Complementary Quantitative Proteomics Reveals that Transcription Factor AP-4 Mediates E-Box-Dependent Complex Formation for Transcriptional Repression of *HDM2*

Contents of Supplementary Information

Detailed information regarding cICAT-labeled proteins (see Table 1) enriched on the *HDM2*-P2 E-box sequence (enrichment ratio ≥1.6). Enriched proteins are arranged according to the functional classification indicated in Table 1.

Detailed information regarding iTRAQ-labeled proteins (see Table 1) enriched on the HDM2-P2 E-box sequence (enrichment ratio ≥1.6). Enriched proteins are arranged according to the functional classification indicated in Table 1.

MS/MS spectra and assignment of peptides (shown in Table 1) identified by single peptide–based protein quantitation using cICAT labeling.

MS/MS spectra and assignment of peptides (shown in Table 1) identified by single peptide–based protein quantitation using iTRAQ labeling.

Instruction for Supplementary Table 1

The following information is instruction for the interpretation of protein and peptide ratios in Supplementary Table 1.

Each protein contains protein and peptide information as follows:

Protein-level Information:

The protein description is shown at the first row. Detailed protein-level information is provided as follows:

1. **Accession No.**: Accession number in Swiss-Prot sequence database v54.2.
2. **Protein Score**: Mascot protein score.
3. **Ratio (L/H)**: Raw ratio between proteins enriched by WT DNA-beads, or L (labeled by light cICAT reagent), and proteins enriched by MU DNA-beads, or H (labeled by heavy cICAT reagent). The value is a weighted average of the ratio of all quantitated peptides (see below).
4. **Normalized Ratio (L/H)**: Normalized ratio of raw Ratio (L/H).
5. **STD**: standard deviation of normalized ratio.
6. **Mass**: Molecular weight (Da) of the protein.
7. **Sequence Coverage (%)**: The number of amino acids spanned by the assigned peptides divided by the sequence length.
8. **Identified Peptide**: The number of peptides assigned to the protein by Mascot. Multiple matches to peptides with the same primary sequence count separately.
9. **Quantitated Peptide**: The number of identified peptides for ratio quantitation.
10. **Identified Unique Peptide**: The number of peptides assigned to the protein by Mascot. Multiple matches to peptides with the same primary sequence count as one.

Peptide-level Information:

Peptide-level information contains detailed information for identified peptides assigned to the protein as follows:

1. **Spectrum No.**: The index number of MS/MS spectrum for Mascot search.
2. **Peptide Score**: Mascot Peptide Score.
3. **Ratio (L/H)**: Raw ratio of peptide pair from light (L) cICAT labeled peptide (represents proteins enriched by WT DNA-beads) and heavy (H) cICAT labeled peptide (represents proteins enriched by MU DNA-beads).
4. **Normalized Ratio (L/H)**: Normalized ratio of raw peptide ratio (L/H).
5. **Precursor *m/z* (Da)**: The precursor ion selected for MS/MS analysis.

6. **Charge**: The charge state of precursor ion.
7. **Mass Error (Da)**: The value of observed peptide mass minus expected peptide mass.
8. **Peptide Sequence**: The peptide sequence of matched peptide.
9. **Modification**: Observed modification of the peptide.
10. **Labeled**: The value is “Yes” if the peptide is labeled with cICAT reagents.
11. **Unique**: The value is “Yes” if the peptide is a non-degenerate peptide.

Supplementary Table 1

bHLH Transcription Factors

Transcription factor AP-4 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q01664	59	2.37	1.96	0.07	38702	8.0	3	2	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
51341	33.38	2.34	1.93	902.4012	3	-0.27	TEKEVIGGLCSLANIPLTPETQR	ICAT-C:13C(9) (C)	YES	YES
54132	31.56	2.44	2.01	956.1966	3	0.1025	EVIGGLCSLANIPLTPETQRDQER	ICAT-C (C)	YES	YES
54139	30.47	N/A	N/A	956.2158	3	0.1601	EVIGGLCSLANIPLTPETQRDQER	ICAT-C (C)	YES	YES

Circadian locomoter output cycles protein kaput - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O15516	64	2.47	2.04	N/A	95244	1.8	1	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
35628	63.57	2.47	2.04	1022.4034	2	-0.0638	EMCTVEEPNEEFTSR	ICAT-C (C); Oxidation (M)	YES	YES

Transcription factors

Nuclear factor of activated T-cells, cytoplasmic 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q13469	65	7.82	6.46	2.10	100083	6.7	8	2	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
7458	31.39	N/A	N/A	616.2552	2	-0.1683	ATIDCAGILK	ICAT-C (C)	YES	YES
33429	35.87	N/A	N/A	986.8950	2	-0.2294	IVSLQTASNPIECSQR	ICAT-C (C)	YES	NO
33430	29.99	7.04	5.82	986.8992	2	-0.2210	IVSLQTASNPIECSQR	ICAT-C (C)	YES	YES
33432	30.81	N/A	N/A	986.9060	2	-0.2073	IVSLQTASNPIECSQR	ICAT-C (C)	YES	YES
33445	39.8	N/A	N/A	986.9597	2	-0.0999	IVSLQTASNPIECSQR	ICAT-C (C)	YES	NO
33447	33.09	N/A	N/A	986.9780	2	-0.0632	IVSLQTASNPIECSQR	ICAT-C (C)	YES	NO
35142	25.22	N/A	N/A	677.7010	3	0.0446	HSCAEALVALPPGASPQR	ICAT-C (C)	YES	YES
44025	28.93	10.01	8.27	776.7252	3	0.0057	HIYPAVEFLGPCEQGERR	ICAT-C (C)	YES	YES

Alpha-globin transcription factor CP2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q12800	1019	4.01	3.32	1.58	57220	12.7	56	32	4

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
24592	53.74	N/A	N/A	849.8016	2	-0.2520	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24593	51.97	N/A	N/A	849.8136	2	-0.2281	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24596	62.52	N/A	N/A	849.8268	2	-0.2017	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24597	74.79	N/A	N/A	849.8286	2	-0.1981	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24598	26.4	N/A	N/A	849.8398	2	-0.1756	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24599	53.06	N/A	N/A	849.8430	2	-0.1691	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24602	63.27	N/A	N/A	849.8728	2	-0.1097	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24603	44.25	N/A	N/A	849.8730	2	-0.1092	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24604	56.79	N/A	N/A	849.8745	2	-0.1062	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24605	48.33	N/A	N/A	849.8895	2	-0.0761	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24606	62.77	N/A	N/A	849.8915	2	-0.0723	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24609	33.45	N/A	N/A	849.9026	2	-0.0500	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24615	54.52	N/A	N/A	849.9968	2	0.1384	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24618	67.33	N/A	N/A	850.0995	2	0.3437	DDVIQICGPADGIR	ICAT-C (C)	YES	NO
24890	36.7	N/A	N/A	854.3255	2	-0.2345	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24894	57.52	N/A	N/A	854.3366	2	-0.2122	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24895	52.97	N/A	N/A	854.3384	2	-0.2086	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24899	47.16	N/A	N/A	854.3810	2	-0.1233	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24900	35.81	N/A	N/A	854.3884	2	-0.1086	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24901	53.05	N/A	N/A	854.3919	2	-0.1016	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24907	51.42	N/A	N/A	854.4010	2	-0.0834	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24922	35.98	N/A	N/A	854.5010	2	0.1166	DDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
27383	27.04	3.55	2.93	896.8951	2	-0.1797	LTIYVCQESLQLR	ICAT-C (C)	YES	YES
27387	35.89	2.84	2.35	896.9276	2	-0.1147	LTIYVCQESLQLR	ICAT-C (C)	YES	YES
27391	46.96	4.02	3.32	896.9391	2	-0.0916	LTIYVCQESLQLR	ICAT-C (C)	YES	YES
27392	28.22	2.86	2.36	896.9440	2	-0.0819	LTIYVCQESLQLR	ICAT-C (C)	YES	YES
27714	40.15	2.80	2.31	901.4402	2	-0.1197	LTIYVCQESLQLR	ICAT-C:13C(9) (C)	YES	YES
27718	45.96	3.92	3.24	901.4422	2	-0.1157	LTIYVCQESLQLR	ICAT-C:13C(9) (C)	YES	YES
35760	39.1	5.21	4.30	1024.4321	2	-0.2679	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35761	53.7	5.24	4.33	1024.4361	2	-0.2599	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35767	43.31	9.89	8.17	1024.4617	2	-0.2088	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35790	39.41	6.09	5.03	1024.5141	2	-0.1040	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35797	28.42	8.22	6.79	1024.5245	2	-0.0831	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35814	70.08	5.01	4.14	1024.8000	2	0.4678	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35815	50.55	5.60	4.62	1024.8000	2	0.4678	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
35823	46.67	5.28	4.36	1024.9000	2	0.6678	ILPFQYVLCAATSPAVK	ICAT-C (C)	YES	YES
36111	28.24	5.32	4.39	1028.9575	2	-0.2473	ILPFQYVLCAATSPAVK	ICAT-C:13C(9) (C)	YES	YES
36139	27.32	6.19	5.12	1029.0244	2	-0.1135	ILPFQYVLCAATSPAVK	ICAT-C:13C(9) (C)	YES	YES
36681	26.8	N/A	N/A	690.3406	3	-0.0736	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES

36688	50.04	3.02	2.49	690.3587	3	-0.0193	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36691	50.98	4.06	3.36	690.3627	3	-0.0073	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36692	43.96	3.48	2.88	690.3633	3	-0.0053	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36693	38.98	N/A	N/A	690.3639	3	-0.0035	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36697	33.97	4.20	3.47	690.3696	3	0.0133	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36702	38.6	3.22	2.66	690.3815	3	0.0491	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36703	27.16	4.65	3.84	690.3842	3	0.0571	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36708	41.04	3.00	2.48	690.4493	3	0.2526	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
36709	41.13	4.24	3.50	690.4585	3	0.2802	LTRDDVIQICGPADGIR	ICAT-C (C)	YES	YES
37022	34.25	3.62	2.99	693.3706	3	-0.0137	LTRDDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	YES
37030	38.05	4.04	3.34	693.3862	3	0.0331	LTRDDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	YES
37031	27.81	3.01	2.49	693.3868	3	0.0347	LTRDDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	YES
37032	25.14	2.74	2.26	693.3898	3	0.0438	LTRDDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	YES
37035	33.27	3.17	2.62	693.4460	3	0.2125	LTRDDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	YES
37037	32.67	4.28	3.53	693.4606	3	0.2563	LTRDDVIQICGPADGIR	ICAT-C:13C(9) (C)	YES	YES
40092	32.77	3.79	3.13	1083.4677	2	-0.2346	IAQLFSISPCQISQIYK	ICAT-C (C)	YES	YES
40119	39.24	4.31	3.56	1083.9000	2	0.6300	IAQLFSISPCQISQIYK	ICAT-C (C)	YES	YES

General transcription factor II-I - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P78347	141	3.81	3.15	0.82	112346	4.9	9	3	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
3521	31.42	N/A	N/A	509.2045	2	-0.1379	CGEALGLK	ICAT-C (C)	YES	YES
15664	25.5	N/A	N/A	721.7855	2	-0.2034	SILSPGGSCGPIK	ICAT-C (C)	YES	YES
15666	53.65	N/A	N/A	721.7917	2	-0.1911	SILSPGGSCGPIK	ICAT-C (C)	YES	YES
15671	46.66	N/A	N/A	721.8449	2	-0.0847	SILSPGGSCGPIK	ICAT-C (C)	YES	YES
15674	50.04	N/A	N/A	721.8538	2	-0.0669	SILSPGGSCGPIK	ICAT-C (C)	YES	YES
15675	61.03	N/A	N/A	721.8656	2	-0.0432	SILSPGGSCGPIK	ICAT-C (C)	YES	YES
42955	29.12	5.10	4.21	758.3438	3	-0.1501	ITINPGCVVVDGMPPGVSFK	ICAT-C (C); Oxidation (M)	YES	YES
44053	29.77	3.86	3.19	777.3068	3	-0.2784	VMVTDADRSILSPGGSCGPIK	ICAT-C (C)	YES	YES
44328	26.35	3.55	2.93	782.7635	3	0.0966	VMVTDADRSILSPGGSCGPIK	ICAT-C (C); Oxidation (M)	YES	YES

Upstream-binding protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9NZI7	903	3.27	2.70	0.45	60453	7.6	45	40	4	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
4550	28.35	3.59	2.97	547.7435	2	-0.1229	LTIYVCR	ICAT-C (C)	YES	YES
24183	48.18	N/A	N/A	843.8274	2	-0.2004	EDLVQICGAADGIR	ICAT-C (C)	YES	YES

24184	58.39	3.20	2.64	843.8419	2	-0.1715	EDLVQICGAADGIR	ICAT-C (C)	YES	YES
24186	50.57	N/A	N/A	843.8783	2	-0.0986	EDLVQICGAADGIR	ICAT-C (C)	YES	YES
24191	65.52	N/A	N/A	843.8894	2	-0.0764	EDLVQICGAADGIR	ICAT-C (C)	YES	YES
24192	74.86	2.93	2.42	843.9062	2	-0.0428	EDLVQICGAADGIR	ICAT-C (C)	YES	YES
24489	34.46	3.79	3.13	848.3862	2	-0.1131	EDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
24502	45.76	3.12	2.58	848.4256	2	-0.0342	EDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
35045	44.01	3.23	2.67	677.0224	3	-0.0220	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35047	57.97	3.26	2.70	677.0248	3	-0.0147	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35049	49.53	3.46	2.86	677.0260	3	-0.0112	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35053	38.2	3.74	3.09	677.0298	3	0.0003	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35055	43.89	3.26	2.69	677.0329	3	0.0095	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35067	44.45	N/A	N/A	677.0407	3	0.0329	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35069	33.09	3.71	3.06	677.0433	3	0.0406	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35071	40.41	3.04	2.51	677.0440	3	0.0428	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35073	43.85	4.09	3.38	677.0457	3	0.0478	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35075	42.17	3.32	2.75	677.0480	3	0.0547	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35079	25.85	3.03	2.50	677.1156	3	0.2575	LTKEDLVQICGAADGIR	ICAT-C (C)	YES	YES
35360	33.41	3.28	2.71	680.0287	3	-0.0333	LTKEDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
35365	40.65	3.24	2.68	680.0329	3	-0.0207	LTKEDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
35374	36.55	3.22	2.66	680.0367	3	-0.0092	LTKEDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
35376	39.33	3.25	2.68	680.0388	3	-0.0031	LTKEDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
35390	34.18	3.09	2.55	680.0579	3	0.0542	LTKEDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
35395	26.02	3.09	2.56	680.1169	3	0.2312	LTKEDLVQICGAADGIR	ICAT-C:13C(9) (C)	YES	YES
40028	44.85	3.42	2.83	721.9427	3	-0.2721	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40029	45.58	3.59	2.96	721.9478	3	-0.2569	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40030	28.25	4.10	3.38	721.9511	3	-0.2469	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40033	34.09	N/A	N/A	721.9982	3	-0.1054	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40040	43.69	3.41	2.81	722.0300	3	-0.0102	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40042	28.16	3.04	2.51	722.0345	3	0.0035	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40043	32.99	3.09	2.55	722.0349	3	0.0045	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40044	36.96	3.42	2.82	722.0350	3	0.0050	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40048	55.13	5.61	4.63	722.0521	3	0.0561	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40050	43.77	3.23	2.67	722.0529	3	0.0587	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40051	33.09	3.26	2.69	722.0566	3	0.0695	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40053	34.55	3.74	3.09	722.0623	3	0.0868	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40054	44.1	3.34	2.76	722.0625	3	0.0874	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40055	59.28	3.25	2.69	722.0665	3	0.0993	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40061	53.85	3.33	2.75	722.2000	3	0.4999	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40062	42.74	3.25	2.68	722.2000	3	0.4999	TSAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
40287	34.97	3.36	2.77	725.0363	3	-0.0215	TSAFIQVHCISTEFTPR	ICAT-C:13C(9) (C)	YES	YES
40288	27.53	3.11	2.57	725.0435	3	0.0001	TSAFIQVHCISTEFTPR	ICAT-C:13C(9) (C)	YES	YES
40292	26.99	3.24	2.67	725.0545	3	0.0333	TSAFIQVHCISTEFTPR	ICAT-C:13C(9) (C)	YES	YES
40296	30.55	3.21	2.65	725.0665	3	0.0693	TSAFIQVHCISTEFTPR	ICAT-C:13C(9) (C)	YES	YES

COUP transcription factor 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P10589	316	2.69	2.22	2.13	46126	15.6	18	5	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
10675	25.38	N/A	N/A	673.9053	2	0.1651	NCPIDQHHR	ICAT-C (C)	YES	NO
14604	48.3	N/A	N/A	712.7716	2	-0.1479	SQCALEEYVR	ICAT-C (C)	YES	NO
14605	33.62	N/A	N/A	712.7728	2	-0.1455	SQCALEEYVR	ICAT-C (C)	YES	NO
14607	40.56	N/A	N/A	712.7786	2	-0.1339	SQCALEEYVR	ICAT-C (C)	YES	NO
14613	33.59	N/A	N/A	712.8306	2	-0.0299	SQCALEEYVR	ICAT-C (C)	YES	NO
14615	37.84	N/A	N/A	712.8387	2	-0.0137	SQCALEEYVR	ICAT-C (C)	YES	NO
14619	36.06	N/A	N/A	712.8552	2	0.0193	SQCALEEYVR	ICAT-C (C)	YES	NO
14620	48.12	N/A	N/A	712.8694	2	0.0476	SQCALEEYVR	ICAT-C (C)	YES	NO
14625	49.89	N/A	N/A	712.9309	2	0.1708	SQCALEEYVR	ICAT-C (C)	YES	NO
15056	28.03	N/A	N/A	717.2904	2	-0.1404	SQCALEEYVR	ICAT-C:13C(9) (C)	YES	NO
15080	32.58	N/A	N/A	717.3628	2	0.0043	SQCALEEYVR	ICAT-C:13C(9) (C)	YES	NO
15100	35.35	N/A	N/A	717.4346	2	0.1479	SQCALEEYVR	ICAT-C:13C(9) (C)	YES	NO
52010	26.9	7.37	6.09	915.6923	3	-0.3139	AIVLFTSDACGLSDAAHIESLQEK	ICAT-C (C)	YES	YES
52016	56.4	2.44	2.01	915.7575	3	-0.1182	AIVLFTSDACGLSDAAHIESLQEK	ICAT-C (C)	YES	YES
52023	48.54	2.91	2.41	915.8335	3	0.1096	AIVLFTSDACGLSDAAHIESLQEK	ICAT-C (C)	YES	YES
52132	33.85	2.55	2.11	918.7587	3	-0.1449	AIVLFTSDACGLSDAAHIESLQEK	ICAT-C:13C(9) (C)	YES	YES
56773	34.96	2.61	2.15	1014.3642	3	-0.3168	YGSQCMQPNNIMGIENICELAAR	2 ICAT-C (C); 2 Oxidation (M)	YES	YES
56774	40.32	N/A	N/A	1014.3977	3	-0.2162	YGSQCMQPNNIMGIENICELAAR	2 ICAT-C (C); 2 Oxidation (M)	YES	YES

COUP transcription factor 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P24468	228	2.16	1.78	0.05	45542	10.4	14	2	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
10675	25.38	N/A	N/A	673.9053	2	0.1651	NCPIDQHHR	ICAT-C (C)	YES	NO
15056	28.03	N/A	N/A	712.7716	2	-0.1479	SQCALEEYVR	ICAT-C:13C(9) (C)	YES	NO
15080	32.58	N/A	N/A	712.7728	2	-0.1455	SQCALEEYVR	ICAT-C:13C(9) (C)	YES	NO
14613	33.59	N/A	N/A	712.7786	2	-0.1339	SQCALEEYVR	ICAT-C (C)	YES	NO
14605	33.62	N/A	N/A	712.8306	2	-0.0299	SQCALEEYVR	ICAT-C (C)	YES	NO
15100	35.35	N/A	N/A	712.8387	2	-0.0137	SQCALEEYVR	ICAT-C:13C(9) (C)	YES	NO
52241	35.7	2.20	1.81	712.8552	2	0.0193	AIVLFTSDACGLSDVAHVESLQEK	ICAT-C (C)	YES	YES
14619	36.06	N/A	N/A	712.8694	2	0.0476	SQCALEEYVR	ICAT-C (C)	YES	NO
52430	36.75	2.12	1.75	712.9309	2	0.1708	AIVLFTSDACGLSDVAHVESLQEK	ICAT-C:13C(9) (C)	YES	YES
14615	37.84	N/A	N/A	717.2904	2	-0.1404	SQCALEEYVR	ICAT-C (C)	YES	NO
14607	40.56	N/A	N/A	717.3628	2	0.0043	SQCALEEYVR	ICAT-C (C)	YES	NO
14620	48.12	N/A	N/A	717.4346	2	0.1479	SQCALEEYVR	ICAT-C (C)	YES	NO
14604	48.3	N/A	N/A	920.4227	3	-0.1385	SQCALEEYVR	ICAT-C (C)	YES	NO
14625	49.89	N/A	N/A	923.4576	3	-0.0640	SQCALEEYVR	ICAT-C (C)	YES	NO

Nuclear factor 1 C-type - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P08651	85	2.04	1.69	0.18	55640	9.8	4	3	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
20865	46.28	2.28	1.89	792.4109	2	-0.0064	KAPGCVLSNPDQK	ICAT-C (C)	YES	YES
20866	33.94	2.19	1.81	528.6121	3	0.0008	KAPGCVLSNPDQK	ICAT-C (C)	YES	YES
41209	42.19	1.94	1.60	735.7402	3	0.0728	DIRPECREDFVLSITGK	ICAT-C (C)	YES	YES
44015	25.03	N/A	N/A	776.4194	3	0.0617	MPSHCLSAQMLAPPPPGLPR	ICAT-C (C)	YES	YES

Cellular tumor antigen p53 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P04637	49	1.09	0.90	0.18	43625	6.9	3	3	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
18905	25.69	1.39	1.14	760.3634	2	-0.0678	SVTCTYSPALNK	ICAT-C:13C(9) (C)	YES	YES
28770	30.92	1.10	0.91	612.6452	3	0.0142	CSDSDGLAPPQHLIR	ICAT-C (C)	YES	YES
29123	32.46	1.06	0.88	615.6532	3	0.0080	CSDSDGLAPPQHLIR	ICAT-C:13C(9) (C)	YES	YES

Nuclear receptor subfamily 2 group F member 6 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P10588	78	5.18	4.28	0.27	42952	14.6	4	3	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
19967	25.45	N/A	N/A	776.7926	2	-0.1896	LQVDSAEYGCLK	ICAT-C (C)	YES	YES
43781	32.27	5.47	4.51	772.6881	3	-0.1267	FGAGGGAAGAVLGIDNVCELAAR	ICAT-C (C)	YES	YES
51908	35.53	4.93	4.07	913.7659	3	-0.0827	AIALFTPDACGLSDPAHVESLQEK	ICAT-C (C)	YES	YES
51912	39.85	5.26	4.35	913.8162	3	0.0684	AIALFTPDACGLSDPAHVESLQEK	ICAT-C (C)	YES	YES

Homeobox protein PKNOX1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P55347	37	4.47	3.69	N/A	47577	3.4	1	1	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
30453	36.76	4.47	3.69	946.3527	2	-0.2158	ILQPMLDSSCSETPK	ICAT-C (C); Oxidation (M)	YES	YES

Transcription factor Sp1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P08047	92	3.14	2.59	N/A	80644	3.9	5	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
57334	28.21	3.14	2.59	1032.3622	3	-0.3824	SSSTGSSSSTGGGGQESQPSPLALLAATCSR	ICAT-C (C)	YES	YES
57336	37.23	N/A	N/A	1032.3725	3	-0.3517	SSSTGSSSSTGGGGQESQPSPLALLAATCSR	ICAT-C (C)	YES	YES
57337	41.71	N/A	N/A	1032.3902	3	-0.2986	SSSTGSSSSTGGGGQESQPSPLALLAATCSR	ICAT-C (C)	YES	YES
57338	26.32	N/A	N/A	1032.4231	3	-0.1999	SSSTGSSSSTGGGGQESQPSPLALLAATCSR	ICAT-C (C)	YES	YES
57341	30.63	N/A	N/A	1032.4577	3	-0.0959	SSSTGSSSSTGGGGQESQPSPLALLAATCSR	ICAT-C (C)	YES	YES

Nuclear factor 1 A-type - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q12857	75	2.54	2.10	0.21	55909	12.4	4	2	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
30140	35.37	N/A	N/A	628.3251	3	0.0093	KPPCCVLSNPDQK	2 ICAT-C (C)	YES	NO
30143	28.91	N/A	N/A	628.3289	3	0.0208	KPPCCVLSNPDQK	2 ICAT-C (C)	YES	NO
50018	28.1	2.48	2.05	661.0809	4	-0.0318	SPQCSNPGLCVQPHHIGVSVK	2 ICAT-C (C)	YES	YES
58217	40.18	2.77	2.29	1068.1475	3	-0.1306	EFVQLVCPDAGQQAGQVGFLNPNGSSQGK	ICAT-C (C)	YES	YES

Breast cancer type 1 susceptibility protein - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P38398	38	2.46	2.03	N/A	207592	0.4	1	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
7078	38.46	2.46	2.03	607.7452	2	-0.1155	FCLSSQFR	ICAT-C (C)	YES	YES

Zinc fingers and homeoboxes protein 3 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9H4I2	60	2.21	1.82	1.12	104592	4.0	3	2	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
16865	27.94	N/A	N/A	733.8430	2	-0.1136	AELCYLTVVTK	ICAT-C (C)	YES	YES
42705	55.79	3.55	2.93	755.3277	3	-0.2269	VPEVTCIPTTATLATHPSAK	ICAT-C (C)	YES	YES
44666	31.3	1.97	1.62	788.4465	3	0.0636	AELCYLTVVTKYPEEQLK	ICAT-C:13C(9) (C)	YES	YES

Transcriptional repressor and corepressor

Transcriptional repressor CTCF - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P49711	34	11.71	9.68	N/A	82732	2.1	2	1	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
31563	25.16	11.71	9.68	641.3046	3	-0.0272	YHDPNFVPAAFVCSK	ICAT-C (C)	YES	YES
31567	25.45	N/A	N/A	641.3147	3	0.0032	YHDPNFVPAAFVCSK	ICAT-C (C)	YES	YES

Transcription factor CP2-like protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9NZI6	331	3.16	2.61	0.38	54593	10.0	24	2	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
24592	43.31	N/A	N/A	849.8016	2	-0.2520	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24593	46.41	N/A	N/A	849.8136	2	-0.2281	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24596	44.78	N/A	N/A	849.8268	2	-0.2017	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24597	67.28	N/A	N/A	849.8286	2	-0.1981	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24599	49.29	N/A	N/A	849.8430	2	-0.1691	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24602	46.94	N/A	N/A	849.8728	2	-0.1097	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24603	34.01	N/A	N/A	849.8730	2	-0.1092	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24604	52.83	N/A	N/A	849.8745	2	-0.1062	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24605	41.72	N/A	N/A	849.8895	2	-0.0761	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24606	47.14	N/A	N/A	849.8915	2	-0.0723	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24609	31.1	N/A	N/A	849.9026	2	-0.0500	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24615	50.67	N/A	N/A	849.9968	2	0.1384	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24618	51.01	N/A	N/A	850.0995	2	0.3437	DDLVQICGPADGIR	ICAT-C (C)	YES	NO
24890	33.33	N/A	N/A	854.3255	2	-0.2345	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24894	43.3	N/A	N/A	854.3366	2	-0.2122	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24895	45.31	N/A	N/A	854.3384	2	-0.2086	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24899	43.5	N/A	N/A	854.3810	2	-0.1233	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24900	30.9	N/A	N/A	854.3884	2	-0.1086	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24901	49.61	N/A	N/A	854.3919	2	-0.1016	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24907	48.04	N/A	N/A	854.4010	2	-0.0834	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
24922	32.64	N/A	N/A	854.5010	2	0.1166	DDLVQICGPADGIR	ICAT-C:13C(9) (C)	YES	NO
34251	26.83	N/A	N/A	666.6114	3	-0.2896	LPPLQYVLCAATSPAVK	ICAT-C (C)	YES	YES
39169	37.86	2.98	2.46	712.0279	3	-0.0057	ASAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES
39180	33.7	3.52	2.91	712.0487	3	0.0566	ASAFIQVHCISTEFTPR	ICAT-C (C)	YES	YES

Zinc finger and BTB domain-containing protein 7A - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
O95365	886	6.85	5.66	1.90	61401	11.6	36	15	5	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
15701	37.04	N/A	N/A	722.2688	2	-0.1998	SVLAACSQYFK	ICAT-C (C)	YES	YES
15706	39.48	6.49	5.36	722.2884	2	-0.1604	SVLAACSQYFK	ICAT-C (C)	YES	YES
15707	26.51	N/A	N/A	722.2937	2	-0.1498	SVLAACSQYFK	ICAT-C (C)	YES	YES
15715	54.97	N/A	N/A	722.3229	2	-0.0916	SVLAACSQYFK	ICAT-C (C)	YES	YES
15728	34.48	N/A	N/A	722.3479	2	-0.0415	SVLAACSQYFK	ICAT-C (C)	YES	YES
15741	56.2	N/A	N/A	722.3607	2	-0.0160	SVLAACSQYFK	ICAT-C (C)	YES	YES
16194	32.55	N/A	N/A	726.8631	2	-0.0414	SVLAACSQYFK	ICAT-C:13C(9) (C)	YES	YES
20500	39.88	6.47	5.35	786.4250	2	0.0178	SVLAACSQYFKK	ICAT-C (C)	YES	YES
28929	51.87	N/A	N/A	921.3913	2	-0.2400	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28931	85.21	N/A	N/A	921.4048	2	-0.2130	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28932	60.34	N/A	N/A	921.4104	2	-0.2018	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28933	40.64	N/A	N/A	921.4205	2	-0.1816	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28934	39.11	N/A	N/A	921.4326	2	-0.1574	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28935	61.58	12.03	9.94	921.4365	2	-0.1496	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28936	67.85	N/A	N/A	921.4442	2	-0.1343	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28941	28.83	N/A	N/A	921.4591	2	-0.1044	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28949	52.22	N/A	N/A	921.4767	2	-0.0693	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28950	74.04	N/A	N/A	921.4800	2	-0.0626	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28954	68.52	N/A	N/A	921.5170	2	0.0114	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28955	45.59	N/A	N/A	921.5210	2	0.0194	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
28957	56.41	N/A	N/A	921.5251	2	0.0275	TQGLLCDVVILVEGR	ICAT-C (C)	YES	YES
37679	27.38	9.22	7.62	697.7247	3	0.0329	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37684	30.2	N/A	N/A	697.7369	3	0.0693	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37686	28.93	8.61	7.11	697.7381	3	0.0730	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37688	27.93	N/A	N/A	697.7445	3	0.0922	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37691	59.02	6.49	5.36	697.8000	3	0.2588	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37702	62.89	8.12	6.70	697.9000	3	0.5588	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37703	30.1	9.04	7.47	697.9000	3	0.5588	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
37704	61.1	7.53	6.22	1046.4000	2	0.6661	LLEIPAVSHVCADLLDR	ICAT-C (C)	YES	YES
38063	29.9	7.03	5.81	700.8000	3	0.2286	LLEIPAVSHVCADLLDR	ICAT-C:13C(9) (C)	YES	YES
56814	40.97	N/A	N/A	762.7799	4	-0.3477	HTGEKPYLCQQCGAAFAHNYDLK	2 ICAT-C (C)	YES	YES
56815	26.76	6.18	5.10	762.8561	4	-0.0429	HTGEKPYLCQQCGAAFAHNYDLK	2 ICAT-C (C)	YES	YES
58066	39.54	4.75	3.93	794.8839	4	-0.0268	KHTGEKPYLCQQCGAAFAHNYDLK	2 ICAT-C (C)	YES	YES
58069	29	4.83	3.99	794.8921	4	0.0063	KHTGEKPYLCQQCGAAFAHNYDLK	2 ICAT-C (C)	YES	YES
58072	44.51	6.93	5.72	794.9161	4	0.1022	KHTGEKPYLCQQCGAAFAHNYDLK	2 ICAT-C (C)	YES	YES
58073	43.54	5.54	4.58	794.9166	4	0.1043	KHTGEKPYLCQQCGAAFAHNYDLK	2 ICAT-C (C)	YES	YES

C-terminal-binding protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q13363	40	2.74	2.27	N/A	47505	4.3	1	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
44029	40.34	2.74	2.27	776.7436	3	0.0939	DVATVAFCDAQSTQEIHEK	ICAT-C:13C(9) (C)	YES	YES

