGEKPYKCDK.C
1487.7911	1486.7839	1486.7277	37.8	618	630	1	K.VFNDSGNLSNHKR.I
2096.9825	2095.9752	2095.9932	-8.55	556	573	1	K.CNVCGKVFNYSGNLSIHK.R
2342.9727	2341.9654	2342.1536	-80.36	57	77	1	K.ELPPIGNSNTGEKCQTVTLER.H
2566.1975	2565.1903	2565.2493	-23.01	161	182	1	K.IYECNQSEKTVNNSSLVSPLQR.I

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1179.6458, 1350.7517, 1365.6962, 1434.8149, 1493.7857, 1657.8508, 1673.8901, 1687.9314, 1707.8239, 1765.7810, 1791.7890, 1838.9497, 2083.0419, 2101.1833, 2211.0887, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2383.9402, 2399.0061, 2501.1843, 2584.1487, 2705.1099, 2717.0329, 3312.2262

20. GDIA_HUMAN **Mass:** 51177 **Score:** 32 **Expect:** 14 **Matches:** 6

Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1179.6458	1178.6386	1178.6659	-23.17	209	218	1	R.IKLYSESLAR.Y
1193.6580	1192.6507	1192.7002	-41.48	300	309	0	R.IICILSHPIK.N
1673.8901	1672.8828	1672.8355	28.3	56	70	1	R.FQLLEGPPESMGRGR.D
1791.7890	1790.7817	1790.9277	-81.49	90	103	1	K.MLLYTEVTRYLDFK.V
1838.9497	1837.9425	1837.8152	69.2	194	208	0	R.TDDYLDQPCLETVNR.I
2211.0887	2210.0814	2210.0711	4.66	119	138	1	K.VPSTETEALASNLMGMFEKR.R

No match to: 842.4951, 856.5073, 870.5331, 881.3265, 886.1516, 901.6158, 917.3060, 1107.5881, 1165.6325, 1234.7160, 1320.6409, 1350.7517, 1365.6962, 1434.8149, 1475.8162, 1487.7911, 1493.7857, 1657.8508, 1687.9314, 1707.8239, 1765.7810, 2083.0419, 2096.9825, 2101.1833, 2225.1085, 2286.0969, 2291.1592, 2293.9587, 2342.9727, 2383.9402, 2399.0061, 2501.1843, 2566.1975, 2584.1487, 2705.1099, 2717.0329, 3312.2262

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 150 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 43
Selected for scoring : 39

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

```
User            : JOY
Email           : joyprashant88@gmail.com
Search title    :
Database        : SwissProt 2015_08 (549008 sequences; 195692017 residues)
Taxonomy        : Homo sapiens (human) (20204 sequences)
Timestamp       : 31 Jul 2015 at 05:29:58 GMT
Top Score       : 58 for ZN248_HUMAN, Zinc finger protein 248 OS=Homo sapiens GN=ZNF248 PE=2 SV=1
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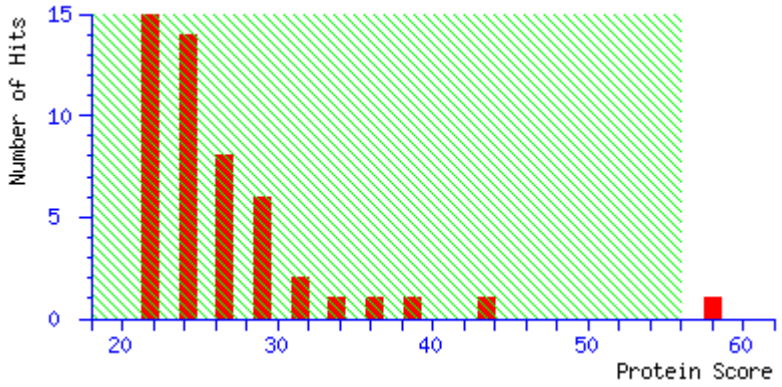
Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant (p<0.05).



Protein Summary Report

Format As [Protein Summary] Help

Significance threshold p< [0.05] Max. number of hits [20]

Preferred taxonomy [All entries]

Re-Search All | Search Unmatched

Index

	Accession	Mass	Score	Description
1.	ZN248_HUMAN	68868	58	Zinc finger protein 248 OS=Homo sapiens GN=ZNF248 PE=2 SV=1
2.	VDAC2_HUMAN	32060	44	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2
3.	OLIG3_HUMAN	29567	40	Oligodendrocyte transcription factor 3 OS=Homo sapiens GN=OLIG3 PE=1 SV=2
4.	YP010_HUMAN	21022	36	Putative uncharacterized protein FLJ32790 OS=Homo sapiens PE=2 SV=2
5.	Z658B_HUMAN	97349	35	Zinc finger protein 658B OS=Homo sapiens GN=ZNF658B PE=2 SV=1
6.	SELN_HUMAN	66229	31	Selenoprotein N OS=Homo sapiens GN=SEPN1 PE=1 SV=5
7.	ZN658_HUMAN	125674	31	Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2
8.	TTC34_HUMAN	61777	30	Tetratricopeptide repeat protein 34 OS=Homo sapiens GN=TTC34 PE=2 SV=2
9.	MCM5_HUMAN	83031	30	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5
10.	UBTD2_HUMAN	26401	29	Ubiquitin domain-containing protein 2 OS=Homo sapiens GN=UBTD2 PE=1 SV=2
11.	OLIG2_HUMAN	32649	29	Oligodendrocyte transcription factor 2 OS=Homo sapiens GN=OLIG2 PE=2 SV=2
12.	GNMT_HUMAN	33178	29	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3
13.	SFTPD_HUMAN	38047	28	Pulmonary surfactant-associated protein D OS=Homo sapiens GN=SFTPD PE=1 SV=3
14.	STIM2_HUMAN	84774	28	Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=2
15.	NTF3_HUMAN	29678	27	Neurotrophin-3 OS=Homo sapiens GN=NTF3 PE=1 SV=1
16.	ZN391_HUMAN	41831	27	Zinc finger protein 391 OS=Homo sapiens GN=ZNF391 PE=2 SV=2
17.	LEG1_HUMAN	15048	26	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2
18.	GBG5_HUMAN	7428	26	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 S
19.	ST20_HUMAN	9189	26	Suppressor of tumorigenicity 20 protein OS=Homo sapiens GN=ST20 PE=2 SV=2
20.	YMEL1_HUMAN	86686	26	ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2

Results List

1. ZN248_HUMAN **Mass:** 68868 **Score:** 58 **Expect:** 0.032 **Matches:** 6

Zinc finger protein 248 OS=Homo sapiens GN=ZNF248 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
940.4691	939.4618	939.5250	-67.25	533 - 540		1	K.SALTKHQR.T
1838.9385	1837.9312	1837.8496	44.4	219 - 234		1	K.NGQGFHDEAAFFTNKR.S
2211.0609	2210.0536	2210.0745	-9.45	139 - 157		1	K.ICDSCEMNLKNISGLIISK.K + Oxidation (M)
2399.0070	2397.9997	2398.0868	-36.31	485 - 504		1	R.THTGEKPFICNECGKSFCVK.S
2528.1127	2527.1054	2527.1186	-5.22	342 - 363		1	K.HQIVHMGGKSYDYNENGSNFSK.K + Oxidation (M)
2717.0256	2716.0183	2716.2082	-69.89	449 - 471		1	K.SNLTEHQRTHTGEKPYECNACGK.S

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2225.0839, 2342.9922, 2425.1176, 2473.1140, 2501.1537, 2584.1504, 2705.0918

2. VDAC2_HUMAN **Mass:** 32060 **Score:** 44 **Expect:** 0.8 **Matches:** 4

Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
940.4691	939.4618	939.4563	5.92	178 - 185		0	R.NNFAVGYR.T
2103.1388	2102.1316	2102.1484	-8.02	248 - 267		0	K.VNNSSLIGVGYTQTLRPGVK.L
2399.0070	2397.9997	2398.0529	-22.19	209 - 229		0	K.VCEDLDTSVNLAWTSGTNCTR.F

2528.1127	2527.1054	2527.1616	-22.22	186 - 208	0	R.TGDFQLHTNVNDGTEFGGSIYQK.V

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2425.1176, 2473.1140, 2501.1537, 2584.1504, 2705.0918, 2717.0256

3. OLIG3_HUMAN **Mass:** 29567 **Score:** 40 **Expect:** 2.2 **Matches:** 5

Oligodendrocyte transcription factor 3 OS=Homo sapiens GN=OLIG3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5230	869.5158	869.5698	-62.15	124 -	131	0	K.IATLLLAR.N
940.4691	939.4618	939.4661	-4.59	63 -	71	1	K.AAGESSKYK.I
2096.9809	2095.9736	2095.8952	37.4	12 -	28	1	R.ASSPDMDEMYLRDHHHR.H
2399.0070	2397.9997	2398.0927	-38.75	37 -	58	1	R.LNSVSSTQGDMMQKMPGESLSR.A + Oxidation (M)
2584.1504	2583.1432	2583.0523	35.2	1 -	23	1	-.MNSDSSSVSSRASSPDMDEMYLR.D + 2 Oxidation (M)

No match to: 806.3781, 842.4891, 881.2678, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2705.0918, 2717.0256

4. YP010_HUMAN **Mass:** 21022 **Score:** 36 **Expect:** 5.7 **Matches:** 3

Putative uncharacterized protein FLJ32790 OS=Homo sapiens PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6185	1319.6112	1319.6503	-29.67	1 -	12	1	-.MAAKSTQDSLPR.D + Oxidation (M)
2211.0609	2210.0536	2210.0927	-17.71	5 -	25	1	K.STQDSLPRDTGEPSALPVQGR.A
2342.9922	2341.9849	2342.1412	-66.75	119 -	140	1	K.GPWPPAQGLAMRTHCPTGPPSK.A

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2225.0839, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

5. Z658B_HUMAN **Mass:** 97349 **Score:** 35 **Expect:** 6.7 **Matches:** 6

Zinc finger protein 658B OS=Homo sapiens GN=ZNF658B PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5230	869.5158	869.4831	37.5	515 -	521	1	K.TRLSTHR.R
1493.7734	1492.7662	1492.8263	-40.26	398 -	410	1	R.SFAHISVLKAHQR.I
1791.7746	1790.7673	1790.8080	-22.71	551 -	565	0	R.IHTGEKPYECNVCGK.T
2342.9922	2341.9849	2342.0532	-29.16	771 -	789	1	R.VHQRIHTGEKPYECDECGK.T
2501.1537	2500.1464	2500.1401	2.54	86 -	107	1	K.CEENFSQSSAHIVHQKTQAGDK.F
2584.1504	2583.1432	2583.1304	4.93	38 -	58	1	K.TTAVEYNKVHMAMTHYECNER.G

No match to: 806.3781, 842.4891, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1519.7469, 1672.8529, 1707.8052, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2399.0070, 2425.1176, 2473.1140, 2528.1127, 2705.0918, 2717.0256

6. SELN_HUMAN **Mass:** 66229 **Score:** 31 **Expect:** 16 **Matches:** 5

Selenoprotein N OS=Homo sapiens GN=SEPN1 PE=1 SV=5

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6185	1319.6112	1319.6795	-51.79	162 -	172	0	R.FQPLLPETMTK.S + Oxidation (M)
1487.7944	1486.7871	1486.8119	-16.66	255 -	266	0	R.LLSMFHPRPFVK.T + Oxidation (M)
1493.7734	1492.7662	1492.7787	-8.37	10 -	25	0	R.GPPSPGPAAQPPAPPR.R
1519.7469	1518.7396	1518.8116	-47.41	162 -	174	1	R.FQPLLPETMTKSK.D
2705.0918	2704.0845	2704.2658	-67.04	446 -	469	1	K.LVHSILLWGALDDQSCUGSGRTLR.E

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2717.0256

7. ZN658_HUMAN **Mass:** 125674 **Score:** 31 **Expect:** 18 **Matches:** 6

Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5230	869.5158	869.4831	37.5	755 -	761	1	K.TRLSTHR.R
1493.7734	1492.7662	1492.8263	-40.26	638 -	650	1	R.SFAHISVLKAHQR.I
1791.7746	1790.7673	1790.8080	-22.71	791 -	805	0	R.IHTGEKPYECNVCGK.T
2342.9922	2341.9849	2342.0532	-29.16	1011 -	1029	1	R.VHQRIHTGEKPYECDECGK.T
2501.1537	2500.1464	2500.1401	2.54	330 -	351	1	K.CEENFSQSSAHIVHQKTQAGDK.F
2584.1504	2583.1432	2583.1304	4.93	282 -	302	1	K.TTAVEYNKVHMAMTHYECNER.G

No match to: 806.3781, 842.4891, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1519.7469, 1672.8529, 1707.8052, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2399.0070, 2425.1176, 2473.1140, 2528.1127, 2705.0918, 2717.0256

8. TTC34_HUMAN **Mass:** 61777 **Score:** 30 **Expect:** 22 **Matches:** 4

Tetratricopeptide repeat protein 34 OS=Homo sapiens GN=TTC34 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4891	841.4818	841.5385	-67.37	72 -	79	0	K.ALLVALSR.R
870.5230	869.5158	869.4719	50.4	353 -	361	1	K.KGDVPGAAR.D
1493.7734	1492.7662	1492.8586	-61.93	142 -	156	1	R.ALAILRARPGGADGR.V
2103.1388	2102.1316	2102.0181	54.0	528 -	546	0	R.HAEAWTAVESGLLVDPDHR.G

No match to: 806.3781, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

9. MCM5_HUMAN **Mass:** 83031 **Score:** 30 **Expect:** 23 **Matches:** 6

DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
940.4691	939.4618	939.4635	-1.75	591 -	598	1	R.SGARQHER.D
1320.6185	1319.6112	1319.6656	-41.24	252 -	262	1	R.YLCDKVVPGNR.V
1407.7819	1406.7746	1406.6898	60.3	139 -	150	1	R.SLKSDMMSHLVK.I + 2 Oxidation (M)
1838.9385	1837.9312	1837.8595	39.0	309 -	324	1	R.SFAGAVSPQEEEEFRR.L
2103.1388	2102.1316	2102.0942	17.8	177 -	195	0	R.NTLTNIAMRPGLEGYALPR.K + Oxidation (M)

2225.0839	2224.0767	2224.2072	-58.67	142 - 162	1	K.SDMMSHLVKIPGIIIAASAVR.A + Oxidation (M)

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 1234.6990, 1350.7203, 1365.6894, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 2083.0122, 2096.9809, 2198.9398, 2211.0609, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

10. UBTD2_HUMAN **Mass:** 26401 **Score:** 29 **Expect:** 25 **Matches:** 4

Ubiquitin domain-containing protein 2 OS=Homo sapiens GN=UBTD2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4891	841.4818	841.5385	-67.39	163 - 169		1	K.DLKLVVR.S
940.4691	939.4618	939.4735	-12.47	205 - 211		1	K.MKFEELK.I + Oxidation (M)
1350.7203	1349.7130	1349.6688	32.8	181 - 193		0	R.LHAAEGVEPGSQR.W
2225.0839	2224.0767	2224.1376	-27.40	215 - 234		0	K.DYVVQVIVSQPVQNPTPVEN.-

No match to: 806.3781, 870.5230, 881.2678, 1234.6990, 1320.6185, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

11. OLIG2_HUMAN **Mass:** 32649 **Score:** 29 **Expect:** 26 **Matches:** 3

Oligodendrocyte transcription factor 2 OS=Homo sapiens GN=OLIG2 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5230	869.5158	869.5698	-62.15	149 - 156		0	K.IATLLLAR.N
1707.8052	1706.7979	1706.7442	31.4	77 - 95		0	K.SSSSSTSSSTSSAAASSTK.K
2705.0918	2704.0845	2704.2650	-66.74	1 - 25		0	-.MDSDASLVSSRPSSPEPDDLFLPAR.S + Oxidation (M)

No match to: 806.3781, 842.4891, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2717.0256

12. GNMT_HUMAN **Mass:** 33178 **Score:** 29 **Expect:** 28 **Matches:** 5

Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
806.3781	805.3708	805.4116	-50.67	162 - 168		0	K.NIASMVR.A + Oxidation (M)
1493.7734	1492.7662	1492.7787	-8.37	30 - 41		1	R.VWQLYIGDTRSR.T
1707.8052	1706.7979	1706.9151	-68.66	47 - 60		1	K.AWLLGLLRQHGCQR.V
2473.1140	2472.1067	2472.2148	-43.70	243 - 264		0	R.LSYYPHCLASFTELLQAAFGGK.C
2528.1127	2527.1054	2527.2377	-52.34	216 - 240		0	K.AHMVTLDYTVQVPGAGQDGSPGLSK.F

No match to: 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1519.7469, 1672.8529, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2501.1537, 2584.1504, 2705.0918, 2717.0256

13. SFTPD_HUMAN **Mass:** 38047 **Score:** 28 **Expect:** 31 **Matches:** 3

Pulmonary surfactant-associated protein D OS=Homo sapiens GN=SFTPD PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4891	841.4818	841.4658	19.1	208 - 216		1	K.GIPGDKGAK.G

2103.1388	2102.1316	2102.0215	52.3	64 - 87	0	K.GDPGLPGAAGQAGMPGQAGPVGPK.G + Oxidation (M)
2584.1504	2583.1432	2583.1550	-4.58	30 - 53	1	R.TMPSACTLVMCSSVESGLPGRDGR.D + Oxidation (M)

No match to: 806.3781, 870.5230, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2705.0918, 2717.0256

14. STIM2_HUMAN **Mass:** 84774 **Score:** 28 **Expect:** 36 **Matches:** 4

Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1791.7746	1790.7673	1790.7273	22.3	290 - 303		1	K.MMDEINYAKEEACR.L + 2 Oxidation (M)
2225.0839	2224.0767	2224.2038	-57.16	165 - 184		1	K.GTTLPRIAVHEPSFMISQLK.I
2342.9922	2341.9849	2341.9856	-0.30	78 - 97		1	K.QMDDDKDGGIEVEESDEFIR.E + Oxidation (M)
2528.1127	2527.1054	2527.1604	-21.74	248 - 268		1	K.MMKDLESLQTAEQSLMDLQER.L + 2 Oxidation (M)

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2584.1504, 2705.0918, 2717.0256

15. NTF3_HUMAN **Mass:** 29678 **Score:** 27 **Expect:** 40 **Matches:** 3

Neurotrophin-3 OS=Homo sapiens GN=NTF3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
940.4691	939.4618	939.4774	-16.56	71 - 79		1	R.EPERGGPAK.S
1487.7944	1486.7871	1486.7892	-1.41	226 - 238		1	R.ALTSENNKLVGWR.W
2103.1388	2102.1316	2102.0942	17.7	80 - 97		1	K.SAFQPVIAMDTELLRQQR.R

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

16. ZN391_HUMAN **Mass:** 41831 **Score:** 27 **Expect:** 42 **Matches:** 3

Zinc finger protein 391 OS=Homo sapiens GN=ZNF391 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1487.7944	1486.7871	1486.8004	-8.97	313 - 325		1	K.GFSRSSSLIIHQR.T
2211.0609	2210.0536	2210.0941	-18.30	205 - 222		1	R.STNLSQHQRTHTQERPYK.C
2342.9922	2341.9849	2342.0419	-24.36	111 - 129		1	K.CNECEKAFSYQSDLLVHSR.I

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2225.0839, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

17. LEG1_HUMAN **Mass:** 15048 **Score:** 26 **Expect:** 51 **Matches:** 2

Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2103.1388	2102.1316	2102.0435	41.9	1 - 19		0	-.MACGLVASNLNLKPGECLR.V
2705.0918	2704.0845	2704.2048	-44.49	50 - 74		1	R.FNAHGDANTIVCNSKDGGAWGTEQR.E

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2717.0256

18. GBG5_HUMAN **Mass:** 7428 **Score:** 26 **Expect:** 51 **Matches:** 2

Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5230	869.5158	869.5447	-33.25	12 -	18	1	K.KVVQQLR.L
940.4691	939.4618	939.4331	30.5	2 -	11	0	M.SGSSSVAAMK.K + Oxidation (M)

No match to: 806.3781, 842.4891, 881.2678, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

19. ST20_HUMAN **Mass:** 9189 **Score:** 26 **Expect:** 51 **Matches:** 2

Suppressor of tumorigenicity 20 protein OS=Homo sapiens GN=ST20 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1707.8052	1706.7979	1706.8839	-50.40	6 -	21	0	R.LTATSVSQVQENGFVK.K
1838.9385	1837.9312	1837.9284	1.52	23 -	38	1	K.LEPKSGWMTFLEVTGK.I + Oxidation (M)

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 940.4691, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1487.7944, 1493.7734, 1519.7469, 1672.8529, 1791.7746, 1803.9416, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2342.9922, 2399.0070, 2425.1176, 2473.1140, 2501.1537, 2528.1127, 2584.1504, 2705.0918, 2717.0256

20. YMEL1_HUMAN **Mass:** 86686 **Score:** 26 **Expect:** 52 **Matches:** 5

ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
940.4691	939.4618	939.4194	45.2	82 -	89	0	R.SMFMEPAK.R
1487.7944	1486.7871	1486.7047	55.4	563 -	574	1	K.EMVTMKELEFSK.D + Oxidation (M)
2342.9922	2341.9849	2342.0828	-41.82	147 -	166	0	K.NISSHWHTSHVSAQSFFENK.Y
2425.1176	2424.1103	2424.0614	20.2	45 -	65	0	R.DVVPEHEAPSSECMFSDFLTK.L
2528.1127	2527.1054	2527.1993	-37.13	145 -	166	1	K.GKNISSHWHTSHVSAQSFFENK.Y

No match to: 806.3781, 842.4891, 870.5230, 881.2678, 1234.6990, 1320.6185, 1350.7203, 1365.6894, 1407.7819, 1434.8006, 1493.7734, 1519.7469, 1672.8529, 1707.8052, 1791.7746, 1803.9416, 1838.9385, 2083.0122, 2096.9809, 2103.1388, 2198.9398, 2211.0609, 2225.0839, 2399.0070, 2473.1140, 2501.1537, 2584.1504, 2705.0918, 2717.0256

Search Parameters

Type of search : **Peptide Mass Fingerprint**
Enzyme : **Trypsin**
Fixed modifications : **Carbamidomethyl (C)**
Variable modifications : **Oxidation (M)**
Mass values : **Monoisotopic**
Protein Mass : **Unrestricted**
Peptide Mass Tolerance : **± 70 ppm**

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Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 34
Selected for scoring   : 19
```

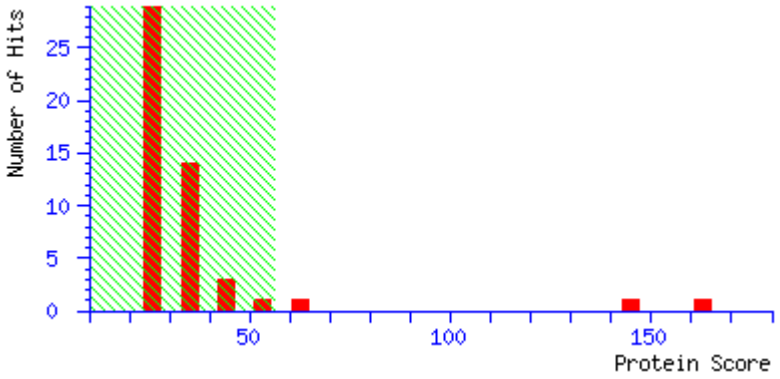
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

```
User            : joy
Email           : joyprashant88@gmail.com
Search title    :
Database        : SwissProt 2015_08 (549008 sequences; 195692017 residues)
Taxonomy        : Homo sapiens (human) (20204 sequences)
Timestamp       : 31 Jul 2015 at 05:37:09 GMT
Top Score       : 163 for Mixture 1, HSP72_HUMAN + GSTM5_HUMAN
```

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant (p<0.05).



Protein Summary Report

Format As | Protein Summary | Help

Significance threshold p< 0.05 Max. number of hits 20

Overview Table

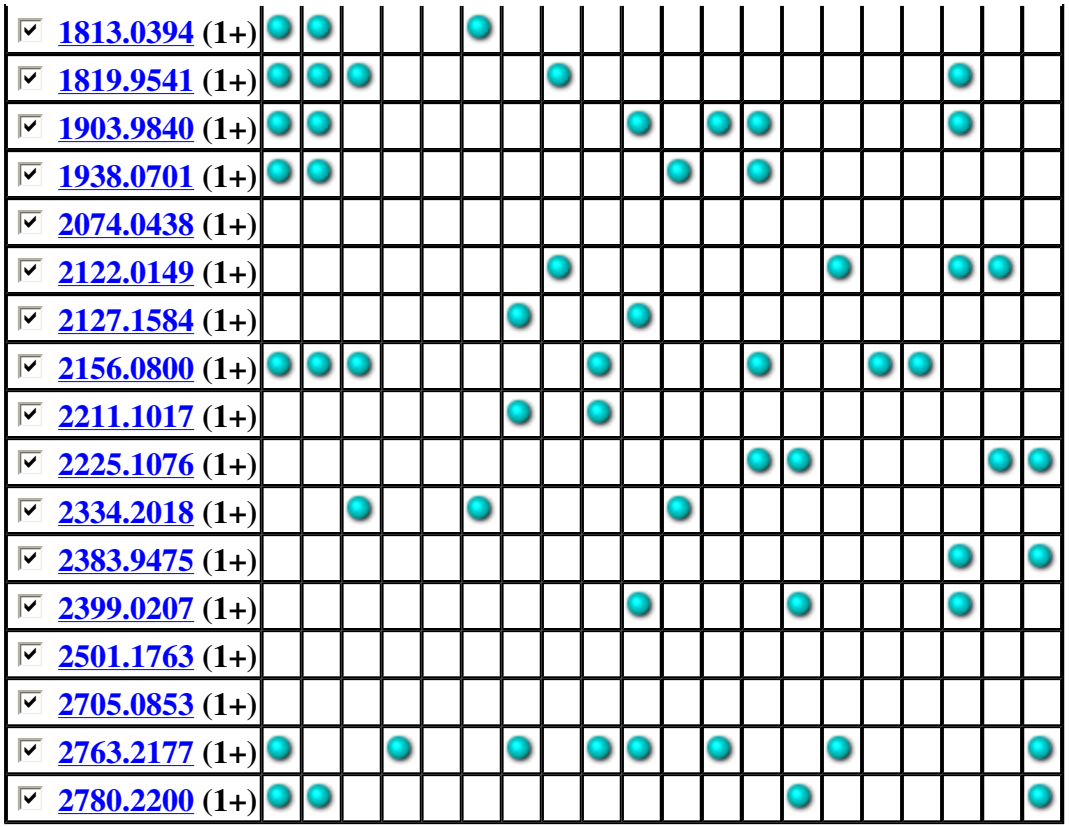
Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.

Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
742.3472 (1+)	●	●																		
842.5066 (1+)														●	●					
856.5039 (1+)	●			●							●	●		●	●				●	
870.5346 (1+)								●												
881.2682 (1+)																				
1179.6541 (1+)	●			●				●			●									
1183.6825 (1+)	●	●				●						●	●			●	●			
1197.7106 (1+)	●		●	●	●							●				●	●			
1229.7276 (1+)	●	●																		●
1253.6649 (1+)	●	●	●			●														
1320.6298 (1+)												●								●
1346.7124 (1+)	●	●				●			●	●					●				●	●
1456.8486 (1+)	●	●			●			●												
1465.9285 (1+)															●	●	●			
1480.8025 (1+)	●	●	●			●					●		●						●	
1487.7539 (1+)	●	●	●						●			●				●	●	●	●	●
1580.8660 (1+)																				
1638.9042 (1+)						●	●					●								
1657.9233 (1+)	●	●																●		
1687.9421 (1+)	●			●	●			●	●							●	●			
1691.7796 (1+)	●	●	●		●		●	●												
1707.7998 (1+)	●			●	●															●
1771.9377 (1+)																				
1788.0271 (1+)	●	●	●		●															



Select All | Select None | Search Selected

Index

	Accession	Mass	Score	Description
1.	Mixture 1		163	HSP72_HUMAN + GSTM5_HUMAN
2.	HSP72_HUMAN	70263	148	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1
3.	HSP7C_HUMAN	71082	58	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1
4.	GSTM5_HUMAN	25829	49	Glutathione S-transferase Mu 5 OS=Homo sapiens GN=GSTM5 PE=1 SV=3
5.	B3GT1_HUMAN	38425	44	Beta-1,3-galactosyltransferase 1 OS=Homo sapiens GN=B3GALT1 PE=2 SV=1
6.	NELFB_HUMAN	66283	42	Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1
7.	MRT4_HUMAN	27657	41	mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2
8.	F13A_HUMAN	83728	38	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4
9.	DPOA2_HUMAN	66762	36	DNA polymerase alpha subunit B OS=Homo sapiens GN=POLA2 PE=1 SV=2
10.	UST_HUMAN	48042	35	Uronyl 2-sulfotransferase OS=Homo sapiens GN=UST PE=2 SV=1
11.	ANKR1_HUMAN	36514	35	Ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=ANKRD1 PE=1 SV=2
12.	MSH2_HUMAN	105418	35	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1

13.	RAD18_HUMAN	57043	35	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=2
14.	TTLL1_HUMAN	49356	34	Probable tubulin polyglutamylase TTLL1 OS=Homo sapiens GN=TTLL1 PE=2 SV=1
15.	GT253_HUMAN	67891	34	Probable inactive glycosyltransferase 25 family member 3 OS=Homo sapiens GN=CERCAM PE=2 SV=1
16.	HS71A_HUMAN	70294	32	Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1
17.	HS71B_HUMAN	70294	32	Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1
18.	KIF5C_HUMAN	109997	32	Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1
19.	RIC8B_HUMAN	59586	32	Synembryn-B OS=Homo sapiens GN=RIC8B PE=1 SV=2
20.	WRN_HUMAN	164410	31	Werner syndrome ATP-dependent helicase OS=Homo sapiens GN=WRN PE=1 SV=2

Results List

1. **Mixture 1** **Total score:** 163 **Expect:** 1e-12 **Matches:** 23

Components: 1. HSP72_HUMAN Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1
2. GSTM5_HUMAN Glutathione S-transferase Mu 5 OS=Homo sapiens GN=GSTM5 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Comp	Peptide
742.3472	741.3400	741.3711	-41.97	90	94	0	1	K.HWPFR.V
856.5039	855.4967	855.4524	51.7	193	199	1	2	K.KISAYMK.S + Oxidation (M)
1179.6541	1178.6469	1178.6084	32.7	44	52	1	2	R.SQWLNEKFK.L
1183.6825	1182.6752	1182.6397	30.0	462	472	0	1	K.FDLTGIPPAPR.G
1197.7106	1196.7033	1196.6805	19.1	135	144	1	2	K.LKLYSEFLGK.R
1229.7276	1228.7203	1228.6776	34.8	161	172	0	1	K.DAGTITGLNVLR.I
1253.6649	1252.6577	1252.6088	39.0	305	314	0	1	R.FEELNADLFR.G
1346.7124	1345.7051	1345.6812	17.8	240	250	1	1	R.MVSHLAEEFKR.K
1456.8486	1455.8413	1455.8046	25.3	332	345	0	1	K.GQIQEIVLVGGSTR.I
1480.8025	1479.7953	1479.7470	32.6	303	314	1	1	R.ARFEELNADLFR.G
1487.7539	1486.7466	1486.6940	35.4	38	50	0	1	R.TTPSYVAFTDTER.L
1657.9233	1656.9160	1656.9159	0.09	157	172	1	1	R.QATKDAGTITGLNVLR.I
1687.9421	1686.9348	1686.8716	37.5	19	32	1	2	R.LLLEYTDSSYVEKK.Y
1691.7796	1690.7723	1690.7183	31.9	224	239	0	1	K.STAGDTHLGGEDFDNR.M
1707.7998	1706.7925	1706.9065	-66.81	169	182	1	2	R.IFEPKCLDAFLNLK.D
1788.0271	1787.0198	1786.9828	20.7	173	189	1	1	R.IINEPTAAAIAYGLDKK.G
1813.0394	1812.0321	1812.0105	11.9	329	345	1	1	K.LDKGQIQEIVLVGGSTR.I
1819.9541	1818.9469	1818.9046	23.2	58	73	1	1	K.NQVAMNPTNTIFDAKR.L
1903.9840	1902.9767	1902.9588	9.42	140	156	0	1	K.VHSAVITVPAYFNDSQR.Q
1938.0701	1937.0629	1937.0370	13.3	455	472	1	1	K.DNNLLGKFDLTGIPPAPR.G
2156.0800	2155.0727	2155.0797	-3.26	38	57	1	1	R.TTPSYVAFTDTERLIGDAAK.N
2763.2177	2762.2105	2762.3778	-60.59	145	167	1	2	K.RPWFAGDKITFVDFLAYDVLDMK.R + Oxidation (M)
2780.2200	2779.2127	2779.2937	-29.13	427	450	0	1	K.QTQTFTTYSDNQSSVLVQVYEGER.A

No match to: 842.5066, 870.5346, 881.2682, 1320.6298, 1465.9285, 1580.8660, 1638.9042, 1771.9377, 2074.0438, 2122.0149, 2127.1584, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853

2. HSP72_HUMAN **Mass:** 70263 **Score:** 148 **Expect:** 3.2e-11 **Matches:** 17

Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
742.3472	741.3400	741.3711	-41.97	90 -	94	0	K.HWPFR.V
1183.6825	1182.6752	1182.6397	30.0	462 -	472	0	K.FDLTGIPPAPR.G
1229.7276	1228.7203	1228.6776	34.8	161 -	172	0	K.DAGTITGLNVLR.I
1253.6649	1252.6577	1252.6088	39.0	305 -	314	0	R.FEELNADLFR.G
1346.7124	1345.7051	1345.6812	17.8	240 -	250	1	R.MVSHLAEEFKR.K
1456.8486	1455.8413	1455.8046	25.3	332 -	345	0	K.GQIQEIVLVGGSTR.I
1480.8025	1479.7953	1479.7470	32.6	303 -	314	1	R.ARFEELNADLFR.G
1487.7539	1486.7466	1486.6940	35.4	38 -	50	0	R.TTPSYVAFTDTER.L
1657.9233	1656.9160	1656.9159	0.09	157 -	172	1	R.QATKDAGTITGLNVLR.I
1691.7796	1690.7723	1690.7183	31.9	224 -	239	0	K.STAGDTHLGGEDFDNR.M
1788.0271	1787.0198	1786.9828	20.7	173 -	189	1	R.IINEPTAAAIAYGLDKK.G
1813.0394	1812.0321	1812.0105	11.9	329 -	345	1	K.LDKGQIQEIVLVGGSTR.I
1819.9541	1818.9469	1818.9046	23.2	58 -	73	1	K.NQVAMNPTNTIFDAKR.L
1903.9840	1902.9767	1902.9588	9.42	140 -	156	0	K.VHSAVITVPAYFNDSQR.Q
1938.0701	1937.0629	1937.0370	13.3	455 -	472	1	K.DNNLLGKFDLTGIPPAPR.G
2156.0800	2155.0727	2155.0797	-3.26	38 -	57	1	R.TTPSYVAFTDTERLIGDAAK.N
2780.2200	2779.2127	2779.2937	-29.13	427 -	450	0	K.QTQTFTTYSDNQSSVLVQVYEGER.A