Protein Wiz - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O95785	117	2.37	1.96	0.40	178563	0.7	12	10	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
28717	29.7	N/A	N/A	917.7852	2	-0.2256	CEFCGEFFENR	2 ICAT-C (C)	YES	YES
28718	40.02	N/A	N/A	917.7912	2	-0.2137	CEFCGEFFENR	2 ICAT-C (C)	YES	YES
28727	33.08	2.68	2.21	917.8454	2	-0.1052	CEFCGEFFENR	2 ICAT-C (C)	YES	YES
28728	37.94	2.57	2.12	917.8552	2	-0.0856	CEFCGEFFENR	2 ICAT-C (C)	YES	YES
28731	43.34	2.52	2.08	917.8563	2	-0.0835	CEFCGEFFENR	2 ICAT-C (C)	YES	YES
29340	36.14	2.52	2.08	926.8788	2	-0.0988	CEFCGEFFENR	2 ICAT-C:13C(9) (C)	YES	YES
29341	33.44	2.56	2.12	926.8896	2	-0.0771	CEFCGEFFENR	2 ICAT-C:13C(9) (C)	YES	YES
32942	25.08	2.74	2.26	654.9663	3	0.0006	CEFCGEFFENRK	2 ICAT-C (C)	YES	YES
32946	29.78	2.41	1.99	654.9698	3	0.0113	CEFCGEFFENRK	2 ICAT-C (C)	YES	YES
32948	26.43	1.33	1.09	654.9708	3	0.0143	CEFCGEFFENRK	2 ICAT-C (C)	YES	YES
32952	29.95	2.32	1.92	654.9836	3	0.0526	CEFCGEFFENRK	2 ICAT-C (C)	YES	YES
32953	36.7	2.29	1.89	654.9849	3	0.0564	CEFCGEFFENRK	2 ICAT-C (C)	YES	YES

Basic transcription machinery

Transcription termination factor 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9UNY4	43	2.09	1.73	0.02	129508	2.3	2	2	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
56918	30.4	2.10	1.74	765.2000	4	0.1493	SLESCPGETVVAEDPAGLKVPLLLHQK	ICAT-C (C)	YES	YES
56988	27.96	2.08	1.72	767.4225	4	0.0092	SLESCPGETVVAEDPAGLKVPLLLHQK	ICAT-C:13C(9) (C)	YES	YES

TATA-box-binding protein - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P20226	210	1.04	0.86	0.04	37674	4.4	10	10	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique

32025	31.4	1.06	0.88	645.3406	3	0.0085	IQNMVGSCDVKFPIR	ICAT-C (C)	YES	YES
32027	32.74	1.01	0.84	645.3441	3	0.0191	IQNMVGSCDVKFPIR	ICAT-C (C)	YES	YES
32029	25.35	1.02	0.84	645.3457	3	0.0240	IQNMVGSCDVKFPIR	ICAT-C (C)	YES	YES
32271	54.99	1.07	0.88	648.3492	3	0.0043	IQNMVGSCDVKFPIR	ICAT-C:13C(9) (C)	YES	YES
32272	51.07	1.01	0.84	648.3514	3	0.0109	IQNMVGSCDVKFPIR	ICAT-C:13C(9) (C)	YES	YES
32274	44.11	1.16	0.96	648.3538	3	0.0180	IQNMVGSCDVKFPIR	ICAT-C:13C(9) (C)	YES	YES
32279	42.65	1.05	0.87	648.3702	3	0.0673	IQNMVGSCDVKFPIR	ICAT-C:13C(9) (C)	YES	YES
32489	28.76	1.02	0.84	650.6732	3	0.0114	IQNMVGSCDVKFPIR	ICAT-C (C); Oxidation (M)	YES	YES
32496	29.65	1.04	0.86	650.6883	3	0.0567	IQNMVGSCDVKFPIR	ICAT-C (C); Oxidation (M)	YES	YES
32820	28.82	1.04	0.86	653.6963	3	0.0505	IQNMVGSCDVKFPIR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES

TATA-binding protein-associated factor 172 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
O14981	97	2.05	1.70	0.10	206756	1.8	4	4	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
17794	46.85	1.91	1.58	744.8646	2	-0.0871	ETCAQTLGVVLK	ICAT-C (C)	YES	YES
49227	29.39	1.96	1.62	649.3223	4	0.0171	AKCDVDETVSSATLSEETEKPK	ICAT-C (C)	YES	YES
49230	52.4	2.11	1.74	649.3312	4	0.0527	AKCDVDETVSSATLSEETEKPK	ICAT-C (C)	YES	YES
49372	27.09	2.12	1.75	651.5934	4	0.0714	AKCDVDETVSSATLSEETEKPK	ICAT-C:13C(9) (C)	YES	YES

SWI/SNF-related proteins

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q12824	69	3.59	2.97	0.73	44113	13.2	5	4	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
53609	30.14	3.65	3.01	946.0000	3	0.6679	NTGDADQWCPLLETLTDAEMEKK	ICAT-C (C)	YES	YES
53802	31.92	4.82	3.98	948.8218	3	0.1033	NTGDADQWCPLLETLTDAEMEKK	ICAT-C:13C(9) (C)	YES	YES
59147	31.13	N/A	N/A	847.4267	4	0.0013	TFPLCFDDHDPAVIHENASQPEVLVPIR	ICAT-C (C)	YES	YES
59149	27.12	3.83	3.16	847.4483	4	0.0876	TFPLCFDDHDPAVIHENASQPEVLVPIR	ICAT-C (C)	YES	YES
59206	33.49	3.06	2.53	849.6996	4	0.0625	TFPLCFDDHDPAVIHENASQPEVLVPIR	ICAT-C:13C(9) (C)	YES	YES

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q8TAQ2	1529	2.51	2.07	0.39	132797	8.1	124	51	4	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
3295	30.03	2.61	2.16	500.1770	2	-0.1501	CFLDFK	ICAT-C (C)	YES	YES
3296	27.18	2.76	2.28	500.1839	2	-0.1362	CFLDFK	ICAT-C (C)	YES	YES

3297	27.44	N/A	N/A	500.1847	2	-0.1346	CFLDFK	ICAT-C (C)	YES	YES
3298	27.62	2.54	2.10	500.1886	2	-0.1269	CFLDFK	ICAT-C (C)	YES	YES
3299	27.5	2.68	2.22	500.1897	2	-0.1248	CFLDFK	ICAT-C (C)	YES	YES
3301	25.95	2.45	2.02	500.1913	2	-0.1215	CFLDFK	ICAT-C (C)	YES	YES
3311	29.15	N/A	N/A	500.2184	2	-0.0674	CFLDFK	ICAT-C (C)	YES	YES
3322	27.21	3.06	2.53	500.2540	2	0.0039	CFLDFK	ICAT-C (C)	YES	YES
3324	27.38	2.47	2.04	500.2572	2	0.0104	CFLDFK	ICAT-C (C)	YES	YES
3334	35.1	2.93	2.42	500.2951	2	0.0861	CFLDFK	ICAT-C (C)	YES	YES
3335	29.45	2.49	2.06	500.3123	2	0.1205	CFLDFK	ICAT-C (C)	YES	YES
3338	28.94	3.47	2.86	500.3212	2	0.1383	CFLDFK	ICAT-C (C)	YES	YES
3340	25.63	2.57	2.12	500.3567	2	0.2094	CFLDFK	ICAT-C (C)	YES	YES
3341	27.86	2.48	2.05	500.4000	2	0.2959	CFLDFK	ICAT-C (C)	YES	YES
3342	27.85	2.64	2.18	500.4589	2	0.4138	CFLDFK	ICAT-C (C)	YES	YES
3404	26.56	2.54	2.10	504.7017	2	-0.1308	CFLDFK	ICAT-C:13C(9) (C)	YES	YES
3406	25.23	2.48	2.05	504.7026	2	-0.1290	CFLDFK	ICAT-C:13C(9) (C)	YES	YES
3410	28.9	N/A	N/A	504.7396	2	-0.0551	CFLDFK	ICAT-C:13C(9) (C)	YES	YES
3412	26.94	2.48	2.05	504.7630	2	-0.0084	CFLDFK	ICAT-C:13C(9) (C)	YES	YES
3419	26.5	2.50	2.07	504.9524	2	0.3705	CFLDFK	ICAT-C:13C(9) (C)	YES	YES
5101	26.88	N/A	N/A	563.2196	2	-0.1619	TPEIYLAYR		NO	NO
5102	35.32	N/A	N/A	563.2242	2	-0.1527	TPEIYLAYR		NO	NO
5103	44.34	N/A	N/A	563.2269	2	-0.1474	TPEIYLAYR		NO	NO
5108	44.32	N/A	N/A	563.2843	2	-0.0326	TPEIYLAYR		NO	NO
5116	27.94	N/A	N/A	563.3826	2	0.1641	TPEIYLAYR		NO	NO
5117	38.6	N/A	N/A	563.3893	2	0.1775	TPEIYLAYR		NO	NO
10136	26.16	N/A	N/A	666.3104	2	-0.1467	SLVALLVETQMK		NO	NO
10148	32.86	N/A	N/A	666.3841	2	0.0007	SLVALLVETQMK		NO	NO
12464	25.03	N/A	N/A	695.2968	2	-0.1113	NLAGDVCAIMR	ICAT-C (C)	YES	YES
12506	27.21	2.00	1.65	695.3713	2	0.0376	NLAGDVCAIMR	ICAT-C (C)	YES	YES
12514	28.68	N/A	N/A	695.3766	2	0.0482	NLAGDVCAIMR	ICAT-C (C)	YES	YES
13507	30	N/A	N/A	703.2573	2	-0.1853	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13513	48.67	2.88	2.38	703.2708	2	-0.1584	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13518	40.03	2.40	1.99	703.2734	2	-0.1530	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13528	39.33	2.99	2.47	703.2798	2	-0.1403	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13531	33.77	N/A	N/A	703.2975	2	-0.1050	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13550	30.69	2.51	2.08	703.3484	2	-0.0031	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13585	26.3	3.20	2.65	703.4290	2	0.1581	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13587	42.35	2.57	2.12	703.4300	2	0.1600	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
13593	39.91	2.71	2.24	703.5000	2	0.3001	NLAGDVCAIMR	ICAT-C (C); Oxidation (M)	YES	YES
14020	36.77	2.60	2.15	707.7901	2	-0.1498	NLAGDVCAIMR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
14021	32.94	2.54	2.10	707.7916	2	-0.1468	NLAGDVCAIMR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
14022	34.95	N/A	N/A	707.7929	2	-0.1444	NLAGDVCAIMR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
14031	25.62	N/A	N/A	707.8499	2	-0.0303	NLAGDVCAIMR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
14051	28.51	2.52	2.08	707.9434	2	0.1568	NLAGDVCAIMR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
21455	28.02	N/A	N/A	534.6001	3	-0.0248	TQDECILHFLR	ICAT-C (C)	YES	NO
21460	34.97	N/A	N/A	534.6052	3	-0.0095	TQDECILHFLR	ICAT-C (C)	YES	NO

21464	25.66	N/A	N/A	534.6074	3	-0.0028	TQDECILHFLR	ICAT-C (C)	YES	NO
21466	26.45	N/A	N/A	534.6084	3	0.0003	TQDECILHFLR	ICAT-C (C)	YES	NO
21467	33.32	N/A	N/A	534.6087	3	0.0011	TQDECILHFLR	ICAT-C (C)	YES	NO
21469	28.64	N/A	N/A	534.6090	3	0.0021	TQDECILHFLR	ICAT-C (C)	YES	NO
21470	34.07	2.44	2.02	534.6095	3	-0.0328	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21471	26.55	N/A	N/A	534.6099	3	0.0046	TQDECILHFLR	ICAT-C (C)	YES	NO
21472	36.27	3.70	3.06	534.6101	3	-0.0309	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21473	28.65	N/A	N/A	534.6105	3	0.0064	TQDECILHFLR	ICAT-C (C)	YES	NO
21476	48.41	2.44	2.01	534.6110	3	-0.0285	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21484	28.66	2.42	2.00	534.6156	3	-0.0144	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21488	42.5	2.39	1.98	534.6179	3	-0.0075	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21496	40.82	2.58	2.13	534.6251	3	0.0140	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21497	33.03	2.47	2.04	534.6261	3	0.0169	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21498	40.95	2.67	2.21	534.6266	3	0.0184	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21499	33.06	2.55	2.11	534.6286	3	0.0244	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21503	34.48	N/A	N/A	801.5000	2	0.1823	TQDECILHFLR	ICAT-C (C)	YES	NO
21505	49.8	2.31	1.91	534.6876	3	0.2016	AGGSLCHILAAAYK	ICAT-C (C)	YES	YES
21506	39.12	N/A	N/A	801.5640	2	0.3102	TQDECILHFLR	ICAT-C (C)	YES	NO
21507	79.91	N/A	N/A	801.6000	2	0.3823	TQDECILHFLR	ICAT-C (C)	YES	NO
21508	67.29	N/A	N/A	801.6000	2	0.3823	TQDECILHFLR	ICAT-C (C)	YES	NO
21509	34.03	N/A	N/A	534.8000	3	0.5750	TQDECILHFLR	ICAT-C (C)	YES	NO
21510	74.71	N/A	N/A	801.7000	2	0.5823	TQDECILHFLR	ICAT-C (C)	YES	NO
21775	29.04	N/A	N/A	805.8000	2	-0.2479	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21778	58.44	N/A	N/A	805.9016	2	-0.0447	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21779	25.16	N/A	N/A	537.6053	3	-0.0392	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21780	25.36	N/A	N/A	537.6063	3	-0.0362	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21781	27.03	N/A	N/A	537.6076	3	-0.0324	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21783	28.25	N/A	N/A	537.6111	3	-0.0218	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21784	29.58	N/A	N/A	537.6124	3	-0.0181	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21785	37.38	N/A	N/A	537.6147	3	-0.0110	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21788	39.43	N/A	N/A	537.6180	3	-0.0013	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21789	39.04	2.47	2.04	537.6185	3	-0.0359	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21790	28.73	N/A	N/A	537.6186	3	0.0007	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21791	34.47	N/A	N/A	537.6186	3	0.0008	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21792	27.91	N/A	N/A	537.6192	3	0.0024	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21795	52.84	N/A	N/A	805.9281	2	0.0083	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21796	32.32	2.37	1.96	537.6228	3	-0.0230	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21797	27.7	N/A	N/A	537.6231	3	0.0140	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21799	28.34	N/A	N/A	537.6235	3	0.0154	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21801	31.24	N/A	N/A	537.6247	3	0.0190	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21803	29.61	N/A	N/A	537.6252	3	0.0205	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21804	33.1	2.91	2.41	537.6269	3	-0.0108	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21805	34.97	2.50	2.07	537.6276	3	-0.0087	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21806	45.55	2.50	2.07	537.6289	3	-0.0047	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21807	26.42	N/A	N/A	537.6305	3	0.0364	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO

21808	38.38	4.54	3.75	537.6311	3	0.0016	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21809	32.2	N/A	N/A	537.6313	3	0.0388	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21810	25.49	2.58	2.13	537.6325	3	0.0058	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21812	34.82	2.45	2.02	537.6341	3	0.0108	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21813	27.52	2.74	2.26	537.6358	3	0.0159	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21814	33.13	2.58	2.13	537.6360	3	0.0164	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21815	39.66	2.70	2.23	537.6395	3	0.0271	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21817	38.71	2.90	2.39	537.6434	3	0.0387	AGGSLCHILAAAYK	ICAT-C:13C(9) (C)	YES	YES
21823	75.25	N/A	N/A	806.1000	2	0.3521	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
21824	28.43	N/A	N/A	537.8000	3	0.5448	TQDECILHFLR	ICAT-C:13C(9) (C)	YES	NO
25245	38.23	N/A	N/A	861.8203	2	-0.2146	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25246	34.94	N/A	N/A	861.8246	2	-0.2061	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25248	66.68	N/A	N/A	861.8377	2	-0.1798	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25249	57.42	N/A	N/A	861.8436	2	-0.1680	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25250	41.77	N/A	N/A	861.8443	2	-0.1667	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25252	38	N/A	N/A	861.8491	2	-0.1570	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25253	27.56	N/A	N/A	861.8529	2	-0.1494	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25254	43.95	N/A	N/A	861.8740	2	-0.1072	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25255	29.93	N/A	N/A	861.8763	2	-0.1026	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25256	43.94	N/A	N/A	861.8807	2	-0.0937	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25257	59.09	N/A	N/A	861.8836	2	-0.0879	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25260	34.19	N/A	N/A	861.9059	2	-0.0434	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25263	41.52	N/A	N/A	861.9273	2	-0.0006	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25270	56.58	N/A	N/A	862.0000	2	0.1448	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25272	40.56	N/A	N/A	862.0297	2	0.2042	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25273	30.8	N/A	N/A	862.0353	2	0.2155	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25275	66.92	N/A	N/A	862.0851	2	0.3149	LNPQEYLTSTACR	ICAT-C (C)	YES	NO
25458	66.72	N/A	N/A	866.3489	2	-0.1875	LNPQEYLTSTACR	ICAT-C:13C(9) (C)	YES	NO
25459	50.52	N/A	N/A	866.3549	2	-0.1755	LNPQEYLTSTACR	ICAT-C:13C(9) (C)	YES	NO
25463	46.09	N/A	N/A	866.3824	2	-0.1205	LNPQEYLTSTACR	ICAT-C:13C(9) (C)	YES	NO
25470	43.11	N/A	N/A	866.4401	2	-0.0051	LNPQEYLTSTACR	ICAT-C:13C(9) (C)	YES	NO
56034	27.27	2.50	2.06	990.2191	3	0.1044	SLVQNNCLSRPNIFLCPEIEPK	2 ICAT-C (C)	YES	YES

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q969G3	71	2.45	2.03	0.12	46621	2.9	4	4	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
21109	27.71	2.41	1.99	530.9492	3	0.0100	LCGLKVEVDMEK	ICAT-C (C)	YES	YES
21111	27.91	2.55	2.11	530.9517	3	0.0176	LCGLKVEVDMEK	ICAT-C (C)	YES	YES
21112	35.25	2.27	1.88	530.9519	3	0.0183	LCGLKVEVDMEK	ICAT-C (C)	YES	YES
21114	32.95	2.51	2.08	530.9530	3	0.0216	LCGLKVEVDMEK	ICAT-C (C)	YES	YES

AT-rich interactive domain-containing protein 1A - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O14497	34	2.72	2.25	0.25	241892	0.6	3	3	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
27361	28.73	3.03	2.50	597.9484	3	-0.0386	NDPFVVDCSDKLGR	ICAT-C (C)	YES	YES
27362	29.61	2.56	2.11	597.9643	3	0.0089	NDPFVVDCSDKLGR	ICAT-C (C)	YES	YES
27366	33.96	2.94	2.43	597.9685	3	0.0214	NDPFVVDCSDKLGR	ICAT-C (C)	YES	YES

AT-rich interactive domain-containing protein 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q68CP9	1226	2.36	1.95	0.51	197268	9.6	51	42	9

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
9795	49.34	N/A	N/A	660.7578	2	-0.1567	GMEILGNLCK	ICAT-C (C); Oxidation (M)	YES	YES
23784	27.56	2.56	2.11	836.3362	2	-0.1759	CLYELNFTVQSK	ICAT-C (C)	YES	YES
23792	25.28	N/A	N/A	836.3738	2	-0.1008	CLYELNFTVQSK	ICAT-C (C)	YES	YES
23798	30.12	N/A	N/A	836.4147	2	-0.0190	CLYELNFTVQSK	ICAT-C (C)	YES	YES
26098	51.21	2.24	1.85	877.7905	2	-0.1873	AEMYSEYLSTCSK	ICAT-C (C); Oxidation (M)	YES	YES
26101	46.87	N/A	N/A	877.8504	2	-0.0676	AEMYSEYLSTCSK	ICAT-C (C); Oxidation (M)	YES	YES
26380	55.09	1.83	1.51	882.3114	2	-0.1759	AEMYSEYLSTCSK	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
43769	53.73	1.53	1.26	1158.4103	2	-0.2314	AEDNGVLICEYVDQDSYR	ICAT-C (C)	YES	YES
43771	56.78	N/A	N/A	1158.4136	2	-0.2250	AEDNGVLICEYVDQDSYR	ICAT-C (C)	YES	YES
43776	62.58	2.52	2.08	1158.4724	2	-0.1074	AEDNGVLICEYVDQDSYR	ICAT-C (C)	YES	YES
43778	74.89	3.32	2.74	1158.4974	2	-0.0573	AEDNGVLICEYVDQDSYR	ICAT-C (C)	YES	YES
43779	62.75	1.79	1.48	1158.5007	2	-0.0508	AEDNGVLICEYVDQDSYR	ICAT-C (C)	YES	YES
43780	34.67	0.76	0.63	1158.5033	2	-0.0455	AEDNGVLICEYVDQDSYR	ICAT-C (C)	YES	YES
43966	39.6	1.62	1.33	1162.9308	2	-0.2208	AEDNGVLICEYVDQDSYR	ICAT-C:13C(9) (C)	YES	YES
43967	51.14	2.46	2.03	1162.9614	2	-0.1595	AEDNGVLICEYVDQDSYR	ICAT-C:13C(9) (C)	YES	YES
43970	42.18	3.12	2.58	1162.9961	2	-0.0901	AEDNGVLICEYVDQDSYR	ICAT-C:13C(9) (C)	YES	YES
43971	58.29	1.79	1.48	1163.0171	2	-0.0480	AEDNGVLICEYVDQDSYR	ICAT-C:13C(9) (C)	YES	YES
44488	41.94	2.22	1.83	590.1405	4	0.3484	KPLVNGICDFDKGDGSHLSK	ICAT-C (C)	YES	YES
44731	49.64	2.55	2.11	592.3061	4	-0.0193	KPLVNGICDFDKGDGSHLSK	ICAT-C:13C(9) (C)	YES	YES
44741	31.56	2.42	2.00	592.3959	4	0.3398	KPLVNGICDFDKGDGSHLSK	ICAT-C:13C(9) (C)	YES	YES
48497	26.42	2.10	1.73	849.7748	3	0.0115	IICQKEEEAKEATGLHVHER	ICAT-C (C)	YES	YES
49472	27.64	2.96	2.44	652.8243	4	-0.0396	HCSKDALLAGLKQDEPGQAGSQK	ICAT-C (C)	YES	YES
49620	25.16	2.95	2.44	655.0965	4	0.0193	HCSKDALLAGLKQDEPGQAGSQK	ICAT-C:13C(9) (C)	YES	YES
53482	36.81	2.32	1.92	707.9000	4	0.1422	SDLRKPLVNGICDFDKGDGSHLSK	ICAT-C (C)	YES	YES
53483	45.95	2.30	1.90	707.9000	4	0.1422	SDLRKPLVNGICDFDKGDGSHLSK	ICAT-C (C)	YES	YES
53641	33.15	2.30	1.90	710.1087	4	-0.0533	SDLRKPLVNGICDFDKGDGSHLSK	ICAT-C:13C(9) (C)	YES	YES
53644	36.5	2.46	2.03	710.1152	4	-0.0272	SDLRKPLVNGICDFDKGDGSHLSK	ICAT-C:13C(9) (C)	YES	YES
55919	65.78	2.30	1.90	987.3599	3	-0.3614	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES

55920	92.46	2.72	2.25	987.3714	3	-0.3268	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES
55922	53.7	2.50	2.06	987.3822	3	-0.2943	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES
55926	48.3	2.65	2.19	987.4376	3	-0.1281	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES
55927	40.59	2.49	2.06	987.4411	3	-0.1179	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES
55928	53.16	N/A	N/A	987.4525	3	-0.0835	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES
55934	39.6	2.43	2.01	987.5368	3	0.1693	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C (C)	YES	YES
56042	85.57	2.31	1.91	990.3692	3	-0.3637	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C:13C(9) (C)	YES	YES
56043	54.2	2.69	2.23	990.3820	3	-0.3253	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C:13C(9) (C)	YES	YES
56044	79.49	2.38	1.96	990.3921	3	-0.2948	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C:13C(9) (C)	YES	YES
56046	89.18	2.69	2.22	990.4356	3	-0.1644	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C:13C(9) (C)	YES	YES
56047	37.02	2.51	2.08	990.4543	3	-0.1085	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C:13C(9) (C)	YES	YES
56053	40.09	2.36	1.95	990.5514	3	0.1829	IQSETNQCSLISNGPSLELGENGASGK	ICAT-C:13C(9) (C)	YES	YES
57203	35.67	N/A	N/A	1028.7356	3	-0.3418	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C)	YES	YES
57209	33.62	3.42	2.83	1028.8076	3	-0.1256	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C)	YES	YES
57318	31.66	N/A	N/A	1031.7432	3	-0.3491	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C:13C(9) (C)	YES	YES
57409	42.45	2.49	2.06	1034.0630	3	-0.3544	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57411	26.42	N/A	N/A	1034.0703	3	-0.3325	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57415	38.7	2.89	2.39	1034.1309	3	-0.1508	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57416	28.84	2.89	2.39	1034.2116	3	0.0912	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57417	33.77	3.22	2.66	1034.2136	3	0.0973	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57418	48.68	3.20	2.64	1034.2236	3	0.1273	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57420	27.39	2.39	1.97	1034.3000	3	0.3565	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C (C); Oxidation (M)	YES	YES
57501	31.4	2.69	2.22	1037.1419	3	-0.1481	IVTISDPNNAGCSATMVAVPAGADPSTVAK	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES

Histone modifiying proteins

Histone-lysine N-methyltransferase, H3 lysine-9 specific 5 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9H9B1	1231	3.15	2.60	1.02	138166	16.2	66	58	11

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
17877	33.96	N/A	N/A	746.8044	2	-0.1924	APLLVLCEDHR	ICAT-C (C)	YES	YES
17887	36.47	N/A	N/A	746.8712	2	-0.0590	APLLVLCEDHR	ICAT-C (C)	YES	YES
17893	37.68	4.79	3.96	746.8883	2	-0.0248	APLLVLCEDHR	ICAT-C (C)	YES	YES
17902	60.52	3.39	2.80	746.9029	2	0.0044	APLLVLCEDHR	ICAT-C (C)	YES	YES
17904	33.21	2.96	2.44	498.2731	3	0.0106	APLLVLCEDHR	ICAT-C (C)	YES	YES
19614	44.84	3.04	2.51	771.8898	2	0.0143	DAEGSTCLHLAAK	ICAT-C (C)	YES	YES
19617	48.11	1.43	1.18	771.8934	2	0.0216	DAEGSTCLHLAAK	ICAT-C (C)	YES	YES
28894	28.93	2.40	1.99	614.3043	3	-0.0392	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES
28897	34.15	3.28	2.71	614.3118	3	-0.0164	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES
28900	26.52	3.28	2.71	614.3151	3	-0.0067	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES
28906	29.51	3.02	2.49	614.3241	3	0.0203	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES
28909	30.02	N/A	N/A	614.3258	3	0.0253	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES
28912	27.75	3.37	2.78	614.3291	3	0.0352	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES

28915	28.98	3.69	3.05	614.3339	3	0.0498	ENRYDCVVLFLSR	ICAT-C (C)	YES	YES
29275	30.11	3.12	2.58	617.3158	3	-0.0347	ENRYDCVVLFLSR	ICAT-C:13C(9) (C)	YES	YES
29285	35.67	3.12	2.57	617.3341	3	0.0202	ENRYDCVVLFLSR	ICAT-C:13C(9) (C)	YES	YES
29529	78.71	3.40	2.81	930.8881	2	-0.2311	SQTACLPFVLAAAVSR	ICAT-C (C)	YES	YES
29530	52.02	4.79	3.95	930.8913	2	-0.2247	SQTACLPFVLAAAVSR	ICAT-C (C)	YES	YES
29533	81.67	3.88	3.20	930.9067	2	-0.1938	SQTACLPFVLAAAVSR	ICAT-C (C)	YES	YES
29538	67.93	4.62	3.81	930.9516	2	-0.1042	SQTACLPFVLAAAVSR	ICAT-C (C)	YES	YES
29540	25.38	8.06	6.66	930.9642	2	-0.0789	SQTACLPFVLAAAVSR	ICAT-C (C)	YES	YES
29547	25.29	3.87	3.20	931.0059	2	0.0046	SQTACLPFVLAAAVSR	ICAT-C (C)	YES	YES
29736	30.44	4.72	3.90	935.3944	2	-0.2487	SQTACLPFVLAAAVSR	ICAT-C:13C(9) (C)	YES	YES
29737	58.35	3.49	2.88	935.4128	2	-0.2118	SQTACLPFVLAAAVSR	ICAT-C:13C(9) (C)	YES	YES
29740	28.12	7.89	6.52	935.4657	2	-0.1060	SQTACLPFVLAAAVSR	ICAT-C:13C(9) (C)	YES	YES
30789	35.76	3.19	2.63	634.6746	3	0.0291	FINHHCEPNLVPVR	ICAT-C (C)	YES	YES
30798	28.57	3.16	2.61	634.8000	3	0.4052	FINHHCEPNLVPVR	ICAT-C (C)	YES	YES
31138	42.42	3.02	2.49	637.5915	3	-0.2507	FINHHCEPNLVPVR	ICAT-C:13C(9) (C)	YES	YES
32620	36.6	3.44	2.84	977.3418	2	-0.2394	YVSQNCVTSPMNIDR	ICAT-C (C)	YES	YES
32626	37.02	3.35	2.77	977.3956	2	-0.1317	YVSQNCVTSPMNIDR	ICAT-C (C)	YES	YES
32630	37.28	3.65	3.02	977.4134	2	-0.0961	YVSQNCVTSPMNIDR	ICAT-C (C)	YES	YES
32631	42.98	3.68	3.04	977.4137	2	-0.0956	YVSQNCVTSPMNIDR	ICAT-C (C)	YES	YES
33291	37.11	3.36	2.77	985.4289	2	-0.0600	YVSQNCVTSPMNIDR	ICAT-C (C); Oxidation (M)	YES	YES
40444	54.52	3.45	2.85	727.0006	3	0.0329	VNNASYCPHCGEESSK	2 ICAT-C (C)	YES	YES
40940	26.59	2.84	2.34	733.0179	3	0.0245	VNNASYCPHCGEESSK	2 ICAT-C:13C(9) (C)	YES	YES
42761	44.33	3.14	2.59	567.2885	4	-0.0188	CDLHAVNIHGDSPLHIAAR	ICAT-C (C)	YES	YES
42762	43.11	N/A	N/A	756.0501	3	-0.0152	CDLHAVNIHGDSPLHIAAR	ICAT-C (C)	YES	YES
42766	45.21	3.66	3.03	567.2938	4	0.0023	CDLHAVNIHGDSPLHIAAR	ICAT-C (C)	YES	YES
42767	33.8	3.70	3.06	567.2963	4	0.0124	CDLHAVNIHGDSPLHIAAR	ICAT-C (C)	YES	YES
42991	51.72	3.18	2.63	569.5485	4	-0.0088	CDLHAVNIHGDSPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
42992	33.45	3.52	2.91	569.5512	4	0.0019	CDLHAVNIHGDSPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
42996	37.11	4.07	3.36	569.5643	4	0.0541	CDLHAVNIHGDSPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
42999	44.72	3.53	2.91	569.6000	4	0.1971	CDLHAVNIHGDSPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
43000	37.31	3.26	2.69	569.6325	4	0.3269	CDLHAVNIHGDSPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
43374	28.22	3.54	2.92	574.3045	4	0.0154	AGALVDPKDAEGSTCLHLAAK	ICAT-C (C)	YES	YES
50391	64.95	2.79	2.31	886.9915	3	-0.2852	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50396	52.06	2.87	2.37	887.0026	3	-0.2519	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50397	31.34	3.16	2.61	887.0029	3	-0.2509	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50399	30.46	3.66	3.02	887.0299	3	-0.1697	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50401	34.05	2.78	2.30	887.0860	3	-0.0017	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50402	56.05	2.99	2.47	887.1000	3	0.0404	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50406	68.37	3.16	2.61	887.1211	3	0.1036	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50408	37.45	N/A	N/A	887.1252	3	0.1161	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50413	37.73	3.86	3.19	887.2096	3	0.3693	EITTLANNQCMATESVDHELGR	ICAT-C (C)	YES	YES
50517	35.37	2.88	2.38	890.0078	3	-0.2664	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C)	YES	YES
50522	33.92	2.53	2.09	890.0921	3	-0.0134	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C)	YES	YES
50532	53.81	2.91	2.40	890.1133	3	0.0500	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C)	YES	YES
50541	48.38	3.17	2.62	890.1283	3	0.0952	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C)	YES	YES

50545	44.04	3.45	2.85	890.2173	3	0.3622	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C)	YES	YES
50546	27.31	3.74	3.09	890.2242	3	0.3827	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C)	YES	YES
50679	65.67	N/A	N/A	892.3282	3	-0.2697	EITTLANNQCMATESVDHELGR	ICAT-C (C); Oxidation (M)	YES	YES
50683	30.97	4.21	3.48	892.3336	3	-0.2538	EITTLANNQCMATESVDHELGR	ICAT-C (C); Oxidation (M)	YES	YES
50698	39.63	N/A	N/A	892.5664	3	0.4448	EITTLANNQCMATESVDHELGR	ICAT-C (C); Oxidation (M)	YES	YES
50867	32.37	3.42	2.82	895.4637	3	0.1063	EITTLANNQCMATESVDHELGR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
56391	32.37	3.02	2.49	1001.1552	3	-0.0293	NKEGETPLQCASLNSQVWSALQMSK	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
60854	28.92	N/A	N/A	1284.9352	3	-0.1560	VKGILSSQAEGLANGPDVLETDGLQEVPLCSCR	2 ICAT-C (C)	YES	YES