No match to: 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1197.7106, 1320.6298, 1465.9285, 1580.8660, 1638.9042, 1687.9421, 1707.7998, 1771.9377, 2074.0438, 2122.0149, 2127.1584, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177

3. HSP7C_HUMAN **Mass:** 71082 **Score:** 58 **Expect:** 0.031 **Matches:** 9

Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1197.7106	1196.7033	1196.6553	40.1	459 -	469	0	K.FELTGIPPAPR.G
1253.6649	1252.6577	1252.6088	39.0	302 -	311	0	R.FEELNADLFR.G
1480.8025	1479.7953	1479.7470	32.6	300 -	311	1	R.ARFEELNADLFR.G
1487.7539	1486.7466	1486.6940	35.4	37 -	49	0	R.TTPSYVAFTDTER.L
1691.7796	1690.7723	1690.7183	31.9	221 -	236	0	K.STAGDTHLGGEDFDNR.M
1788.0271	1787.0198	1786.9828	20.7	172 -	188	1	R.IINEPTAAAIAYGLDKK.V
1819.9541	1818.9469	1819.0316	-46.58	329 -	345	1	K.SQIHDIVLVGGSTRIPK.I
2156.0800	2155.0727	2155.0797	-3.26	37 -	56	1	R.TTPSYVAFTDTERLIGDAAK.N
2334.2018	2333.1945	2333.1685	11.1	50 -	71	1	R.LIGDAAKNQVAMNPTNTVFDAK.R + Oxidation (M)

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1229.7276, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1707.7998, 1771.9377, 1813.0394, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2211.1017, 2225.1076, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

4. GSTM5_HUMAN **Mass:** 25829 **Score:** 49 **Expect:** 0.23 **Matches:** 6

Glutathione S-transferase Mu 5 OS=Homo sapiens GN=GSTM5 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5039	855.4967	855.4524	51.7	193 - 199		1	K.KISAYMK.S + Oxidation (M)
1179.6541	1178.6469	1178.6084	32.7	44 - 52		1	R.SQWLNEKFK.L
1197.7106	1196.7033	1196.6805	19.1	135 - 144		1	K.LKLYSEFLGK.R
1687.9421	1686.9348	1686.8716	37.5	19 - 32		1	R.LLLEYTDSSYVEKK.Y
1707.7998	1706.7925	1706.9065	-66.81	169 - 182		1	R.IFEPKCLDAFLNLK.D
2763.2177	2762.2105	2762.3778	-60.59	145 - 167		1	K.RPWFAGDKITFVDFLAYDVLDMK.R + Oxidation (M)

No match to: 742.3472, 842.5066, 870.5346, 881.2682, 1183.6825, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1480.8025, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1691.7796, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2780.2200

5. B3GT1_HUMAN **Mass:** 38425 **Score:** 44 **Expect:** 0.86 **Matches:** 6

Beta-1,3-galactosyltransferase 1 OS=Homo sapiens GN=B3GALT1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1197.7106	1196.7033	1196.6012	85.3	162 - 171		1	R.WVATFCSKAK.Y
1456.8486	1455.8413	1455.7511	62.0	202 - 214		0	R.YFTGYVINGGPIR.D
1687.9421	1686.9348	1686.8044	77.3	156 - 169		1	K.TLMGMRWVATFCSK.A
1691.7796	1690.7723	1690.8461	-43.62	300 - 313		0	R.VITVHQISPEEMHR.I + Oxidation (M)
1707.7998	1706.7925	1706.8012	-5.11	95 - 108		1	R.QAIRETWGDENNFK.G
1788.0271	1787.0198	1786.8447	98.0	176 - 190		0	K.TDSDIFVNMDNLIYK.L

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1465.9285, 1480.8025, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1771.9377, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

6. NELFB_HUMAN **Mass:** 66283 **Score:** 42 **Expect:** 1.3 **Matches:** 7

Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1183.6825	1182.6752	1182.6972	-18.57	515 - 525		1	R.VAPSKLEALQK.A
1253.6649	1252.6577	1252.6485	7.29	130 - 139		1	K.LVMADKELYR.A + Oxidation (M)
1346.7124	1345.7051	1345.6837	15.9	77 - 89		1	R.VSAIASEGKAEER.Y
1480.8025	1479.7953	1479.9038	-73.33	507 - 519		1	R.LLIHLHPRVAPSK.L
1638.9042	1637.8970	1637.8963	0.39	211 - 223		1	K.NVKLYDMVLQFLR.T
1813.0394	1812.0321	1811.8950	75.7	420 - 434		0	R.MACEVGLYYVLHITK.Q + Oxidation (M)
2334.2018	2333.1945	2333.1750	8.36	526 - 547		1	K.ALEPTGQSGEAVKELYSQLGEK.L

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1197.7106, 1229.7276, 1320.6298, 1456.8486, 1465.9285, 1487.7539, 1580.8660, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

7. MRT4_HUMAN **Mass:** 27657 **Score:** 41 **Expect:** 1.5 **Matches:** 5

mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1638.9042	1637.8970	1637.8447	31.9	164	177	1	K.RGVVTLLSDYEVCK.E
1691.7796	1690.7723	1690.8640	-54.22	192	205	1	K.LFGYEMAEFKVTIK.Y + Oxidation (M)
2127.1584	2126.1511	2126.0329	55.6	33	49	1	K.CVDTYKYLFIFSVANMR.N
2211.1017	2210.0944	2209.9626	59.6	110	126	1	K.EEVNEWFTKYTEMDYAR.A
2763.2177	2762.2105	2762.0145	71.0	215	239	0	R.FQQMGDDLPESASESTEESDSEDDD.-

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1480.8025, 1487.7539, 1580.8660, 1657.9233, 1687.9421, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2156.0800, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2780.2200

8. F13A_HUMAN **Mass:** 83728 **Score:** 38 **Expect:** 3.4 **Matches:** 7

Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5346	869.5273	869.5083	21.9	254	261	1	R.GNPIKVSR.V
1179.6541	1178.6469	1178.5965	42.7	706	716	0	K.LIASMSSDSLR.H
1456.8486	1455.8413	1455.7470	64.8	717	728	0	R.HVYGELDVQIQR.R
1687.9421	1686.9348	1686.9192	9.23	115	130	0	K.GTYIPVPIVSELQSGK.W
1691.7796	1690.7723	1690.8275	-32.62	448	463	0	K.DGTHVVENVDATHIGK.L
1819.9541	1818.9469	1818.9224	13.4	447	463	1	K.KDGTHVVENVDATHIGK.L
2122.0149	2121.0076	2121.0777	-33.04	639	658	0	R.GTQVVGSDMTVTVQFTNPLK.E

No match to: 742.3472, 842.5066, 856.5039, 881.2682, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1465.9285, 1480.8025, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1903.9840, 1938.0701, 2074.0438, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

9. DPOA2_HUMAN **Mass:** 66762 **Score:** 36 **Expect:** 5 **Matches:** 6

DNA polymerase alpha subunit B OS=Homo sapiens GN=POLA2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1346.7124	1345.7051	1345.7136	-6.29	404	414	1	K.QCLRTIIEGTR.S
1487.7539	1486.7466	1486.8004	-36.18	574	586	1	R.LYLRRPAADGAER.Q
1687.9421	1686.9348	1686.8546	47.6	550	564	1	K.DVLGCVCVNPGRLTK.G
2156.0800	2155.0727	2155.1750	-47.45	408	427	1	R.TIIEGTRSSGSHLVFVPSLR.D
2211.1017	2210.0944	2210.1042	-4.42	293	312	0	K.EYSLFPGQVVIMEGINTTGR.K
2763.2177	2762.2105	2762.3156	-38.07	386	407	1	K.HEQVENCLLTSPFEDIFKQCLR.T

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1456.8486, 1465.9285, 1480.8025, 1580.8660, 1638.9042, 1657.9233, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2780.2200

10. UST_HUMAN **Mass:** 48042 **Score:** 35 **Expect:** 6.7 **Matches:** 5

Uronyl 2-sulfotransferase OS=Homo sapiens GN=UST PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1346.7124	1345.7051	1345.7275	-16.61	144	154	1	R.LTKNEQMELIK.N
1903.9840	1902.9767	1902.9986	-11.46	327	342	1	K.TVPSPEAVQILYQRMR.Y + Oxidation (M)
2127.1584	2126.1511	2126.0342	55.0	245	260	1	R.LFYIIPYFCGQHPRCR.E
2399.0207	2398.0135	2398.0569	-18.12	226	244	0	R.YLDINECILENYPECSNPR.L
2763.2177	2762.2105	2762.2772	-24.18	5	32	0	K.QQHPGGGADPWPHGAPMGGAPPGLGSWK.R + Oxidation (M)

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1456.8486, 1465.9285, 1480.8025, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1938.0701, 2074.0438, 2122.0149, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2501.1763, 2705.0853, 2780.2200

11. ANKR1_HUMAN **Mass:** 36514 **Score:** 35 **Expect:** 6.7 **Matches:** 5

Ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=ANKRD1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5039	855.4967	855.5542	-67.21	204	211	1	K.LLLNKGAK.I
1179.6541	1178.6469	1178.7135	-56.55	218	228	0	K.LLSTALHVAVR.T
1480.8025	1479.7953	1479.7066	59.9	249	261	1	K.DREGDTPLHDAVR.L
1938.0701	1937.0629	1936.9265	70.4	30	46	1	R.DGEYEAAVTLEKQEDLK.T
2334.2018	2333.1945	2333.2379	-18.60	42	61	1	K.QEDLKTLLAHPVTLGEQQWK.S

No match to: 742.3472, 842.5066, 870.5346, 881.2682, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

12. MSH2_HUMAN **Mass:** 105418 **Score:** 35 **Expect:** 6.7 **Matches:** 8

DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5039	855.4967	855.4273	81.1	839	845	0	K.HVIECAK.Q
1183.6825	1182.6752	1182.6608	12.2	502	512	1	R.DLGLDPGKQIK.L
1197.7106	1196.7033	1196.5925	92.7	556	565	0	K.LTSLNEEYTK.N
1320.6298	1319.6225	1319.6834	-46.12	160	171	0	R.QVGVGYVDSIQR.K
1487.7539	1486.7466	1486.7092	25.2	111	122	1	K.ASKENDWYLAYK.A
1638.9042	1637.8970	1637.8236	44.8	22	35	0	R.FFQGMPEKPTTTVR.L
1903.9840	1902.9767	1903.0163	-20.78	913	929	1	K.AEVIAKNNSFVNEIISR.I
2763.2177	2762.2105	2762.3466	-49.29	250	275	0	K.GEQMNSAVLPEMENQVAVSSLSAVIK.F + 2 Oxidation (M)

No match to: 742.3472, 842.5066, 870.5346, 881.2682, 1179.6541, 1229.7276, 1253.6649, 1346.7124, 1456.8486, 1465.9285, 1480.8025, 1580.8660, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2780.2200

13. RAD18_HUMAN **Mass:** 57043 **Score:** 35 **Expect:** 7 **Matches:** 6

E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1183.6825	1182.6752	1182.5955	67.5	319	328	0	K.LNESVMVFTK.D + Oxidation (M)
1480.8025	1479.7953	1479.7304	43.8	371	383	1	K.TVTITKEDESTEK.L
1903.9840	1902.9767	1902.9332	22.9	1	17	1	-.MDSLAESRWPPGLAVMK.T + Oxidation (M)
1938.0701	1937.0629	1936.9135	77.1	202	218	0	K.VDCPVCGVNIPESHINK.H
2156.0800	2155.0727	2155.1538	-37.62	84	102	1	K.SLNFARNHLLQFALESPAK.S
2225.1076	2224.1003	2223.9942	47.7	278	295	0	R.HQEFVHMYNAQCDALHPK.S

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 2074.0438, 2122.0149, 2127.1584, 2211.1017, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

14. TTLL1_HUMAN **Mass:** 49356 **Score:** 34 **Expect:** 9 **Matches:** 5

Probable tubulin polyglutamylase TTLL1 OS=Homo sapiens GN=TTLL1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.5066	841.4993	841.4406	69.8	400	407	0	R.QGQSLGPR.A
856.5039	855.4967	855.4603	42.5	366	372	1	K.WNKSPPK.E
2225.1076	2224.1003	2224.1537	-23.99	199	215	1	R.LYVLVSTYRPLRCYMYK.L
2399.0207	2398.0135	2398.2492	-98.30	320	341	0	K.LKPWLIEVNASPSLTSSTANDR.I
2780.2200	2779.2127	2779.4731	-93.67	281	304	1	K.LFDEIHWIIVQSLKAVAPVMNNDK.H

No match to: 742.3472, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1480.8025, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2334.2018, 2383.9475, 2501.1763, 2705.0853, 2763.2177

15. GT253_HUMAN **Mass:** 67891 **Score:** 34 **Expect:** 9 **Matches:** 6

Probable inactive glycosyltransferase 25 family member 3 OS=Homo sapiens GN=CERCAM PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.5066	841.4993	841.4657	39.9	449	455	1	R.KQVNPEK.E
856.5039	855.4967	855.4351	71.9	113	118	1	K.HWTKER.H
1346.7124	1345.7051	1345.6812	17.8	117	126	1	K.ERHQFLMELK.Q + Oxidation (M)
1465.9285	1464.9212	1464.7977	84.3	317	329	0	K.IGFDEVFVISLAR.R
2122.0149	2121.0076	2120.9949	5.97	267	284	1	R.YGYMNVPVKSHQGLEDER.V
2763.2177	2762.2105	2762.3196	-39.52	495	516	1	R.RMLPVDEFLPIMFDQHPNEQYK.A + Oxidation (M)

No match to: 742.3472, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1456.8486, 1480.8025, 1487.7539, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2780.2200

16. HS71A_HUMAN **Mass:** 70294 **Score:** 32 **Expect:** 12 **Matches:** 6

Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1183.6825	1182.6752	1182.6397	30.0	459	469	0	R.FELSGIPPAPR.G
1197.7106	1196.7033	1196.6877	13.0	160	171	0	K.DAGVIAGLNVLR.I
1465.9285	1464.9212	1464.8049	79.4	329	342	0	K.AQIHDLVLVGGSTR.I
1487.7539	1486.7466	1486.6940	35.4	37	49	0	R.TTPSYVAFTDTER.L
1687.9421	1686.9348	1686.8940	24.2	172	187	0	R.IINEPTAAAIAYGLDR.T
2156.0800	2155.0727	2155.0797	-3.26	37	56	1	R.TTPSYVAFTDTERLIGDAAK.N

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1480.8025, 1580.8660, 1638.9042, 1657.9233, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

17. HS71B_HUMAN **Mass:** 70294 **Score:** 32 **Expect:** 12 **Matches:** 6

Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1183.6825	1182.6752	1182.6397	30.0	459	469	0	R.FELSGIPPAPR.G
1197.7106	1196.7033	1196.6877	13.0	160	171	0	K.DAGVIAGLNVLR.I
1465.9285	1464.9212	1464.8049	79.4	329	342	0	K.AQIHDLVLVGGSTR.I
1487.7539	1486.7466	1486.6940	35.4	37	49	0	R.TTPSYVAFTDTER.L
1687.9421	1686.9348	1686.8940	24.2	172	187	0	R.IINEPTAAAIAYGLDR.T
2156.0800	2155.0727	2155.0797	-3.26	37	56	1	R.TTPSYVAFTDTERLIGDAAK.N

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1480.8025, 1580.8660, 1638.9042, 1657.9233, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2211.1017, 2225.1076, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

18. KIF5C_HUMAN **Mass:** 109997 **Score:** 32 **Expect:** 12 **Matches:** 7

Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1487.7539	1486.7466	1486.6432	69.6	642	653	0	K.SLTDYMQNMEQK.R
1657.9233	1656.9160	1656.8947	12.9	15	28	1	R.FRPLNEAEILRGDK.F
1819.9541	1818.9469	1818.8894	31.6	447	461	1	K.QQMLDQDELLASTRR.D + Oxidation (M)
1903.9840	1902.9767	1902.9920	-8.02	11	25	1	K.VMCRFRPLNEAEILR.G
2122.0149	2121.0076	2121.0048	1.30	173	191	1	R.FVSSPEEVMDVIDEGKANR.H
2383.9475	2382.9402	2383.0672	-53.29	168	188	1	K.GCTERFVSSPEEVMDVIDEGK.A
2399.0207	2398.0135	2398.1732	-66.63	619	639	1	K.MNASERELAACQLLISQHEAK.I

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1346.7124, 1456.8486, 1465.9285, 1480.8025, 1580.8660, 1638.9042, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1938.0701, 2074.0438, 2127.1584, 2156.0800, 2211.1017, 2225.1076, 2334.2018, 2501.1763, 2705.0853, 2763.2177, 2780.2200

19. RIC8B_HUMAN **Mass:** 59586 **Score:** 32 **Expect:** 12 **Matches:** 6

Synembryn-B OS=Homo sapiens GN=RIC8B PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5039	855.4967	855.5430	-54.14	79	86	0	K.VLVPVTTK.E
1346.7124	1345.7051	1345.7493	-32.82	108	119	0	K.VSEFPVIVESLK.C
1480.8025	1479.7953	1479.8596	-43.45	409	421	1	K.LVRLMTHVDLGVK.Q
1487.7539	1486.7466	1486.7878	-27.72	95	107	1	R.LAKLNELDDSLEK.V
2122.0149	2121.0076	2121.1438	-64.24	255	273	1	R.VMAAVLRHCLLIVGPTEDK.T
2225.1076	2224.1003	2224.1158	-6.95	356	375	1	K.GSSYREGLTPVLSLLTECSR.A

No match to: 742.3472, 842.5066, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1229.7276, 1253.6649, 1320.6298, 1456.8486, 1465.9285, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1707.7998, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2127.1584, 2156.0800, 2211.1017, 2334.2018, 2383.9475, 2399.0207, 2501.1763, 2705.0853, 2763.2177, 2780.2200

20. WRN_HUMAN **Mass:** 164410 **Score:** 31 **Expect:** 17 **Matches:** 9

Werner syndrome ATP-dependent helicase OS=Homo sapiens GN=WRN PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1229.7276	1228.7203	1228.6452	61.2	911	920	0	R.QIILSHFEDK.Q
1320.6298	1319.6225	1319.6278	-4.04	242	252	0	K.EEEILLSDMNK.Q
1346.7124	1345.7051	1345.7136	-6.29	1190	1200	1	K.MRPTTVENVKR.I + Oxidation (M)
1487.7539	1486.7466	1486.6068	94.0	1374	1386	0	R.CFPGSEEICSSSK.R
1707.7998	1706.7925	1706.8668	-43.52	211	225	0	K.LYAATDAYAGFIIYR.N
2225.1076	2224.1003	2224.2752	-78.64	591	610	0	K.IGLVISPLISLMEDQVLQLK.M + Oxidation (M)
2383.9475	2382.9402	2383.1266	-78.24	835	854	1	R.QVIHYGAPKDMESYYQEIGR.A
2763.2177	2762.2105	2762.4645	-91.97	1281	1305	1	R.ILPLMTIGMHLSQAVKAGCPLDLER.A
2780.2200	2779.2127	2779.3350	-43.98	566	590	1	R.DNVAVMATGYGKSLCFQYPPVYVGK.I + Oxidation (M)

No match to: 742.3472, 842.5066, 856.5039, 870.5346, 881.2682, 1179.6541, 1183.6825, 1197.7106, 1253.6649, 1456.8486, 1465.9285, 1480.8025, 1580.8660, 1638.9042, 1657.9233, 1687.9421, 1691.7796, 1771.9377, 1788.0271, 1813.0394, 1819.9541, 1903.9840, 1938.0701, 2074.0438, 2122.0149, 2127.1584, 2156.0800, 2211.1017, 2334.2018, 2399.0207, 2501.1763, 2705.0853

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 41
Selected for scoring : 37

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

```
User            : JOY
Email           : joyprashant88@gmail.com
Search title    :
Database        : SwissProt 2015_08 (549008 sequences; 195692017 residues)
Taxonomy        : Homo sapiens (human) (20204 sequences)
Timestamp       : 31 Jul 2015 at 06:12:58 GMT
Top Score       : 43 for TF3C1_HUMAN, General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4
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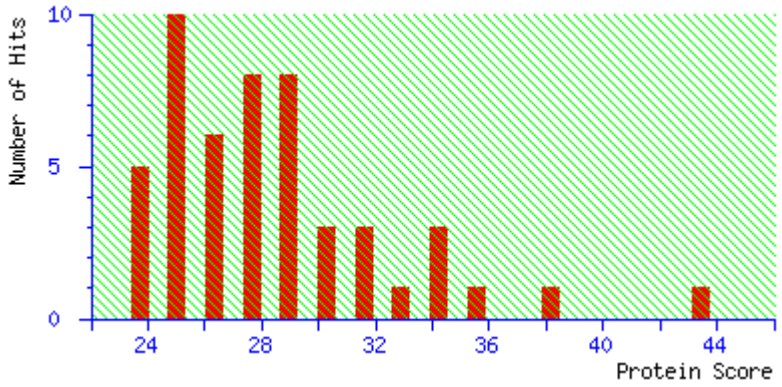
Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant (p<0.05).



Protein Summary Report

Format As [Protein Summary] Help

Significance threshold p< [0.05] Max. number of hits [20]

Preferred taxonomy [All entries]

Re-Search All | Search Unmatched

Index

	Accession	Mass	Score	Description
1.	TF3C1_HUMAN	241062	43	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4
2.	K22E_HUMAN	65678	38	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
3.	IFIT2_HUMAN	55282	35	Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens GN=IFIT2 PE=1 SV=1
4.	CJ120_HUMAN	39756	35	Uncharacterized protein C10orf120 OS=Homo sapiens GN=C10orf120 PE=2 SV=1
5.	CIART_HUMAN	41702	34	Circadian-associated transcriptional repressor OS=Homo sapiens GN=CIART PE=1 SV=1
6.	CV034_HUMAN	16872	34	Uncharacterized protein C22orf34 OS=Homo sapiens GN=C22orf34 PE=2 SV=1
7.	OLIG3_HUMAN	29567	33	Oligodendrocyte transcription factor 3 OS=Homo sapiens GN=OLIG3 PE=1 SV=2
8.	ZN621_HUMAN	50199	32	Zinc finger protein 621 OS=Homo sapiens GN=ZNF621 PE=2 SV=1
9.	MORC1_HUMAN	114178	32	MORC family CW-type zinc finger protein 1 OS=Homo sapiens GN=MORC1 PE=2 SV=2
10.	PLXD1_HUMAN	215293	31	Plexin-D1 OS=Homo sapiens GN=PLXND1 PE=1 SV=3
11.	CHSTC_HUMAN	48669	30	Carbohydrate sulfotransferase 12 OS=Homo sapiens GN=CHST12 PE=1 SV=2
12.	SHRM3_HUMAN	218321	30	Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2
13.	PKHJ1_HUMAN	17711	30	Pleckstrin homology domain-containing family J member 1 OS=Homo sapiens GN=PLEKHJ1 PE=2 SV=1
14.	TM225_HUMAN	26267	30	Transmembrane protein 225 OS=Homo sapiens GN=TMEM225 PE=2 SV=1
15.	DC1L2_HUMAN	54351	30	Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1
16.	Z280D_HUMAN	111211	29	Zinc finger protein 280D OS=Homo sapiens GN=ZNF280D PE=1 SV=3
17.	MK15_HUMAN	60251	29	Mitogen-activated protein kinase 15 OS=Homo sapiens GN=MAPK15 PE=1 SV=1
18.	HIDE1_HUMAN	24966	29	Protein HIDE1 OS=Homo sapiens GN=HIDE1 PE=2 SV=2
19.	MYOF_HUMAN	236100	29	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1
20.	ASCC3_HUMAN	252898	29	Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3

Results List

1. TF3C1_HUMAN **Mass:** 241062 **Score:** 43 **Expect:** 0.92 **Matches:** 9

General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
842.4920	841.4847	841.5498	-77.25	658	-	664	1	K.SIVRLVR.N
870.5361	869.5288	869.4759	60.8	116	-	121	2	R.YFKERK.N
1838.9523	1837.9451	1837.9661	-11.47	1803	-	1818	0	R.LVAMGSAWPWLLHSVR.L + Oxidation (M)
2096.9866	2095.9793	2095.9932	-6.62	131	-	147	2	K.SLQPRCTMVEAFDRWGK.K + Oxidation (M)
2210.0795	2209.0722	2209.1352	-28.50	598	-	616	2	K.TGRHSSGQDKPHETYRLLK.R
2342.9947	2341.9875	2342.2203	-99.41	497	-	517	2	K.DTRASANLRPKTQPHHSTPTK.G
2399.0057	2397.9985	2398.2618	-109.80	500	-	521	2	R.ASANLRPKTQPHHSTPTKGGWK.V
2584.1753	2583.1680	2583.4510	-109.54	231	-	252	2	R.LPTGAQQHSILLLLNRFHVDRR.S
2872.3294	2871.3222	2871.4403	-41.14	1102	-	1129	1	R.EVVDEGLIPGDGLGAAGLDSSFYGHLKR.N

No match to: 881.2605, 1320.6282, 1487.8178, 1493.7815, 2056.0437, 2225.1093, 2501.1727, 2651.3524, 2831.1880

2. K22E_HUMAN **Mass:** 65678 **Score:** 38 **Expect:** 3.4 **Matches:** 6

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1320.6282	1319.6209	1319.5756	34.3	46	-	61	0	R.HGGGGGGFGGGGFGSR.S
1838.9523	1837.9451	1837.9072	20.6	71	-	92	0	K.SISISVAGGGGGFGAAGGFGGR.G

2056.0437	2055.0365	2054.9995	18.0	13 - 35	2	R.GGGGGGFRGFSSGSAVVSGGSRR.S
2399.0057	2397.9985	2398.0113	-5.33	93 - 122	0	R.GGGFGGGSSFGGGSGFSGGGFGGGGFGGGR.F
2501.1727	2500.1655	2500.0600	42.2	516 - 544	1	K.AAFGGSGGRGSSSGGGYSSGSSSYGSGGR.Q
2651.3524	2650.3451	2650.3828	-14.20	62 - 92	1	R.SLVGLGGTKSISISVAGGGGGFGAAGGFGGR.G

No match to: 842.4920, 870.5361, 881.2605, 1487.8178, 1493.7815, 2096.9866, 2210.0795, 2225.1093, 2342.9947, 2584.1753, 2831.1880, 2872.3294

3. IFIT2_HUMAN **Mass:** 55282 **Score:** 35 **Expect:** 6.1 **Matches:** 5

Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens GN=IFIT2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4847	841.4446	47.7	252 -	258	1	R.SAAKFYR.R
1838.9523	1837.9451	1838.0149	-38.00	235 -	251	1	K.LVEEALEKAPGVTDVLR.S
2210.0795	2209.0722	2209.2946	-100.66	200 -	218	2	R.QAIRLNPDNQYLKVLLALK.L
2584.1753	2583.1680	2583.2726	-40.50	371 -	390	2	K.QLLHLRYGNFQLYQMKCEDK.A
2872.3294	2871.3222	2871.2480	25.8	15 -	37	1	R.QLKCHFTWNLMEGENSLDDFEDK.V + Oxidation (M)

No match to: 870.5361, 881.2605, 1320.6282, 1487.8178, 1493.7815, 2056.0437, 2096.9866, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2651.3524, 2831.1880

4. CJ120_HUMAN **Mass:** 39756 **Score:** 35 **Expect:** 6.7 **Matches:** 5

Uncharacterized protein C10orf120 OS=Homo sapiens GN=C10orf120 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5361	869.5288	869.5083	23.6	26 -	32	1	R.KNEKPVR.I
1320.6282	1319.6209	1319.6252	-3.25	15 -	25	1	K.QRASDTMVQER.K
2096.9866	2095.9793	2096.0547	-35.97	129 -	146	1	K.HSSPCAICVPLEKIWTAK.V
2210.0795	2209.0722	2208.8978	79.0	211 -	228	2	R.KEDNYDTHNCDDANQDKK.E
2225.1093	2224.1020	2224.1496	-21.40	128 -	146	2	K.KHSSPCAICVPLEKIWTAK.V

No match to: 842.4920, 881.2605, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2342.9947, 2399.0057, 2501.1727, 2584.1753, 2651.3524, 2831.1880, 2872.3294

5. CIART_HUMAN **Mass:** 41702 **Score:** 34 **Expect:** 7.3 **Matches:** 4

Circadian-associated transcriptional repressor OS=Homo sapiens GN=CIART PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4848	841.4592	30.3	361 -	367	1	R.KMTIGHR.E
1320.6282	1319.6209	1319.6252	-3.25	82 -	95	1	K.QRGSASPMAGSGAK.R + Oxidation (M)
1838.9523	1837.9451	1837.9105	18.8	148 -	163	1	R.GLSSFQQSVAMDRIQR.I + Oxidation (M)
2651.3524	2650.3451	2650.4193	-27.97	177 -	199	1	R.YLGTLLQVEGMLKTWFPQIAAQK.S + Oxidation (M)

No match to: 870.5361, 881.2605, 1487.8178, 1493.7815, 2056.0437, 2096.9866, 2210.0795, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2584.1753, 2831.1880, 2872.3294

6. CV034_HUMAN **Mass:** 16872 **Score:** 34 **Expect:** 8 **Matches:** 3

Uncharacterized protein C22orf34 OS=Homo sapiens GN=C22orf34 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6282	1319.6209	1319.6768	-42.38	136 -	147	1	R.SAPRASLCPPHK.G
1838.9523	1837.9451	1838.0122	-36.55	123 -	139	2	K.VSTRSITVPSPQRSAPR.A
2501.1727	2500.1655	2500.1731	-3.06	22 -	44	1	R.DGLGTILRGGAEEGSYDNWPHTR.K

No match to: 842.4920, 870.5361, 881.2605, 1487.8178, 1493.7815, 2056.0437, 2096.9866, 2210.0795, 2225.1093, 2342.9947, 2399.0057, 2584.1753, 2651.3524, 2831.1880, 2872.3294

7. OLIG3_HUMAN **Mass:** 29567 **Score:** 33 **Expect:** 9.9 **Matches:** 4

Oligodendrocyte transcription factor 3 OS=Homo sapiens GN=OLIG3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5361	869.5288	869.5698	-47.18	124 -	131	0	K.IATLLLAR.N
2096.9866	2095.9793	2095.8952	40.1	12 -	28	1	R.ASSPDMDEMYLRDHHHR.H
2399.0057	2397.9985	2398.0927	-39.28	37 -	58	1	R.LNSVSSTQGDMMQKMPGESLSR.A + Oxidation (M)
2584.1753	2583.1680	2583.0523	44.8	1 -	23	1	-.MNSDSSSVSSRASSPDMDEMYLR.D + 2 Oxidation (M)