Histone-lysine N-methyltransferase, H3 lysine-9 specific 3 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q96KQ7	870	2.97	2.45	0.56	132287	16.1	49	37	7	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
18136	43.91	N/A	N/A	749.8865	2	-0.0212	VALMVLCETHR	ICAT-C (C)	YES	YES
18137	71.97	3.39	2.80	749.8898	2	-0.0146	VALMVLCETHR	ICAT-C (C)	YES	YES
18138	65	4.01	3.31	749.8956	2	-0.0030	VALMVLCETHR	ICAT-C (C)	YES	YES
18144	53.14	N/A	N/A	749.9079	2	0.0216	VALMVLCETHR	ICAT-C (C)	YES	YES
18146	66.43	2.71	2.24	749.9225	2	0.0509	VALMVLCETHR	ICAT-C (C)	YES	YES
18438	34.06	3.37	2.79	754.4006	2	-0.0232	VALMVLCETHR	ICAT-C:13C(9) (C)	YES	YES
18439	55.98	N/A	N/A	754.4070	2	-0.0103	VALMVLCETHR	ICAT-C:13C(9) (C)	YES	YES
18441	27.48	3.45	2.85	754.4197	2	0.0152	VALMVLCETHR	ICAT-C:13C(9) (C)	YES	YES
26624	48.74	2.76	2.28	590.6400	3	0.0091	CKHSAEAIALEQSR	ICAT-C (C)	YES	YES
27887	27	3.81	3.15	603.6305	3	-0.0229	ESYHDCVLLFLSR	ICAT-C (C)	YES	YES
27889	36.73	5.14	4.24	603.6353	3	-0.0087	ESYHDCVLLFLSR	ICAT-C (C)	YES	YES
27891	36.18	3.80	3.14	603.6361	3	-0.0062	ESYHDCVLLFLSR	ICAT-C (C)	YES	YES
27896	28.08	N/A	N/A	603.6425	3	0.0130	ESYHDCVLLFLSR	ICAT-C (C)	YES	YES
27897	31.77	3.56	2.94	603.6426	3	0.0134	ESYHDCVLLFLSR	ICAT-C (C)	YES	YES
27898	30.2	N/A	N/A	603.6430	3	-0.0178	TPLMEAVVNNHLEVAR	Oxidation (M)	NO	YES
29963	40.86	3.36	2.78	626.6589	3	-0.0432	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
29965	27.75	2.98	2.46	626.6614	3	-0.0359	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
29968	30.04	3.07	2.54	626.6711	3	-0.0065	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
29973	33.7	3.05	2.52	626.6781	3	0.0144	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
29975	30.09	2.78	2.30	626.6818	3	0.0254	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
29980	46.92	3.07	2.53	939.7064	2	0.4001	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
29982	45.63	3.01	2.49	626.9000	3	0.6800	FINHLCDPNIIPVR	ICAT-C (C)	YES	YES
30266	31.63	3.21	2.65	629.6679	3	-0.0465	FINHLCDPNIIPVR	ICAT-C:13C(9) (C)	YES	YES
30276	31.18	3.00	2.48	629.6841	3	0.0020	FINHLCDPNIIPVR	ICAT-C:13C(9) (C)	YES	YES
30277	32.6	2.83	2.34	629.6843	3	0.0029	FINHLCDPNIIPVR	ICAT-C:13C(9) (C)	YES	YES
30280	31.69	2.79	2.30	629.6959	3	0.0377	FINHLCDPNIIPVR	ICAT-C:13C(9) (C)	YES	YES
44055	41.06	3.14	2.59	583.2837	4	-0.0328	CDLHAVNYHGDTPLHIAAR	ICAT-C (C)	YES	YES
44068	41.15	3.39	2.80	583.3746	4	0.3307	CDLHAVNYHGDTPLHIAAR	ICAT-C (C)	YES	YES
44230	46.66	3.12	2.58	585.5450	4	-0.0177	CDLHAVNYHGDTPLHIAAR	ICAT-C:13C(9) (C)	YES	YES

44233	28.32	3.41	2.82	585.5552	4	0.0229	CDLHAVNYHGDTPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
44234	25.38	3.09	2.56	585.5566	4	0.0284	CDLHAVNYHGDTPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
44238	34.05	3.21	2.65	585.6354	4	0.3438	CDLHAVNYHGDTPLHIAAR	ICAT-C:13C(9) (C)	YES	YES
44967	42.61	2.69	2.23	793.3340	3	-0.2623	GSVEICHVLLQAGANINAVDK	ICAT-C (C)	YES	YES
45150	30.74	2.70	2.23	796.3381	3	-0.2800	GSVEICHVLLQAGANINAVDK	ICAT-C:13C(9) (C)	YES	YES
47725	28.54	N/A	N/A	626.9000	4	0.2915	YYGNISRFINHLCDPNIIPVR		NO	YES
49692	26.09	N/A	N/A	874.6745	3	-0.2594	CMATESVDGELSGCNAAILKR	2 ICAT-C (C)	YES	YES
49693	44.27	N/A	N/A	874.6754	3	-0.2567	CMATESVDGELSGCNAAILKR	2 ICAT-C (C)	YES	YES
49696	63.78	2.55	2.11	874.6821	3	-0.2366	CMATESVDGELSGCNAAILKR	2 ICAT-C (C)	YES	YES
49713	31.04	2.91	2.40	874.7936	3	0.0979	CMATESVDGELSGCNAAILKR	2 ICAT-C (C)	YES	YES
49718	40.89	2.83	2.33	874.8817	3	0.3620	CMATESVDGELSGCNAAILKR	2 ICAT-C (C)	YES	YES
49719	27.25	N/A	N/A	874.8823	3	0.3639	CMATESVDGELSGCNAAILKR	2 ICAT-C (C)	YES	YES
49964	49.06	2.49	2.06	879.9989	3	-0.2811	CMATESVDGELSGCNAAILKR	2 ICAT-C (C); Oxidation (M)	YES	YES
49966	31.69	4.35	3.59	880.0196	3	-0.2191	CMATESVDGELSGCNAAILKR	2 ICAT-C (C); Oxidation (M)	YES	YES
49982	37.47	3.08	2.55	880.2157	3	0.3692	CMATESVDGELSGCNAAILKR	2 ICAT-C (C); Oxidation (M)	YES	YES
50002	45.45	2.07	1.71	880.7647	3	-0.0491	CMATESVDGELSGCNAAILKR	2 ICAT-C:13C(9) (C)	YES	YES
50308	37.87	2.37	1.96	886.0971	3	-0.0468	CMATESVDGELSGCNAAILKR	2 ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
53430	32.55	N/A	N/A	941.4537	3	0.1004	EDDSYLFDLDNKDGEVYCIDAR	ICAT-C (C)	YES	YES
61273	38.19	N/A	N/A	1014.6774	4	0.6191	RPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGR	2 ICAT-C (C)	YES	YES
61300	37.83	N/A	N/A	1019.0000	4	-0.1511	RPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGR	2 ICAT-C:13C(9) (C)	YES	YES

Histone deacetylase complex subunit SAP130 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9H0E3	52	2.34	1.93	0.25	110255	2.0	3	3	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
51034	36.37	2.69	2.22	898.1171	3	-0.0509	VHLCAAQLLQLTNLEHDVYER	ICAT-C (C)	YES	YES
51037	32.8	2.30	1.90	673.9000	4	0.1907	VHLCAAQLLQLTNLEHDVYER	ICAT-C (C)	YES	YES
51271	29.22	2.23	1.84	676.1172	4	0.0293	VHLCAAQLLQLTNLEHDVYER	ICAT-C:13C(9) (C)	YES	YES

Histone deacetylase 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q13547	175	2.01	1.66	0.22	55068	11.6	14	5	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
7634	36.58	1.98	1.63	618.2670	2	-0.1550	LGCFNLTIK	ICAT-C (C)	YES	YES
7635	29.81	2.09	1.73	618.2683	2	-0.1524	LGCFNLTIK	ICAT-C (C)	YES	YES
7896	28.07	2.00	1.66	622.7904	2	-0.1383	LGCFNLTIK	ICAT-C:13C(9) (C)	YES	YES
50831	46.76	N/A	N/A	895.0511	3	-0.1136	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C (C)	YES	NO
50844	48.2	N/A	N/A	895.2000	3	0.3330	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C (C)	YES	NO
51028	43.26	N/A	N/A	898.0594	3	-0.1189	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C:13C(9) (C)	YES	NO
51182	38.57	N/A	N/A	900.3234	3	-0.2917	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C (C); Oxidation (M)	YES	NO

51194	33.38	N/A	N/A	900.3746	3	-0.1381	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C (C); Oxidation (M)	YES	NO
51212	43.18	N/A	N/A	900.5000	3	0.2381	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C (C); Oxidation (M)	YES	NO
51388	29.43	N/A	N/A	903.3395	3	-0.2735	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
51648	33.29	N/A	N/A	908.6613	3	-0.3031	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C:13C(9) (C); 2 Oxidation (M)	YES	NO
51649	36.58	N/A	N/A	908.6666	3	-0.2873	VMEMFQPSAVVLQCGSDSLSGDR	ICAT-C:13C(9) (C); 2 Oxidation (M)	YES	NO
57604	30.74	N/A	N/A	782.0910	4	-0.0248	VCYYYDGDVGNYYYGQGHPMKPHR	ICAT-C (C); Oxidation (M)	YES	YES
57605	35.37	N/A	N/A	782.1185	4	0.0852	VCYYYDGDVGNYYYGQGHPMKPHR	ICAT-C (C); Oxidation (M)	YES	YES

Histone deacetylase 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q92769	164	2.01	1.66	0.19	55329	11.5	16	8	3	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
7223	30.49	1.74	1.44	611.2633	2	-0.1466	LGCFNLTVK	ICAT-C (C)	YES	YES
7227	32.33	2.26	1.86	611.2705	2	-0.1322	LGCFNLTVK	ICAT-C (C)	YES	YES
7236	34.14	N/A	N/A	611.2998	2	-0.0737	LGCFNLTVK	ICAT-C (C)	YES	YES
7241	28.93	N/A	N/A	611.3275	2	-0.0184	LGCFNLTVK	ICAT-C (C)	YES	YES
50822	31.92	N/A	N/A	894.9871	3	-0.3056	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C)	YES	YES
50829	49.48	1.94	1.60	895.0454	3	-0.1309	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C)	YES	YES
51180	28.81	2.12	1.75	900.3209	3	-0.2993	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C); Oxidation (M)	YES	YES
51182	27.59	N/A	N/A	900.3234	3	-0.2916	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C); Oxidation (M)	YES	NO
51389	25.18	N/A	N/A	903.3837	3	-0.1409	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
51493	29.18	N/A	N/A	905.6507	3	-0.3048	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C); 2 Oxidation (M)	YES	YES
51498	33.87	N/A	N/A	905.6917	3	-0.1816	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C); 2 Oxidation (M)	YES	YES
51499	50.75	2.32	1.92	905.7268	3	-0.0764	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C (C); 2 Oxidation (M)	YES	YES
51651	31.36	N/A	N/A	908.7013	3	-0.1832	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C:13C(9) (C); 2 Oxidation (M)	YES	YES
51653	46.46	2.20	1.81	908.7087	3	-0.1608	VMEMYQPSAVVLQCGADSLSGDR	ICAT-C:13C(9) (C); 2 Oxidation (M)	YES	YES
57718	30.52	2.03	1.68	785.5979	4	-0.0127	VCYYYDGDIGNYYYGQGHPMKPHR	ICAT-C (C); Oxidation (M)	YES	YES
57773	30.63	1.96	1.62	787.8524	4	-0.0250	VCYYYDGDIGNYYYGQGHPMKPHR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES

DNA damage response proteins

DNA-(apurinic or apyrimidinic site) lyase - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P27695	766	9.80	8.10	3.21	35532	21.7	33	25	6	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
12460	55.87	11.28	9.32	695.2865	2	-0.1286	ICSWNVDGLR	ICAT-C (C)	YES	YES
12493	28.99	13.38	11.05	695.3631	2	0.0245	ICSWNVDGLR	ICAT-C (C)	YES	YES
13123	29.4	14.64	12.09	699.8811	2	0.0304	ICSWNVDGLR	ICAT-C:13C(9) (C)	YES	YES
25076	31.35	N/A	N/A	858.3176	2	-0.2240	EEAPDILCLQETK	ICAT-C (C)	YES	YES
25083	51.62	12.14	10.02	858.3791	2	-0.1012	EEAPDILCLQETK	ICAT-C (C)	YES	YES

25084	41.21	14.40	11.90	858.3851	2	-0.0890	EEAPDILCLQETK	ICAT-C (C)	YES	YES
25085	49.88	N/A	N/A	858.3890	2	-0.0813	EEAPDILCLQETK	ICAT-C (C)	YES	YES
42640	34.33	10.07	8.32	754.8000	3	0.2016	LDYFLLSHSLLPALCDSK	ICAT-C (C)	YES	YES
42644	30.17	10.65	8.80	754.9000	3	0.5016	LDYFLLSHSLLPALCDSK	ICAT-C (C)	YES	YES
42647	47.7	8.99	7.42	1131.9000	2	0.6089	LDYFLLSHSLLPALCDSK	ICAT-C (C)	YES	YES
44582	36.26	N/A	N/A	590.9866	4	-0.3347	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44593	88.3	8.84	7.30	787.7553	3	-0.0081	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44594	35.51	N/A	N/A	787.7568	3	-0.0036	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44596	34.67	N/A	N/A	787.7583	3	0.0010	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44597	43.42	N/A	N/A	787.7591	3	0.0033	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44598	34.25	N/A	N/A	591.0773	4	0.0278	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44601	30.42	9.41	7.78	591.0795	4	0.0367	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44604	40.47	8.57	7.08	591.1000	4	0.1187	KPLVLCGDLNVAHEEIDLR	ICAT-C (C)	YES	YES
44796	44.87	9.04	7.46	790.7657	3	-0.0073	KPLVLCGDLNVAHEEIDLR	ICAT-C:13C(9) (C)	YES	YES
44797	44.78	8.60	7.11	593.3275	4	-0.0016	KPLVLCGDLNVAHEEIDLR	ICAT-C:13C(9) (C)	YES	YES
45689	29.49	18.74	15.48	805.3345	3	-0.2383	GLDWVKEEAPDILCLQETK	ICAT-C (C)	YES	YES
45701	41.44	8.46	6.99	805.6000	3	0.5583	GLDWVKEEAPDILCLQETK	ICAT-C (C)	YES	YES
51225	38.63	13.73	11.34	675.7762	4	-0.3670	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51244	35.88	N/A	N/A	675.8533	4	-0.0587	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51246	28.87	11.25	9.30	675.8595	4	-0.0340	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51247	72.3	10.31	8.51	900.8119	3	-0.0291	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51250	45.73	10.27	8.49	675.8823	4	0.0571	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51253	70.29	9.90	8.18	675.9000	4	0.1281	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51263	47.31	21.71	17.93	676.0000	4	0.5281	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51265	40.79	10.13	8.37	901.0000	3	0.5353	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C (C)	YES	YES
51410	35.24	11.09	9.16	678.1202	4	-0.0215	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C:13C(9) (C)	YES	YES
51411	50.38	10.47	8.65	678.1221	4	-0.0136	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C:13C(9) (C)	YES	YES
51415	50.67	10.26	8.47	678.1349	4	0.0376	KPLVLCGDLNVAHEEIDLRNPK	ICAT-C:13C(9) (C)	YES	YES

Telomeric repeat-binding factor 2-interacting protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9NYB0	66	6.94	5.73	2.57	44233	3.5	3	3	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
23181	35.74	7.23	5.97	551.9749	3	-0.0003	LSTLILHGGGTVCR	ICAT-C (C)	YES	YES
23184	49.11	8.08	6.67	551.9813	3	0.0187	LSTLILHGGGTVCR	ICAT-C (C)	YES	YES
23186	37.18	3.26	2.70	551.9827	3	0.0231	LSTLILHGGGTVCR	ICAT-C (C)	YES	YES

High mobility group protein B3 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O15347	85	6.68	5.51	0.32	22965	14.0	8	2	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
23619	35.13	N/A	N/A	833.8023	2	-0.1743	MSAYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
23621	25.51	N/A	N/A	833.8088	2	-0.1613	MSAYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
23623	34.23	N/A	N/A	833.8218	2	-0.1352	MSAYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
23637	27.41	N/A	N/A	833.9079	2	0.0369	MSAYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
23639	25.4	N/A	N/A	833.9141	2	0.0493	MSAYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
23655	39.16	N/A	N/A	833.9957	2	0.2125	MSAYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
39438	28.62	6.43	5.31	714.7040	3	0.0023	RPPSGFFLFCSEFRPK	ICAT-C (C)	YES	YES
39656	29.3	6.88	5.69	717.7006	3	-0.0382	RPPSGFFLFCSEFRPK	ICAT-C:13C(9) (C)	YES	YES

DNA topoisomerase 2-binding protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q92547	40	3.35	2.77	N/A	170571	1.4	1	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
48917	39.79	3.35	2.77	858.7750	3	0.0124	LKPDDSGVNIAEAAAQNVYCLR	ICAT-C (C)	YES	YES

Mediator of DNA damage checkpoint protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q14676	278	2.32	1.92	1.35	226529	3.9	18	16	3

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
28172	34.24	N/A	N/A	909.8387	2	-0.2427	MPDCSVALPFPSISK	ICAT-C (C)	YES	YES
28175	42.74	4.67	3.86	909.8534	2	-0.2133	MPDCSVALPFPSISK	ICAT-C (C)	YES	YES
28178	26.34	4.56	3.77	909.9153	2	-0.0895	MPDCSVALPFPSISK	ICAT-C (C)	YES	YES
28181	44.58	5.88	4.86	909.9363	2	-0.0476	MPDCSVALPFPSISK	ICAT-C (C)	YES	YES
28750	33.38	N/A	N/A	612.3452	3	0.0321	DCGSLNGTQILRPPK	ICAT-C:13C(9) (C)	YES	YES
44992	31.74	3.32	2.74	793.6778	3	-0.2123	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
44993	25.16	2.04	1.68	793.6825	3	-0.1982	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
44994	36.77	1.98	1.63	793.6841	3	-0.1935	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
44997	28.69	2.08	1.71	793.7362	3	-0.0371	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
45000	28.03	2.25	1.86	793.7555	3	0.0207	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
45001	36.01	2.25	1.86	793.7756	3	0.0810	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
45002	29.07	2.32	1.92	793.7845	3	0.1077	VVITCPQDFPHCSIPLR	2 ICAT-C (C)	YES	YES
45380	29.1	2.11	1.75	799.6981	3	-0.2119	VVITCPQDFPHCSIPLR	2 ICAT-C:13C(9) (C)	YES	YES
45382	28.94	1.93	1.59	799.7071	3	-0.1849	VVITCPQDFPHCSIPLR	2 ICAT-C:13C(9) (C)	YES	YES
45387	28.32	2.23	1.84	799.7513	3	-0.0522	VVITCPQDFPHCSIPLR	2 ICAT-C:13C(9) (C)	YES	YES
45395	34.45	2.26	1.87	799.7999	3	0.0937	VVITCPQDFPHCSIPLR	2 ICAT-C:13C(9) (C)	YES	YES
45397	41.27	2.41	1.99	799.8042	3	0.1064	VVITCPQDFPHCSIPLR	2 ICAT-C:13C(9) (C)	YES	YES
60585	38.3	5.46	4.51	949.7116	4	-0.0723	VSRGDQESPDACLPPTVPEAPAPPQKPLNSQSQK	ICAT-C (C)	YES	YES

High mobility group protein B2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P26583	497	12.11	10.01	N/A	24019	13.4	22	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
23619	35.48	N/A	N/A	833.8023	2	-0.1743	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23621	25.51	N/A	N/A	833.8088	2	-0.1613	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23623	32.97	N/A	N/A	833.8218	2	-0.1352	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23637	27.92	N/A	N/A	833.9079	2	0.0369	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23639	25.4	N/A	N/A	833.9141	2	0.0493	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23655	32.85	N/A	N/A	833.9957	2	0.2125	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
24074	69.23	N/A	N/A	841.7971	2	-0.1796	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24076	57.08	N/A	N/A	841.8104	2	-0.1529	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24077	80.37	N/A	N/A	841.8113	2	-0.1512	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24078	50.55	N/A	N/A	841.8201	2	-0.1337	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24079	31.71	N/A	N/A	841.8586	2	-0.0566	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24080	35.05	N/A	N/A	841.8611	2	-0.0516	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24082	32.22	N/A	N/A	841.8913	2	0.0088	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24100	39.78	N/A	N/A	841.9819	2	0.1900	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24101	77.81	N/A	N/A	841.9830	2	0.1922	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24103	80.64	N/A	N/A	842.1000	2	0.4262	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24104	46.66	N/A	N/A	842.1000	2	0.4262	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24337	38.82	N/A	N/A	846.3261	2	-0.1517	MSSYAFFVQTCR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
24338	30.46	N/A	N/A	846.3313	2	-0.1414	MSSYAFFVQTCR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
24359	32.32	N/A	N/A	846.4975	2	0.1910	MSSYAFFVQTCR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
39557	28.58	12.11	10.01	537.2821	4	0.0053	RPPSAFFLFCSEHRPK	ICAT-C (C)	YES	YES
39560	26.48	N/A	N/A	537.2929	4	0.0485	RPPSAFFLFCSEHRPK	ICAT-C (C)	YES	YES

High mobility group protein B1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P09429	603	6.50	5.37	0.48	24878	13.0	30	9	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
23619	35.48	N/A	N/A	833.8023	2	-0.1743	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23621	25.51	N/A	N/A	833.8088	2	-0.1613	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23623	32.97	N/A	N/A	833.8218	2	-0.1352	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23637	27.92	N/A	N/A	833.9079	2	0.0369	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
23639	25.4	N/A	N/A	833.9141	2	0.0493	MSSYAFFVQTCR	ICAT-C (C)	YES	NO

23655	32.85	N/A	N/A	833.9957	2	0.2125	MSSYAFFVQTCR	ICAT-C (C)	YES	NO
24074	69.23	N/A	N/A	841.7971	2	-0.1796	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24076	57.08	N/A	N/A	841.8104	2	-0.1529	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24077	80.37	N/A	N/A	841.8113	2	-0.1512	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24078	50.55	N/A	N/A	841.8201	2	-0.1337	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24079	31.71	N/A	N/A	841.8586	2	-0.0566	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24080	35.05	N/A	N/A	841.8611	2	-0.0516	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24082	32.22	N/A	N/A	841.8913	2	0.0088	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24100	39.78	N/A	N/A	841.9819	2	0.1900	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24101	77.81	N/A	N/A	841.9830	2	0.1922	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24103	80.64	N/A	N/A	842.1000	2	0.4262	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24104	46.66	N/A	N/A	842.1000	2	0.4262	MSSYAFFVQTCR	ICAT-C (C); Oxidation (M)	YES	NO
24337	38.82	N/A	N/A	846.3261	2	-0.1517	MSSYAFFVQTCR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
24338	30.46	N/A	N/A	846.3313	2	-0.1414	MSSYAFFVQTCR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
24359	32.32	N/A	N/A	846.4975	2	0.1910	MSSYAFFVQTCR	ICAT-C:13C(9) (C); Oxidation (M)	YES	NO
40237	38.11	7.18	5.93	724.6235	3	-0.2498	RPPSAFFLFCSEYRPK	ICAT-C (C)	YES	YES
40245	33.92	6.17	5.10	724.6981	3	-0.0260	RPPSAFFLFCSEYRPK	ICAT-C (C)	YES	YES
40258	28.15	7.19	5.94	724.7183	3	0.0345	RPPSAFFLFCSEYRPK	ICAT-C (C)	YES	YES
40262	30.69	N/A	N/A	724.7249	3	0.0543	RPPSAFFLFCSEYRPK	ICAT-C (C)	YES	YES
40271	40.38	6.26	5.17	724.9000	3	0.5796	RPPSAFFLFCSEYRPK	ICAT-C (C)	YES	YES
40273	36.95	6.88	5.68	724.9000	3	0.5796	RPPSAFFLFCSEYRPK	ICAT-C (C)	YES	YES
40481	34.16	7.15	5.91	727.6247	3	-0.2764	RPPSAFFLFCSEYRPK	ICAT-C:13C(9) (C)	YES	YES
40489	33.43	6.09	5.03	727.7011	3	-0.0474	RPPSAFFLFCSEYRPK	ICAT-C:13C(9) (C)	YES	YES
40500	30.12	6.18	5.11	727.7350	3	0.0543	RPPSAFFLFCSEYRPK	ICAT-C:13C(9) (C)	YES	YES
40502	30.21	6.86	5.67	727.7383	3	0.0644	RPPSAFFLFCSEYRPK	ICAT-C:13C(9) (C)	YES	YES

DNA polymerase epsilon subunit 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P56282	34	10.49	8.66	N/A	59499	3.2	2	1	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
40675	30.38	10.49	8.66	730.0246	3	-0.0110	TLADIICEYPDIHQSSR	ICAT-C (C)	YES	YES
40679	28.04	N/A	N/A	730.0464	3	0.0543	TLADIICEYPDIHQSSR	ICAT-C (C)	YES	YES

Proliferating cell nuclear antigen - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
P12004	202	3.77	3.12	1.43	28750	18.0	14	8	3	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**

14913	61.61	3.26	2.69	716.2879	2	-0.1574	CAGNEDIITLR	ICAT-C (C)	YES	YES
14916	29.19	N/A	N/A	716.2908	2	-0.1518	CAGNEDIITLR	ICAT-C (C)	YES	YES
14939	26.71	2.59	2.14	716.3561	2	-0.0210	CAGNEDIITLR	ICAT-C (C)	YES	YES
14942	36.16	4.29	3.54	716.3618	2	-0.0096	CAGNEDIITLR	ICAT-C (C)	YES	YES
26104	27.93	N/A	N/A	877.8591	2	-0.1995	DLSHIGDAVVISCAK	ICAT-C (C)	YES	YES
26129	27.17	6.67	5.51	585.6487	3	0.0209	DLSHIGDAVVISCAK	ICAT-C (C)	YES	YES
26130	40.17	N/A	N/A	585.6513	3	0.0288	DLSHIGDAVVISCAK	ICAT-C (C)	YES	YES
26131	43.36	4.93	4.07	585.6529	3	0.0335	DLSHIGDAVVISCAK	ICAT-C (C)	YES	YES
26132	37.09	N/A	N/A	585.6581	3	0.0493	DLSHIGDAVVISCAK	ICAT-C (C)	YES	YES
26133	40.29	2.87	2.37	878.1000	2	0.2822	DLSHIGDAVVISCAK	ICAT-C (C)	YES	YES
50159	30.12	N/A	N/A	884.3155	3	-0.3625	LMDLDVEQLGIPEQEYSCVVK	ICAT-C (C); Oxidation (M)	YES	YES
50167	28.63	5.26	4.35	884.3871	3	-0.1476	LMDLDVEQLGIPEQEYSCVVK	ICAT-C (C); Oxidation (M)	YES	YES
50169	36.01	5.53	4.57	884.3983	3	-0.1138	LMDLDVEQLGIPEQEYSCVVK	ICAT-C (C); Oxidation (M)	YES	YES
50178	30.94	N/A	N/A	884.6000	3	0.4912	LMDLDVEQLGIPEQEYSCVVK	ICAT-C (C); Oxidation (M)	YES	YES

Poly [ADP-ribose] polymerase 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9UGN5	45	2.09	1.73	0.11	66164	2.1	2	2	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
24291	29.97	2.02	1.67	845.8025	2	-0.1587	ALMEACNEFYTR	ICAT-C (C); Oxidation (M)	YES	YES
24310	36.17	2.18	1.80	845.8951	2	0.0267	ALMEACNEFYTR	ICAT-C (C); Oxidation (M)	YES	YES

Others

Coiled-coil domain-containing protein 95 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q8NBZ0	295	2.13	1.76	0.52	26462	7.8	15	14	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
37821	55.61	2.18	1.80	1047.9092	2	-0.2352	MAVGPPDCPVGGPLTFPGR	ICAT-C (C)	YES	YES
37822	30.51	2.79	2.30	1047.9110	2	-0.2316	MAVGPPDCPVGGPLTFPGR	ICAT-C (C)	YES	YES
37823	28.19	2.00	1.65	1047.9259	2	-0.2018	MAVGPPDCPVGGPLTFPGR	ICAT-C (C)	YES	YES
38227	68.13	2.04	1.69	701.9319	3	-0.2954	MAVGPPDCPVGGPLTFPGR	ICAT-C:13C(9) (C)	YES	YES
38229	38.24	2.15	1.78	1052.4251	2	-0.2337	MAVGPPDCPVGGPLTFPGR	ICAT-C:13C(9) (C)	YES	YES
38234	40	2.29	1.89	1052.4881	2	-0.1076	MAVGPPDCPVGGPLTFPGR	ICAT-C:13C(9) (C)	YES	YES
38235	53.99	2.05	1.70	1052.4944	2	-0.0951	MAVGPPDCPVGGPLTFPGR	ICAT-C:13C(9) (C)	YES	YES
38415	33.26	2.15	1.77	704.2522	3	-0.2992	MAVGPPDCPVGGPLTFPGR	ICAT-C (C); Oxidation (M)	YES	YES
38417	27.56	2.46	2.03	704.2595	3	-0.2773	MAVGPPDCPVGGPLTFPGR	ICAT-C (C); Oxidation (M)	YES	YES
38418	32.15	2.20	1.82	704.2609	3	-0.2732	MAVGPPDCPVGGPLTFPGR	ICAT-C (C); Oxidation (M)	YES	YES
38419	28.04	2.01	1.66	704.2623	3	-0.2689	MAVGPPDCPVGGPLTFPGR	ICAT-C (C); Oxidation (M)	YES	YES
38422	58.4	N/A	N/A	704.3042	3	-0.1432	MAVGPPDCPVGGPLTFPGR	ICAT-C (C); Oxidation (M)	YES	YES

38435	41.62	3.99	3.30	704.4082	3	0.1688	MAVGPPDCPVGGPLTFPGR	ICAT-C (C); Oxidation (M)	YES	YES
38695	29.04	2.69	2.22	707.3148	3	-0.1417	MAVGPPDCPVGGPLTFPGR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES
38696	35.52	2.31	1.91	707.3233	3	-0.1161	MAVGPPDCPVGGPLTFPGR	ICAT-C:13C(9) (C); Oxidation (M)	YES	YES

ZZ-type zinc finger-containing protein 3 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q8IYH5	94	2.38	1.96	0.20	101960	5.3	5	3	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
27031	31.09	2.40	1.98	891.3317	2	-0.1925	STVGLNGLDESFCGR	ICAT-C (C)	YES	YES
27033	31.15	2.12	1.75	891.3497	2	-0.1566	STVGLNGLDESFCGR	ICAT-C (C)	YES	YES
27042	40.84	2.51	2.07	891.4093	2	-0.0374	STVGLNGLDESFCGR	ICAT-C (C)	YES	YES
29462	45.3	N/A	N/A	929.4309	2	-0.0400	CDNCGIEPIQGVR	2 ICAT-C (C)	YES	YES
48604	28.48	N/A	N/A	639.4154	4	-0.6457	KEDSYIDHKVPCTDSQVQVK	ICAT-C:13C(9) (C)	YES	YES

Uncharacterized protein C14orf43 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q6PJG2	158	3.23	2.67	0.14	114918	2.4	7	6	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
11759	27	N/A	N/A	687.2997	2	-0.0962	CLFGGQEPAPK	ICAT-C (C)	YES	YES
25987	60.39	3.22	2.66	584.2992	3	0.0039	CGVEFSEPSLATKR	ICAT-C (C)	YES	YES
25989	56.25	3.27	2.70	584.3035	3	0.0166	CGVEFSEPSLATKR	ICAT-C (C)	YES	YES
25992	34.55	2.98	2.47	584.3076	3	0.0290	CGVEFSEPSLATKR	ICAT-C (C)	YES	YES
25993	46.96	3.01	2.49	584.3077	3	0.0294	CGVEFSEPSLATKR	ICAT-C (C)	YES	YES
26296	38.71	3.32	2.74	587.3079	3	-0.0002	CGVEFSEPSLATKR	ICAT-C:13C(9) (C)	YES	YES
26303	30.8	3.20	2.64	587.3165	3	0.0256	CGVEFSEPSLATKR	ICAT-C:13C(9) (C)	YES	YES

SAPS domain family member 3 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q5H9R7	40	1.97	1.63	N/A	97608	2.4	1	1	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
51316	39.91	1.97	1.63	901.7852	3	0.0657	YKYPNISCELLTSDVSQMNDR	ICAT-C (C)	YES	YES

Cytoskeleton-associated protein 5 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q14008	46	N/A	N/A	N/A	225366	0.5	2	0	0	

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
7395	46.57	N/A	N/A	615.3453	2	-0.0201	CLTGLAVGLR	ICAT-C (C)	YES	YES
7406	28.79	N/A	N/A	615.4253	2	0.1398	CLTGLAVGLR	ICAT-C (C)	YES	YES

Spliceosome RNA helicase BAT1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q13838	157	NaN	NaN	N/A	48960	7.0	12	0	0

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
7865	45.2	NaN	NaN	622.3638	2	-0.0206	DFLLKPELLR		NO	YES
7866	27.62	NaN	NaN	622.3646	2	-0.0190	DFLLKPELLR		NO	YES
7867	35.16	NaN	NaN	622.3675	2	-0.0131	DFLLKPELLR		NO	YES
7869	34.28	NaN	NaN	622.3697	2	-0.0088	DFLLKPELLR		NO	YES
7870	55.81	NaN	NaN	622.3698	2	-0.0086	DFLLKPELLR		NO	YES
7871	29.85	NaN	NaN	622.3723	2	-0.0036	DFLLKPELLR		NO	YES
7872	44.71	NaN	NaN	622.3747	2	0.0014	DFLLKPELLR		NO	YES
7873	27.93	NaN	NaN	622.3768	2	0.0055	DFLLKPELLR		NO	YES
7875	39.72	NaN	NaN	622.3819	2	0.0157	DFLLKPELLR		NO	YES
7876	30.77	NaN	NaN	622.3821	2	0.0161	DFLLKPELLR		NO	YES
7884	33.1	NaN	NaN	622.5000	2	0.2519	DFLLKPELLR		NO	YES
46365	43.53	NaN	NaN	816.4859	3	0.0841	CIALAQLLVEQNFPAIAIHR	ICAT-C (C)	YES	YES

Zinc finger protein 462 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q96JM2	95	4.39	3.62	0.61	161426	1.1	3	3	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
32949	52.74	3.97	3.28	654.9728	3	-0.0089	HDIDAYYTHCLAASR	ICAT-C (C)	YES	YES
32955	36.66	5.15	4.25	654.9893	3	0.0407	HDIDAYYTHCLAASR	ICAT-C (C)	YES	YES
38686	43.9	4.25	3.51	530.6000	4	0.3644	RHDIDAYYTHCLAASR	ICAT-C (C)	YES	YES

Bromodomain-containing protein 7 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9NPI1	223	4.03	3.33	0.95	74092	9.8	10	8	3

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
42017	41.83	5.76	4.75	748.0639	3	-0.0062	LSTRPPPNMICLLGPSYR	ICAT-C (C)	YES	YES
42020	32.05	3.86	3.19	748.0739	3	0.0236	LSTRPPPNMICLLGPSYR	ICAT-C (C)	YES	YES
42024	30.72	4.72	3.90	748.0883	3	0.0667	LSTRPPPNMICLLGPSYR	ICAT-C (C)	YES	YES
45805	39.98	2.62	2.17	808.4153	3	0.0508	LMCTNAMIYNKPETIYYK	ICAT-C (C)	YES	YES

46219	36.09	4.91	4.05	813.7672	3	0.1115	LMCTNAMIYNKPETIYYK	ICAT-C (C); Oxidation (M)	YES	YES
46519	32.23	N/A	N/A	818.9802	3	-0.2444	LMCTNAMIYNKPETIYYK	ICAT-C (C); 2 Oxidation (M)	YES	YES
58295	25.99	N/A	N/A	804.3575	4	-0.2958	RKPDGTTTLGLLHPVDPIVGEPGYCPVR	ICAT-C (C)	YES	YES
58296	55.43	3.48	2.87	804.4387	4	0.0287	RKPDGTTTLGLLHPVDPIVGEPGYCPVR	ICAT-C (C)	YES	YES
58297	54.27	4.20	3.47	804.4539	4	0.0896	RKPDGTTTLGLLHPVDPIVGEPGYCPVR	ICAT-C (C)	YES	YES
58340	40.31	4.19	3.46	806.7167	4	0.1106	RKPDGTTTLGLLHPVDPIVGEPGYCPVR	ICAT-C:13C(9) (C)	YES	YES

UPF0609 protein C4orf27 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9NWY4	111	3.75	3.10	1.37	39383	8.1	6	5	2	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
21237	31.89	5.23	4.32	532.9158	3	-0.0356	FCEADVSSDLRK	ICAT-C (C)	YES	YES
21239	32.14	1.95	1.61	532.9257	3	-0.0061	FCEADVSSDLRK	ICAT-C (C)	YES	YES
30729	49.45	5.25	4.34	950.8873	2	-0.2275	NCIIVPNGDNVFAAVK	ICAT-C (C)	YES	YES
30731	49.88	4.67	3.85	950.8969	2	-0.2085	NCIIVPNGDNVFAAVK	ICAT-C (C)	YES	YES
30736	27.34	4.10	3.38	950.9524	2	-0.0974	NCIIVPNGDNVFAAVK	ICAT-C (C)	YES	YES
30742	29.89	N/A	N/A	950.9659	2	-0.0704	NCIIVPNGDNVFAAVK	ICAT-C (C)	YES	YES

Chromatin accessibility complex protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9NRG0	330	3.23	2.67	1.22	14701	11.5	10	9	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
34101	50.44	2.32	1.92	996.3794	2	-0.2380	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34103	35.46	2.23	1.84	996.3907	2	-0.2153	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34104	34.29	5.32	4.39	996.4080	2	-0.1808	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34105	82.77	3.47	2.86	996.4173	2	-0.1621	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34108	55.91	4.79	3.96	996.4505	2	-0.0958	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34109	59.7	2.87	2.37	996.4719	2	-0.0529	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34111	62.83	N/A	N/A	996.4941	2	-0.0085	ATELFVQCLATYSYR	ICAT-C (C)	YES	YES
34297	25.2	2.13	1.76	1000.9084	2	-0.2101	ATELFVQCLATYSYR	ICAT-C:13C(9) (C)	YES	YES
34298	69.4	3.49	2.88	1000.9282	2	-0.1705	ATELFVQCLATYSYR	ICAT-C:13C(9) (C)	YES	YES
34305	52.86	4.78	3.95	1000.9938	2	-0.0393	ATELFVQCLATYSYR	ICAT-C:13C(9) (C)	YES	YES

Zinc finger protein 335 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide	
Q9H4Z2	57	3.09	2.55	0.92	144802	2.1	2	2	1	
Spectrum No.	**Peptide Score**	**Ratio(L/H)**	**Normalized Ratio (L/H)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**

57574	26.25	3.93	3.25	1040.9604	3	0.4492	TPVEAGVSQSDAENAAPSCPDEHDTLPR	ICAT-C (C)	YES	YES
57633	57.25	2.63	2.17	1043.7288	3	-0.2758	TPVEAGVSQSDAENAAPSCPDEHDTLPR	ICAT-C:13C(9) (C)	YES	YES

YEATS domain-containing protein 2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9ULM3	97	2.73	2.26	0.43	150688	6.3	6	4	3

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
27075	29.26	N/A	N/A	892.4215	2	-0.1053	ACIVANYYASAGLLK	ICAT-C (C)	YES	YES
27082	28.49	N/A	N/A	892.4369	2	-0.0745	ACIVANYYASAGLLK	ICAT-C (C)	YES	YES
46180	25.57	2.62	2.16	813.4284	3	0.1116	VTFCSHGNSAFQPIASSCK	2 ICAT-C (C)	YES	YES
47931	43.31	2.74	2.26	838.4511	3	0.0835	VKTEPETPGPSCLSQEGQTAVK	ICAT-C (C)	YES	YES
48083	42.55	2.65	2.19	841.4559	3	0.0678	VKTEPETPGPSCLSQEGQTAVK	ICAT-C:13C(9) (C)	YES	YES
60267	26.57	3.53	2.92	1231.0767	3	0.3947	HSLGEDCIYPQSSESDISDAPPSLPLTIPAPVK	ICAT-C (C)	YES	YES

E3 ubiquitin-protein ligase UHRF2 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q96PU4	182	2.33	1.92	0.22	89928	3.6	7	5	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
19340	44.97	N/A	N/A	768.3372	2	-0.0787	AQVFSCPACR	2 ICAT-C (C)	YES	NO
40997	41.87	2.18	1.80	733.6225	3	-0.2543	ALALNCDAPLDDKIGAESR	ICAT-C (C)	YES	YES
41007	28.94	N/A	N/A	733.7114	3	0.0124	ALALNCDAPLDDKIGAESR	ICAT-C (C)	YES	YES
41014	53.46	2.53	2.09	733.7305	3	0.0697	ALALNCDAPLDDKIGAESR	ICAT-C (C)	YES	YES
41017	47.31	1.99	1.65	733.7393	3	0.0960	ALALNCDAPLDDKIGAESR	ICAT-C (C)	YES	YES
41273	37.82	2.46	2.03	736.7307	3	0.0401	ALALNCDAPLDDKIGAESR	ICAT-C:13C(9) (C)	YES	YES
41277	32.7	2.35	1.94	736.7392	3	0.0654	ALALNCDAPLDDKIGAESR	ICAT-C:13C(9) (C)	YES	YES

Protein S100-A8 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P05109	56	10.79	8.91	N/A	10828	11.8	2	1	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
21120	50.28	N/A	N/A	796.3338	2	-0.1546	LLETECPQYIR	ICAT-C (C)	YES	YES
21128	31.13	10.79	8.91	796.3953	2	-0.0315	LLETECPQYIR	ICAT-C (C)	YES	YES

Serine/threonine-protein kinase VRK1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q99986	124	5.02	4.14	0.61	45447	5.3	4	3	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
46498	53.17	N/A	N/A	818.7148	3	-0.0167	CHDGTIEFTSIDAHNGVAPSR	ICAT-C (C)	YES	YES
46499	49.85	4.62	3.82	818.7166	3	-0.0113	CHDGTIEFTSIDAHNGVAPSR	ICAT-C (C)	YES	YES
46502	49.25	5.80	4.79	614.2966	4	0.0177	CHDGTIEFTSIDAHNGVAPSR	ICAT-C (C)	YES	YES
46724	46.24	4.95	4.09	821.7184	3	-0.0362	CHDGTIEFTSIDAHNGVAPSR	ICAT-C:13C(9) (C)	YES	YES

Deoxynucleotidyltransferase terminal-interacting protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9H147	481	5.81	4.80	1.30	36990	10.6	16	12	2

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
17761	29.55	N/A	N/A	496.6004	3	-0.0271	GCLDLKLEELK	ICAT-C (C)	YES	YES
42055	31.16	7.62	6.30	748.9185	3	-0.2990	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42056	36.53	7.21	5.96	748.9264	3	-0.2753	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42057	47.34	5.25	4.33	748.9274	3	-0.2724	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42058	81.88	6.97	5.76	1122.8998	2	-0.2478	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42067	33.93	6.03	4.98	748.9718	3	-0.1393	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42070	92.82	5.94	4.90	1122.9602	2	-0.1270	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42072	37.32	8.15	6.73	748.9803	3	-0.1138	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42074	25.47	6.05	5.00	748.9835	3	-0.1042	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42076	40.41	6.29	5.20	748.9929	3	-0.0761	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42118	99.19	5.42	4.48	1123.2000	2	0.3526	DNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
42319	34.31	6.64	5.49	1127.4153	2	-0.2469	DNVGEEVDAEQLIQEACR	ICAT-C:13C(9) (C)	YES	YES
54176	69.73	3.13	2.58	957.0503	3	-0.2746	AALNVRDNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
54183	51.99	N/A	N/A	957.1728	3	0.0932	AALNVRDNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
54184	38.34	N/A	N/A	957.1732	3	0.0941	AALNVRDNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES
54190	41.28	N/A	N/A	957.2808	3	0.4170	AALNVRDNVGEEVDAEQLIQEACR	ICAT-C (C)	YES	YES

PR domain zinc finger protein 16 - Homo sapiens (Human)

Accession No.	Protein Score	Ratio(L/H)	Normalized Ratio (L/H)	STD	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9HAZ2	44	2.25	1.85	0.02	140172	0.8	2	2	1

Spectrum No.	Peptide Score	Ratio(L/H)	Normalized Ratio (L/H)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
15820	31.03	2.26	1.87	723.2746	2	-0.1422	SYTQFSNLCR	ICAT-C (C)	YES	YES
16308	44.37	2.23	1.85	727.7847	2	-0.1522	SYTQFSNLCR	ICAT-C:13C(9) (C)	YES	YES

Instruction for Supplementary Table 2

The following information is instruction for the interpretation of protein and peptide ratios in Supplementary Table 2.

Each protein contains protein and peptide information as follows:

Protein-level Information:

The protein description is shown at the first row. Detailed protein-level information is provided as follows:

1. **Accession Number**: Accession number in Swiss-Prot sequence database v54.2.
2. **Protein Score**: Mascot protein score.
3. **Normalized Ratio (114/117), (115/117), and (116/117)**: Normalized protein ratio between proteins enriched by WT DNA-beads, which were labeled by iTRAQ^{114} and iTRAQ^{115}, and proteins enriched by MU DNA-beads, which were labeled by iTRAQ^{116} and iTRAQ^{117}. The value is a weighted average of the ratio of all quantitated peptides (see below).
4. **STD**: standard deviation of normalized ratio.
5. **Mass**: Molecular weight (Da) of the protein.
6. **Sequence Coverage (%)**: The number of amino acids spanned by the assigned peptides divided by the sequence length.
7. **Identified Peptide**: The number of peptides assigned to the protein by Mascot. Multiple matches to peptides with the same primary sequence count separately.
8. **Quantitated Peptide**: The number of identified peptides for ratio quantitation.
9. **Identified Unique Peptide**: The number of peptides assigned to the protein by Mascot. Multiple matches to peptides with the same primary sequence count as one.

Peptide-level Information:

Peptide-level information contains detailed information for identified peptides assigned to the protein as follows:

1. **Spectrum No.**: The index number of MS/MS spectrum for Mascot search.
2. **Peptide Score**: Mascot Peptide Score.
3. **Int. 114~117**: Ion intensity of each reporter ion in MS/MS analysis.
4. **Ratio (114/117), (115/117), and (116/117)**: Peptide ratio of indicated reporter ion pairs of the peptide.
5. **Precursor *m/z* (Da)**: The precursor ion selected for MS/MS analysis.
6. **Charge**: The charge state of precursor ion.

7. **Mass Error (Da)**: The value of observed peptide mass minus expected peptide mass.
8. **Peptide Sequence**: The peptide sequence of matched peptide.
9. **Modification**: Observed modification of the peptide.
10. **Labeled**: The value is “Yes” if the peptide is labeled with iTRAQ reagents.
11. **Unique**: The value is “Yes” if the peptide is a non-degenerate peptide.

Supplementary Table 2

bHLH transcription factors

Transcription factor AP-4 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q01664	199	2.46	1.96	1.32	0.60	0.39	0.34	38702	5.3	5	3	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
87636	53.63	37.38	31.22	18.81	9.12	5.06	3.72	2.15	790.7753	3	0.0319	AAILQQTAEYIFSLEQEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
87637	54.08	76.72	64.06	46.10	28.86	3.28	2.41	1.66	790.7926	3	0.0838	AAILQQTAEYIFSLEQEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
87639	61.56	74.79	60.41	37.86	40.24	2.29	1.63	0.98	790.7970	3	0.0971	AAILQQTAEYIFSLEQEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
87643	77.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	790.8073	3	0.1278	AAILQQTAEYIFSLEQEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
87653	58.37	151.97	151.69	108.76	85.95	2.18	1.92	1.32	790.9000	3	0.4060	AAILQQTAEYIFSLEQEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Upstream stimulatory factor 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q15853	108	3.36	3.22	1.11	0.90	0.71	0.09	36932	4.6	4	4	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
72199	44.39	294.04	348.07	180.86	151.51	2.40	2.50	1.24	652.3550	3	0.0619	AQLQQHNLEMVGEGTR	iTRAQ4plex (N-term)	YES	YES
72201	48.68	312.40	329.81	121.14	119.22	3.24	3.01	1.06	652.3651	3	0.0924	AQLQQHNLEMVGEGTR	iTRAQ4plex (N-term)	YES	YES
72207	44.09	301.80	360.24	159.97	156.44	2.38	2.50	1.07	652.3819	3	0.1427	AQLQQHNLEMVGEGTR	iTRAQ4plex (N-term)	YES	YES
72771	53.75	777.50	824.93	232.30	223.72	4.29	4.01	1.08	657.6907	3	0.0742	AQLQQHNLEMVGEGTR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES

Transcription factors

Nuclear factor of activated T-cells, cytoplasmic 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q13469	88	2.00	2.05	1.05	0.58	0.49	0.04	100083	1.8	3	3	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
74755	53.19	100.34	132.80	73.46	72.56	1.71	1.99	1.05	673.0717	3	0.0442	IEITPSHELIQAVGPLR	iTRAQ4plex (N-term)	YES	YES
74763	44.00	174.97	201.55	132.89	136.82	1.58	1.60	1.01	673.0848	3	0.0835	IEITPSHELIQAVGPLR	iTRAQ4plex (N-term)	YES	YES
74766	58.36	193.71	214.63	94.97	90.51	2.64	2.58	1.09	673.0945	3	0.1128	IEITPSHELIQAVGPLR	iTRAQ4plex (N-term)	YES	YES

Alpha-globin transcription factor CP2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q12800	522	2.26	2.00	0.96	0.34	0.33	0.08	57220	12.9	18	9	5

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
33816	47.96	1270.56	1322.22	636.93	712.02	2.20	2.02	0.93	679.4238	2	0.0475	LGELPEINGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
33820	41.66	538.36	582.23	225.35	249.28	2.67	2.54	0.94	679.4272	2	0.0542	LGELPEINGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
52633	72.67	1773.24	1788.11	941.33	1024.85	2.14	1.90	0.96	807.4601	2	-0.0012	LFTNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
52648	80.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	807.4803	2	0.0392	LFTNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
52649	45.43	777.34	782.89	455.53	576.72	1.66	1.48	0.82	807.4803	2	0.0392	LFTNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
52654	70.68	306.21	339.56	172.50	196.90	1.92	1.87	0.91	807.4835	2	0.0456	LFTNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
52655	84.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	807.4855	2	0.0496	LFTNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
52660	59.50	1247.45	1177.28	646.11	736.75	2.09	1.74	0.91	807.4974	2	0.0735	LFTNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
57724	44.45	767.46	826.81	416.99	404.41	2.34	2.22	1.07	564.6604	3	0.0459	AETNDSYHIILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

57727	44.95	1201.37	1181.30	606.82	615.51	2.41	2.09	1.03	564.6644	3	0.0582	AETNDSYHIILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
65765	54.64	1124.05	1047.37	526.45	516.26	2.69	2.21	1.06	611.3322	3	0.0613	LQYTEHQQLEGWR	iTRAQ4plex (N-term)	YES	YES
65769	42.83	410.86	407.03	183.93	211.32	2.40	2.09	0.91	611.3368	3	0.0751	LQYTEHQQLEGWR	iTRAQ4plex (N-term)	YES	YES
86413	65.05	116.55	172.58	114.20	122.69	1.17	1.53	0.97	775.4138	3	0.0629	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86414	53.71	188.46	327.14	186.21	152.29	1.53	2.33	1.27	775.4156	3	0.0685	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86415	66.25	587.87	856.66	442.12	393.25	1.85	2.37	1.17	775.4198	3	0.0811	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86416	86.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	775.4209	3	0.0843	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86417	52.70	99.71	164.57	82.18	85.14	1.45	2.10	1.01	775.4307	3	0.1136	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86422	54.88	161.21	239.34	134.01	131.73	1.51	1.97	1.06	775.4484	3	0.1666	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO

General transcription factor II-I - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P78347	757	1.74	1.63	0.98	0.33	0.36	0.13	112346	23.4	40	28	20

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
16164	47.56	1964.94	2052.90	1293.12	1374.76	1.76	1.62	0.98	568.8741	2	0.0129	AGISFIIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
16167	66.84	2406.44	2428.13	1382.48	1418.36	2.09	1.86	1.02	568.8764	2	0.0173	AGISFIIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
16170	40.49	411.67	466.49	233.73	208.02	2.44	2.44	1.17	568.8828	2	0.0302	AGISFIIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
16171	49.28	696.18	791.19	475.11	479.83	1.79	1.79	1.03	568.8984	2	0.0614	AGISFIIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
25164	43.88	1719.54	1723.00	1113.71	1134.16	1.87	1.65	1.02	626.3247	2	-0.0029	EQVNDLFSR	iTRAQ4plex (N-term)	YES	YES
25193	47.86	914.96	901.97	646.46	655.01	1.72	1.50	1.03	626.3511	2	0.0499	EQVNDLFSR	iTRAQ4plex (N-term)	YES	YES
25195	40.03	1191.06	1246.96	924.86	1023.13	1.44	1.32	0.94	626.3524	2	0.0525	EQVNDLFSR	iTRAQ4plex (N-term)	YES	YES
27665	45.21	1992.15	1942.69	1084.38	1246.26	1.97	1.69	0.91	640.8679	2	0.0197	VENLFNEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
27673	42.48	331.92	453.95	274.07	246.21	1.66	2.00	1.16	640.8935	2	0.0709	VENLFNEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
31085	51.29	600.69	715.72	414.93	394.61	1.88	1.97	1.10	662.4055	2	0.0276	ILDSAEFIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
31087	56.54	1697.75	1612.56	1073.74	1064.07	1.97	1.65	1.05	662.4090	2	0.0344	ILDSAEFIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
37120	59.55	374.57	421.44	208.64	200.19	2.31	2.29	1.09	699.3852	2	0.0416	APSYLEISSMR	iTRAQ4plex (N-term)	YES	YES
37916	54.78	1156.01	1049.28	627.54	684.71	2.08	1.67	0.95	703.9309	2	0.0412	STVVPVPYEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
38313	46.84	1621.53	1623.28	1030.89	1123.99	1.78	1.57	0.96	706.4094	2	0.0443	FAEALGSTEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42493	52.26	1729.08	1895.90	1260.72	1266.37	1.69	1.63	1.04	489.2937	3	0.0413	KQVEELFER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42496	43.08	594.03	698.50	466.28	460.32	1.59	1.65	1.06	489.2954	3	0.0464	KQVEELFER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
45424	70.25	711.25	787.50	500.21	531.70	1.65	1.61	0.98	753.9290	2	0.0553	MSVDAVEIETLR	iTRAQ4plex (N-term)	YES	YES
46251	46.34	902.52	1023.84	577.26	590.00	1.89	1.89	1.02	758.9087	2	0.0427	EFSFEAWNAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
47649	71.45	878.38	830.88	425.95	519.00	2.09	1.74	0.85	768.4518	2	-0.0071	FAQALGLTEAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
47654	64.35	814.36	881.78	454.77	530.65	1.89	1.81	0.89	768.4554	2	-0.0001	FAQALGLTEAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
47667	74.89	1183.60	1319.93	713.57	828.57	1.76	1.73	0.90	768.4786	2	0.0464	FAQALGLTEAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
47670	77.52	1290.98	1301.07	699.55	775.22	2.06	1.82	0.94	768.4804	2	0.0499	FAQALGLTEAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
50992	50.11	1028.47	1026.46	704.29	729.28	1.74	1.53	1.01	530.3050	3	0.0431	HPENYDLATLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
50994	40.84	993.92	1053.84	723.10	822.41	1.49	1.39	0.92	530.3070	3	0.0491	HPENYDLATLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
53447	57.21	1253.74	1212.92	743.56	800.33	1.93	1.65	0.97	542.6449	3	-0.0094	KPEMFETAIK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
53448	43.91	983.29	1035.68	655.50	638.47	1.90	1.76	1.07	542.6510	3	0.0088	KPEMFETAIK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
54537	53.04	1669.66	1616.81	1085.46	1116.54	1.85	1.57	1.01	547.9842	3	0.0135	KPEMFETAIK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
56906	43.36	1192.25	1237.32	751.73	789.93	1.86	1.70	0.99	560.6945	3	0.0632	KQVEEIFNLK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
56909	41.24	627.66	666.76	424.32	477.24	1.62	1.52	0.93	560.7014	3	0.0840	KQVEEIFNLK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
57156	41.22	708.73	613.34	637.93	707.68	1.24	0.94	0.94	561.9888	3	-0.0123	KFAEALGSTEAK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
65647	41.07	327.18	390.79	349.75	417.87	0.97	1.02	0.87	610.3448	3	-0.0156	KFGEAIGMGFPVK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
65653	40.68	576.56	672.01	448.01	530.17	1.34	1.38	0.88	610.3515	3	0.0045	KFGEAIGMGFPVK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
65813	41.44	928.29	985.58	664.91	701.09	1.63	1.53	0.99	611.3697	3	0.0458	EDLQLDKPASGVK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
71044	53.58	522.31	534.44	344.39	415.97	1.55	1.40	0.86	645.0409	3	0.0700	TPTQTNGSNVPFKPR	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
74419	43.17	116.98	150.96	101.62	92.28	1.57	1.78	1.15	670.3613	3	-0.0202	RPELLTHSTTEVTQPR	iTRAQ4plex (N-term)	YES	YES
74422	42.3	188.68	266.20	184.34	134.44	1.73	2.15	1.43	670.3637	3	-0.0131	RPELLTHSTTEVTQPR	iTRAQ4plex (N-term)	YES	YES
80861	51.59	219.22	189.17	124.92	151.19	1.79	1.36	0.86	721.4510	3	0.0767	KPELVISYLPPGMASK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80862	57.32	140.83	158.59	131.88	148.91	1.17	1.16	0.92	721.4590	3	0.1007	KPELVISYLPPGMASK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80863	52.74	453.09	495.47	348.60	343.82	1.63	1.57	1.06	721.4605	3	0.1051	KPELVISYLPPGMASK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90989	42.94	187.92	203.85	132.17	100.85	2.30	2.20	1.37	834.4447	3	0.0613	FEAHPNDLYVEGLPENIPFR	iTRAQ4plex (N-term)	YES	YES

Upstream-binding protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9NZI7	582	1.88	1.73	0.98	0.19	0.19	0.10	60453	18.1	20	12	7

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
16296	42.41	907.87	1056.56	674.43	639.59	1.75	1.80	1.10	569.8595	2	0.0407	IQVDTFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
51716	52.75	1030.67	966.62	565.38	610.59	2.08	1.72	0.96	800.4513	2	-0.0030	LFSNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
51724	50.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	800.4773	2	0.0489	LFSNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
51727	65.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	800.4872	2	0.0686	LFSNFSGADLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
71325	63.7	820.86	907.18	495.73	520.79	1.95	1.89	0.99	646.7066	3	0.0632	LEPIIEDAVEHEQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
71329	48.19	306.14	293.21	150.69	206.93	1.83	1.54	0.76	646.7135	3	0.0838	LEPIIEDAVEHEQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
71334	50.87	537.45	577.56	377.44	403.44	1.64	1.56	0.97	646.7258	3	0.1205	LEPIIEDAVEHEQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
71770	47.47	861.24	837.85	525.26	577.53	1.84	1.58	0.95	650.0415	3	0.0933	LQYTEHQQLEGWK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81689	41.66	182.56	172.04	102.83	104.20	2.16	1.79	1.03	728.1075	3	0.0462	LALVFNIPLHQINQVYR	iTRAQ4plex (N-term)	YES	YES
81692	40.03	160.39	180.63	93.62	98.61	2.01	1.99	0.99	728.1129	3	0.0624	LALVFNIPLHQINQVYR	iTRAQ4plex (N-term)	YES	YES
81693	51.02	155.68	165.79	97.63	94.44	2.04	1.91	1.08	728.1151	3	0.0690	LALVFNIPLHQINQVYR	iTRAQ4plex (N-term)	YES	YES
81699	60.05	154.66	166.97	93.48	96.63	1.98	1.88	1.01	728.1321	3	0.1200	LALVFNIPLHQINQVYR	iTRAQ4plex (N-term)	YES	YES
81701	61.67	85.11	94.65	42.57	48.99	2.14	2.10	0.91	728.1362	3	0.1323	LALVFNIPLHQINQVYR	iTRAQ4plex (N-term)	YES	YES
83104	53.65	200.67	216.40	120.31	154.37	1.60	1.52	0.81	740.1137	3	0.1519	TNPSQLNAVEFLWDPAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86413	65.05	116.55	172.58	114.20	122.69	1.17	1.53	0.97	775.4138	3	0.0629	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86414	53.71	188.46	327.14	186.21	152.29	1.53	2.33	1.27	775.4156	3	0.0685	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86415	66.25	587.87	856.66	442.12	393.25	1.85	2.37	1.17	775.4198	3	0.0811	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86416	86.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	775.4209	3	0.0843	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86417	52.7	99.71	164.57	82.18	85.14	1.45	2.10	1.01	775.4307	3	0.1136	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO
86422	54.88	161.21	239.34	134.01	131.73	1.51	1.97	1.06	775.4484	3	0.1666	LHDETLTYLNQGQSYEIR	iTRAQ4plex (N-term)	YES	NO

COUP transcription factor 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P10589	143	2.13	1.94	1.17	0.56	0.49	0.21	46126	16.8	7	3	4

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
29854	43.81	2751.62	2668.99	1632.44	1689.87	2.01	1.72	1.01	654.8979	2	0.0483	IFQEQVEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
29855	53.47	2511.68	2515.94	1604.31	1744.29	1.78	1.57	0.96	654.8999	2	0.0523	IFQEQVEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
32032	49.94	287.94	302.77	201.44	200.63	1.77	1.64	1.05	668.4014	2	0.0414	LLFSAVEWAR	iTRAQ4plex (N-term)	YES	YES
32038	42.43	237.93	253.27	152.63	117.88	2.49	2.34	1.35	668.4049	2	0.0484	LLFSAVEWAR	iTRAQ4plex (N-term)	YES	YES
61257	47.07	256.77	211.72	132.96	141.81	2.24	1.62	0.98	878.5058	2	0.0283	TVSSSVIEQLFFVR	iTRAQ4plex (N-term)	YES	NO
61276	66.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	878.5308	2	0.0782	TVSSSVIEQLFFVR	iTRAQ4plex (N-term)	YES	NO
101859	45.59	42.42	29.01	15.56	18.27	2.87	1.73	0.89	943.3000	4	0.3777	GGGGGAGEQQQQAGSGAPHTPQTPGQPGAPATPGTAGDK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

COUP transcription factor 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P24468	136	1.99	1.78	0.97	-	-	-	45542	7.7	5	1	3

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
29854	43.81	2751.62	2668.99	1632.44	1689.87	2.01	1.72	1.01	654.8979	2	0.0483	IFQEQVEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
29855	53.47	2511.68	2515.94	1604.31	1744.29	1.78	1.57	0.96	654.8999	2	0.0523	IFQEQVEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
33441	62.75	945.78	961.18	547.87	585.38	1.99	1.78	0.97	677.3616	2	0.0053	MLFSAVEWAR	iTRAQ4plex (N-term)	YES	YES
61257	47.07	256.77	211.72	132.96	141.81	2.24	1.62	0.98	878.5058	2	0.0283	TVSSSVIEQLFFVR	iTRAQ4plex (N-term)	YES	NO
61276	66.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	878.5308	2	0.0782	TVSSSVIEQLFFVR	iTRAQ4plex (N-term)	YES	NO

Nuclear factor 1 C-type - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide

P08651	175	1.73	1.75	0.91	0.06	0.05	0.03	55640	10.4	6	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
37041	45.35	850.15	892.39	722.98	758.57	1.38	1.28	0.99	698.8873	2	-0.0252	EDFVLSITGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
37052	76.46	1011.61	1019.59	795.23	866.19	1.44	1.28	0.96	698.9044	2	0.0089	EDFVLSITGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
37065	60.91	739.60	720.23	616.45	643.54	1.42	1.22	1.00	698.9293	2	0.0586	EDFVLSITGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
48420	54.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	773.4587	2	0.0669	ELDLYLAYFVR	iTRAQ4plex (N-term)	YES	YES
100697	45.96	125.26	137.17	78.58	87.33	1.77	1.71	0.94	857.4732	4	0.0934	TPVVTGTGPNFSLGELQGHLAYDLNPASTGLR	iTRAQ4plex (N-term)	YES	YES
100700	54.04	129.88	155.81	81.21	95.19	1.68	1.78	0.89	857.5048	4	0.2201	TPVVTGTGPNFSLGELQGHLAYDLNPASTGLR	iTRAQ4plex (N-term)	YES	YES

Cellular tumor antigen p53 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P04637	96	1.13	1.29	1.47	-	-	-	43625	4.8	3	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
82919	42.74	20.52	24.18	19.84	19.08	1.33	1.38	1.08	738.0990	3	0.0043	RPILTIITLEDSSGNLLGR	iTRAQ4plex (N-term)	YES	YES
82923	56.82	49.71	64.70	77.10	54.47	1.13	1.29	1.47	738.1145	3	0.0509	RPILTIITLEDSSGNLLGR	iTRAQ4plex (N-term)	YES	YES
82926	54.83	9.79	10.63	25.91	11.82	1.02	0.98	2.28	738.1287	3	0.0933	RPILTIITLEDSSGNLLGR	iTRAQ4plex (N-term)	YES	YES

Zinc finger and BTB domain-containing protein 7B - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O15156	67	4.25	4.19	1.28	0.74	0.95	0.26	57990	6.3	2	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
30028	48.88	971.72	1064.07	343.45	300.48	3.99	3.85	1.19	437.5968	3	0.0410	FLHSYDLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
97861	46.43	327.34	383.02	119.69	80.23	5.04	5.19	1.55	750.4330	4	0.1712	ANHLVPEVPTVPAHPLTYEEEEVAGR	iTRAQ4plex (N-term)	YES	YES

Transcription factor Sp3 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q02447	110	2.60	1.98	1.02	0.07	0.03	0.02	81876	5.6	3	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
78827	63.35	1230.81	1059.70	570.26	573.28	2.65	2.01	1.04	705.0438	3	0.0769	VQVVDEEGDQQHQEGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78839	46.74	1333.66	1166.91	625.12	646.70	2.55	1.96	1.01	705.0672	3	0.1469	VQVVDEEGDQQHQEGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
101217	44.26	15.41	29.69	12.85	11.39	1.67	2.83	1.18	889.4814	4	0.1548	IKEEEPDPEEWQLSGDSTLNTNDLTHLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Steroid hormone receptor ERR1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P11474	50	1.76	1.99	1.18	-	-	-	55404	2.7	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
60621	49.72	128.69	165.26	101.88	90.25	1.76	1.99	1.18	582.3354	3	0.0932	EALHEALLEYEAGR	iTRAQ4plex (N-term)	YES	YES