No match to: 842.4920, 881.2605, 1320.6282, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2210.0795, 2225.1093, 2342.9947, 2501.1727, 2651.3524, 2831.1880, 2872.3294

8. ZN621_HUMAN **Mass:** 50199 **Score:** 32 **Expect:** 13 **Matches:** 4

Zinc finger protein 621 OS=Homo sapiens GN=ZNF621 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4847	841.4844	0.43	112 -	119	0	R.MPVGGLLR.N
1838.9523	1837.9451	1837.8635	44.4	67 -	82	0	R.GEAPWGPDPWDTEILR.G
2096.9866	2095.9793	2096.0771	-46.68	166 -	182	2	K.LIRHQMSHTGEKPFKCK.E
2210.0795	2209.0722	2209.0408	14.2	228 -	245	2	R.IHTGEKPYECKECGKAFR.R

No match to: 870.5361, 881.2605, 1320.6282, 1487.8178, 1493.7815, 2056.0437, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2584.1753, 2651.3524, 2831.1880, 2872.3294

9. MORC1_HUMAN **Mass:** 114178 **Score:** 32 **Expect:** 14 **Matches:** 6

MORC family CW-type zinc finger protein 1 OS=Homo sapiens GN=MORC1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6282	1319.6209	1319.6213	-0.33	755 -	765	0	K.QELCNDVLAMK.R
2096.9866	2095.9793	2095.9165	29.9	864 -	879	0	K.MCFNQIQNTYMVQYEK.K
2210.0795	2209.0722	2209.1855	-51.26	345 -	363	2	R.ELKTARTLSLFYGVNVENR.S
2225.1093	2224.1020	2224.0115	40.7	864 -	880	1	K.MCFNQIQNTYMVQYEKK.I
2584.1753	2583.1680	2583.2428	-28.94	217 -	238	2	K.TDKEDILMAGALEDFPARWSFR.A + Oxidation (M)
2872.3294	2871.3222	2871.4219	-34.73	775 -	801	1	K.SLLNVPMEDVNLSSGHIARVSVSGSCK.V + Oxidation (M)

No match to: 842.4920, 870.5361, 881.2605, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2342.9947, 2399.0057, 2501.1727, 2651.3524, 2831.1880

10. PLXD1_HUMAN **Mass:** 215293 **Score:** 31 **Expect:** 15 **Matches:** 9

Plexin-D1 OS=Homo sapiens GN=PLXND1 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
870.5361	869.5288	869.4719	65.4	5	-	14	0	R.AAGGAPLSAR.A
1320.6282	1319.6209	1319.5841	27.9	1622	-	1633	0	R.DLDDTSVVEDGR.K
1493.7815	1492.7742	1492.7562	12.1	1170	-	1182	0	R.LDYLPNPQFSTAK.R
2096.9866	2095.9793	2096.0803	-48.19	1165	-	1182	2	R.GSRFRLDYLPNPQFSTAK.R
2210.0795	2209.0722	2209.1049	-14.77	1324	-	1342	2	R.KGFAELQTDMTDLTKELNR.S
2225.1093	2224.1020	2224.1045	-1.11	1320	-	1338	2	R.EEIRKGFAELQTDMTDLTK.E
2342.9947	2341.9875	2342.2529	-113.31	1435	-	1455	2	K.DFAVRDRCSLASLLTIALHGK.L
2651.3524	2650.3451	2650.2730	27.2	1398	-	1420	0	K.IPESCRPNMEEGISLFSSLLNNK.H + Oxidation (M)
2831.1880	2830.1807	2830.4423	-92.43	941	-	968	0	R.YTVSEEIVCVTGPAPGPLSGVVTVNASK.E

No match to: 842.4920, 881.2605, 1487.8178, 1838.9523, 2056.0437, 2399.0057, 2501.1727, 2584.1753, 2872.3294

11. CHSTC_HUMAN **Mass:** 48669 **Score:** 30 **Expect:** 18 **Matches:** 5

Carbohydrate sulfotransferase 12 OS=Homo sapiens GN=CHST12 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1320.6282	1319.6209	1319.7350	-86.46	246	-	256	1	R.DPFVRLISAFR.S
2056.0437	2055.0365	2054.9909	22.2	145	-	162	0	R.AFDDIPNSELSHLIVDDR.H
2342.9947	2341.9875	2342.2681	-119.81	269	-	289	2	R.KFAVPMLRLYANHTSLPASAR.E
2399.0057	2397.9985	2398.2209	-92.73	395	-	414	1	K.LYEADFVLFGYPKPENLLRD.-
2584.1753	2583.1680	2583.2235	-21.48	80	-	102	2	K.QSDLPRKETEQPPAPGSMEESVR.G + Oxidation (M)

No match to: 842.4920, 870.5361, 881.2605, 1487.8178, 1493.7815, 1838.9523, 2096.9866, 2210.0795, 2225.1093, 2501.1727, 2651.3524, 2831.1880, 2872.3294

12. SHRM3_HUMAN **Mass:** 218321 **Score:** 30 **Expect:** 18 **Matches:** 8

Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1320.6282	1319.6209	1319.6569	-27.25	57	-	69	1	K.VEEGGKADTLSSK.L
1838.9523	1837.9451	1837.8411	56.6	283	-	300	1	R.SGSMDNTSARGGLLEGMR.Q
2096.9866	2095.9793	2096.1239	-68.99	986	-	1005	1	R.HSVTPAEGDLARPVPPAARR.G
2342.9947	2341.9875	2342.0352	-20.38	622	-	640	0	R.LSEPWEGDFQEDHNANLWR.R
2584.1753	2583.1680	2583.3517	-71.11	660	-	682	2	K.SAFSSLQNIPESLRRHSSLELGR.G
2651.3524	2650.3451	2650.3813	-13.67	44	-	69	2	K.GGLEHGEPLIISKVEEGGKADTLSSK.L
2831.1880	2830.1807	2830.3264	-51.47	850	-	876	2	K.NGELKLEEASRQPCGQQLSGGASDSGR.G
2872.3294	2871.3222	2871.3596	-13.04	1019	-	1044	1	R.SYSEPEKMNEVGIVEEAEPAPLGPQR.N + Oxidation (M)

No match to: 842.4920, 870.5361, 881.2605, 1487.8178, 1493.7815, 2056.0437, 2210.0795, 2225.1093, 2399.0057, 2501.1727

13. PKHJ1_HUMAN **Mass:** 17711 **Score:** 30 **Expect:** 22 **Matches:** 3

Pleckstrin homology domain-containing family J member 1 OS=Homo sapiens GN=PLEKHJ1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1838.9523	1837.9451	1837.9297	8.35	106	-	119	2	R.ASYEFMRRSLIFYR.N
2399.0057	2397.9985	2398.2096	-88.05	7	-	28	2	K.ELQALSRQPAEMAAELGMRGPK.K + Oxidation (M)

2651.3524	2650.3451	2650.2842	23.0	3 - 25	2	R.YNEKELQALSRQPAEMAAELGMR.G + Oxidation (M)

No match to: 842.4920, 870.5361, 881.2605, 1320.6282, 1487.8178, 1493.7815, 2056.0437, 2096.9866, 2210.0795, 2225.1093, 2342.9947, 2501.1727, 2584.1753, 2831.1880, 2872.3294

14. TM225_HUMAN **Mass:** 26267 **Score:** 30 **Expect:** 22 **Matches:** 3

Transmembrane protein 225 OS=Homo sapiens GN=TMEM225 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4848	841.4229	73.6	1 -	7	0	-.MVHVSNR.S
2584.1753	2583.1680	2583.4202	-97.63	65 -	87	1	K.VVRIMMTSSLGLSFLLNLILGMK.F + 3 Oxidation (M)
2872.3294	2871.3222	2871.2787	15.1	45 -	67	1	K.MNHSPWMMCCPALWPEDDLKVVR.I

No match to: 870.5361, 881.2605, 1320.6282, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2096.9866, 2210.0795, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2651.3524, 2831.1880

15. DC1L2_HUMAN **Mass:** 54351 **Score:** 30 **Expect:** 22 **Matches:** 4

Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4847	841.4731	13.8	163 -	169	1	K.MKIPPEK.M
870.5361	869.5288	869.4793	56.9	165 -	171	1	K.IPPEKMR.E
2096.9866	2095.9793	2096.0902	-52.90	421 -	440	1	K.NNAASEGVLASFFNSLLSKK.T
2210.0795	2209.0722	2209.0301	19.1	243 -	259	1	K.EHDYRDEHLDFIQSHLR.R

No match to: 881.2605, 1320.6282, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2584.1753, 2651.3524, 2831.1880, 2872.3294

16. Z280D_HUMAN **Mass:** 111211 **Score:** 29 **Expect:** 24 **Matches:** 5

Zinc finger protein 280D OS=Homo sapiens GN=ZNF280D PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4848	841.4520	38.9	675 -	680	1	R.FCIFKK.H
870.5361	869.5288	869.5446	-18.25	329 -	335	1	K.ILKNNIR.F
1320.6282	1319.6209	1319.6227	-1.34	332 -	341	1	K.NNIRFMNHMK.H + Oxidation (M)
2210.0795	2209.0722	2208.8701	91.5	349 -	365	0	K.QSSESWENHTTCQHCYR.Q
2872.3294	2871.3222	2871.2764	15.9	10 -	32	2	K.SNSKMAELFMECEEEELEPWQKK.V

No match to: 881.2605, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2096.9866, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2584.1753, 2651.3524, 2831.1880

17. MK15_HUMAN **Mass:** 60251 **Score:** 29 **Expect:** 25 **Matches:** 4

Mitogen-activated protein kinase 15 OS=Homo sapiens GN=MAPK15 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4848	841.4406	52.5	317 -	323	0	R.EADVRPR.A
1320.6282	1319.6209	1319.7422	-91.92	251 -	262	0	R.ASVLHQLGSRPR.Q
2210.0795	2209.0722	2209.2556	-82.99	481 -	500	2	R.VASVQQVPPRLPPEARPGRR.M
2651.3524	2650.3451	2650.4707	-47.38	284 -	306	2	R.LLVFAPDKRLSATQALQHPYVQR.F

No match to: 870.5361, 881.2605, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2096.9866, 2225.1093, 2342.9947, 2399.0057, 2501.1727, 2584.1753, 2831.1880, 2872.3294

18. HIDE1_HUMAN **Mass:** 24966 **Score:** 29 **Expect:** 27 **Matches:** 3

Protein HIDE1 OS=Homo sapiens GN=HIDE1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2225.1093	2224.1020	2224.2442	-63.90	1 -	21	0	-.MPWTILLFAAGSLAIPAPSIR.L
2399.0057	2397.9985	2398.1877	-78.90	207 -	227	2	R.TRKRPTSTSSSPETPEFSTFR.A
2501.1727	2500.1655	2500.1653	0.08	209 -	230	2	R.KRPTSTSSSPETPEFSTFRACQ.-

No match to: 842.4920, 870.5361, 881.2605, 1320.6282, 1487.8178, 1493.7815, 1838.9523, 2056.0437, 2096.9866, 2210.0795, 2342.9947, 2584.1753, 2651.3524, 2831.1880, 2872.3294

19. MYOF_HUMAN **Mass:** 236100 **Score:** 29 **Expect:** 27 **Matches:** 8

Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1320.6282	1319.6209	1319.6034	13.3	1447 -	1456	0	K.EEEIVDWWSK.F
1487.8178	1486.8106	1486.6861	83.7	1806 -	1818	0	K.SITGEEMSDIYVK.G + Oxidation (M)
2210.0795	2209.0722	2209.0548	7.91	314 -	333	1	K.GYMKVSMFVLGTGDEPPPER.R
2225.1093	2224.1020	2224.0834	8.38	1211 -	1229	1	K.VIMELFDNDQVGKDEFLGR.S
2342.9947	2341.9875	2342.1906	-86.74	37 -	55	1	K.KVDNELNPVWNEILEFDLR.G
2399.0057	2397.9985	2398.0787	-33.45	1041 -	1060	0	R.AMEELQDQEGWEYASLIGWK.F + Oxidation (M)
2501.1727	2500.1655	2500.2591	-37.45	1966 -	1987	2	K.VEMTLEILNEKEADERPAGKGR.D + Oxidation (M)
2872.3294	2871.3222	2871.3030	6.66	273 -	297	1	R.ADCLMGEFKIDVGFVYDEPGHAVMR.K + Oxidation (M)

No match to: 842.4920, 870.5361, 881.2605, 1493.7815, 1838.9523, 2056.0437, 2096.9866, 2584.1753, 2651.3524, 2831.1880

20. ASCC3_HUMAN **Mass:** 252898 **Score:** 29 **Expect:** 28 **Matches:** 7

Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4920	841.4847	841.5385	-63.87	2126 -	2132	1	R.ELIALKR.V
1320.6282	1319.6209	1319.7285	-81.50	1978 -	1988	1	K.WKPIMKGPHAR.G
1838.9523	1837.9451	1837.8675	42.2	1748 -	1761	0	K.QDALDYITWTYFFR.R
2210.0795	2209.0722	2209.1215	-22.29	770 -	788	1	K.QVRELFPDGFSIHHAGMLR.Q
2225.1093	2224.1020	2224.1899	-39.48	1153 -	1171	2	K.DMRKDEIGHILHHVNIGLK.V
2584.1753	2583.1680	2583.2971	-49.99	1172 -	1193	1	K.VKQCVHQIPSVMMEASIQPITR.T + 2 Oxidation (M)
2651.3524	2650.3451	2650.3768	-11.97	2074 -	2095	1	K.LHADQEYVLQVSLQRVHFGFHK.G

No match to: 870.5361, 881.2605, 1487.8178, 1493.7815, 2056.0437, 2096.9866, 2342.9947, 2399.0057, 2501.1727, 2831.1880, 2872.3294

Search Parameters

Type of search : Peptide Mass Fingerprint

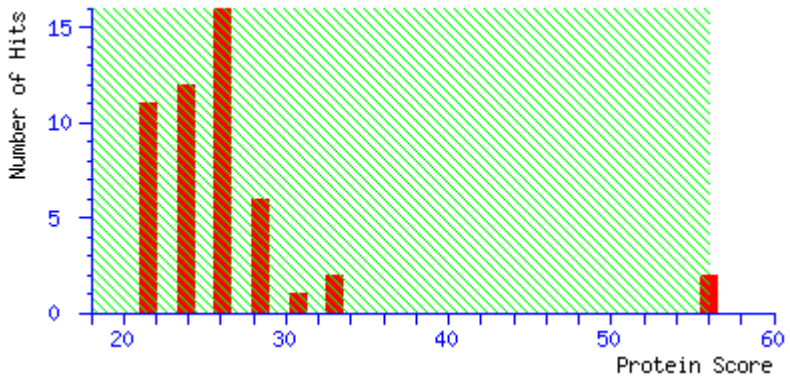
Enzyme	: Trypsin
Fixed modifications	: Carbamidomethyl (C)
Variable modifications	: Oxidation (M)
Mass values	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 120 ppm
Peptide Charge State	: 1+
Max Missed Cleavages	: 2
Number of queries	: 18
Selected for scoring	: 14

MATRIX SCIENCE Mascot Search Results