Transcriptional adapter 2-alpha - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O75478	57	N/A	2.10	N/A	N/A	-	N/A	51463	3.6	2	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
79729	40.45	32.18	41.22	28.96	16.66	2.38	2.69	1.81	711.7353	3	0.0960	DIDFVEDDSDILHALK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

79730	45.71	27.09	45.46	30.46	23.58	1.42	2.10	1.35	711.7398	3	0.1094	DIDFVEDDSDILHALK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Transcriptional repressor and corepressor

Zinc finger and BTB domain-containing protein 7A - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O95365	56	3.32	3.09	0.93	0.26	0.17	0.16	61401	5.0	2	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
66751	43.53	470.81	509.74	142.99	188.06	3.09	2.95	0.79	617.3562	3	0.0812	ADDKGVMDYYLK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
83041	40.27	756.20	790.24	262.46	269.40	3.47	3.19	1.01	739.4004	3	0.1216	YFSGAHDGDVYPAWSQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

C-terminal-binding protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q13363	177	1.68	1.71	1.01	0.38	0.12	0.11	47505	6.6	5	5	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
42555	46.95	682.69	765.29	497.87	497.83	1.69	1.67	1.04	733.9210	2	0.0254	IGSGFDNIDIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80242	54.16	104.20	90.22	52.48	56.55	2.27	1.73	0.97	716.0855	3	0.0608	VLNEAVGALMYHTITLTR	iTRAQ4plex (N-term)	YES	YES
80244	66.88	64.73	113.62	49.92	64.64	1.24	1.91	0.80	716.0885	3	0.0698	VLNEAVGALMYHTITLTR	iTRAQ4plex (N-term)	YES	YES
80248	55.98	89.49	125.31	77.87	73.37	1.51	1.86	1.11	716.0946	3	0.0881	VLNEAVGALMYHTITLTR	iTRAQ4plex (N-term)	YES	YES
80251	58.89	99.64	117.94	70.05	78.73	1.56	1.63	0.93	716.0991	3	0.1018	VLNEAVGALMYHTITLTR	iTRAQ4plex (N-term)	YES	YES

Protein Wiz - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O95785	801	1.68	1.61	1.01	0.30	0.25	0.12	178563	9.4	35	26	11

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
10862	58.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	529.3621	2	0.0310	LLPAEVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
10864	45.83	1155.91	1204.53	813.15	877.20	1.63	1.49	0.97	529.3623	2	0.0313	LLPAEVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
32558	41.44	539.71	614.55	374.32	379.54	1.76	1.76	1.03	671.9131	2	0.0217	FVGNIYTLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
32559	60.52	1418.63	1368.60	826.78	893.43	1.96	1.67	0.96	671.9148	2	0.0251	FVGNIYTLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
37881	43.88	51.12	43.78	39.04	35.20	1.79	1.35	1.16	703.8676	2	0.0213	EDMTPLNLSSR	iTRAQ4plex (N-term)	YES	YES
37886	52.82	596.24	638.23	373.28	394.56	1.87	1.76	0.99	703.8818	2	0.0497	EDMTPLNLSSR	iTRAQ4plex (N-term)	YES	YES
44322	50.92	466.09	545.40	357.47	376.37	1.53	1.58	0.99	497.6435	3	0.0227	GLGHPPSSPLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
44336	45.99	182.31	184.42	123.38	123.26	1.83	1.63	1.04	497.6527	3	0.0502	GLGHPPSSPLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
44339	47.02	496.25	537.74	321.77	327.98	1.87	1.78	1.02	497.6551	3	0.0575	GLGHPPSSPLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
47030	45.04	1334.06	1397.27	997.94	1078.70	1.53	1.41	0.96	764.4574	2	0.0415	TYIQTELPFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
55972	49.09	62.90	55.18	68.79	49.85	1.56	1.20	1.44	555.3491	3	0.0240	RPSLGLAPGGLAVVGR	iTRAQ4plex (N-term)	YES	YES
55973	49.9	70.31	84.73	68.72	59.82	1.45	1.54	1.20	555.3604	3	0.0579	RPSLGLAPGGLAVVGR	iTRAQ4plex (N-term)	YES	YES
55974	70.05	171.14	192.98	189.64	230.27	0.92	0.91	0.86	555.3627	3	0.0646	RPSLGLAPGGLAVVGR	iTRAQ4plex (N-term)	YES	YES
55976	46.44	136.38	181.02	159.32	156.65	1.07	1.26	1.06	555.3639	3	0.0683	RPSLGLAPGGLAVVGR	iTRAQ4plex (N-term)	YES	YES
58944	57.87	898.07	1046.38	729.64	749.12	1.48	1.52	1.01	571.6904	3	-0.0068	KTPLALAGSPTPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
58954	48.9	608.81	709.72	527.10	548.57	1.37	1.41	1.00	571.6979	3	0.0158	KTPLALAGSPTPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60593	49.68	596.40	629.92	450.77	369.09	1.99	1.86	1.27	582.0267	3	0.0296	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60595	42.58	627.17	591.53	434.51	427.86	1.81	1.50	1.06	582.0300	3	0.0396	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60596	49.93	215.24	238.05	169.75	162.12	1.64	1.60	1.09	582.0303	3	0.0403	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60597	45.66	605.16	742.02	459.69	488.57	1.53	1.65	0.98	582.0319	3	0.0452	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60600	58.2	396.31	384.75	221.16	237.66	2.06	1.76	0.97	582.0408	3	0.0719	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60603	54.11	506.34	582.97	423.57	444.36	1.41	1.43	0.99	582.0512	3	0.1031	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60604	49.9	136.42	129.00	128.22	107.10	1.57	1.31	1.25	582.0586	3	0.1253	GLPDAHLGLPPGLAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73264	54.15	336.88	356.22	189.21	229.13	1.82	1.69	0.86	661.3910	3	0.0674	AADGGERPLAASPPGTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73265	53.39	1924.76	2161.90	1402.26	1470.74	1.62	1.60	0.99	661.3912	3	0.0682	AADGGERPLAASPPGTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

73266	51.69	663.78	661.19	407.21	436.01	1.88	1.65	0.97	661.3913	3	0.0685	AADGGERPLAASPPGTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73268	48.72	1462.88	1406.04	858.66	891.95	2.02	1.71	1.00	661.3944	3	0.0777	AADGGERPLAASPPGTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73281	53.72	1259.37	1331.48	974.65	981.81	1.58	1.47	1.03	661.4056	3	0.1113	AADGGERPLAASPPGTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73290	50.98	1945.11	1894.41	1284.97	1276.28	1.88	1.61	1.05	661.4150	3	0.1395	AADGGERPLAASPPGTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90560	41.95	205.44	227.98	125.22	140.14	1.81	1.77	0.93	621.3325	4	0.0665	EMLPGALHGELHPSEGPWGAPR	iTRAQ4plex (N-term)	YES	YES
90589	62.31	334.73	363.31	223.64	233.57	1.77	1.69	1.00	621.4000	4	0.3364	EMLPGALHGELHPSEGPWGAPR	iTRAQ4plex (N-term)	YES	YES
90592	56.52	151.43	128.34	87.87	90.92	2.06	1.53	1.01	621.4000	4	0.3364	EMLPGALHGELHPSEGPWGAPR	iTRAQ4plex (N-term)	YES	YES
90874	42.04	149.80	160.25	94.38	83.59	2.21	2.08	1.18	625.3265	4	0.0477	EMLPGALHGELHPSEGPWGAPR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
90878	51.27	300.14	342.78	210.32	197.19	1.88	1.89	1.11	625.3438	4	0.1165	EMLPGALHGELHPSEGPWGAPR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
92044	43.7	1403.12	1393.81	591.06	677.01	2.56	2.24	0.91	637.7000	4	0.3496	KLPPPPGSPLGHSPTASPPPTAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Paired amphipathic helix protein Sin3b - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O75182	87	1.77	1.74	1.13	0.49	0.71	0.17	132983	3.2	3	3	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
79482	51.11	61.71	64.62	55.88	59.42	1.28	1.18	0.98	710.1065	3	0.1158	LPVHVEDALTYLDQVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
93652	45.41	45.23	38.35	31.62	28.54	1.96	1.46	1.15	661.5960	4	0.1220	SLLNEIESVYDEHQEQHSEGR	iTRAQ4plex (N-term)	YES	YES
93659	49.5	61.42	79.05	43.09	33.98	2.23	2.53	1.32	661.6048	4	0.1573	SLLNEIESVYDEHQEQHSEGR	iTRAQ4plex (N-term)	YES	YES

Methyl-CpG-binding domain protein 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9UBB5	147	1.64	1.68	1.07	0.19	0.25	0.29	43228	3.2	4	3	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
62631	73.55	29.99	50.27	31.06	26.55	1.39	2.06	1.22	593.0282	3	0.0568	KLEEALMADILSR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
62637	59.79	43.05	47.26	39.02	31.20	1.70	1.65	1.30	593.0365	3	0.0819	KLEEALMADILSR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
62640	58.67	45.89	55.41	28.22	39.67	1.43	1.52	0.74	593.0405	3	0.0939	KLEEALMADILSR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
62641	68.73	53.93	53.57	40.41	37.13	1.79	1.57	1.13	593.0420	3	0.0983	KLEEALMADILSR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Nuclear receptor coactivator 5 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9HCD5	45	N/A	1.64	N/A	N/A	-	N/A	65496	3.1	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
75327	44.97	22.22	38.89	25.75	25.80	1.06	1.64	1.04	677.3972	3	0.0508	GGHPPAIQSLINLLADNR	iTRAQ4plex (N-term)	YES	YES

Basic transcription machinery

Transcription termination factor 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9UNY4	261	1.30	1.21	0.97	0.22	0.18	0.11	129508	7.7	18	14	9

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
5624	40.5	1977.16	1942.06	1586.46	1695.67	1.44	1.24	0.97	481.8390	2	0.0219	LSILTK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
5626	40.26	1603.69	1515.58	1215.77	1328.78	1.49	1.24	0.95	481.8429	2	0.0297	LSILTK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
11462	45.27	316.14	393.20	357.13	430.54	0.91	0.99	0.86	534.3480	2	-0.0292	VVALHLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
28793	46.52	774.10	895.20	743.74	814.64	1.17	1.19	0.95	647.9059	2	0.0437	STALTWLSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
28794	50.1	494.26	537.10	473.85	527.14	1.16	1.11	0.94	647.9061	2	0.0440	STALTWLSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
34734	42.9	306.38	331.06	253.60	256.26	1.48	1.40	1.03	456.9422	3	0.0406	ITSEAIGQLHR	iTRAQ4plex (N-term)	YES	YES
34745	47.43	366.52	373.84	275.16	279.24	1.62	1.46	1.03	456.9470	3	0.0549	ITSEAIGQLHR	iTRAQ4plex (N-term)	YES	YES

34751	41.58	363.71	314.55	290.47	279.61	1.61	1.22	1.08	456.9576	3	0.0866	ITSEAIGQLHR	iTRAQ4plex (N-term)	YES	YES
40586	46.63	690.74	663.19	583.24	556.09	1.53	1.30	1.09	480.6375	3	0.0520	IILDEAHNVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
40589	59.88	968.81	959.38	819.81	863.15	1.39	1.21	0.99	480.6413	3	0.0633	IILDEAHNVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
40591	47.24	363.57	371.51	291.29	304.52	1.47	1.33	1.00	480.6431	3	0.0689	IILDEAHNVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42228	53.79	161.43	178.58	125.35	133.18	1.50	1.46	0.98	488.2619	3	0.0481	MDLVEAFNHSR	iTRAQ4plex (N-term)	YES	YES
42234	40.76	208.88	255.95	184.47	194.44	1.33	1.43	0.99	488.2647	3	0.0566	MDLVEAFNHSR	iTRAQ4plex (N-term)	YES	YES
50073	41.34	643.94	753.04	706.24	782.47	1.02	1.05	0.94	524.9812	3	-0.0021	RGTQPVGSLELK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
50078	41.5	246.65	217.62	219.08	255.92	1.19	0.92	0.89	524.9883	3	0.0192	RGTQPVGSLELK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
50875	41.74	124.97	151.39	70.73	113.67	1.36	1.45	0.65	793.9714	2	0.0122	ISSLLAELEAIQR	iTRAQ4plex (N-term)	YES	YES
50884	41.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	793.9979	2	0.0651	ISSLLAELEAIQR	iTRAQ4plex (N-term)	YES	YES
54393	42.14	1156.10	1245.11	1051.58	1134.43	1.26	1.19	0.97	547.3201	3	0.0443	EKGDQLFDQK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

TATA-box-binding protein - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P20226	490	0.98	0.96	1.05	0.25	0.28	0.23	37674	19.5	18	6	4

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
3678	41.68	1960.18	1791.08	1970.48	2157.54	1.12	0.90	0.95	460.8009	2	0.0137	LGFPAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
30206	70.24	962.06	897.07	1064.35	1237.21	0.96	0.79	0.90	656.8865	2	-0.0058	TTALIFSSGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
30228	42.82	930.30	935.01	1160.75	1275.83	0.90	0.80	0.95	656.9111	2	0.0436	TTALIFSSGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
35469	45.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	688.9872	2	0.0552	IVLLIFVSGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
35470	61.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	688.9897	2	0.0603	IVLLIFVSGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
35471	70.61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	688.9898	2	0.0604	IVLLIFVSGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78323	69.56	99.87	106.66	110.71	127.91	0.96	0.91	0.90	701.0708	3	0.0520	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78334	45.58	93.32	84.18	107.54	89.08	1.29	1.03	1.26	701.0831	3	0.0889	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78336	40.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	701.0869	3	0.1001	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78338	41.75	37.75	62.35	78.14	82.42	0.57	0.82	0.99	701.0881	3	0.1040	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78340	58.18	29.44	28.18	35.47	22.38	1.62	1.37	1.65	701.0898	3	0.1090	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78342	61.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	701.0922	3	0.1161	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78344	58.22	44.42	28.82	50.31	49.71	1.10	0.63	1.05	701.0990	3	0.1366	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78348	48.34	27.95	52.53	59.35	41.28	0.84	1.38	1.50	701.1028	3	0.1480	AEIYEAFENIYPILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78393	63.95	160.62	168.80	184.12	202.55	0.98	0.91	0.95	701.5000	3	0.3555	AEIYEAFENIYPILK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
98559	55.59	28.27	36.38	30.76	28.58	1.22	1.38	1.12	770.9321	4	0.0854	LEGLVLTHQQFSSYEPELFPGLIYR	iTRAQ4plex (N-term)	YES	YES
98560	74.5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	770.9435	4	0.1308	LEGLVLTHQQFSSYEPELFPGLIYR	iTRAQ4plex (N-term)	YES	YES
98561	72.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	770.9440	4	0.1327	LEGLVLTHQQFSSYEPELFPGLIYR	iTRAQ4plex (N-term)	YES	YES

SWI/SNF-related proteins

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q12824	317	1.84	1.77	1.04	0.29	0.26	0.12	44113	14.0	15	13	5

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
48185	52.48	1354.70	1314.90	941.84	920.30	1.82	1.55	1.07	772.3990	2	0.0455	DAFTWNMNEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48187	47.74	1610.86	1657.23	1086.72	1131.44	1.76	1.59	1.00	772.4020	2	0.0514	DAFTWNMNEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
49210	42.81	202.63	218.28	121.00	134.34	1.86	1.77	0.94	780.4063	2	0.0651	DAFTWNMNEK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
50321	40.36	794.23	838.71	463.71	518.29	1.89	1.76	0.93	789.4364	2	-0.0001	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50324	41.74	186.80	209.90	130.88	149.90	1.54	1.52	0.91	789.4426	2	0.0125	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50335	52.89	527.36	581.92	387.08	357.00	1.82	1.77	1.13	789.4558	2	0.0388	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50336	53.45	185.66	216.79	138.11	109.57	2.09	2.15	1.31	789.4559	2	0.0390	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50337	52.85	436.21	489.48	282.40	307.80	1.75	1.73	0.96	789.4562	2	0.0395	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50341	53.16	449.42	529.17	300.99	286.93	1.93	2.00	1.09	789.4581	2	0.0434	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50343	43.87	633.58	670.76	415.34	395.64	1.98	1.84	1.09	789.4589	2	0.0450	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50352	68.05	1158.55	1222.28	722.75	687.25	2.08	1.93	1.10	789.4646	2	0.0565	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES
50355	48.93	443.50	474.99	285.77	268.67	2.04	1.92	1.11	789.4706	2	0.0683	AVSISTEPPTYLR	iTRAQ4plex (N-term)	YES	YES

66019	51.54	173.95	202.45	169.83	187.16	1.15	1.18	0.95	612.6593	3	0.0522	ASEVEEILDGNDEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
69766	41.51	342.84	407.80	321.71	319.12	1.33	1.39	1.05	636.7241	3	0.0897	DHGYTTLATSVTLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
84832	53.99	601.01	649.37	357.82	440.25	1.69	1.60	0.85	757.7719	3	0.1297	ASEVEEILDGNDEKYK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q8TAQ2	1430	1.64	1.61	1.06	0.40	0.36	0.30	132797	19.1	60	30	19

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
15406	46.41	70.47	76.47	77.32	56.44	1.54	1.47	1.43	563.3058	2	0.0105	TPEIYLAYR		NO	NO
20502	48.85	2864.03	2948.75	2328.53	2415.27	1.46	1.33	1.00	599.8521	2	0.0412	SALEEFSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
20504	62.06	3328.82	3259.24	2588.62	2705.25	1.52	1.31	1.00	599.8536	2	0.0441	SALEEFSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
20506	51.93	4096.12	3993.92	3070.19	3298.85	1.53	1.32	0.97	599.8550	2	0.0470	SALEEFSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
20508	52.79	1179.19	1240.69	956.90	1031.70	1.41	1.31	0.97	599.8609	2	0.0589	SALEEFSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
20887	46.12	1121.26	1086.83	678.24	666.39	2.08	1.77	1.06	602.3194	2	0.0366	NFMIDTYR	iTRAQ4plex (N-term)	YES	NO
20890	43.71	616.53	623.50	325.78	351.72	2.16	1.93	0.96	602.3220	2	0.0419	NFMIDTYR	iTRAQ4plex (N-term)	YES	NO
20893	46.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	602.3283	2	0.0546	NFMIDTYR	iTRAQ4plex (N-term)	YES	NO
30033	68.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	655.8958	2	0.0496	ALPEFFNGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30043	41.87	1214.74	1313.17	1037.27	1044.01	1.44	1.37	1.03	655.8991	2	0.0563	ALPEFFNGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30050	50.82	1077.14	1293.22	943.17	931.26	1.43	1.51	1.05	655.9027	2	0.0634	ALPEFFNGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30067	51.84	3234.50	2974.87	2134.90	2250.96	1.77	1.44	0.99	656.1000	2	0.4580	ALPEFFNGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30110	50.99	1153.56	1072.25	860.40	881.21	1.62	1.32	1.02	656.3650	2	0.0040	ALPEFFNGK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30112	55.92	1348.67	1516.66	1281.50	1321.82	1.26	1.25	1.01	656.3681	2	0.0103	ALPEFFNGK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30132	67.99	2038.43	2028.42	1521.47	1671.51	1.51	1.32	0.95	656.3837	2	0.0415	ALPEFFNGK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30137	58.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	656.3892	2	0.0525	ALPEFFNGK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30143	42.87	547.26	687.21	563.94	586.94	1.15	1.27	1.00	656.3912	2	0.0565	ALPEFFNGK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
30149	58.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	656.3971	2	0.0682	ALPEFFNGK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
41249	45.02	2458.53	2323.33	1728.18	1769.91	1.71	1.43	1.02	724.9227	2	0.0394	YIQAEPPTNK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
47157	41.57	357.24	387.80	196.90	216.75	2.03	1.94	0.95	765.4187	2	0.0355	NVEMFMTIEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
49516	63.01	121.79	160.70	68.45	57.76	2.60	3.02	1.23	522.2834	3	0.0625	TQDECILHFLR	iTRAQ4plex (N-term); Methylthio (C)	YES	NO
51335	56.07	72.22	89.00	88.35	87.94	1.01	1.10	1.05	531.9927	3	0.0920	EEVPTALVEAHVR	iTRAQ4plex (N-term)	YES	YES
53007	42.63	42.23	38.26	40.13	41.16	1.27	1.01	1.02	540.6607	3	0.0031	SLVALLVETQMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
53021	47.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	540.6828	3	0.0693	SLVALLVETQMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
53667	45.51	739.27	786.73	633.60	646.70	1.41	1.32	1.02	543.6655	3	0.0570	SKTPEIYLAYR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
54128	41.89	57.76	62.18	45.93	36.87	1.93	1.83	1.30	545.9912	3	-0.0003	SLVALLVETQMK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
59478	50.45	1017.44	1178.12	735.52	786.72	1.60	1.63	0.97	575.3210	3	0.0444	EKPTDMQNFGLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
59491	46.75	208.23	238.46	169.91	158.12	1.63	1.64	1.12	575.3315	3	0.0760	EKPTDMQNFGLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
59496	47.81	426.67	466.40	335.81	355.42	1.48	1.43	0.98	575.3362	3	0.0900	EKPTDMQNFGLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
59502	45.77	220.20	240.22	186.65	186.36	1.46	1.40	1.04	575.3396	3	0.1004	EKPTDMQNFGLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60323	48.12	1025.58	1121.04	789.64	763.35	1.66	1.60	1.08	580.6524	3	0.0438	EKPTDMQNFGLR	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
69777	45.19	178.14	193.16	105.94	147.04	1.50	1.43	0.75	636.7528	3	0.0874	SLVALLVETQMKK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
69779	46.53	374.79	410.61	298.93	308.14	1.50	1.45	1.01	636.7551	3	0.0945	SLVALLVETQMKK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
71212	52.77	113.04	147.78	82.85	66.12	2.11	2.43	1.31	646.0253	3	0.1408	YYEAADTVTQFDNVR	iTRAQ4plex (N-term)	YES	YES
73911	52.74	344.58	321.23	241.09	205.83	2.07	1.70	1.22	500.0330	4	0.0008	MKEEVPTALVEAHVR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73912	41.81	498.65	517.45	426.09	348.31	1.77	1.61	1.27	500.0349	4	0.0087	MKEEVPTALVEAHVR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73946	42.29	127.28	135.94	114.74	109.70	1.43	1.35	1.09	500.0771	4	0.1775	MKEEVPTALVEAHVR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
73958	54.89	123.21	139.30	110.56	109.89	1.38	1.38	1.05	500.1000	4	0.2690	MKEEVPTALVEAHVR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
74568	48.21	154.00	199.94	193.17	183.11	1.04	1.19	1.10	504.0771	4	0.1823	MKEEVPTALVEAHVR	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
81287	80.99	36.39	30.31	17.58	16.18	2.78	2.04	1.13	725.0745	3	0.0022	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81290	62.38	74.16	91.76	60.11	65.20	1.40	1.53	0.96	725.0800	3	0.0187	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81292	55.99	26.36	31.75	22.21	23.97	1.36	1.44	0.97	725.0822	3	0.0255	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81293	51.21	56.57	71.30	43.17	67.99	1.03	1.14	0.66	725.0874	3	0.0410	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81296	54.77	278.90	355.10	240.48	226.82	1.52	1.70	1.10	725.0905	3	0.0503	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81299	70.21	109.61	119.73	90.20	96.82	1.40	1.34	0.97	725.0951	3	0.0640	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81300	86.05	98.26	137.00	70.26	96.70	1.25	1.54	0.76	725.0964	3	0.0681	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81301	58.66	38.79	60.28	13.25	32.34	1.48	2.03	0.43	725.0969	3	0.0695	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81305	55.17	35.24	38.21	22.87	22.93	1.90	1.81	1.04	725.1016	3	0.0836	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

81308	54.68	47.93	53.68	48.11	44.78	1.32	1.30	1.12	725.1045	3	0.0924	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81311	63.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	725.1102	3	0.1093	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81313	72.09	112.40	130.24	68.13	83.80	1.66	1.69	0.85	725.1111	3	0.1121	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81314	72.34	71.34	83.11	54.58	40.46	2.18	2.23	1.41	725.1127	3	0.1170	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81315	62.81	90.93	103.61	65.10	72.97	1.54	1.54	0.93	725.1179	3	0.1326	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81317	55.08	84.35	82.42	85.53	42.07	2.48	2.13	2.12	725.1250	3	0.1539	DIGEGNLSTAAAAALAAAAVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
83605	41.07	463.69	515.36	364.57	341.08	1.68	1.64	1.11	745.4143	3	0.0892	EGQEEVLKEVVESEGER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
89375	60.04	59.04	48.20	41.78	60.07	1.21	0.87	0.72	813.8424	3	0.1389	SLSSLVVQLLQFQEEVFGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
99251	48.86	93.27	86.50	64.57	60.01	1.92	1.57	1.12	796.2000	4	0.1439	NNASHVVYPVPGNLEEEEWVRPVMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
99357	42.11	179.97	201.32	131.37	124.89	1.78	1.75	1.10	800.2000	4	0.1490	NNASHVVYPVPGNLEEEEWVRPVMK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
101850	45.89	84.38	80.80	72.76	38.64	2.70	2.27	1.96	941.4770	4	0.1755	WILDTDTFNEWMNEEDYEVNDDKNPVSR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
101851	40.01	52.78	60.89	32.10	34.49	1.89	1.92	0.97	941.7174	4	0.1531	WILDTDTFNEWMNEEDYEVNDDKNPVSR	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q969G3	1142	1.88	1.76	1.03	0.30	0.28	0.08	46621	28.5	44	28	10

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
16211	45.09	3594.84	3457.89	2577.95	2680.53	1.66	1.40	1.00	569.3285	2	0.0434	VEVDMEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
24898	66.43	2341.02	2299.19	1569.76	1595.06	1.81	1.57	1.03	624.8068	2	-0.0125	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24899	65.78	1560.43	1578.42	1015.46	1050.73	1.83	1.63	1.01	624.8134	2	0.0007	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24900	63.7	646.21	689.55	364.90	379.89	2.10	1.97	1.00	624.8179	2	0.0097	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24901	75.25	710.14	792.96	457.67	412.61	2.12	2.09	1.16	624.8232	2	0.0204	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24903	55.75	99.27	86.66	47.84	52.76	2.32	1.79	0.94	624.8269	2	0.0277	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24904	57.29	1302.52	1323.82	784.09	804.39	2.00	1.79	1.02	624.8278	2	0.0295	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24905	51.39	400.54	423.21	229.57	273.25	1.81	1.68	0.88	624.8291	2	0.0322	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24906	53.38	2176.18	2191.01	1373.43	1388.01	1.94	1.72	1.03	624.8305	2	0.0350	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24907	53.91	568.15	592.60	318.36	333.08	2.11	1.93	1.00	624.8315	2	0.0370	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24908	65.25	541.51	524.39	344.99	313.95	2.13	1.82	1.14	624.8316	2	0.0371	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24909	59.77	1625.00	1600.00	939.51	941.12	2.13	1.85	1.04	624.8367	2	0.0473	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
24917	54.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	624.8495	2	0.0729	AEAALEEESR	iTRAQ4plex (N-term)	YES	YES
29279	51.18	1061.17	991.40	611.34	650.50	2.01	1.66	0.98	651.3635	2	0.0548	IEYNESMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
29281	53.05	2630.36	2382.24	1628.12	1730.35	1.88	1.50	0.98	651.3657	2	0.0592	IEYNESMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48188	52.4	149.78	161.10	99.10	89.38	2.07	1.96	1.15	772.4037	2	-0.0194	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48190	70.37	737.04	748.25	459.68	473.57	1.92	1.72	1.01	772.4056	2	-0.0157	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48194	40.78	151.63	168.54	81.33	73.17	2.56	2.50	1.16	772.4121	2	-0.0027	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48208	98.02	488.06	546.92	299.36	300.98	2.00	1.98	1.04	772.4225	2	0.0181	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48210	53.72	1307.90	1355.26	857.01	862.08	1.87	1.71	1.04	772.4255	2	0.0242	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48212	55.7	388.92	403.90	262.61	274.78	1.75	1.60	1.00	772.4292	2	0.0314	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48222	74.04	901.83	958.68	614.53	674.39	1.65	1.55	0.95	772.4389	2	0.0509	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48223	63.46	659.11	694.30	413.77	400.69	2.03	1.88	1.08	772.4389	2	0.0510	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48236	84.48	874.73	913.54	574.60	612.23	1.76	1.62	0.98	772.4444	2	0.0620	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
48239	75.11	949.96	1002.21	603.66	632.83	1.85	1.72	0.99	772.4466	2	0.0663	IAAEIAQAEEQAR	iTRAQ4plex (N-term)	YES	YES
61466	58.84	240.18	340.82	194.48	173.91	1.71	2.13	1.16	587.0076	3	-0.0119	KLEAELLQIEER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61475	53.81	211.68	265.85	182.99	167.50	1.56	1.73	1.14	587.0125	3	0.0027	KLEAELLQIEER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61498	68.76	344.36	382.17	243.36	213.67	1.99	1.94	1.19	587.0280	3	0.0490	KLEAELLQIEER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61501	60.63	329.62	419.03	274.75	278.22	1.46	1.64	1.03	587.0320	3	0.0613	KLEAELLQIEER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61502	52.8	205.80	210.12	152.54	156.93	1.62	1.46	1.01	587.0321	3	0.0613	KLEAELLQIEER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61506	56.5	99.14	93.12	97.57	100.52	1.22	1.01	1.01	587.0400	3	0.0852	KLEAELLQIEER	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61515	44.87	653.44	728.11	463.66	431.41	1.87	1.83	1.12	587.2000	3	-0.4189	KLEAELLQIEER	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
63956	73.12	60.73	63.36	33.95	34.41	2.18	2.00	1.03	600.6875	3	0.0246	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
63957	56.51	31.92	54.23	28.63	31.66	1.24	1.86	0.94	600.6886	3	0.0277	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
63963	59.83	29.34	32.91	11.48	15.45	2.34	2.32	0.77	600.7003	3	0.0628	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
63968	85.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	900.5523	2	0.0739	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
63969	47.51	22.64	18.13	17.45	12.20	2.29	1.62	1.49	600.7041	3	0.0744	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
63972	44.11	21.49	25.39	10.92	15.48	1.71	1.78	0.73	600.7060	3	0.0800	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
63974	42.48	8.68	16.19	9.73	8.55	1.25	2.06	1.19	600.7101	3	0.0923	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES

63978	88.55	35.99	50.28	19.19	23.09	1.92	2.37	0.87	600.7172	3	0.1136	LISEILSESVVPDVR	iTRAQ4plex (N-term)	YES	YES
73525	43.08	787.41	829.59	480.95	525.53	1.85	1.72	0.95	663.3749	3	0.0774	FLESTDSFNNELKR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78432	50.74	648.59	670.30	465.67	462.37	1.73	1.58	1.05	702.0552	3	0.0225	KFLESTDSFNNELK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90751	55.08	1372.28	1536.03	1259.33	1222.79	1.39	1.37	1.07	831.4703	3	0.1124	SQSSIVPEEEQAANKGEEK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
94188	58.12	769.10	794.86	508.10	521.34	1.82	1.66	1.02	893.4783	3	0.1161	DLTDEEKQEYLNEYEAEK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

AT-rich interactive domain-containing protein 1A - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
O14497	367	1.79	1.76	0.96	0.28	0.24	0.09	241892	3.9	12	10	6

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
7043	45.9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	494.3566	2	0.0255	ALLALAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
19983	60.81	1900.48	1825.87	1256.49	1311.63	1.79	1.51	1.00	595.9012	2	0.0353	LVLETLSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
28283	43.47	774.99	850.57	571.24	564.44	1.70	1.64	1.05	644.8685	2	0.0271	YLAFTEEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
28297	54.24	645.73	813.46	398.14	500.27	1.59	1.77	0.83	644.8802	2	0.0504	YLAFTEEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
44068	40.42	314.29	335.31	261.68	297.89	1.30	1.22	0.92	496.6290	3	0.0850	FPFGISPAQSHR	iTRAQ4plex (N-term)	YES	YES
46301	67.82	182.42	179.24	96.46	103.48	2.18	1.88	0.97	759.3865	2	0.0345	EEAGGEAAAAAAAER	iTRAQ4plex (N-term)	YES	YES
46306	117.5	747.27	836.39	435.89	444.55	2.08	2.05	1.02	759.3911	2	0.0438	EEAGGEAAAAAAAER	iTRAQ4plex (N-term)	YES	YES
46310	73.91	735.82	809.16	398.73	462.25	1.97	1.90	0.90	759.4025	2	0.0666	EEAGGEAAAAAAAER	iTRAQ4plex (N-term)	YES	YES
46312	75.22	903.58	970.90	574.54	557.18	2.00	1.89	1.07	759.4077	2	0.0769	EEAGGEAAAAAAAER	iTRAQ4plex (N-term)	YES	YES
53802	60.87	274.61	319.74	194.83	217.91	1.56	1.59	0.93	544.3047	3	0.0536	VQEFDSGLLHWR	iTRAQ4plex (N-term)	YES	YES
53806	45.27	259.04	297.93	152.76	200.83	1.59	1.61	0.79	544.3098	3	0.0691	VQEFDSGLLHWR	iTRAQ4plex (N-term)	YES	YES
98514	44.35	418.56	471.77	273.66	327.21	1.58	1.57	0.87	769.6446	4	-0.0030	KHVTTAEGTPGTTDQEGPPPDGPPEK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

AT-rich interactive domain-containing protein 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q68CP9	1357	1.80	1.67	1.05	0.34	0.30	0.14	197268	13.4	66	50	21

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
12947	46.73	726.52	724.22	512.34	541.22	1.66	1.45	0.99	544.8445	2	-0.0100	DALLAGLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
12956	57.11	1829.76	1862.02	1419.50	1439.26	1.57	1.41	1.03	544.8643	2	0.0296	DALLAGLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
12960	46.89	1564.21	1739.71	1353.31	1403.36	1.38	1.35	1.00	544.8656	2	0.0321	DALLAGLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
15776	50.74	681.12	643.97	476.86	542.90	1.55	1.29	0.91	565.8973	2	0.0122	LTAALILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
15778	56.02	675.05	697.66	498.75	545.86	1.53	1.39	0.95	565.9022	2	0.0220	LTAALILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
15779	60.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	565.9052	2	0.0281	LTAALILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
15780	44.56	460.85	607.71	390.45	389.82	1.46	1.69	1.04	565.9078	2	0.0333	LTAALILK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
18861	47.28	84.17	91.61	45.39	57.87	1.80	1.72	0.82	589.3310	2	-0.0150	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18862	45.32	182.13	243.74	112.60	134.69	1.67	1.97	0.87	589.3324	2	-0.0123	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18870	49.61	56.65	67.67	31.88	30.50	2.29	2.41	1.09	589.3401	2	0.0031	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18871	42.02	114.03	148.30	96.73	68.50	2.06	2.35	1.47	589.3421	2	0.0072	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18875	47.39	186.54	222.82	134.04	152.75	1.51	1.59	0.91	589.3456	2	0.0143	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18877	54.25	210.53	223.34	136.85	130.62	1.99	1.86	1.09	589.3467	2	0.0164	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18881	45.29	28.29	35.35	32.22	18.51	1.89	2.08	1.81	589.3489	2	0.0209	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18896	43.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	589.3585	2	0.0401	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
18898	48.29	60.63	68.35	34.96	27.36	2.74	2.72	1.33	589.3625	2	0.0479	GLAFLDELR	iTRAQ4plex (N-term)	YES	YES
19213	63.79	3255.08	3045.88	2289.84	2376.91	1.69	1.39	1.00	591.3656	2	0.0108	VTTLGGFAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
22223	40.91	102.67	116.61	75.77	62.47	2.03	2.03	1.26	609.8148	2	0.0140	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22224	42.1	106.98	100.87	58.89	56.25	2.35	1.95	1.09	609.8164	2	0.0174	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22225	41.48	95.01	99.45	62.96	57.07	2.06	1.89	1.15	609.8187	2	0.0218	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22230	57.18	387.76	361.76	237.49	236.95	2.02	1.66	1.04	609.8221	2	0.0287	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22231	57.28	248.71	264.42	158.67	150.60	2.04	1.91	1.10	609.8227	2	0.0300	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22232	65.11	301.56	321.82	205.92	211.41	1.76	1.65	1.01	609.8232	2	0.0309	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22236	52.94	734.52	774.10	566.83	558.72	1.62	1.51	1.06	609.8278	2	0.0401	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22238	54.64	642.41	679.30	445.86	420.26	1.89	1.76	1.11	609.8290	2	0.0425	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES
22241	61.58	657.76	661.78	498.31	457.91	1.77	1.57	1.13	609.8335	2	0.0514	DIVDDNEVR	iTRAQ4plex (N-term)	YES	YES

25805	47.11	1497.36	1481.82	1092.41	1065.36	1.74	1.51	1.07	629.8425	2	-0.0094	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
25812	47.88	173.21	189.47	107.40	90.98	2.35	2.26	1.23	629.8515	2	0.0085	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
25819	55.18	476.73	463.69	297.03	276.17	2.13	1.82	1.12	629.8575	2	0.0205	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
25826	57.95	266.70	264.91	173.59	150.92	2.18	1.91	1.20	629.8629	2	0.0313	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
25830	59.5	541.71	614.38	343.91	339.91	1.97	1.96	1.05	629.8653	2	0.0362	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
25831	40.22	639.66	666.79	402.81	389.21	2.03	1.86	1.08	629.8657	2	0.0370	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
25835	42.27	1048.78	1110.78	784.96	793.57	1.63	1.52	1.03	629.8698	2	0.0452	LGINDIEGQR	iTRAQ4plex (N-term)	YES	YES
31576	49.46	1310.75	1312.31	1106.73	1153.89	1.40	1.24	1.00	444.2858	3	0.0706	TVFPNHTVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
34052	42.67	682.64	667.98	477.19	425.86	1.98	1.70	1.17	454.2686	3	0.0571	ELDLHGLYTR	iTRAQ4plex (N-term)	YES	YES
34070	67.92	3761.61	3719.42	2633.00	2654.80	1.75	1.52	1.03	680.9223	2	0.0335	VAIESAVQQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
34073	62.31	1751.26	1837.02	1344.00	1340.68	1.61	1.49	1.04	680.9282	2	0.0453	VAIESAVQQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
39442	76.51	1955.17	2041.73	1350.11	1416.20	1.70	1.57	0.99	712.9083	2	0.0469	NLSFEEGNVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
39446	61.28	1396.41	1479.42	972.61	1018.75	1.69	1.58	0.99	712.9126	2	0.0557	NLSFEEGNVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
39910	61.37	2238.27	2486.65	1586.83	1686.11	1.64	1.60	0.98	716.4268	2	0.0378	GGILTSTGFYK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
39911	70.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	716.4323	2	0.0487	GGILTSTGFYK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
41329	46.27	209.21	239.64	162.82	133.43	1.94	1.95	1.27	483.9579	3	-0.0077	KGLAFLDELR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
46746	41.59	906.39	880.26	523.63	556.56	2.01	1.72	0.98	508.6420	3	0.0656	FSFITHLQDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
51710	43.69	391.02	398.90	291.02	296.51	1.63	1.46	1.02	533.9558	3	0.0500	ENEMHVGSLLNGR	iTRAQ4plex (N-term)	YES	YES
51715	55.19	422.51	474.33	345.75	370.97	1.41	1.39	0.97	533.9685	3	0.0881	ENEMHVGSLLNGR	iTRAQ4plex (N-term)	YES	YES
51757	49.62	320.62	418.90	297.09	270.21	1.46	1.69	1.15	534.2855	3	0.0550	ENEMHVGSLLNGR	Deamidated (NQ); iTRAQ4plex (N-term)	YES	YES
51764	45.93	273.56	322.04	286.59	220.78	1.53	1.59	1.35	534.3006	3	0.1004	ENEMHVGSLLNGR	Deamidated (NQ); iTRAQ4plex (N-term)	YES	YES
53316	46.22	736.58	721.04	469.98	404.13	2.25	1.94	1.21	541.9922	3	0.0498	AIVNHPSAALMALR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
53318	46.22	591.56	622.19	386.90	301.97	2.42	2.24	1.33	541.9925	3	0.0509	AIVNHPSAALMALR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
63136	56.2	138.16	141.85	96.08	117.53	1.45	1.31	0.85	595.6815	3	0.0008	FLLLSAHSHFISLR	iTRAQ4plex (N-term)	YES	YES
69796	46.34	97.58	120.86	75.94	102.46	1.18	1.28	0.77	637.0045	3	0.0630	NQWGEIVEEFNFPR	iTRAQ4plex (N-term)	YES	YES
69807	41.24	30.25	37.33	28.70	28.67	1.30	1.42	1.04	637.0231	3	0.1188	NQWGEIVEEFNFPR	iTRAQ4plex (N-term)	YES	YES
80395	51.36	364.44	378.01	207.61	262.28	1.72	1.57	0.82	538.5444	4	0.0163	VEDSSSNGQAHIHVVGVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80422	40.86	845.25	887.42	569.76	621.47	1.68	1.55	0.95	538.7839	4	-0.0097	VEDSSSNGQAHIHVVGVK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80423	57.21	619.97	701.64	443.78	467.33	1.64	1.63	0.99	538.7843	4	-0.0082	VEDSSSNGQAHIHVVGVK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80429	44.55	535.16	592.04	334.08	367.37	1.80	1.75	0.95	538.8000	4	0.0545	VEDSSSNGQAHIHVVGVK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80432	67.74	550.57	571.51	387.21	392.00	1.73	1.58	1.03	538.8068	4	0.0816	VEDSSSNGQAHIHVVGVK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86940	47.25	279.57	321.54	225.69	193.52	1.78	1.81	1.21	782.1276	3	0.0568	AVVAQHVAPPPGIVEIDSEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86944	61.79	108.66	116.93	85.95	82.02	1.64	1.55	1.09	782.1428	3	0.1023	AVVAQHVAPPPGIVEIDSEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86951	59.81	303.25	337.39	217.02	211.90	1.77	1.73	1.07	782.1557	3	0.1411	AVVAQHVAPPPGIVEIDSEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86954	66	464.46	526.88	346.29	331.89	1.73	1.73	1.09	782.1609	3	0.1567	AVVAQHVAPPPGIVEIDSEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86955	47.52	307.19	290.37	210.64	187.23	2.03	1.69	1.17	782.1619	3	0.1598	AVVAQHVAPPPGIVEIDSEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
88378	41.95	28.70	64.93	44.63	41.93	0.85	1.68	1.11	599.7967	4	0.0110	SHEGTSGEWIWESLFHPPR	iTRAQ4plex (N-term)	YES	YES
88381	46.78	22.30	35.15	17.10	22.20	1.24	1.72	0.80	599.8149	4	0.0837	SHEGTSGEWIWESLFHPPR	iTRAQ4plex (N-term)	YES	YES
90491	48.85	920.23	888.64	517.04	558.84	2.03	1.73	0.96	620.5783	4	0.0515	WFQTPSQVFYHAATEHGGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90492	58.76	323.16	341.78	295.40	295.37	1.35	1.26	1.04	620.5876	4	0.0887	WFQTPSQVFYHAATEHGGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Histone modifiying proteins

Histone-lysine N-methyltransferase H3 lysine-9 specific 5 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q9H9B1	226	2.05	1.91	0.99	0.43	0.42	0.38	138166	5.9	12	7	6			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
18446	42.28	1103.10	1144.80	905.72	949.10	1.43	1.31	0.99	586.3519	2	0.0329	TVIEMFK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
39700	41.91	1862.31	1784.29	1249.72	1340.98	1.71	1.45	0.97	476.6479	3	0.0345	KLPAPGADVK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42032	41.66	370.02	398.93	168.32	190.03	2.40	2.28	0.92	730.4008	2	0.0322	VNPQDGTNTLTR	iTRAQ4plex (N-term)	YES	YES
42037	56.04	2278.67	2316.63	1286.76	1323.78	2.13	1.90	1.01	730.4123	2	0.0551	VNPQDGTNTLTR	iTRAQ4plex (N-term)	YES	YES
42047	47.92	819.31	784.71	384.06	433.93	2.33	1.97	0.92	730.4259	2	0.0823	VNPQDGTNTLTR	iTRAQ4plex (N-term)	YES	YES
67346	41.25	29.54	23.00	7.99	16.62	2.19	1.50	0.50	621.3694	3	0.0238	VLLMLVDGIDPNFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67354	72.57	47.84	57.87	42.78	22.02	2.68	2.86	2.02	621.3755	3	0.0421	VLLMLVDGIDPNFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67358	40.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	621.3813	3	0.0595	VLLMLVDGIDPNFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77073	40.78	277.12	294.17	176.10	196.78	1.74	1.62	0.93	691.0629	3	0.1008	TPLMEAAENNHLEAVK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES

81434	54.51	538.76	611.80	368.43	355.81	1.87	1.87	1.08	726.1070	3	0.0629	ETLESALIALDSEKPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81437	57.15	357.21	489.50	270.70	304.33	1.45	1.75	0.93	726.1193	3	0.0998	ETLESALIALDSEKPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81443	44.08	476.02	448.87	259.32	264.88	2.22	1.84	1.02	726.1378	3	0.1553	ETLESALIALDSEKPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Histone-lysine N-methyltransferase H3 lysine-9 specific 3 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q96KQ7	922	2.02	1.83	1.01	0.32	0.31	0.11	132287	5.3	29	23	5

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
19728	43.46	1978.80	1909.85	1400.49	1390.07	1.76	1.49	1.05	594.8324	2	-0.0129	ALVIQESER	iTRAQ4plex (N-term)	YES	YES
19730	43.01	2539.57	2471.38	1894.35	1954.28	1.60	1.37	1.01	594.8343	2	-0.0090	ALVIQESER	iTRAQ4plex (N-term)	YES	YES
19734	44.6	1111.39	1130.40	678.22	681.35	2.01	1.80	1.04	594.8386	2	-0.0005	ALVIQESER	iTRAQ4plex (N-term)	YES	YES
19746	45.29	995.94	1003.17	615.62	605.29	2.03	1.80	1.06	594.8516	2	0.0255	ALVIQESER	iTRAQ4plex (N-term)	YES	YES
19748	46.46	1956.05	1947.34	1299.77	1256.56	1.92	1.68	1.08	594.8539	2	0.0300	ALVIQESER	iTRAQ4plex (N-term)	YES	YES
19750	46.58	2677.66	2566.94	1650.49	1560.16	2.12	1.79	1.10	594.8580	2	0.0383	ALVIQESER	iTRAQ4plex (N-term)	YES	YES
30680	43.3	557.61	619.41	376.70	387.43	1.78	1.74	1.01	440.2530	3	0.0387	VFMLHQDLR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
30686	61.62	887.26	937.15	597.42	583.18	1.88	1.75	1.07	440.2580	3	0.0536	VFMLHQDLR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
30689	49.41	414.96	452.14	270.72	253.37	2.02	1.94	1.11	440.2617	3	0.0648	VFMLHQDLR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
51137	110.34	1647.96	1651.85	897.68	987.95	2.06	1.82	0.95	795.9161	2	0.0047	LNSGGGLSEELGSAR	iTRAQ4plex (N-term)	YES	YES
51147	60.79	861.32	883.93	427.42	433.88	2.45	2.21	1.03	795.9330	2	0.0383	LNSGGGLSEELGSAR	iTRAQ4plex (N-term)	YES	YES
51150	129.43	937.08	996.09	437.41	498.32	2.32	2.17	0.91	795.9406	2	0.0536	LNSGGGLSEELGSAR	iTRAQ4plex (N-term)	YES	YES
51152	67.96	763.99	800.40	371.39	381.49	2.47	2.28	1.01	795.9407	2	0.0539	LNSGGGLSEELGSAR	iTRAQ4plex (N-term)	YES	YES
51153	54.53	393.18	441.22	178.72	219.52	2.21	2.18	0.85	795.9410	2	0.0544	LNSGGGLSEELGSAR	iTRAQ4plex (N-term)	YES	YES
51162	125.11	1198.83	1158.45	604.86	671.62	2.20	1.87	0.94	795.9534	2	0.0791	LNSGGGLSEELGSAR	iTRAQ4plex (N-term)	YES	YES
66254	60.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	614.3450	3	0.0523	FINHLCDPNIIPVR	iTRAQ4plex (N-term); Methylthio (C)	YES	YES
67381	49.6	579.79	610.64	327.66	324.64	2.20	2.04	1.05	621.6753	3	-0.0061	KLNSGGGLSEELGSAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67393	61.71	929.59	970.59	564.60	629.62	1.82	1.68	0.93	621.6909	3	0.0408	KLNSGGGLSEELGSAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67397	67.74	1086.45	1027.69	650.37	697.71	1.92	1.60	0.97	621.6936	3	0.0490	KLNSGGGLSEELGSAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67410	44.85	299.86	307.06	168.76	186.10	1.99	1.79	0.94	621.7025	3	0.0757	KLNSGGGLSEELGSAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67413	75	388.86	357.10	321.14	327.19	1.47	1.19	1.02	621.7037	3	0.0792	KLNSGGGLSEELGSAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
67416	75.95	268.10	245.18	161.35	159.49	2.08	1.67	1.05	621.7091	3	0.0953	KLNSGGGLSEELGSAR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
71284	48.12	165.78	160.92	106.09	114.06	1.79	1.53	0.97	646.3712	3	0.0596	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term)	YES	YES
71290	41.26	48.90	55.17	29.87	48.60	1.24	1.23	0.64	646.3748	3	0.0705	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term)	YES	YES
72081	53.91	305.21	339.36	278.94	261.11	1.44	1.41	1.11	651.7102	3	0.0817	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
72084	76.14	392.24	388.03	253.56	223.20	2.17	1.89	1.18	651.7111	3	0.0844	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
72086	47.71	285.51	274.28	254.70	234.26	1.50	1.27	1.13	651.7131	3	0.0903	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
72089	50.24	223.35	232.71	165.03	162.34	1.70	1.56	1.06	651.7164	3	0.1003	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
72095	89.17	90.72	113.82	58.88	64.24	1.74	1.93	0.95	651.7256	3	0.1278	TPLMEAVVNNHLEVAR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES

Histone deacetylase complex subunit SAP130 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9H0E3	79	1.37	1.22	0.97	0.05	0.12	0.15	110255	2.3	2	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
46050	54.68	766.10	745.11	599.69	701.27	1.35	1.15	0.89	757.4826	2	0.0387	LTNLQEGIIPK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
53019	57.8	454.38	481.25	418.27	396.70	1.41	1.32	1.10	540.6781	3	0.0473	ITLPSHPALGTPK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Histone deacetylase 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q13547	808	1.71	1.47	1.01	0.55	0.28	0.10	55068	19.7	32	15	7

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
23810	60.07	1893.41	1829.58	888.51	1056.19	2.21	1.88	0.88	412.9107	3	0.0161	VMTVSFHK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO

23821	42.33	1664.80	1659.96	729.93	919.49	2.24	1.96	0.83	412.9133	3	0.0241	VMTVSFHK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
29336	42.28	2221.77	2261.71	1522.13	1544.24	1.78	1.59	1.03	651.8543	2	0.0051	YYAVNYPLR	iTRAQ4plex (N-term)	YES	YES
29364	41.6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	651.8772	2	0.0508	YYAVNYPLR	iTRAQ4plex (N-term)	YES	YES
29365	40.79	711.81	709.69	463.30	413.44	2.13	1.87	1.17	651.8790	2	0.0545	YYAVNYPLR	iTRAQ4plex (N-term)	YES	YES
46364	45.4	1311.97	1351.49	872.32	934.39	1.73	1.57	0.97	759.8677	2	-0.0063	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46367	56.83	916.58	920.94	612.97	590.50	1.92	1.70	1.08	759.8807	2	0.0197	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46368	55.88	1311.75	1362.77	866.52	838.64	1.93	1.77	1.08	759.8817	2	0.0216	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46371	48.69	570.05	647.44	416.54	426.61	1.65	1.65	1.02	759.8885	2	0.0351	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46373	59.54	989.03	948.56	647.71	654.90	1.86	1.57	1.03	759.8930	2	0.0441	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46375	53.58	1207.18	1190.99	767.16	768.29	1.94	1.68	1.04	759.9009	2	0.0600	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46377	55.63	1207.64	1167.85	769.26	823.22	1.81	1.54	0.97	759.9061	2	0.0704	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46378	55.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	759.9069	2	0.0721	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46411	50.96	3136.77	3111.50	1979.05	2060.83	1.88	1.64	1.00	760.1040	2	0.4661	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
59031	47.86	1784.40	1830.24	1335.78	1404.06	1.57	1.42	0.99	572.3112	3	0.0518	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
59032	50.18	740.84	758.02	589.64	585.71	1.56	1.41	1.05	572.3141	3	0.0605	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
59829	41.14	1265.58	1271.14	1037.56	1068.04	1.46	1.29	1.01	577.6239	3	-0.0050	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
59845	49.53	1955.22	1938.92	1601.91	1664.98	1.45	1.27	1.00	577.6585	3	0.0988	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
73647	45.26	173.83	208.69	130.85	127.90	1.68	1.77	1.07	664.3516	3	0.0186	QQTDIAVNWAGGLHHAK	Deamidated (NQ); iTRAQ4plex (K)	YES	YES
73652	41.97	307.08	346.23	246.37	265.57	1.43	1.42	0.97	664.3577	3	0.0371	QQTDIAVNWAGGLHHAK	Deamidated (NQ); iTRAQ4plex (K)	YES	YES
79792	42.95	122.46	126.98	121.75	147.39	1.03	0.94	0.86	534.3274	4	0.1483	QQTDIAVNWAGGLHHAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
79796	55.55	203.12	244.19	250.62	307.48	0.82	0.86	0.85	534.3369	4	0.1861	QQTDIAVNWAGGLHHAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90401	40.07	252.96	302.15	256.45	228.16	1.37	1.44	1.17	826.1154	3	0.0674	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90403	65.44	1012.47	976.52	731.89	785.09	1.59	1.35	0.97	826.1213	3	0.0852	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90404	48.49	357.21	339.41	242.49	244.75	1.80	1.51	1.03	826.1219	3	0.0870	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90409	51.72	558.76	561.78	393.67	443.72	1.55	1.38	0.92	826.1280	3	0.1054	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90418	76.46	777.09	995.73	690.05	715.95	1.34	1.51	1.00	826.1443	3	0.1541	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
90740	50.67	688.15	792.69	636.49	618.57	1.37	1.39	1.07	831.4426	3	0.0541	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
90743	58.96	717.43	728.36	558.49	557.14	1.59	1.42	1.04	831.4493	3	0.0743	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
90745	72.29	476.14	443.02	351.09	353.76	1.66	1.36	1.03	831.4525	3	0.0839	DGIDDESYEAIFKPVMSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
91525	75.63	659.89	455.57	273.96	280.22	2.91	1.77	1.02	841.1147	3	0.0701	LHISPSNMTNQNTNEYLEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
91528	47.65	619.55	472.27	229.67	291.19	2.63	1.76	0.82	841.1339	3	0.1278	LHISPSNMTNQNTNEYLEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Histone deacetylase 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q92769	631	1.29	1.28	0.94	0.21	0.20	0.04	55329	13.7	24	8	5

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
23810	60.07	1893.41	1829.58	888.51	1056.19	2.21	1.88	0.88	412.9107	3	0.0161	VMTVSFHK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
23821	42.33	1664.80	1659.96	729.93	919.49	2.24	1.96	0.83	412.9133	3	0.0241	VMTVSFHK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
46364	45.4	1311.97	1351.49	872.32	934.39	1.73	1.57	0.97	759.8677	2	-0.0063	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46367	56.83	916.58	920.94	612.97	590.50	1.92	1.70	1.08	759.8807	2	0.0197	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46368	55.88	1311.75	1362.77	866.52	838.64	1.93	1.77	1.08	759.8817	2	0.0216	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46371	48.69	570.05	647.44	416.54	426.61	1.65	1.65	1.02	759.8885	2	0.0351	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46373	59.54	989.03	948.56	647.71	654.90	1.86	1.57	1.03	759.8930	2	0.0441	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46375	53.58	1207.18	1190.99	767.16	768.29	1.94	1.68	1.04	759.9009	2	0.0600	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46377	55.63	1207.64	1167.85	769.26	823.22	1.81	1.54	0.97	759.9061	2	0.0704	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46378	55.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	759.9069	2	0.0721	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
46411	50.96	3136.77	3111.50	1979.05	2060.83	1.88	1.64	1.00	760.1040	2	0.4661	YGEYFPGTGDLR	iTRAQ4plex (N-term)	YES	NO
59031	47.86	1784.40	1830.24	1335.78	1404.06	1.57	1.42	0.99	572.3112	3	0.0518	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
59032	50.18	740.84	758.02	589.64	585.71	1.56	1.41	1.05	572.3141	3	0.0605	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
59829	41.14	1265.58	1271.14	1037.56	1068.04	1.46	1.29	1.01	577.6239	3	-0.0050	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
59845	49.53	1955.22	1938.92	1601.91	1664.98	1.45	1.27	1.00	577.6585	3	0.0988	SIRPDNMSEYSK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	NO
74371	53.51	432.75	462.72	377.80	410.54	1.30	1.23	0.96	670.0527	3	0.1496	QQTDMAVNWAGGLHHAK	iTRAQ4plex (K)	YES	YES
80427	55.26	375.66	467.24	468.67	535.44	0.87	0.95	0.91	538.7991	4	0.0785	QQTDMAVNWAGGLHHAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80436	54.44	330.40	330.25	297.75	327.27	1.25	1.10	0.95	538.8140	4	0.1381	QQTDMAVNWAGGLHHAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80439	57.82	128.70	114.85	114.16	128.75	1.23	0.97	0.92	538.8243	4	0.1794	QQTDMAVNWAGGLHHAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
89892	56.74	310.36	332.00	214.55	256.01	1.50	1.41	0.87	819.7798	3	0.0013	DGIDDESYGQIFKPIISK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

89896	72.87	623.95	752.37	540.46	603.93	1.28	1.35	0.93	819.8065	3	0.0812	DGIDDESYGQIFKPIISK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
89898	64.43	1655.26	1587.07	1104.83	1124.70	1.82	1.53	1.02	819.8088	3	0.0881	DGIDDESYGQIFKPIISK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
89899	62.46	530.85	507.50	358.82	417.35	1.57	1.32	0.90	615.1170	4	0.1224	DGIDDESYGQIFKPIISK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
89900	59.18	893.83	1108.41	800.95	829.85	1.33	1.45	1.01	819.8290	3	0.1489	DGIDDESYGQIFKPIISK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

DNA damage response proteins

DNA-(apurinic or apyrimidinic site) lyase - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
P27695	782	4.58	4.18	1.19	1.43	1.62	0.19	35532	21.7	29	26	6

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
27179	75.18	454.40	479.94	139.16	76.26	7.36	6.84	1.90	638.3237	2	0.0104	GAVAEDGDELR	iTRAQ4plex (N-term)	YES	YES
27182	76.92	402.32	434.23	98.07	95.15	5.22	4.96	1.07	638.3289	2	0.0208	GAVAEDGDELR	iTRAQ4plex (N-term)	YES	YES
27185	98.06	949.24	1038.00	259.48	212.29	5.52	5.31	1.27	638.3326	2	0.0282	GAVAEDGDELR	iTRAQ4plex (N-term)	YES	YES
27186	58.7	371.62	368.98	101.07	63.08	7.27	6.36	1.67	638.3351	2	0.0332	GAVAEDGDELR	iTRAQ4plex (N-term)	YES	YES
27187	75.37	510.60	570.11	122.06	99.94	6.31	6.20	1.27	638.3364	2	0.0358	GAVAEDGDELR	iTRAQ4plex (N-term)	YES	YES
27191	79.55	1096.76	1112.22	327.08	261.17	5.18	4.63	1.30	638.3386	2	0.0402	GAVAEDGDELR	iTRAQ4plex (N-term)	YES	YES
27710	47.82	1339.93	1353.62	496.55	424.30	3.90	3.47	1.22	641.3490	2	-0.0012	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27711	44.89	259.16	291.89	59.01	53.05	6.03	5.98	1.16	641.3492	2	-0.0008	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27728	58.34	769.53	823.28	237.02	208.51	4.56	4.29	1.18	641.3650	2	0.0308	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27732	62.53	1192.39	1180.30	366.95	339.31	4.34	3.78	1.13	641.3688	2	0.0384	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27733	67.23	1380.74	1412.91	409.19	348.17	4.90	4.41	1.22	641.3724	2	0.0456	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27735	40.03	607.47	576.60	179.72	169.34	4.43	3.70	1.11	641.3737	2	0.0483	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27737	46.75	1086.93	1153.66	396.42	320.01	4.19	3.92	1.29	641.3741	2	0.0490	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27739	62.92	1234.59	1320.42	444.88	392.66	3.88	3.66	1.18	641.3785	2	0.0577	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
27747	41.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	641.3841	2	0.0690	EGYSGVGLLSR	iTRAQ4plex (N-term)	YES	YES
48509	68.11	1308.76	1412.26	568.50	470.01	3.44	3.27	1.26	516.6140	3	0.0007	KGAVAEDGDELR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48510	81.06	1510.18	1640.97	614.62	486.70	3.83	3.66	1.32	516.6171	3	0.0101	KGAVAEDGDELR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48518	53.95	1131.76	1161.98	525.18	487.21	2.87	2.59	1.12	516.6344	3	0.0620	KGAVAEDGDELR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48524	64.9	1383.27	1436.47	578.61	554.53	3.08	2.82	1.09	516.6423	3	0.0856	KGAVAEDGDELR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77228	57.81	653.30	585.06	174.23	167.57	4.81	3.79	1.08	692.3757	3	0.0632	GAVAEDGDELRTEPEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77229	50.33	2694.74	2662.91	682.46	625.63	5.32	4.63	1.14	692.3760	3	0.0640	GAVAEDGDELRTEPEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77238	56.55	2178.28	1885.87	472.24	444.86	6.05	4.61	1.11	692.3829	3	0.0848	GAVAEDGDELRTEPEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77239	40.36	595.27	586.72	166.60	158.92	4.62	4.01	1.09	692.3835	3	0.0864	GAVAEDGDELRTEPEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77242	46.9	1137.17	991.60	235.18	250.43	5.61	4.30	0.98	692.3886	3	0.1017	GAVAEDGDELRTEPEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77254	45.23	1586.62	1518.95	468.75	375.39	5.22	4.40	1.30	692.4037	3	0.1470	GAVAEDGDELRTEPEAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
87612	48.26	92.56	121.76	25.49	12.73	8.98	10.40	2.09	790.4768	3	0.1672	LDYFLLSHSLLPALCDSK	iTRAQ4plex (K); iTRAQ4plex (N-term); Methylthio (C)	YES	YES
95312	57.81	1081.61	1169.49	248.32	250.66	5.33	5.07	1.03	918.8508	3	0.1038	LPAELQELPGLSHQYWSAPSDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
95317	45.34	536.38	531.13	104.19	99.78	6.64	5.79	1.09	918.8686	3	0.1572	LPAELQELPGLSHQYWSAPSDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
95340	47.01	62.49	75.61	22.76	21.90	3.52	3.75	1.08	689.7000	4	0.3601	LPAELQELPGLSHQYWSAPSDK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Telomeric repeat-binding factor 2-interacting protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9NYB0	93	3.18	4.39	1.18	0.76	2.67	0.01	44233	11.5	3	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
84088	46.76	142.56	171.98	52.23	46.48	3.79	4.02	1.17	749.7043	3	-0.0117	KAEEDPEAADSGEPQNK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
84100	41.36	49.55	72.69	12.46	9.37	6.53	8.44	1.39	749.7525	3	0.1329	KAEEDPEAADSGEPQNK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
98200	54.55	170.80	260.21	87.98	77.78	2.71	3.64	1.18	759.9446	4	0.2091	LGPASAADTGSEAKPGALAEGAAEPEPQR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

High mobility group protein B3 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide

O15347	132	2.45	2.33	1.18	0.30	0.24	0.16	22965	7.0	4	4	1			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
75668	45.82	240.52	224.23	115.46	112.58	2.64	2.16	1.07	680.0421	3	-0.0216	KNPEVPVNFAEFSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
75671	61.67	185.10	195.05	98.09	90.39	2.53	2.35	1.13	680.0521	3	0.0085	KNPEVPVNFAEFSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
75685	46.65	124.10	144.87	58.31	58.23	2.63	2.70	1.04	680.0759	3	0.0799	KNPEVPVNFAEFSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
75689	56.14	170.67	216.65	139.35	104.51	2.02	2.25	1.39	680.0902	3	0.1228	KNPEVPVNFAEFSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