```
User            : JOY
Email           : joyprashant88@gmail.com
Search title    :
Database        : SwissProt 2015_08 (549008 sequences; 195692017 residues)
Taxonomy        : Homo sapiens (human) (20204 sequences)
Timestamp       : 31 Jul 2015 at 07:28:19 GMT
Top Score       : 56 for CC74A_HUMAN, Coiled-coil domain-containing protein 74A OS=Homo sapiens GN=CCDC74A PE=2 SV=1
```

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant (p<0.05).



Protein Summary Report

Format As [Protein Summary] Help

Significance threshold p< [0.05] Max. number of hits [20]

Preferred taxonomy [All entries]

Re-Search All | Search Unmatched

Index

	Accession	Mass	Score	Description
1.	CC74A_HUMAN	41808	56	Coiled-coil domain-containing protein 74A OS=Homo sapiens GN=CCDC74A PE=2 SV=1
2.	CC74B_HUMAN	42028	56	Coiled-coil domain-containing protein 74B OS=Homo sapiens GN=CCDC74B PE=2 SV=1
3.	ANKL2_HUMAN	104905	32	Ankyrin repeat and LEM domain-containing protein 2 OS=Homo sapiens GN=ANKLE2 PE=1 SV=4
4.	FANK1_HUMAN	38716	32	Fibronectin type 3 and ankyrin repeat domains protein 1 OS=Homo sapiens GN=FANK1 PE=2 SV=3
5.	FRITZ_HUMAN	86170	31	WD repeat-containing and planar cell polarity effector protein fritz homolog OS=Homo sapiens GN=
6.	DHB4_HUMAN	80092	29	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3
7.	DCA12_HUMAN	51056	28	DDB1- and CUL4-associated factor 12 OS=Homo sapiens GN=DCAF12 PE=1 SV=1
8.	DGKB_HUMAN	92133	28	Diacylglycerol kinase beta OS=Homo sapiens GN=DGKB PE=2 SV=2
9.	RCC2_HUMAN	56790	28	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2
10.	RN152_HUMAN	23141	28	E3 ubiquitin-protein ligase RNF152 OS=Homo sapiens GN=RNF152 PE=1 SV=1
11.	GPCP1_HUMAN	76899	27	Glycerophosphocholine phosphodiesterase GPCPD1 OS=Homo sapiens GN=GPCPD1 PE=1 SV=2
12.	FGF12_HUMAN	27610	27	Fibroblast growth factor 12 OS=Homo sapiens GN=FGF12 PE=1 SV=1
13.	DYRL1_HUMAN	21720	27	Dihydrofolate reductase, mitochondrial OS=Homo sapiens GN=DHFRL1 PE=1 SV=1
14.	KCNA2_HUMAN	57137	27	Potassium voltage-gated channel subfamily A member 2 OS=Homo sapiens GN=KCNA2 PE=1 SV=2
15.	DHAK_HUMAN	59252	26	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=
16.	TBC3D_HUMAN	62889	26	TBC1 domain family member 3D OS=Homo sapiens GN=TBC1D3D PE=2 SV=1
17.	TBC3I_HUMAN	62907	26	TBC1 domain family member 3I OS=Homo sapiens GN=TBC1D3I PE=3 SV=1
18.	TBC3L_HUMAN	62889	26	TBC1 domain family member 3L OS=Homo sapiens GN=TBC1D3L PE=2 SV=1
19.	TBC3A_HUMAN	62889	26	TBC1 domain family member 3 OS=Homo sapiens GN=TBC1D3 PE=1 SV=6
20.	TBC3C_HUMAN	62889	26	TBC1 domain family member 3C OS=Homo sapiens GN=TBC1D3C PE=2 SV=3

Results List

1. CC74A_HUMAN **Mass:** 41808 **Score:** 56 **Expect:** 0.051 **Matches:** 6

Coiled-coil domain-containing protein 74A OS=Homo sapiens GN=CCDC74A PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1179.6053	1178.5980	1178.7387	-119.32	345	355	1	R.AILPALKQTPK.N
1487.7381	1486.7309	1486.7416	-7.23	318	330	1	R.DQEATHFPKVSTK.S
1940.8842	1939.8769	1939.9534	-39.45	1	21	0	-.MSGAGVAAGTRPPSSPTPGSR.R
2096.9062	2095.8989	2096.0545	-74.23	1	22	1	-.MSGAGVAAGTRPPSSPTPGSRR.R
2705.0587	2704.0514	2703.3704	252	109	134	1	R.ASAPLGARWVCINGVWVEPGGPSPAR.L
2716.9800	2715.9728	2715.4529	191	25	48	1	R.QRPSVGVQSLRPQSPQLRQSDPQK.R

No match to: 842.4895, 856.5082, 870.5299, 1045.5718, 1061.5298, 1097.5233, 1259.6726, 1657.7713, 1765.7071, 1791.7057, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 3312.2134

2. CC74B_HUMAN **Mass:** 42028 **Score:** 56 **Expect:** 0.052 **Matches:** 6

Coiled-coil domain-containing protein 74B OS=Homo sapiens GN=CCDC74B PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1179.6053	1178.5980	1178.7387	-119.32	347	357	1	R.AILPALKQTPK.N
1487.7381	1486.7309	1486.7416	-7.23	318	330	1	R.DQEATHFPKVSTK.S
1940.8842	1939.8769	1939.9534	-39.45	1	21	0	-.MSGAGVAAGTRPPSSPTPGSR.R
2096.9062	2095.8989	2096.0545	-74.23	1	22	1	-.MSGAGVAAGTRPPSSPTPGSRR.R

2705.0587	2704.0514	2703.3704	252	109 - 134	1	R.ASAPLGARWVCINGVWVEPGGPSPAR.L
2716.9800	2715.9728	2715.4529	191	25 - 48	1	R.QRPSVGVQSLRPQSPQLRQSDPQK.R

No match to: 842.4895, 856.5082, 870.5299, 1045.5718, 1061.5298, 1097.5233, 1259.6726, 1657.7713, 1765.7071, 1791.7057, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 3312.2134

3. ANKL2_HUMAN **Mass:** 104905 **Score:** 32 **Expect:** 13 **Matches:** 8

Ankyrin repeat and LEM domain-containing protein 2 OS=Homo sapiens GN=ANKLE2 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5082	855.5009	855.4603	47.5	237 - 243		1	R.FKAFSTR.E
870.5299	869.5227	869.5447	-25.29	710 - 717		1	R.TLAGKRPK.A
1045.5718	1044.5645	1044.5927	-27.02	306 - 314		1	R.TQDLTAKLR.K
1061.5298	1060.5225	1060.5877	-61.46	758 - 766		1	K.TKDQILTSR.I
1179.6053	1178.5980	1178.5891	7.54	627 - 638		0	K.ATTSGSNSISVR.A
1765.7071	1764.6998	1764.7955	-54.20	320 - 334		0	K.GEEDTFSDLIWSNPR.Y
1940.8842	1939.8769	1939.8833	-3.30	639 - 654		1	R.AFLDEDDMSLEEIKNR.Q + Oxidation (M)
2716.9800	2715.9728	2715.3075	245	834 - 857		0	K.LDQDVLAALECADVDPHQFPAVHR.W

No match to: 842.4895, 1097.5233, 1259.6726, 1487.7381, 1657.7713, 1791.7057, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2705.0587, 3312.2134

4. FANK1_HUMAN **Mass:** 38716 **Score:** 32 **Expect:** 13 **Matches:** 4

Fibronectin type 3 and ankyrin repeat domains protein 1 OS=Homo sapiens GN=FANK1 PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5299	869.5227	869.5447	-25.31	129 - 136		1	R.ILQGGRVK.V
1791.7057	1790.6984	1790.8695	-95.56	179 - 194		0	K.DSLMLACYAGHLDVVK.Y
2096.9062	2095.8989	2096.1275	-109.03	1 - 19		1	-.MEPQKIMPPSKPHPPVVGK.V
2705.0587	2704.0514	2703.4629	218	277 - 300		1	R.NGKTPLMVAVLNNHEELVQLLLDK.G + Oxidation (M)

No match to: 842.4895, 856.5082, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1940.8842, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800, 3312.2134

5. FRITZ_HUMAN **Mass:** 86170 **Score:** 31 **Expect:** 16 **Matches:** 5

WD repeat-containing and planar cell polarity effector protein fritz homolog OS=Homo sapiens GN=WDPCP PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5299	869.5227	869.4395	95.6	584 - 589		1	R.YQRFEK.A
1179.6053	1178.5980	1178.6546	-48.05	202 - 211		1	R.LEKLSALDYK.I
1940.8842	1939.8769	1940.0043	-65.70	212 - 227		1	K.IFYYEIPGPINKTTER.H
2705.0587	2704.0514	2704.3378	-105.90	346 - 368		1	R.NVTEDKLILGCEDSSLILYETHR.R
3312.2134	3311.2061	3310.6908	156	424 - 452		1	R.ETLQFSKLFDASSSLVQMQWIAPQVVSQK.G + Oxidation (M)

No match to: 842.4895, 856.5082, 1045.5718, 1061.5298, 1097.5233, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800

6. DHB4_HUMAN **Mass:** 80092 **Score:** 29 **Expect:** 26 **Matches:** 5

Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5082	855.5009	855.4702	35.9	637	644	0	K.DIGPEVVK.K
1097.5233	1096.5160	1096.6492	-121.43	635	644	1	R.LKDIGPEVVK.K
1940.8842	1939.8769	1940.0268	-77.29	646	663	1	K.VNAVFEWHITKGGNIGAK.W
2211.0244	2210.0171	2210.2211	-92.31	404	422	1	K.VLHGEQYLELYKPLPRAGK.L
2705.0587	2704.0514	2703.3869	246	332	356	0	K.LPPFSYAYTELEAIMYALGVGASIK.D

No match to: 842.4895, 870.5299, 1045.5718, 1061.5298, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 2096.9062, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800, 3312.2134

7. DCA12_HUMAN **Mass:** 51056 **Score:** 28 **Expect:** 31 **Matches:** 4

DDB1- and CUL4-associated factor 12 OS=Homo sapiens GN=DCAF12 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1097.5233	1096.5160	1096.5149	1.05	57	65	0	R.LQNETSYSR.V
1765.7071	1764.6998	1764.8240	-70.37	204	219	0	R.DGSMGLWEVTDDVLTK.S
2211.0244	2210.0171	2210.0161	0.43	204	223	1	R.DGSMGLWEVTDDVLTKSDAR.H + Oxidation (M)
2716.9800	2715.9728	2715.4344	198	57	80	1	R.LQNETSYSRVLHGYAAQQLPSLLK.E

No match to: 842.4895, 856.5082, 870.5299, 1045.5718, 1061.5298, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1791.7057, 1940.8842, 2096.9062, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2705.0587, 3312.2134

8. DGKB_HUMAN **Mass:** 92133 **Score:** 28 **Expect:** 35 **Matches:** 7

Diacylglycerol kinase beta OS=Homo sapiens GN=DGKB PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4156	79.2	154	159	0	K.LEFMFR.L
1045.5718	1044.5645	1044.5063	55.8	91	99	0	K.FPHSSPMVK.S + Oxidation (M)
1487.7381	1486.7309	1486.8289	-65.97	100	113	1	K.SKPALLSGGLRMNK.G + Oxidation (M)
1657.7713	1656.7640	1656.8260	-37.40	7	20	0	K.WAHLSPSEFSQLQK.Y
1765.7071	1764.6998	1764.8352	-76.71	550	563	1	K.DIENSTEIMLDRWK.F + Oxidation (M)
1791.7057	1790.6984	1790.9171	-122.14	772	787	1	K.ITHKNQAPMLMGPPPK.T + 2 Oxidation (M)
2286.0187	2285.0114	2285.1734	-70.88	776	796	1	K.NQAPMLMGPPPKTGLFCSLVK.R

No match to: 856.5082, 870.5299, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2584.1023, 2705.0587, 2716.9800, 3312.2134

9. RCC2_HUMAN **Mass:** 56790 **Score:** 28 **Expect:** 36 **Matches:** 4

Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4770	6.28	69	77	0	R.AARPATAGK.A
1940.8842	1939.8769	1939.8920	-7.82	416	431	1	R.ESTMYPKAVQDLCGWR.I
2716.9800	2715.9728	2715.3803	218	152	176	1	R.TVVSGSCAAHSLLITTEGKLWSWGR.N
3312.2134	3311.2061	3310.6503	168	471	501	1	K.SSTAAQEVKTLDGIFSEQVAMGYSHSLVIAR.D + Oxidation (M)

No match to: 856.5082, 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071,

1791.7057, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2705.0587

10. RN152_HUMAN **Mass:** 23141 **Score:** 28 **Expect:** 36 **Matches:** 3

E3 ubiquitin-protein ligase RNF152 OS=Homo sapiens GN=RNF152 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
870.5299	869.5227	869.4971	29.5	121	128	0	R.LLPGSQQK.S
1940.8842	1939.8769	1939.9972	-62.01	111	128	1	R.ALLPGDMGCRLLPGSQQK.S
2225.0398	2224.0325	2223.9680	29.0	27	43	1	K.LLDCKHTCCSVCLQQMR.T + Oxidation (M)

No match to: 842.4895, 856.5082, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 2096.9062, 2211.0244, 2239.0429, 2286.0187, 2584.1023, 2705.0587, 2716.9800, 3312.2134

11. GPCP1_HUMAN **Mass:** 76899 **Score:** 27 **Expect:** 38 **Matches:** 5

Glycerophosphocholine phosphodiesterase GPCPD1 OS=Homo sapiens GN=GPCPD1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5082	855.5009	855.4702	36.0	632	638	0	K.QELPELK.S
1097.5233	1096.5160	1096.6492	-121.40	630	638	1	R.LKQELPELK.S
1179.6053	1178.5980	1178.6699	-61.02	519	528	0	K.YPILFLTQGK.S
2211.0244	2210.0171	2210.2674	-113.26	399	417	1	K.ELTFDQLQLLKLTHVTALK.S
2705.0587	2704.0514	2703.3789	249	174	197	1	R.VSPTVLHKMSNSLEISLISDNEFK.C + Oxidation (M)

No match to: 842.4895, 870.5299, 1045.5718, 1061.5298, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800, 3312.2134

12. FGF12_HUMAN **Mass:** 27610 **Score:** 27 **Expect:** 41 **Matches:** 3

Fibroblast growth factor 12 OS=Homo sapiens GN=FGF12 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1179.6053	1178.5980	1178.5527	38.4	18	28	1	R.ESNSDRVSASK.R
2716.9800	2715.9728	2716.2037	-85.00	123	146	0	K.ASLYVAMNGEGYLYSSDVFTPECK.F + Oxidation (M)
3312.2134	3311.2061	3310.6478	169	192	219	1	K.TKPSSHFVPKPIEVCMYREPSLHEIGEK.Q + Oxidation (M)

No match to: 842.4895, 856.5082, 870.5299, 1045.5718, 1061.5298, 1097.5233, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2705.0587

13. DYRL1_HUMAN **Mass:** 21720 **Score:** 27 **Expect:** 42 **Matches:** 3

Dihydrofolate reductase, mitochondrial OS=Homo sapiens GN=DHFRL1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1765.7071	1764.6998	1764.9457	-139.32	124	138	1	K.EAMNHLGHLKLFVTR.I
2705.0587	2704.0514	2704.4258	-138.45	100	123	1	K.LTERPELANKVDMIWIVGGSSVYK.E
2716.9800	2715.9728	2715.3513	229	110	133	1	K.VDMIWIVGGSSVYKEAMNHLGHLK.L + 2 Oxidation (M)

No match to: 842.4895, 856.5082, 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 3312.2134

14. KCNA2_HUMAN **Mass:** 57137 **Score:** 27 **Expect:** 44 **Matches:** 4

Potassium voltage-gated channel subfamily A member 2 OS=Homo sapiens GN=KCNA2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5082	855.5009	855.4702	35.9	438	445	0	K.IPSSPDLK.K
1097.5233	1096.5160	1096.5488	-29.85	66	73	1	R.MRYFDPLR.N
1657.7713	1656.7640	1656.9087	-87.29	50	64	1	K.TLAQFPETLLGDPKK.R
2096.9062	2095.8989	2095.9368	-18.07	420	437	0	R.ETEGEEQAQYLQVTSCPK.I

No match to: 842.4895, 870.5299, 1045.5718, 1061.5298, 1179.6053, 1259.6726, 1487.7381, 1765.7071, 1791.7057, 1940.8842, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2705.0587, 2716.9800, 3312.2134

15. DHAK_HUMAN **Mass:** 59252 **Score:** 26 **Expect:** 50 **Matches:** 4

Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1097.5233	1096.5160	1096.6063	-82.32	153	162	0	R.GLCGTVLIHK.V
1940.8842	1939.8769	1939.9123	-18.26	352	372	0	R.VAPAEPQEAPDSTAAGGSASK.R
2096.9062	2095.8989	2096.0134	-54.62	352	373	1	R.VAPAEPQEAPDSTAAGGSASKR.M
3312.2134	3311.2061	3310.8648	103	295	325	1	K.IARALVGTFMSALEMPGISLTLLLVDEPLLK.L

No match to: 842.4895, 856.5082, 870.5299, 1045.5718, 1061.5298, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2705.0587, 2716.9800

16. TBC3D_HUMAN **Mass:** 62889 **Score:** 26 **Expect:** 50 **Matches:** 4

TBC1 domain family member 3D OS=Homo sapiens GN=TBC1D3D PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4592	27.4	342	348	1	K.HLRASMK.K
856.5082	855.5009	855.4199	94.7	138	144	0	R.SSEHIQR.I
2705.0587	2704.0514	2703.3268	268	449	470	1	R.FLQWNSMPRLPTDLDVEGPWFR.H
3312.2134	3311.2061	3310.6080	181	219	249	0	R.HSLQGFHSPNGGTVQGLQDQQEHVVATSQPK.T

No match to: 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800

17. TBC3I_HUMAN **Mass:** 62907 **Score:** 26 **Expect:** 50 **Matches:** 4

TBC1 domain family member 3I OS=Homo sapiens GN=TBC1D3I PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4592	27.4	342	348	1	K.HLRASMK.K
856.5082	855.5009	855.4199	94.7	138	144	0	R.SSEHIQR.I
2705.0587	2704.0514	2703.3268	268	449	470	1	R.FLQWNSMPRLPTDLDVEGPWFR.H
3312.2134	3311.2061	3310.6080	181	219	249	0	R.HSLQGFHSPNGGTVQGLQDQQEHVVATSQPK.T

No match to: 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800

18. TBC3L_HUMAN **Mass:** 62889 **Score:** 26 **Expect:** 50 **Matches:** 4

TBC1 domain family member 3L OS=Homo sapiens GN=TBC1D3L PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4592	27.4	342 -	348	1	K.HLRASMK.K
856.5082	855.5009	855.4199	94.7	138 -	144	0	R.SSEHIQR.I
2705.0587	2704.0514	2703.3268	268	449 -	470	1	R.FLQWNSMPRLPTDLDVEGPWFR.H
3312.2134	3311.2061	3310.6080	181	219 -	249	0	R.HSLQGFHSPNGGTVQGLQDQQEHVVATSQPK.T

No match to: 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800

19. TBC3A_HUMAN **Mass:** 62889 **Score:** 26 **Expect:** 53 **Matches:** 4

TBC1 domain family member 3 OS=Homo sapiens GN=TBC1D3 PE=1 SV=6

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4592	27.4	342 -	348	1	K.HLRASMK.K
856.5082	855.5009	855.4199	94.7	138 -	144	0	R.SSEHIQR.I
2705.0587	2704.0514	2703.3268	268	449 -	470	1	R.FLQWNSMPRLPTDLDVEGPWFR.H
3312.2134	3311.2061	3310.6080	181	219 -	249	0	R.HSLQGFHSPNGGTVQGLQDQQEHVVATSQPK.T

No match to: 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800

20. TBC3C_HUMAN **Mass:** 62889 **Score:** 26 **Expect:** 53 **Matches:** 4

TBC1 domain family member 3C OS=Homo sapiens GN=TBC1D3C PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.4895	841.4823	841.4592	27.4	342 -	348	1	K.HLRASMK.K
856.5082	855.5009	855.4199	94.7	138 -	144	0	R.SSEHIQR.I
2705.0587	2704.0514	2703.3268	268	449 -	470	1	R.FLQWNSMPRLPTDLDVEGPWFR.H
3312.2134	3311.2061	3310.6080	181	219 -	249	0	R.HSLQGFHSPNGGTVQGLQDQQEHVVATSQPK.T

No match to: 870.5299, 1045.5718, 1061.5298, 1097.5233, 1179.6053, 1259.6726, 1487.7381, 1657.7713, 1765.7071, 1791.7057, 1940.8842, 2096.9062, 2211.0244, 2225.0398, 2239.0429, 2286.0187, 2584.1023, 2716.9800

Search Parameters

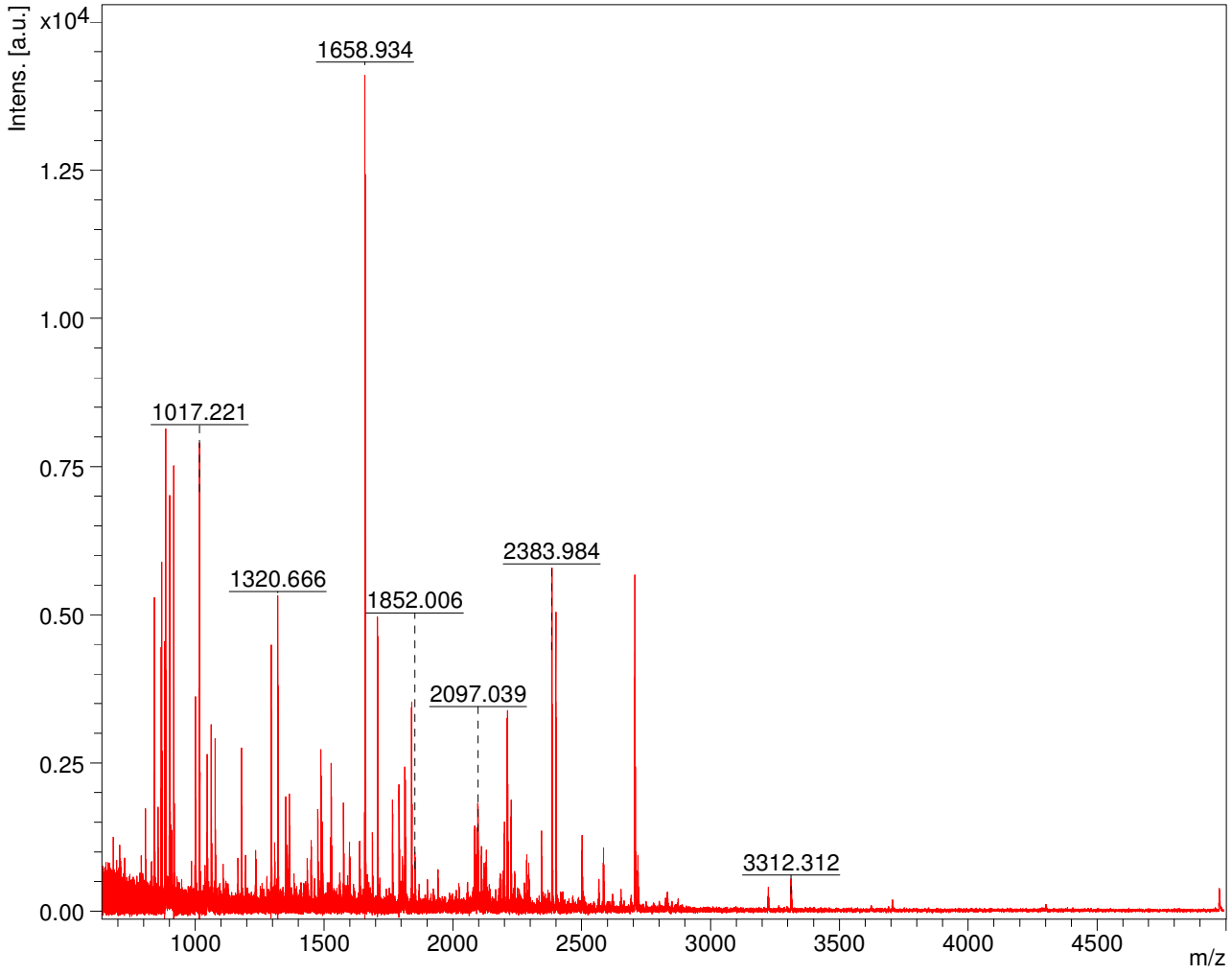
Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 280 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 22
Selected for scoring : 16

Mascot: http://www.matrixscience.com/

D:\DATA\CDFD MALDI RESULTS\CDFD\2015\July\27072015\A2 RU SPOTID 20 27072015\0_A2\1

Comment 1

Comment 2



m/z	S/N	Quality Fac.	Res.	Intens.	Area
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856.532	8.8	1514	5280	1605.92	479
868.419	23.5	4144	5229	4321.13	1339
870.551	30.0	11335	5204	5507.58	1706
881.269	20.1	834	3377	3636.98	1714
886.164	37.1	1991	3109	6721.48	3434
901.623	34.7	2577	4050	6249.54	2507
917.303	37.9	6369	4355	6779.05	2641
1001.542	18.9	2592	4315	3155.10	1419
1017.221	42.8	4440	4683	7054.21	2985
1046.043	10.8	248	2389	1742.97	1486
1061.561	18.2	1883	5100	2918.57	1213
1077.250	13.9	555	4072	2215.19	1184
1179.670	18.2	9629	6455	2720.49	1102
1234.736	6.6	462	4942	952.54	521
1294.746	34.0	10057	7015	4765.46	2101
1320.666	38.6	27984	6958	5350.78	2443
1350.771	13.6	12111	6923	1854.29	885
1356.805	6.1	355	3853	830.61	693
1365.717	12.9	4319	5937	1753.42	967
1475.853	13.7	5467	7418	1775.81	936
1487.839	19.8	14049	6502	2556.58	1498
1493.822	10.8	7348	7023	1382.44	769
1524.807	6.3	130	5559	795.66	563
1527.839	16.5	3469	5666	2074.85	1476
1575.846	13.3	2941	5786	1636.49	1199
1598.841	8.2	659	6254	1004.57	709
1638.934	9.2	1781	6660	1094.46	750
1658.934	120.2	107535	7253	14254.27	9561
1688.027	9.2	2148	5146	1075.01	1025
1707.860	42.5	90289	7383	4972.56	3461
1765.828	13.2	2952	6042	1496.10	1324
1791.788	16.8	7955	6272	1882.75	1664
1803.993	6.1	1375	5203	680.94	727
1813.973	19.2	11646	6540	2131.66	1836
1839.004	31.9	34470	8222	3495.90	2559
1852.006	6.4	1165	5111	690.97	790
2083.074	13.2	1388	5723	1120.39	1329

m/z	S/N	Quality Fac.	Res.	Intens.	Area
2091.981	9.8	597	4669	822.95	1198
2094.129	6.9	367	5484	576.41	714
2097.039	15.8	3835	6424	1324.64	1420
2110.069	10.2	1703	6246	838.55	929
2121.078	7.8	2079	7118	634.59	616
2129.109	8.3	1337	4728	668.44	981