DNA topoisomerase 2-binding protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q92547	41	2.43	2.45	1.14	-	-	-	170571	0.7	1	1	1			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
53520	40.55	65.50	75.01	36.34	33.29	2.43	2.45	1.14	543.0226	3	-0.0137	KPILLPSWIK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Mediator of DNA damage checkpoint protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q14676	427	1.28	1.34	1.01	0.21	0.44	0.14	226529	7.3	15	10	8			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
22474	45.11	608.65	617.34	733.08	753.39	1.00	0.89	1.01	610.8464	2	-0.0263	VLFTGVVDAR	iTRAQ4plex (N-term)	YES	YES
22491	42.57	588.57	671.70	598.95	606.38	1.20	1.20	1.03	610.8680	2	0.0167	VLFTGVVDAR	iTRAQ4plex (N-term)	YES	YES
48594	41.75	202.51	224.65	141.08	173.43	1.44	1.41	0.85	517.0017	3	0.0555	EVPPGSAIIHIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48595	42.32	571.19	690.69	406.94	406.00	1.74	1.85	1.04	517.0044	3	0.0636	EVPPGSAIIHIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
62788	59.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	593.6933	3	0.0621	GIPILSLDWLHQSR	iTRAQ4plex (N-term)	YES	YES
62789	51.73	8.73	13.27	7.05	4.67	2.31	3.09	1.57	593.6935	3	0.0626	GIPILSLDWLHQSR	iTRAQ4plex (N-term)	YES	YES
77592	41.57	33.29	35.41	20.35	15.05	2.73	2.56	1.41	695.4432	3	0.0179	VGLPLLSPEFLLTGVLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
81250	40.17	50.84	57.82	37.41	56.26	1.12	1.12	0.69	724.7446	3	0.0654	SQLPAEGDAGAEWAAAVLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86008	72.16	38.12	43.90	27.68	19.71	2.39	2.42	1.46	770.7760	3	0.0601	AVLALGGSLAGSAAEASHLVTDR	iTRAQ4plex (N-term)	YES	YES
86009	82.59	124.80	160.07	115.16	115.66	1.33	1.50	1.04	770.7788	3	0.0683	AVLALGGSLAGSAAEASHLVTDR	iTRAQ4plex (N-term)	YES	YES
86015	67.22	22.36	32.17	16.10	26.24	1.05	1.33	0.64	770.7866	3	0.0917	AVLALGGSLAGSAAEASHLVTDR	iTRAQ4plex (N-term)	YES	YES
86019	64.07	100.17	141.62	78.86	100.31	1.23	1.53	0.82	770.7957	3	0.1191	AVLALGGSLAGSAAEASHLVTDR	iTRAQ4plex (N-term)	YES	YES
90944	66.87	276.61	369.34	270.15	240.47	1.42	1.67	1.17	833.8281	3	0.1626	AHEVGAQGGPPVAQVEQDLPISR	iTRAQ4plex (N-term)	YES	YES
102063	55.19	183.45	227.62	146.04	171.20	1.32	1.45	0.89	982.3085	4	0.1726	TPKPVEPAASDLEPFTPTDQSVTPEAIAQGGQSK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
102066	45.13	207.02	199.10	215.27	229.11	1.12	0.94	0.98	982.5313	4	0.0798	TPKPVEPAASDLEPFTPTDQSVTPEAIAQGGQSK	Deamidated (NQ); 2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Telomeric repeat-binding factor 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q15554	188	3.96	3.64	1.12	0.63	0.40	0.07	55517	9.0	8	7	3			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
43755	62.96	1921.51	2074.46	684.30	642.13	3.69	3.51	1.11	742.4124	2	0.0392	YGEGNWAAISK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
43757	57.17	1085.84	1107.85	358.48	332.76	4.03	3.62	1.12	742.4168	2	0.0480	YGEGNWAAISK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60491	40.43	318.24	388.18	130.84	119.72	3.28	3.52	1.14	581.3679	3	0.0291	DIMQALLVRPLGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60495	45.94	275.23	288.62	100.96	108.17	3.14	2.90	0.97	581.3732	3	0.0449	DIMQALLVRPLGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60496	46.54	321.52	324.10	94.91	82.40	4.82	4.28	1.20	581.3742	3	0.0480	DIMQALLVRPLGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60499	47.56	460.94	503.01	154.93	149.53	3.81	3.66	1.08	581.3894	3	0.0936	DIMQALLVRPLGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
92629	51.26	486.60	569.77	178.30	170.41	3.53	3.63	1.09	859.7879	3	0.0851	KDENESSAPADGEGGSELQPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
92630	60.8	703.79	660.75	217.97	190.53	4.56	3.77	1.19	859.7905	3	0.0928	KDENESSAPADGEGGSELQPK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

High mobility group protein 1-like 10 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9UGV6	48	2.08	2.31	1.02	-	-	-	24203	6.2	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
49776	47.54	364.78	460.88	212.78	216.96	2.08	2.31	1.02	523.3099	3	0.0469	GEHPGLSIGDVAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

DNA repair protein RAD50 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q92878	83	1.96	1.81	1.05	0.27	0.25	0.09	153797	1.8	4	4	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
48819	44.08	436.42	428.96	267.76	258.52	2.08	1.80	1.08	518.3071	3	0.0819	GYEEEIIHFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
48823	44.31	61.68	66.22	36.92	31.27	2.43	2.30	1.23	518.3118	3	0.0960	GYEEEIIHFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
69822	45.35	474.32	534.00	323.19	323.92	1.81	1.79	1.04	637.0546	3	0.0746	LIQDQQEQIQHLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
69823	58.38	658.23	688.31	414.43	417.66	1.95	1.79	1.03	637.0624	3	0.0981	LIQDQQEQIQHLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Others

Calcineurin-binding protein Cabin-1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9Y6J0	51	2.07	1.75	1.00	-	-	-	246197	0.9	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
85508	51.37	325.74	313.01	186.05	194.31	2.07	1.75	1.00	765.0775	3	0.0631	IAALNASSTIEDDHEGSFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Ephexin-1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q8N5V2	40	1.93	1.63	1.09	-	-	-	82445	1.8	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
60397	40.5	292.39	280.68	196.22	186.89	1.93	1.63	1.09	581.0227	3	0.1432	KMSRTEQMISIQK	Deamidated (NQ); iTRAQ4plex (K); Oxidation (M)	YES	YES

ZZ-type zinc finger-containing protein 3 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q8IYH5	82	1.77	1.60	1.08	0.10	0.18	0.06	101960	3.4	3	3	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
32198	48.01	885.32	883.86	642.40	633.21	1.73	1.52	1.06	446.6136	3	0.0119	LNIGHLPSAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
32201	43.69	267.11	294.40	189.09	172.20	1.92	1.86	1.14	446.6235	3	0.0418	LNIGHLPSAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
94091	55.2	37.28	35.88	29.93	24.62	1.87	1.58	1.27	892.1461	3	0.0491	VVQLPEIVWDQYTHSLGNFER	iTRAQ4plex (N-term)	YES	YES

Neuron navigator 3 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q8IVL0	40	1.93	2.01	1.12	-	-	-	255461	0.4	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
20476	40.38	377.09	445.75	258.65	240.92	1.93	2.01	1.12	599.3889	2	0.0382	LKPPVSEGVK	iTRAQ4plex (K)	YES	YES

Uncharacterized protein C6orf174 precursor - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q5TF21	152	1.78	1.67	0.90	0.17	0.17	0.09	103136	1.4	7	7	1			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
42961	45.69	123.38	131.10	51.59	70.55	2.16	2.02	0.76	736.4125	2	0.0249	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42962	44.3	250.18	240.98	136.30	167.63	1.84	1.56	0.85	736.4183	2	0.0365	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42968	47.1	593.16	641.95	387.27	439.93	1.66	1.59	0.92	736.4234	2	0.0466	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42972	53.19	172.09	195.55	106.22	112.02	1.90	1.90	0.99	736.4248	2	0.0494	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42974	53.21	259.59	270.58	164.52	170.33	1.88	1.73	1.01	736.4267	2	0.0532	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42983	42.03	234.96	251.84	137.65	169.55	1.71	1.61	0.85	736.4343	2	0.0684	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42988	45.04	468.85	507.48	284.30	333.70	1.73	1.65	0.89	736.4365	2	0.0729	AAAAAAAAQMHAK	Deamidated (NQ); iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Cytoskeleton-associated protein 5 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q14008	173	2.07	2.12	1.02	0.14	0.38	0.31	225366	3.4	7	3	3			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
43775	40.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	742.4454	2	0.0436	VNDFLAEIFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
43779	41.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	742.4516	2	0.0560	VNDFLAEIFK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
59076	52.89	33.36	32.25	25.77	8.81	4.68	3.98	3.05	572.6691	3	0.0164	GKPAAPGGAGNTGTK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
59794	45.97	152.18	191.13	93.13	96.62	1.94	2.15	1.00	577.3350	3	0.0509	ALAVMVDHLESEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
59802	58.13	341.15	392.47	173.51	195.80	2.15	2.18	0.92	577.3442	3	0.0783	ALAVMVDHLESEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
61482	68.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	587.0171	3	0.1005	DLMHGLITLMLDSR	iTRAQ4plex (N-term)	YES	YES
75279	54.57	50.09	45.60	47.03	32.84	1.88	1.51	1.49	677.0672	3	0.0550	GLEEALVYVENAHVAGK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Spliceosome RNA helicase BAT1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
Q13838	214	1.88	1.83	1.24	-	-	-	48960	15.9	13	1	1			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**
18992	53.5	289.96	301.78	229.31	230.38	1.55	1.42	1.04	590.3288	2	0.0521	MLEQLDMR	iTRAQ4plex (N-term)	YES	NO
22702	48.18	799.63	818.28	855.23	883.70	1.12	1.01	1.01	612.3799	2	0.0287	ELAFQISK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
22705	47.47	1407.00	1349.97	1320.66	1398.22	1.24	1.05	0.98	612.3826	2	0.0341	ELAFQISK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
22709	48.23	1052.64	1268.07	1250.42	1311.46	0.99	1.05	0.99	612.3874	2	0.0438	ELAFQISK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
24862	43.42	568.02	598.88	535.43	547.31	1.28	1.19	1.02	624.3779	2	-0.0106	ILVATNLFGR	iTRAQ4plex (N-term)	YES	NO
24871	41.91	529.24	638.02	473.93	532.04	1.23	1.30	0.93	624.3861	2	0.0058	ILVATNLFGR	iTRAQ4plex (N-term)	YES	NO
24872	44.47	151.00	150.01	98.80	112.40	1.66	1.45	0.92	624.3920	2	0.0175	ILVATNLFGR	iTRAQ4plex (N-term)	YES	NO
39549	43.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	713.4543	2	0.0304	VAVFFGGLSIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
39553	40.21	1199.46	1126.97	1134.38	1227.83	1.21	1.00	0.96	713.4637	2	0.0494	VAVFFGGLSIK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
60991	47.74	437.79	410.63	338.07	401.38	1.35	1.11	0.88	584.3601	3	0.0562	LTLHGLQQYYVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
60993	42.24	512.07	596.57	489.99	514.35	1.23	1.26	0.99	584.3606	3	0.0579	LTLHGLQQYYVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
61000	42	307.40	329.77	294.30	265.43	1.43	1.35	1.15	584.3741	3	0.0984	LTLHGLQQYYVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
89482	57.4	148.71	164.63	116.58	97.59	1.88	1.83	1.24	815.4205	3	0.1160	VNIAFNYDMPEDSDTYLHR	iTRAQ4plex (N-term)	YES	YES

GTP-binding nuclear protein Ran - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide			
P62826	45	2.86	1.68	1.21	-	-	-	24408	8.3	1	1	1			
Spectrum No.	**Peptide Score**	**Int. 114**	**Int. 115**	**Int. 116**	**Int. 117**	**Ratio (114/117)**	**Ratio (115/117)**	**Ratio (116/117)**	**Precusor *m/z* (Da)**	**Charge**	**Mass Error (Da)**	**Peptide Sequence**	**Modification**	**Labeled**	**Unique**

82251	45.32	76.97	51.27	38.65	33.21	2.86	1.68	1.21	549.8300	4	0.0936	YVATLGVEVHPLVFHTNR	iTRAQ4plex (N-term)	YES	YES

Thymocyte nuclear protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9P016	138	2.52	2.19	0.95	-	-	-	25681	8.9	5	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
22334	66.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	609.9074	2	0.0375	FIPLAELK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
22335	66.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	609.9076	2	0.0380	FIPLAELK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
22336	47.26	1491.91	1504.69	652.87	697.12	2.64	2.35	0.98	609.9076	2	0.0380	FIPLAELK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
22338	65.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	609.9153	2	0.0533	FIPLAELK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO
56952	41.8	835.52	824.14	371.80	409.44	2.52	2.19	0.95	560.9972	3	0.0279	TKTENSGEALAK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Zinc finger protein 462 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q96JM2	76	2.02	1.90	1.03	0.20	0.17	0.06	161426	2.1	2	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
45364	60.36	648.24	687.88	383.22	374.07	2.14	2.00	1.07	753.4277	2	0.0245	VNLDQLEQMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
93412	48.26	423.86	456.78	264.31	281.65	1.86	1.76	0.98	657.5946	4	-0.0101	LQSTAELTSHLNIHNEEFQK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Bromodomain-containing protein 7 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9NPI1	207	1.77	1.69	0.99	0.38	0.24	0.10	74092	6.9	8	8	3

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
64784	47.91	681.16	742.08	441.55	488.39	1.72	1.65	0.94	605.6840	3	0.0701	EMHLAEQVTNNLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
64792	47.79	761.34	932.99	517.24	574.79	1.64	1.76	0.94	605.6907	3	0.0903	EMHLAEQVTNNLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80261	45.46	187.29	185.35	148.84	135.12	1.71	1.49	1.15	716.3520	3	0.0551	TLQEMEMSLPEDEGHTR	iTRAQ4plex (N-term)	YES	YES
80265	58.95	217.07	246.30	190.49	182.18	1.47	1.47	1.09	716.3838	3	0.1504	TLQEMEMSLPEDEGHTR	iTRAQ4plex (N-term)	YES	YES
80266	58.28	58.77	61.36	37.68	44.24	1.64	1.51	0.89	716.3842	3	0.1516	TLQEMEMSLPEDEGHTR	iTRAQ4plex (N-term)	YES	YES
80868	41.94	103.94	152.85	96.77	111.49	1.15	1.49	0.90	721.6960	3	0.0922	TLQEMEMSLPEDEGHTR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
80872	51.14	91.12	94.05	83.02	88.17	1.28	1.16	0.98	721.7082	3	0.1288	TLQEMEMSLPEDEGHTR	iTRAQ4plex (N-term); Oxidation (M)	YES	YES
85406	53.79	614.51	574.62	326.96	315.71	2.40	1.98	1.08	763.7549	3	0.0779	NNDYQSIEELKDNFK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

UPF0609 protein C4orf27 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9NWY4	240	1.80	1.72	1.04	0.45	0.46	0.14	39383	15.0	10	8	4

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
34292	72.72	910.16	941.94	560.36	551.84	2.04	1.86	1.06	682.3672	2	0.0451	TIVEAASDEER	iTRAQ4plex (N-term)	YES	YES
53573	43.03	242.04	247.99	151.95	166.91	1.79	1.61	0.95	543.3343	3	0.0474	TFHGAGLVVPVDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
53576	59.74	278.00	300.09	209.27	234.28	1.46	1.39	0.93	543.3383	3	0.0592	TFHGAGLVVPVDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
53578	56.04	306.61	369.29	245.80	247.57	1.53	1.62	1.03	543.3389	3	0.0611	TFHGAGLVVPVDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
53579	42.16	379.64	418.05	341.78	301.20	1.56	1.51	1.18	543.3416	3	0.0693	TFHGAGLVVPVDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
64040	52.41	50.67	66.44	18.09	27.12	2.31	2.66	0.69	601.0448	3	0.0010	VAGQLLPLAYNLLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
64672	49.28	78.82	108.99	43.22	62.95	1.55	1.88	0.72	605.0020	3	0.0192	NLFAEIIEEHLANR	iTRAQ4plex (N-term)	YES	YES
64676	41.57	25.35	32.26	7.68	11.62	2.69	3.02	0.69	605.0087	3	0.0391	NLFAEIIEEHLANR	iTRAQ4plex (N-term)	YES	YES
64689	92.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	605.0203	3	0.0741	NLFAEIIEEHLANR	iTRAQ4plex (N-term)	YES	YES
64708	47.02	96.98	101.02	40.39	44.08	2.72	2.49	0.95	605.0420	3	0.1392	NLFAEIIEEHLANR	iTRAQ4plex (N-term)	YES	YES

Chromatin accessibility complex protein 1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9NRG0	47	2.92	2.50	1.08	-	-	-	14701	6.1	1	1	1

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
10073	47.04	225.61	219.64	98.43	95.35	2.92	2.50	1.08	521.8515	2	0.0217	LISLPLSR	iTRAQ4plex (N-term)	YES	YES

YEATS domain-containing protein 2 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9ULM3	198	1.82	1.62	1.01	0.38	0.31	0.17	150688	6.1	10	7	5

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
33256	43.14	218.74	213.08	129.15	136.98	1.97	1.69	0.98	675.9684	2	0.0342	LLLIPQGAILR	iTRAQ4plex (N-term)	YES	YES
33259	42.9	199.13	193.54	119.31	136.44	1.80	1.54	0.91	675.9845	2	0.0664	LLLIPQGAILR	iTRAQ4plex (N-term)	YES	YES
38648	52.4	347.31	384.46	261.54	205.85	2.08	2.03	1.32	708.4298	2	0.0549	ATEQLVNDILR	iTRAQ4plex (N-term)	YES	YES
42202	41.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	487.9855	3	0.0398	IGITLQPVALHR	iTRAQ4plex (N-term)	YES	YES
76135	62.32	161.64	168.09	108.47	119.95	1.66	1.52	0.94	684.0546	3	0.0499	TTLFTQAAHGGQASLMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
76138	40.72	434.93	453.35	288.68	326.56	1.64	1.51	0.92	684.0604	3	0.0673	TTLFTQAAHGGQASLMK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
76842	41.2	562.45	527.26	339.70	366.19	1.90	1.57	0.97	689.3943	3	0.0740	TTLFTQAAHGGQASLMK	iTRAQ4plex (K); iTRAQ4plex (N-term); Oxidation (M)	YES	YES
78685	48.15	5.83	8.40	8.01	12.63	0.57	0.72	0.66	703.7842	3	0.0860	IDHLETIQQLLTAVVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
78687	48.21	12.80	10.08	4.94	11.77	1.34	0.93	0.44	703.7922	3	0.1098	IDHLETIQQLLTAVVK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
86996	44.75	42.96	52.16	41.71	57.07	0.93	0.99	0.76	782.7652	3	0.0387	TYTGLQTLGAETVVDVELHR	iTRAQ4plex (N-term)	YES	YES

Serine/threonine-protein kinase VRK1 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q99986	278	2.42	2.28	1.04	0.42	0.40	0.13	45447	17.2	12	11	7

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
11935	44.04	445.87	456.61	228.73	220.25	2.50	2.25	1.08	537.3603	2	0.0333	TVLQLSLR	iTRAQ4plex (N-term)	YES	YES
19674	53.9	265.35	282.55	154.78	146.75	2.23	2.09	1.10	594.3968	2	0.0262	DILLQGLK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
29849	64.89	593.50	574.99	289.92	292.38	2.51	2.14	1.03	654.8865	2	0.0586	ENIASLMDK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
31092	56.08	546.11	594.49	234.42	254.86	2.65	2.54	0.96	662.4131	2	0.0315	ASNLLLNYK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
31096	51.17	993.93	1053.38	580.39	565.83	2.17	2.02	1.07	662.4233	2	0.0518	ASNLLLNYK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
31097	65.25	2157.63	2268.60	1195.89	1218.92	2.19	2.02	1.02	662.4295	2	0.0642	ASNLLLNYK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
32789	41.22	411.13	443.29	209.63	168.12	3.02	2.87	1.30	449.2911	3	-0.0182	KTVLQLSLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
32790	40.77	574.17	641.50	245.31	265.32	2.67	2.63	0.96	449.2937	3	-0.0102	KTVLQLSLR	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77902	75.22	182.41	229.66	82.37	110.06	2.05	2.27	0.78	697.7535	3	0.0802	DDGKLDLSVVENGGLK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
77905	49.42	213.90	254.79	115.60	117.54	2.25	2.36	1.02	697.7565	3	0.0891	DDGKLDLSVVENGGLK	2 iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80813	53.72	179.46	176.86	81.97	94.13	2.35	2.04	0.91	721.0955	3	0.1155	HLAEQFAVGEIITDMAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
80819	46.89	115.50	125.03	101.72	101.30	1.41	1.34	1.05	721.1116	3	0.1638	HLAEQFAVGEIITDMAK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Metastasis-associated protein MTA3 - Homo sapiens (Human)

Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9BTC8	95	1.82	1.74	1.22	0.26	0.07	0.35	67461	6.1	5	2	2

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
25920	45.09	1200.23	1238.68	1305.23	1350.03	1.10	1.00	1.01	630.3527	2	-0.0458	TLLADQGEIR	iTRAQ4plex (N-term)	YES	NO
60322	42.33	104.84	108.08	89.10	65.88	1.96	1.78	1.41	580.6502	3	0.0454	DITLFHAMDTLYR	iTRAQ4plex (N-term)	YES	YES
60324	60.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	580.6561	3	0.0632	DITLFHAMDTLYR	iTRAQ4plex (N-term)	YES	YES
60329	42.91	63.48	75.93	42.66	49.00	1.60	1.68	0.91	580.6683	3	0.0995	DITLFHAMDTLYR	iTRAQ4plex (N-term)	YES	YES
73380	41.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	662.3942	3	0.1350	SLTSIIEYYYMWK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	NO

Deoxynucleotidyltransferase terminal-interacting protein 1 - Homo sapiens (Human)

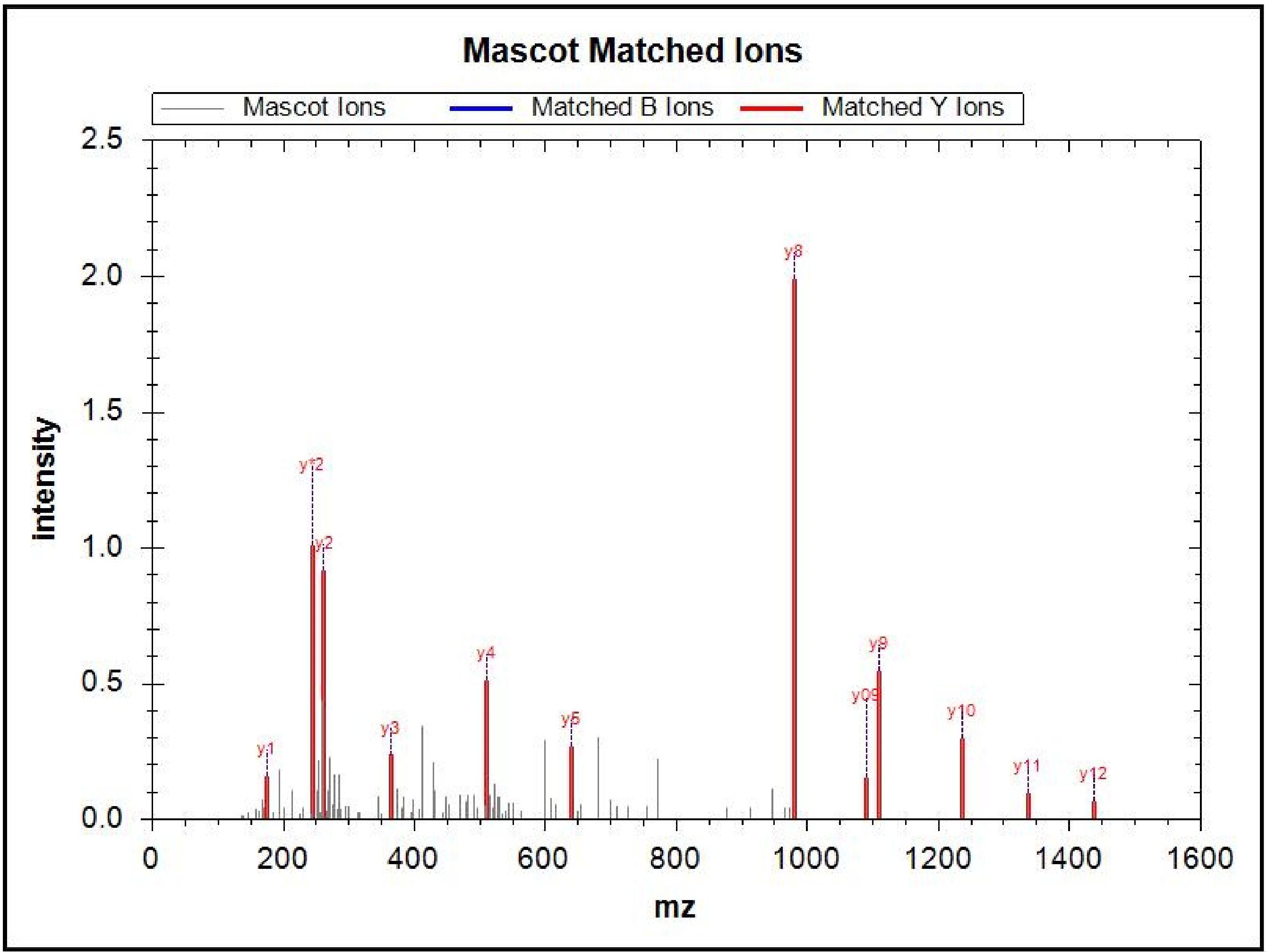
Accession No.	Protein Score	Normalized Ratio (114/117)	Normalized Ratio (115/117)	Normalized Ratio (116/117)	STD (114/117)	STD (115/117)	STD (116/117)	Mass	Sequence Coverage (%)	Identified Peptide	Quantitated Peptide	Identified Unique Peptide
Q9H147	132	2.01	1.83	0.98	0.63	0.99	0.20	36990	14.6	5	5	4

Spectrum No.	Peptide Score	Int. 114	Int. 115	Int. 116	Int. 117	Ratio (114/117)	Ratio (115/117)	Ratio (116/117)	Precusor *m/z* (Da)	Charge	Mass Error (Da)	Peptide Sequence	Modification	Labeled	Unique
20377	43.06	903.54	872.77	512.72	540.06	2.07	1.76	0.99	598.8574	2	0.0310	LLFSDGEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
42618	45.33	532.80	509.85	505.75	540.73	1.22	1.02	0.97	734.4094	2	0.0191	LNESTTFVLGSR	iTRAQ4plex (N-term)	YES	YES
52441	46.22	780.14	793.06	317.79	380.91	2.53	2.26	0.87	805.9722	2	0.0517	SFVLPSWMVEK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
83094	65.7	108.39	130.59	65.31	53.93	2.48	2.63	1.26	740.0842	3	0.0060	AVLQPSINEEIQTVFNK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES
83113	46.78	84.51	124.56	47.39	36.74	2.84	3.68	1.34	740.1318	3	0.1488	AVLQPSINEEIQTVFNK	iTRAQ4plex (K); iTRAQ4plex (N-term)	YES	YES

Supplementary Figure 1

Query 35628 Hit 1

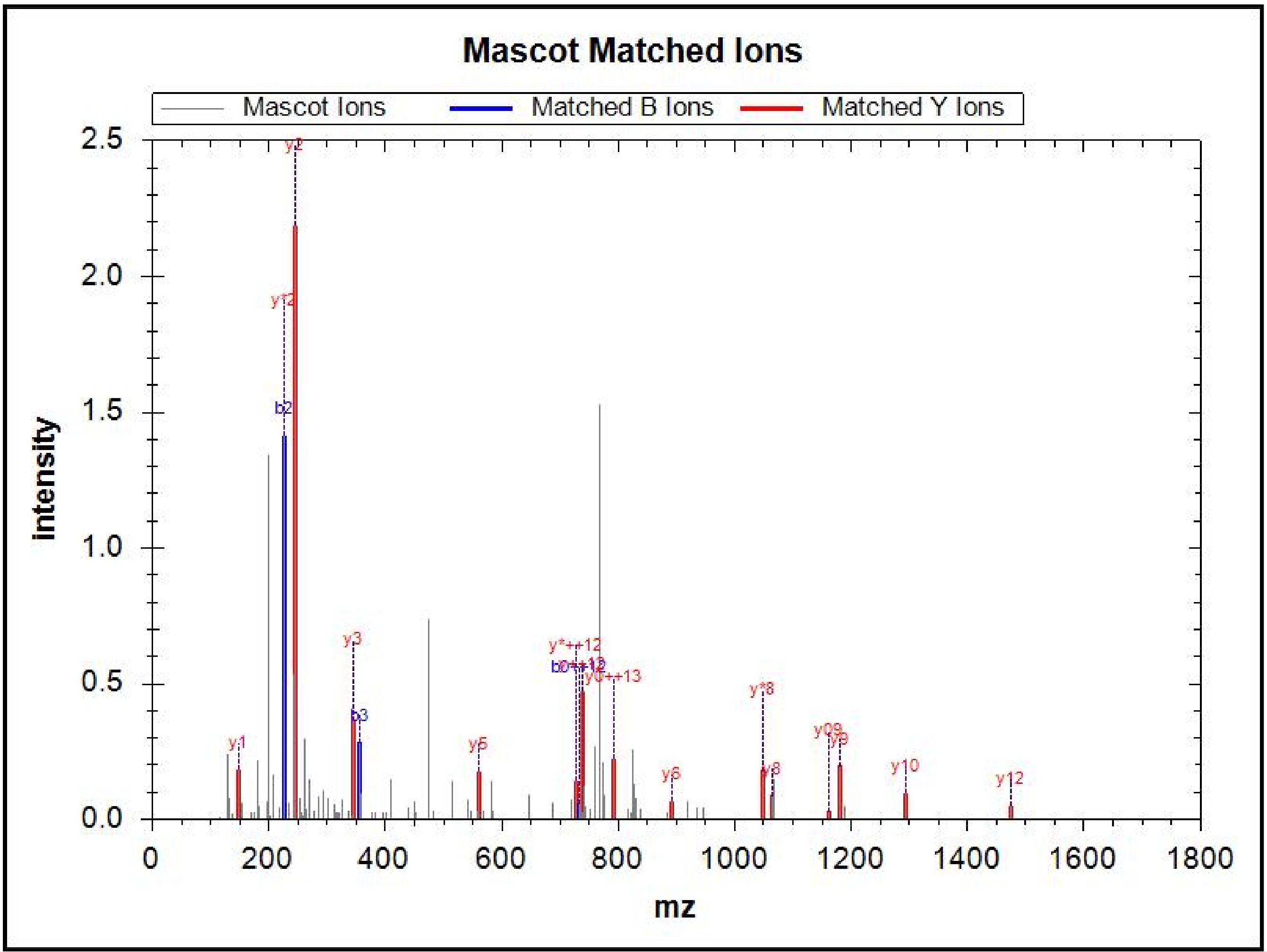
MS/MS Fragmentation of EMCTVEEPNEEFTSR
Found in O15516, Circadian locomoter output cycles protein kaput - Homo sapiens (Human)
Match to Query 35628: 2042.792from(1022.403,2+)
Title: File: SCX225.wiff, Sample: ICAT (sample number 1), Elution: 22.384 min, Period: 1, Cycle(s): 1286 (Experiment 2)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 2042.792
Variable modifications:
M2 :Oxidation (M), with neutral losses 63.99828
C3 :ICAT-C (C)
Ions Score: 63.57 **Expect:** 0.000



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	130.05	65.53			112.04	56.52	E							15
2	277.09	139.05			259.07	130.04	M	1,914.82	957.91	1,897.79	949.40	1,896.81	948.91	14
3	607.22	304.11			589.21	295.11	C	1,767.79	884.40	1,750.76	875.88	1,749.77	875.39	13
4	708.27	354.64			690.26	345.63	T	1,437.65	719.33	1,420.62	710.81	1,419.64	710.32	12
5	807.34	404.17			789.33	395.17	V	1,336.60	668.80	1,319.57	660.29	1,318.59	659.80	11
6	936.38	468.69			918.37	459.69	E	1,237.53	619.27	1,220.51	610.76	1,219.52	610.26	10
7	1,065.42	533.22			1,047.41	524.21	E	1,108.49	554.75	1,091.46	546.24	1,090.48	545.74	9
8	1,162.48	581.74			1,144.46	572.74	P	979.45	490.23	962.42	481.71	961.44	481.22	8
9	1,276.52	638.76	1,259.49	630.25	1,258.51	629.76	N	882.40	441.70	865.37	433.19	864.38	432.70	7
10	1,405.56	703.28	1,388.53	694.77	1,387.55	694.28	E	768.35	384.68	751.33	376.17	750.34	375.67	6
11	1,534.60	767.81	1,517.58	759.29	1,516.59	758.80	E	639.31	320.16	622.28	311.65	621.30	311.15	5
12	1,681.67	841.34	1,664.65	832.83	1,663.66	832.33	F	510.27	255.64	493.24	247.12	492.26	246.63	4
13	1,782.72	891.86	1,765.69	883.35	1,764.71	882.86	T	363.20	182.10	346.17	173.59	345.19	173.10	3
14	1,869.75	935.38	1,852.73	926.87	1,851.74	926.37	S	262.15	131.58	245.12	123.07	244.14	122.57	2
15							R	175.12	88.06	158.09	79.55			1

Query 30453 Hit 1

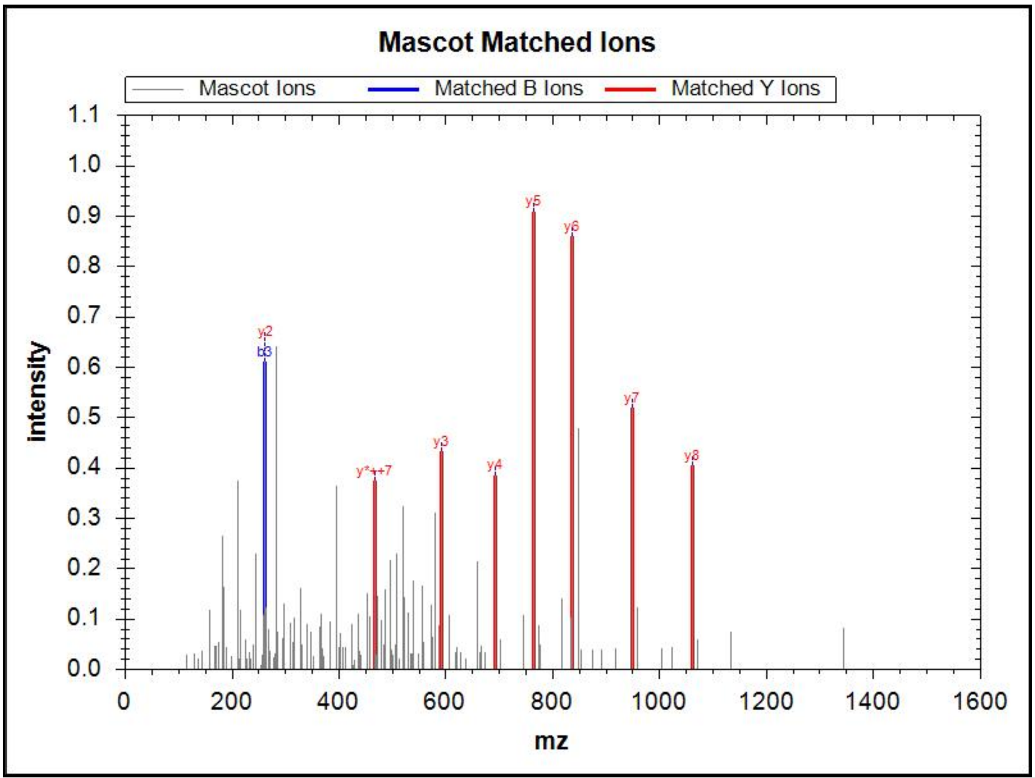
MS/MS Fragmentation of ILQPMLDSSCSETPK
Found in P55347, Homeobox protein PKNOX1 - Homo sapiens (Human)
Match to Query 30453: 1890.691from(946.3527,2+)
Title: File: SCX224.wiff, Sample: ICAT (sample number 1), Elution: 23.273 min, Period: 1, Cycle(s): 1287 (Experiment 4)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 1890.691
Variable modifications:
M5 :Oxidation (M), with neutral losses 63.99828
C10 :ICAT-C (C)
Ions Score: 36.76 **Expect:** 0.021