2199.011	14.3	5046	6744	1084.16	1173
2211.144	39.1	31832	8131	2924.61	2736
2225.169	20.6	18688	8556	1522.71	1371
2286.158	10.2	2575	7620	698.79	735
2294.056	7.1	1396	6228	483.58	603
2343.039	13.8	3148	6525	890.33	1082
2383.984	71.7	14754	8106	4384.98	4630
2399.057	60.1	54459	8057	3617.98	3779
2501.233	17.0	4588	6227	917.67	1304
2584.211	13.6	4063	7060	671.33	876
2705.183	89.0	23820	8840	3901.79	4530
2717.102	13.9	2854	8184	601.55	758
3223.271	7.9	1367	8428	196.73	333
3312.312	11.6	896	7096	271.59	556
4973.240	12.2	590	9489	102.03	309

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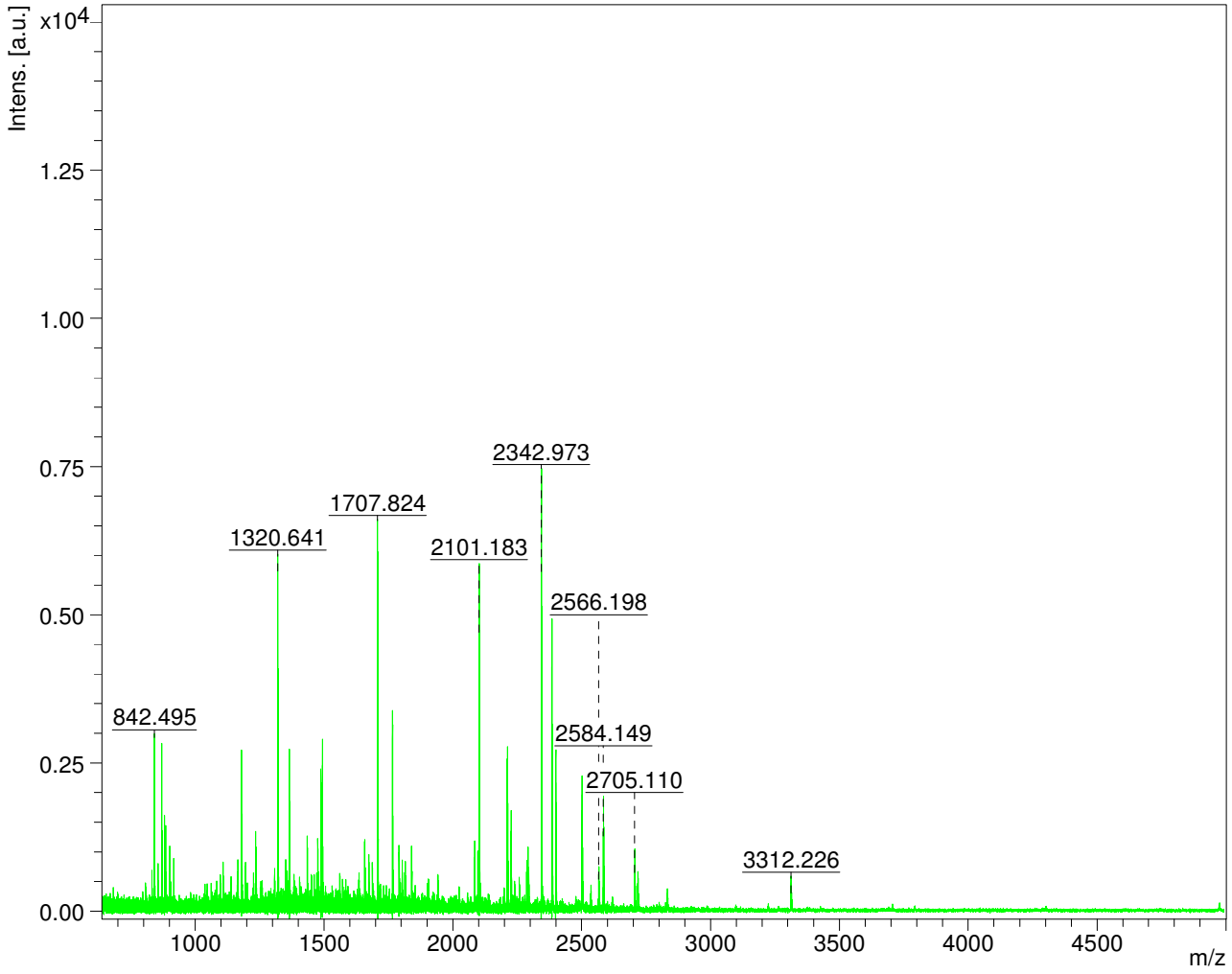

m/z	S/N	Quality Fac.	Res.	Intens.	Area
842.495	29.7	8802	5165	2908.37	850
856.507	7.8	430	4833	764.28	243
870.533	27.9	6590	5413	2746.70	806
881.326	12.6	454	2230	1221.97	904
886.152	10.2	311	2792	995.16	566
901.616	9.5	1257	4144	930.55	364
917.306	6.6	303	3376	640.56	319
1107.588	7.2	202	5295	766.73	333
1165.633	6.1	1600	5731	663.04	288
1179.646	25.3	3742	7146	2725.20	1008
1193.658	7.3	412	6092	788.20	336
1234.716	12.7	949	6452	1366.11	594
1320.641	51.9	29916	6634	5719.45	2675
1350.752	6.5	687	6662	718.21	345
1365.696	21.7	6836	6701	2416.13	1186
1434.815	9.5	1147	6651	1069.64	572
1475.816	9.4	1053	5640	1043.37	694
1487.791	20.6	3591	6556	2293.22	1336
1493.786	24.3	4290	6788	2692.08	1513
1657.851	9.7	1630	6266	1036.45	778
1673.890	7.1	2383	7010	761.60	525
1687.931	6.1	711	6623	646.17	476
1707.824	62.4	111274	7804	6567.80	4282
1765.781	30.7	32200	7442	3148.79	2289
1791.789	8.1	666	5845	810.37	757
1838.950	9.6	3752	7366	943.84	751
2083.042	10.7	699	5162	806.57	1056
2096.983	9.5	337	6171	708.46	781
2101.183	62.6	35100	7707	4682.34	4171
2211.089	33.6	13954	7464	2149.49	2107
2225.108	20.9	28326	8710	1317.68	1149
2286.097	8.5	854	6167	493.50	611
2291.159	10.4	880	6022	602.23	764
2293.959	6.3	946	6935	365.00	402
2342.973	105.5	75141	8192	5707.12	5573
2383.940	70.4	18569	7934	3600.04	3755
2399.006	39.6	33448	8384	1992.43	1970
2501.184	37.5	4451	7008	1680.02	2115
2566.198	12.3	1448	8688	516.73	552

m/z	S/N	Quality Fac.	Res.	Intens.	Area
2584.149	30.2	6816	8019	1247.24	1432
2705.110	17.1	4130	8113	628.30	766
2717.033	11.0	3361	7417	399.85	535
3312.226	14.3	4050	9169	285.27	447

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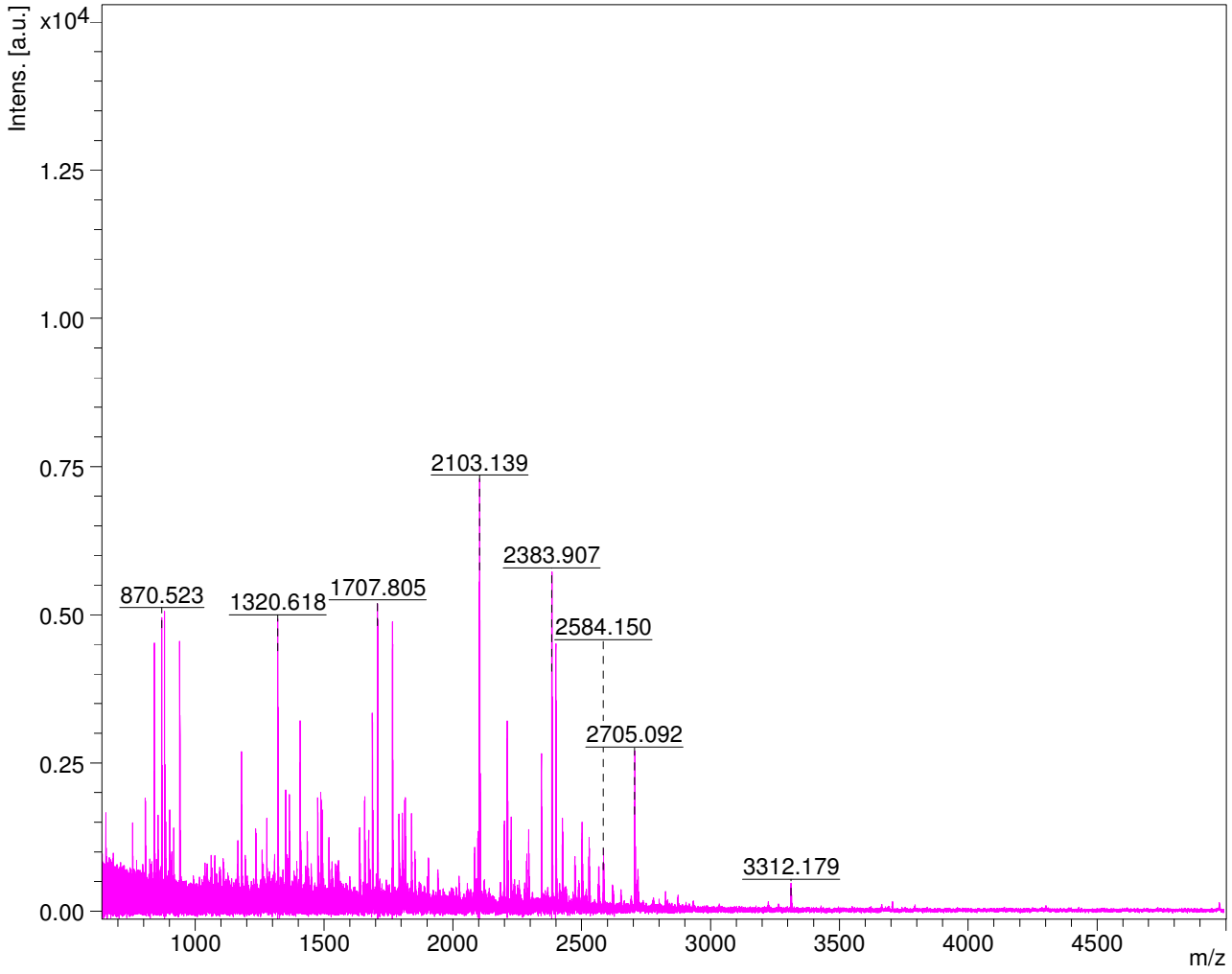

m/z	S/N	Quality Fac.	Res.	Intens.	Area
806.378	8.3	190	4334	1747.74	560
842.489	21.3	3256	5706	4424.22	1202
870.523	23.1	2927	5932	4760.14	1301
881.268	19.6	1081	3743	4023.15	1692
940.469	22.7	2054	5281	4627.10	1569
1179.637	14.2	5581	6746	2534.36	986
1234.699	6.0	415	4373	1028.18	637
1277.741	7.4	2245	5780	1271.77	641
1320.618	25.9	7722	6011	4372.18	2242
1350.720	10.9	3200	6156	1846.66	967
1365.689	9.5	2777	6392	1587.21	818
1407.782	18.2	5094	7146	3009.85	1484
1434.801	6.4	4182	6892	1048.33	539
1475.794	9.1	1303	5247	1478.11	1051
1487.794	10.9	2628	6051	1756.15	1111
1493.773	8.0	1511	5782	1294.53	858
1519.747	6.7	2608	6728	1073.63	643
1638.888	8.1	2019	6596	1234.25	869
1657.837	10.6	1606	5477	1611.27	1383
1672.853	6.3	704	4908	956.31	936
1687.992	20.5	11745	6761	3070.51	2202
1707.805	32.0	35609	6801	4798.11	3567
1765.774	30.0	34555	6381	4325.21	3665
1791.775	8.2	843	5050	1168.39	1268
1803.942	7.1	694	4346	1006.61	1286
1813.913	10.5	1445	5493	1481.40	1515
1838.938	8.0	1496	6314	1107.86	1013
2083.012	6.5	376	4812	704.68	985
2096.981	8.1	1099	5202	869.77	1138
2103.139	53.3	26472	6849	5733.48	5794
2198.940	11.5	2666	6571	1082.02	1204
2211.061	26.4	14653	7178	2456.12	2543
2225.084	11.9	4130	7192	1093.72	1127
2286.089	7.3	2646	5964	618.71	801
2293.968	11.1	2746	6341	934.69	1145
2342.992	23.3	3242	6357	1838.63	2354
2383.907	53.8	14239	6835	4023.79	4832
2399.007	44.5	23553	7348	3272.68	3729
2425.118	13.9	1760	5587	989.13	1480

m/z	S/N	Quality Fac.	Res.	Intens.	Area
2473.114	7.2	616	4639	491.54	903
2501.154	15.2	2786	5526	992.03	1580
2528.113	12.3	1506	6439	781.00	1078
2565.135	8.0	810	6816	481.25	645
2584.150	11.3	2867	7449	674.50	843
2705.092	31.2	6384	7197	1614.18	2239
2717.026	8.4	2587	6756	428.02	647
3312.179	9.0	1494	9472	243.43	390

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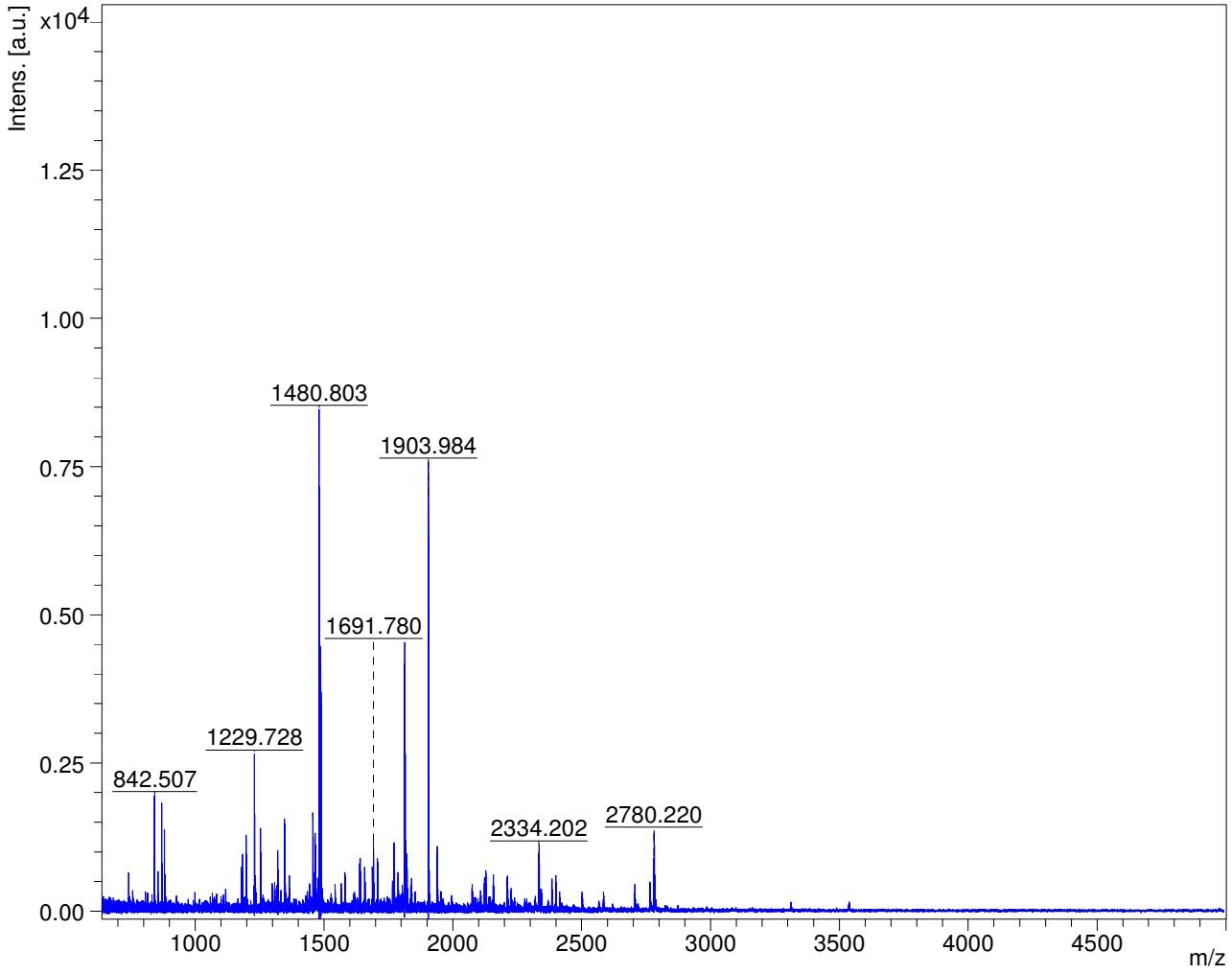

m/z	S/N	Quality Fac.	Res.	Intens.	Area
742.347	8.4	454	3533	555.35	196
842.507	29.7	8374	4915	1944.17	608
856.504	8.6	996	4037	568.23	211
870.535	27.5	7780	5231	1814.41	562
881.268	17.7	1855	3895	1153.92	469
1179.654	9.9	3483	5471	675.78	311
1183.683	14.1	4146	6396	957.27	392
1197.711	19.9	7494	6156	1344.71	586
1229.728	39.5	12558	6698	2679.26	1136
1253.665	21.3	9158	6878	1450.48	619
1320.630	12.9	3274	6207	886.96	444
1346.712	17.1	347	3217	1178.90	1146
1456.849	21.8	14396	6253	1516.60	897
1465.928	15.9	1234	3402	1113.19	1218
1480.803	121.3	61160	6159	8475.02	5229
1487.754	61.2	32000	6032	4278.27	2728
1580.866	7.5	857	4442	516.60	493
1638.904	10.7	1413	6233	736.84	543
1657.923	9.1	1728	5118	627.90	579
1687.942	8.8	858	5620	601.95	524
1691.780	13.3	2139	5073	909.44	876
1707.800	11.0	3096	6399	750.17	585
1771.938	13.8	1465	4965	919.28	990
1788.027	6.5	487	4172	429.63	558
1813.039	63.1	39096	6113	4156.03	3861
1819.954	10.5	709	4687	690.10	835
1903.984	113.0	71321	6904	6982.19	6270
1938.070	15.6	10685	6209	918.31	933
2074.044	6.2	1713	5553	314.81	385
2122.015	8.3	1972	6225	399.84	446
2127.158	11.4	10317	6542	544.71	586
2156.080	9.5	3741	6758	439.43	465
2211.102	11.5	3389	7675	505.15	512
2225.108	6.6	1691	6149	286.61	348
2334.202	21.8	23709	6798	845.29	988
2383.947	9.8	2593	5707	355.96	528
2399.021	11.3	3780	5984	405.26	567
2501.176	6.8	1277	5918	218.65	326
2705.085	11.0	3538	6414	278.82	434

m/z	S/N	Quality Fac.	Res.	Intens.	Area
2763.218	13.5	1003	6021	320.82	545
2780.220	39.2	9994	7860	916.55	1257

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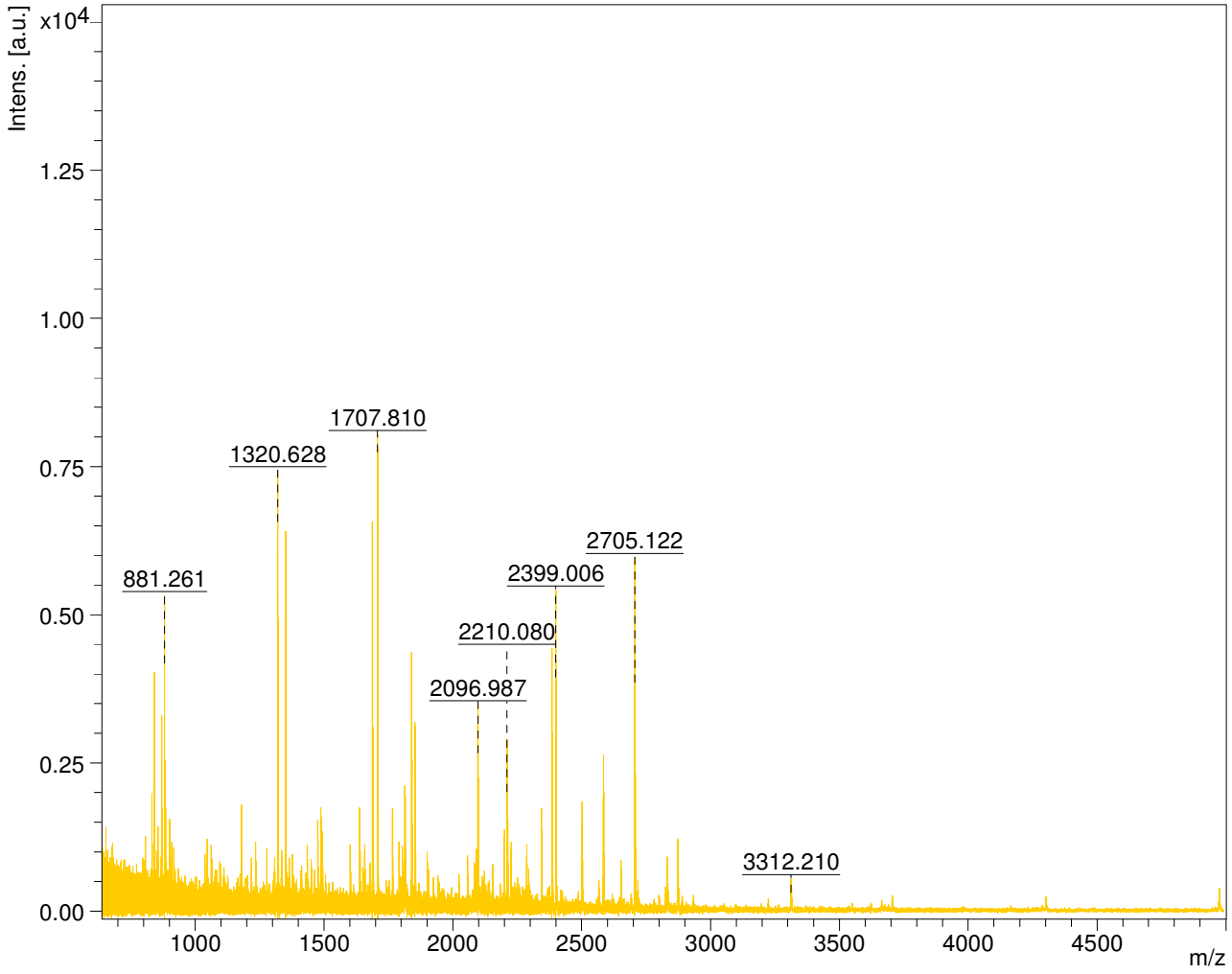

m/z	S/N	Quality Fac.	Res.	Intens.	Area
832.475	8.0	1121	5368	1681.61	469
842.492	18.1	2633	4944	3746.84	1155
870.536	14.3	4996	5562	2944.01	835
881.261	20.4	1049	3726	4164.30	1773
1179.644	9.0	1966	5807	1515.80	663
1320.628	42.2	8663	5967	6549.31	3380
1350.735	39.9	17398	6208	6107.02	3183
1475.801	8.0	1294	5182	1175.04	848
1487.818	10.2	1701	5421	1483.26	1047
1493.782	7.2	1449	5683	1052.60	709
1638.908	11.2	3583	6429	1554.48	1120
1688.011	44.8	29277	6876	6233.89	4457
1707.810	55.8	23809	6701	7722.95	5791
1765.792	9.8	1177	5092	1321.23	1375
1813.920	11.8	1484	5396	1553.09	1615
1838.952	30.6	15152	6785	4021.04	3458
1851.963	21.6	26362	6854	2819.52	2453
2056.044	6.1	2772	6605	660.55	675
2096.987	25.3	11117	6300	2647.95	2887
2198.965	9.0	1136	5227	839.11	1164
2210.080	21.5	1496	6273	1996.20	2330
2225.109	8.7	1960	7562	800.01	784
2286.088	8.3	3942	6291	709.04	874
2342.995	16.4	13216	7162	1328.94	1505
2383.924	40.3	26004	7067	3148.96	3689
2399.006	51.3	39591	7457	3927.51	4368
2501.173	19.9	13042	7071	1364.75	1743
2584.175	27.7	21446	7505	1748.12	2136
2651.352	8.6	2454	6526	507.27	743
2705.122	69.4	70850	8262	3839.54	4673
2831.188	9.1	778	4761	440.19	967
2872.329	15.8	5607	7286	724.62	1087
3312.210	9.7	4053	8088	291.65	521
4973.032	10.0	461	10254	104.84	294

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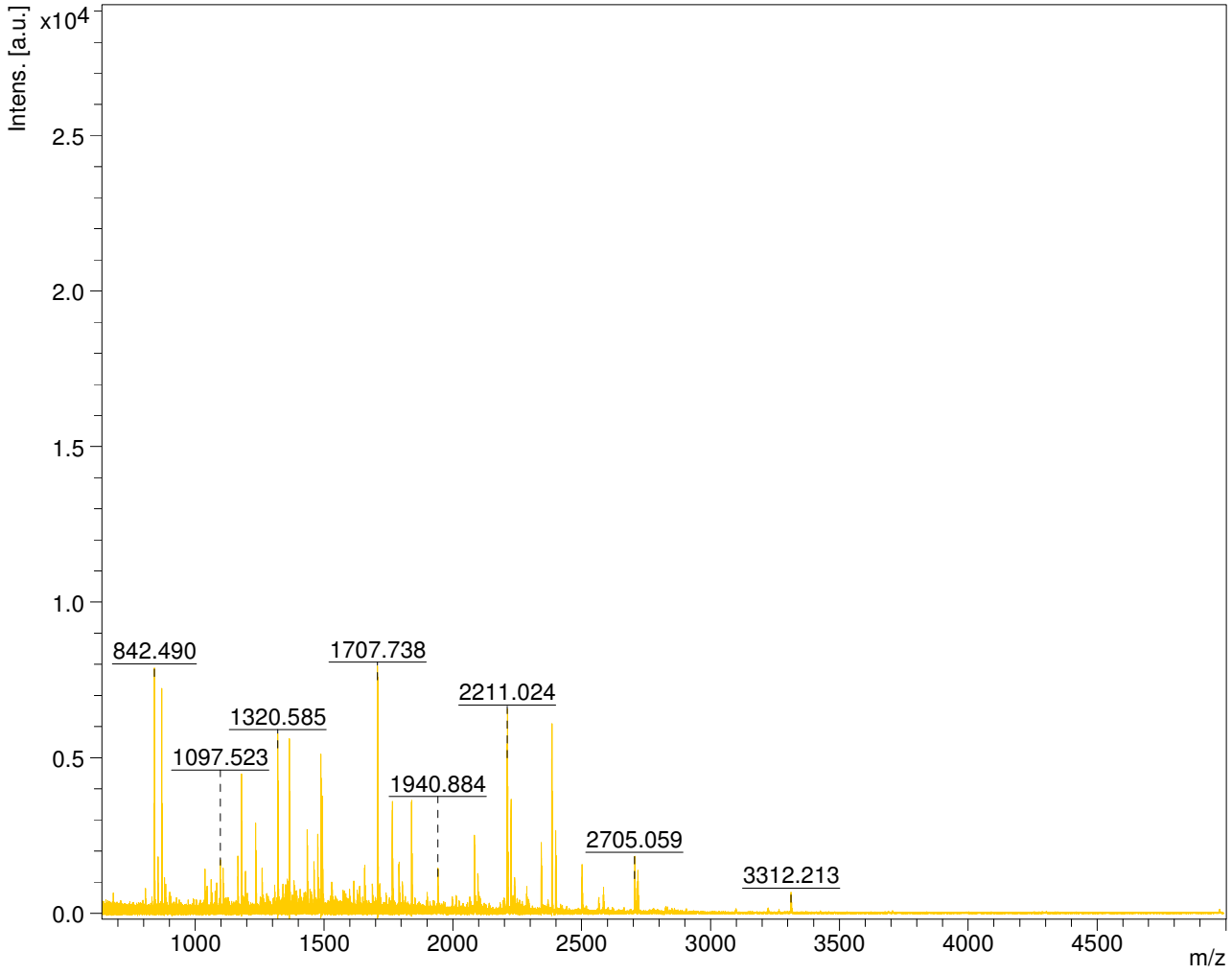
Comment 2



m/z	S/N	Quality Fac.	Res.	Intens.	Area
842.490	57.6	16102	5035	7564.52	2245
856.508	13.5	5104	5571	1779.92	502
870.530	54.9	29645	5619	7278.03	2073
1037.548	6.7	1216	6659	921.46	290
1045.572	6.1	263	5360	844.07	322
1061.530	6.2	195	4840	855.32	374
1097.523	10.8	1830	5546	1506.82	613
1107.561	9.3	439	5301	1302.84	563
1165.592	11.6	4919	6669	1656.09	623
1179.605	29.8	12063	6275	4281.12	1744
1193.621	9.0	389	6532	1286.51	512
1234.673	20.2	2485	6901	2922.83	1190
1259.673	8.1	569	5952	1171.04	558
1320.585	35.9	9689	6339	5268.05	2560
1357.712	6.3	760	6705	933.00	450
1365.640	34.8	15956	6808	5118.56	2469
1434.758	15.9	4584	6966	2332.37	1200
1460.772	9.5	1482	6028	1397.29	855
1475.758	15.9	6040	6571	2326.13	1342
1487.738	34.0	19640	7209	4951.46	2652
1493.719	23.5	5396	7029	3415.35	1867
1657.771	9.4	1648	6974	1311.62	886
1707.738	54.4	25833	7359	7464.74	5082
1765.707	23.5	15232	7047	3140.08	2397
1791.706	10.6	1234	6554	1389.07	1173
1838.871	25.8	25335	7970	3297.60	2428
1940.884	9.9	2066	6794	1135.82	1041
2082.937	19.4	1679	6856	1807.14	1781
2096.906	8.5	698	6352	781.26	839
2211.024	63.0	22169	7851	4954.30	4684
2225.040	34.2	11563	7794	2641.70	2524
2239.043	8.0	704	5899	604.96	760
2286.019	6.5	1160	6563	458.98	532
2342.901	24.3	7496	8080	1607.02	1595
2383.866	69.7	6730	8027	4340.34	4468
2398.930	29.3	9755	8316	1796.88	1790
2501.123	18.9	3499	6831	1003.91	1267
2584.102	10.3	2436	7744	491.94	584
2705.059	26.3	3084	7969	1072.07	1327

m/z	S/N	Quality Fac.	Res.	Intens.	Area
2716.980	20.0	2627	7895	801.77	1007
3312.213	15.5	1874	8375	312.65	521