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	114.09	57.55					I							15
2	227.18	114.09					L	1,714.83	857.92	1,697.81	849.41	1,696.82	848.91	14
3	355.23	178.12	338.21	169.61			Q	1,601.75	801.38	1,584.72	792.86	1,583.74	792.37	13
4	452.29	226.65	435.26	218.13			P	1,473.69	737.35	1,456.66	728.83	1,455.68	728.34	12
5	535.32	268.17	518.30	259.65			M	1,376.64	688.82	1,359.61	680.31	1,358.63	679.82	11
6	648.41	324.71	631.38	316.19			L	1,293.60	647.30	1,276.57	638.79	1,275.59	638.30	10
7	763.43	382.22	746.41	373.71	745.42	373.22	D	1,180.52	590.76	1,163.49	582.25	1,162.50	581.76	9
8	850.47	425.74	833.44	417.22	832.46	416.73	S	1,065.49	533.25	1,048.46	524.73	1,047.48	524.24	8
9	937.50	469.25	920.47	460.74	919.49	460.25	S	978.46	489.73	961.43	481.22	960.45	480.73	7
10	1,267.64	634.32	1,250.61	625.81	1,249.62	625.32	C	891.42	446.22	874.40	437.70	873.41	437.21	6
11	1,354.67	677.84	1,337.64	669.32	1,336.66	668.83	S	561.29	281.15	544.26	272.63	543.28	272.14	5
12	1,483.71	742.36	1,466.68	733.85	1,465.70	733.35	E	474.26	237.63	457.23	229.12	456.25	228.63	4
13	1,584.76	792.88	1,567.73	784.37	1,566.75	783.88	T	345.21	173.11	328.19	164.60	327.20	164.10	3
14	1,681.81	841.41	1,664.78	832.90	1,663.80	832.40	P	244.17	122.59	227.14	114.07			2
15							K	147.11	74.06	130.09	65.55			1

Query 57334 Hit 1

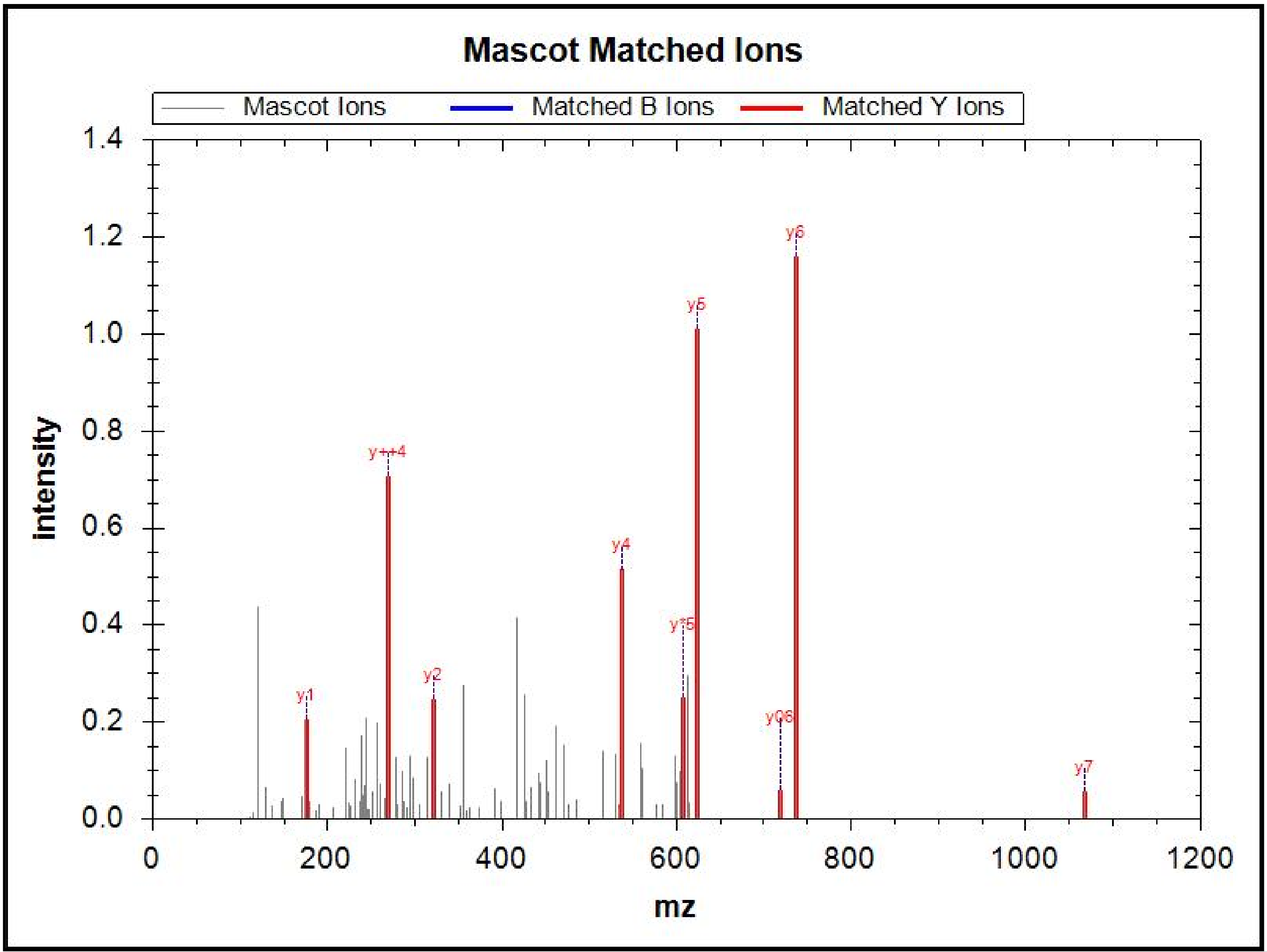
MS/MS Fragmentation of SSSTGSSSSTGGGGQESQPSPLALLAATCSR
Found in P08047, Transcription factor Sp1 - Homo sapiens (Human)
Match to Query 57334: 3094.065from(1032.362,3+)
Title: File: SCX222.wiff, Sample: ICAT (sample number 1), Elution: 41.219 min, Period: 1, Cycle(s): 1638 (Experiment 2)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 3094.065
Variable modifications:
C29 :ICAT-C (C)
Ions Score: 28.21 **Expect:** 0.220



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	88.04	44.52			70.03	35.52	S							31
2	175.07	88.04			157.06	79.03	S	3,008.42	1,504.71	2,991.40	1,496.20	2,990.41	1,495.71	30
3	262.10	131.56			244.09	122.55	S	2,921.39	1,461.20	2,904.36	1,452.69	2,903.38	1,452.19	29
4	363.15	182.08			345.14	173.07	T	2,834.36	1,417.68	2,817.33	1,409.17	2,816.35	1,408.68	28
5	420.17	210.59			402.16	201.58	G	2,733.31	1,367.16	2,716.28	1,358.65	2,715.30	1,358.15	27
6	507.20	254.11			489.19	245.10	S	2,676.29	1,338.65	2,659.26	1,330.13	2,658.28	1,329.64	26
7	594.24	297.62			576.23	288.62	S	2,589.26	1,295.13	2,572.23	1,286.62	2,571.25	1,286.13	25
8	681.27	341.14			663.26	332.13	S	2,502.23	1,251.62	2,485.20	1,243.10	2,484.21	1,242.61	24
9	768.30	384.65			750.29	375.65	S	2,415.19	1,208.10	2,398.17	1,199.59	2,397.18	1,199.09	23
10	869.35	435.18			851.34	426.17	T	2,328.16	1,164.58	2,311.13	1,156.07	2,310.15	1,155.58	22
11	926.37	463.69			908.36	454.68	G	2,227.11	1,114.06	2,210.09	1,105.55	2,209.10	1,105.06	21
12	983.39	492.20			965.38	483.19	G	2,170.09	1,085.55	2,153.07	1,077.04	2,152.08	1,076.54	20
13	1,040.41	520.71			1,022.40	511.70	G	2,113.07	1,057.04	2,096.04	1,048.53	2,095.06	1,048.03	19
14	1,097.43	549.22			1,079.42	540.22	G	2,056.05	1,028.53	2,039.02	1,020.01	2,038.04	1,019.52	18
15	1,225.49	613.25	1,208.47	604.74	1,207.48	604.24	Q	1,999.03	1,000.02	1,982.00	991.50	1,981.02	991.01	17
16	1,354.54	677.77	1,337.51	669.26	1,336.52	668.77	E	1,870.97	935.99	1,853.94	927.47	1,852.96	926.98	16
17	1,441.57	721.29	1,424.54	712.77	1,423.56	712.28	S	1,741.93	871.47	1,724.90	862.95	1,723.92	862.46	15
18	1,569.63	785.32	1,552.60	776.80	1,551.62	776.31	Q	1,654.89	827.95	1,637.87	819.44	1,636.88	818.95	14
19	1,666.68	833.84	1,649.65	825.33	1,648.67	824.84	P	1,526.84	763.92	1,509.81	755.41	1,508.83	754.92	13
20	1,753.71	877.36	1,736.68	868.85	1,735.70	868.35	S	1,429.78	715.40	1,412.76	706.88	1,411.77	706.39	12
21	1,850.76	925.89	1,833.74	917.37	1,832.75	916.88	P	1,342.75	671.88	1,325.72	663.37	1,324.74	662.87	11
22	1,963.85	982.43	1,946.82	973.91	1,945.84	973.42	L	1,245.70	623.35	1,228.67	614.84	1,227.69	614.35	10
23	2,034.88	1,017.95	2,017.86	1,009.43	2,016.87	1,008.94	A	1,132.61	566.81	1,115.59	558.30	1,114.60	557.81	9
24	2,147.97	1,074.49	2,130.94	1,065.97	2,129.96	1,065.48	L	1,061.58	531.29	1,044.55	522.78	1,043.57	522.29	8
25	2,261.05	1,131.03	2,244.03	1,122.52	2,243.04	1,122.02	L	948.49	474.75	931.47	466.24	930.48	465.74	7
26	2,332.09	1,166.55	2,315.06	1,158.04	2,314.08	1,157.54	A	835.41	418.21	818.38	409.69	817.40	409.20	6
27	2,403.13	1,202.07	2,386.10	1,193.55	2,385.12	1,193.06	A	764.37	382.69	747.35	374.18	746.36	373.68	5
28	2,504.17	1,252.59	2,487.15	1,244.08	2,486.16	1,243.59	T	693.33	347.17	676.31	338.66	675.32	338.17	4
29	2,834.31	1,417.66	2,817.28	1,409.15	2,816.30	1,408.65	C	592.29	296.65	575.26	288.13	574.28	287.64	3
30	2,921.34	1,461.18	2,904.32	1,452.66	2,903.33	1,452.17	S	262.15	131.58	245.12	123.07	244.14	122.57	2
31							R	175.12	88.06	158.09	79.55			1

Query 7078 Hit 1

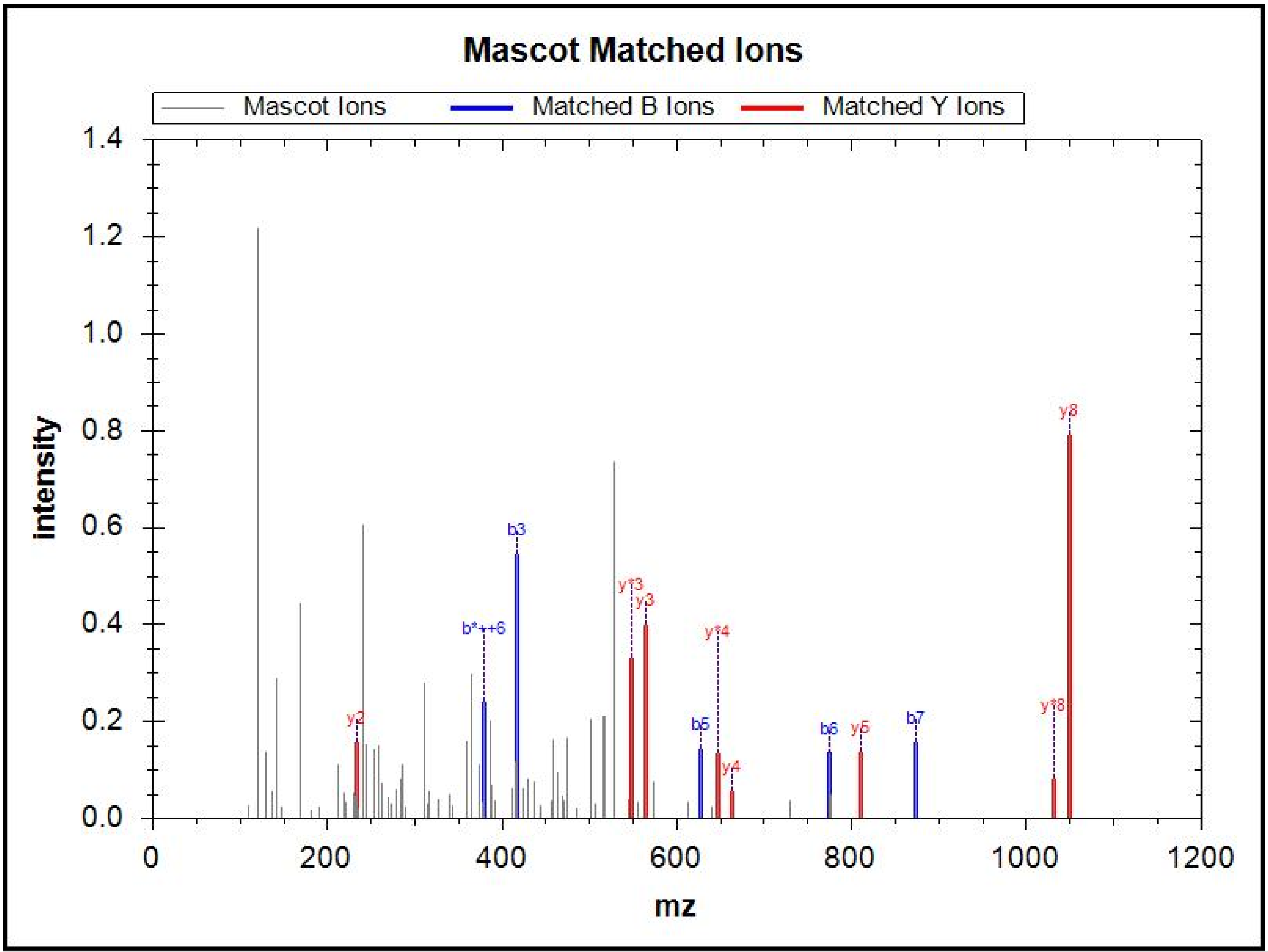
MS/MS Fragmentation of **FCLSSQFR**
Found in **P38398**, Breast cancer type 1 susceptibility protein - Homo sapiens (Human)
Match to Query 7078: 1213.476from(607.7452,2+)
Title: File: SCX230.wiff, Sample: ICAT (sample number 1), Elution: 29.058 min, Period: 1, Cycle(s): 1438 (Experiment 2)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 1213.476
Variable modifications:
C2 :ICAT-C (C)
Ions Score: 38.46 **Expect:** 0.011



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	148.08	74.54					F							8
2	478.21	239.61					C	**1,067.53**	534.27	1,050.50	525.76	1,049.52	525.26	7
3	591.30	296.15					L	**737.39**	369.20	720.37	360.69	**719.38**	360.20	6
4	678.33	339.67			660.32	330.66	S	**624.31**	312.66	**607.28**	304.15	606.30	303.65	5
5	765.36	383.18			747.35	374.18	S	**537.28**	**269.14**	520.25	260.63	519.27	260.14	4
6	893.42	447.21	876.39	438.70	875.41	438.21	Q	450.25	225.63	433.22	217.11			3
7	1,040.49	520.75	1,023.46	512.23	1,022.48	511.74	F	**322.19**	161.60	305.16	153.08			2
8							R	**175.12**	88.06	158.09	79.55			1

Query 31563 Hit 1

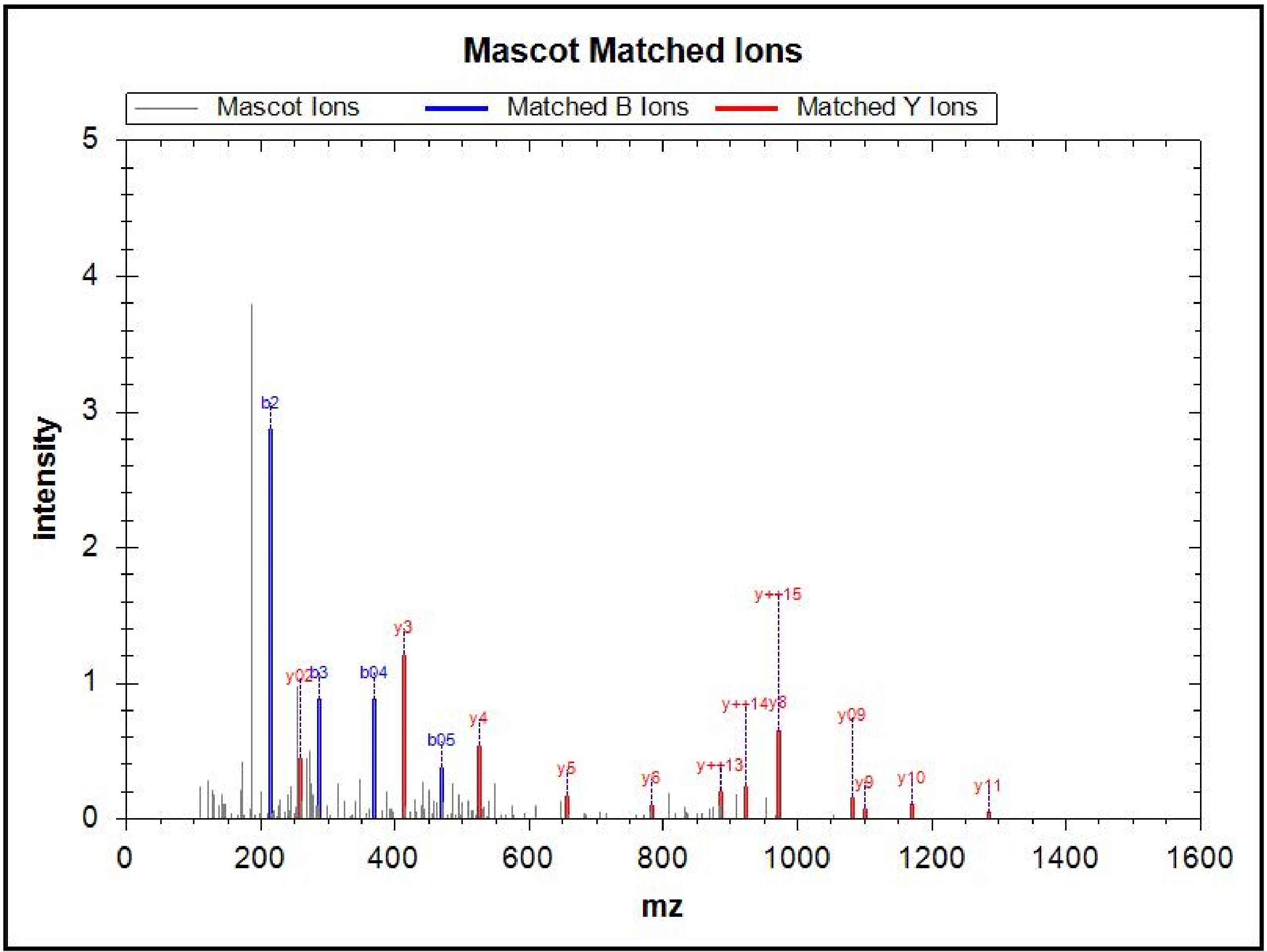
MS/MS Fragmentation of **YHDPNFVPAAFVCSK**
Found in **P49711**, Transcriptional repressor CTCF - Homo sapiens (Human)
Match to Query 31563: 1920.892from(641.3046,3+)
Title: File: SCX243.wiff, Sample: ICAT (sample number 1), Elution: 32.768 min, Period: 1, Cycle(s): 1450 (Experiment 3)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 1920.892
Variable modifications:
C13 :ICAT-C (C)
Ions Score: 25.16 **Expect:** 0.255



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	164.07	82.54					Y							15
2	301.13	151.07					H	1,758.86	879.94	1,741.84	871.42	1,740.85	870.93	14
3	**416.16**	208.58			398.15	199.58	D	1,621.80	811.41	1,604.78	802.89	1,603.79	802.40	13
4	513.21	257.11			495.20	248.10	P	1,506.78	753.89	1,489.75	745.38	1,488.77	744.89	12
5	**627.25**	314.13	610.23	305.62	609.24	305.12	N	1,409.72	705.37	1,392.70	696.85	1,391.71	696.36	11
6	**774.32**	387.66	757.29	**379.15**	756.31	378.66	F	1,295.68	648.34	1,278.66	639.83	1,277.67	639.34	10
7	**873.39**	437.20	856.36	428.68	855.38	428.19	V	1,148.61	574.81	1,131.59	566.30	1,130.60	565.80	9
8	970.44	485.72	953.42	477.21	952.43	476.72	P	**1,049.54**	525.28	**1,032.52**	516.76	1,031.53	516.27	8
9	1,041.48	521.24	1,024.45	512.73	1,023.47	512.24	A	952.49	476.75	935.47	468.24	934.48	467.74	7
10	1,112.52	556.76	1,095.49	548.25	1,094.51	547.76	A	881.45	441.23	864.43	432.72	863.44	432.23	6
11	1,259.58	630.30	1,242.56	621.78	1,241.57	621.29	F	**810.42**	405.71	793.39	397.20	792.41	396.71	5
12	1,358.65	679.83	1,341.63	671.32	1,340.64	670.82	V	**663.35**	332.18	**646.32**	323.67	645.34	323.17	4
13	1,688.79	844.90	1,671.76	836.38	1,670.78	835.89	C	**564.28**	282.64	**547.25**	274.13	546.27	273.64	3
14	1,775.82	888.41	1,758.79	879.90	1,757.81	879.41	S	**234.14**	117.58	217.12	109.06	216.13	108.57	2
15							K	147.11	74.06	130.09	65.55			1

Query 44029 Hit 1

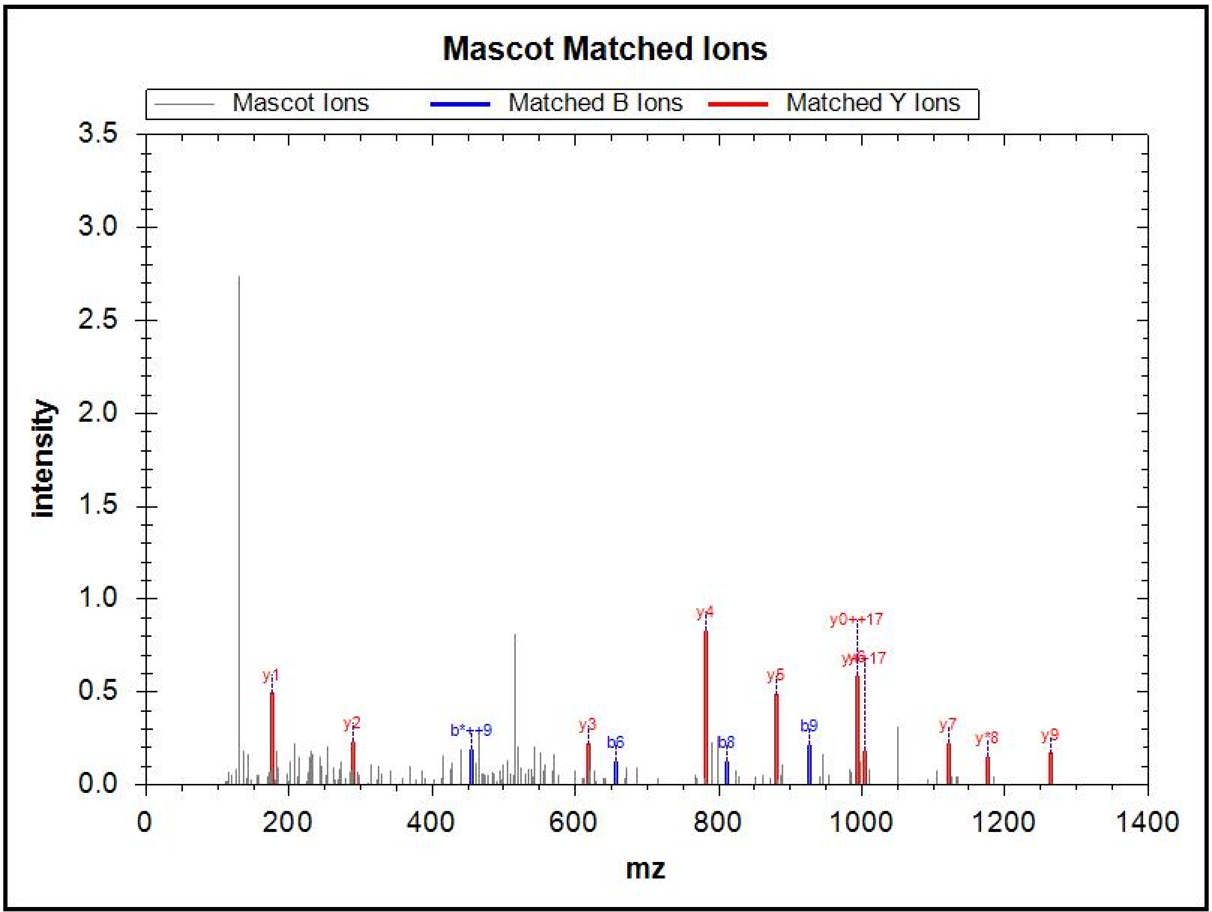
MS/MS Fragmentation of **DVATVAFCDAQSTQEIHEK**
Found in **Q13363**, C-terminal-binding protein 1 - Homo sapiens (Human)
Match to Query 44029: 2327.209from(776.7436,3+)
Title: File: SCX36_1.wiff, Sample: hung (sample number 1), Elution: 33.812 min, Period: 1, Cycle(s): 1475 (Experiment 3)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 2327.209
Variable modifications:
C8 :ICAT-C:13C(9) (C)
Ions Score: 40.34 **Expect:** 0.008



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	116.03	58.52			98.02	49.52	D							19
2	**215.10**	108.05			197.09	99.05	V	2,213.10	1,107.05	2,196.07	1,098.54	2,195.08	1,098.05	18
3	**286.14**	143.57			268.13	134.57	A	2,114.03	1,057.52	2,097.00	1,049.00	2,096.02	1,048.51	17
4	387.19	194.10			**369.18**	185.09	T	2,042.99	1,022.00	2,025.96	1,013.49	2,024.98	1,012.99	16
5	486.26	243.63			**468.25**	234.63	V	1,941.94	**971.47**	1,924.92	962.96	1,923.93	962.47	15
6	557.29	279.15			539.28	270.14	A	1,842.87	**921.94**	1,825.85	913.43	1,824.86	912.94	14
7	704.36	352.68			686.35	343.68	F	1,771.84	**886.42**	1,754.81	877.91	1,753.83	877.42	13
8	1,043.53	522.27			1,025.52	513.26	C	1,624.77	812.89	1,607.74	804.37	1,606.76	803.88	12
9	1,158.55	579.78			1,140.54	570.78	D	**1,285.60**	643.30	1,268.58	634.79	1,267.59	634.30	11
10	1,229.59	615.30			1,211.58	606.29	A	**1,170.57**	585.79	1,153.55	577.28	1,152.56	576.79	10
11	1,357.65	679.33	1,340.62	670.82	1,339.64	670.32	Q	**1,099.54**	550.27	1,082.51	541.76	**1,081.53**	541.27	9
12	1,444.68	722.84	1,427.66	714.33	1,426.67	713.84	S	**971.48**	486.24	954.45	477.73	953.47	477.24	8
13	1,545.73	773.37	1,528.70	764.86	1,527.72	764.36	T	884.45	442.73	867.42	434.21	866.44	433.72	7
14	1,673.79	837.40	1,656.76	828.88	1,655.78	828.39	Q	**783.40**	392.20	766.37	383.69	765.39	383.20	6
15	1,802.83	901.92	1,785.80	893.41	1,784.82	892.91	E	**655.34**	328.17	638.31	319.66	637.33	319.17	5
16	1,915.92	958.46	1,898.89	949.95	1,897.90	949.46	I	**526.30**	263.65	509.27	255.14	508.29	254.65	4
17	2,052.97	1,026.99	2,035.95	1,018.48	2,034.96	1,017.99	H	**413.21**	207.11	396.19	198.60	395.20	198.11	3
18	2,182.02	1,091.51	2,164.99	1,083.00	2,164.01	1,082.51	E	276.16	138.58	259.13	130.07	**258.14**	129.58	2
19							K	147.11	74.06	130.09	65.55			1

Query 48917 Hit 1

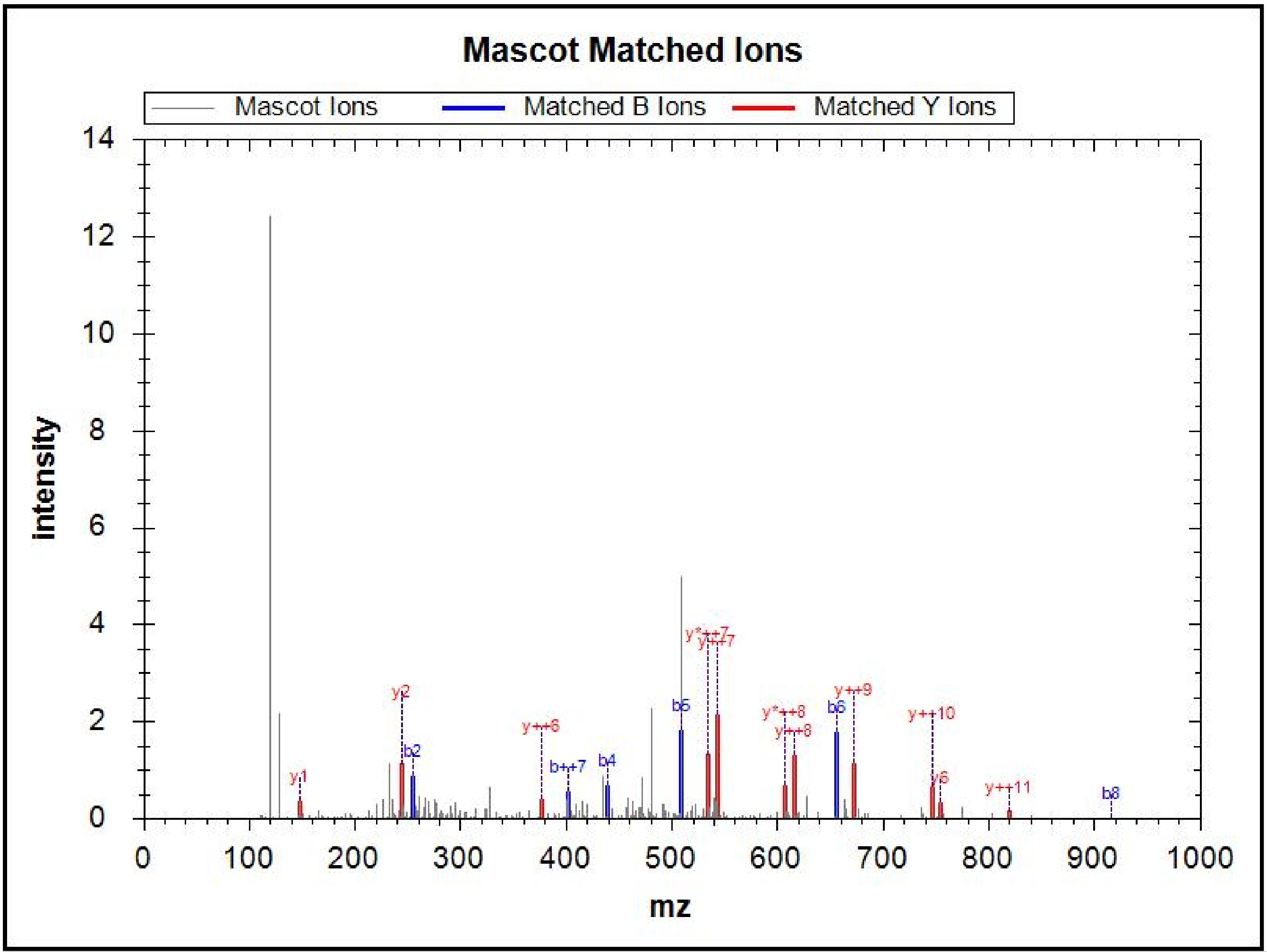
MS/MS Fragmentation of **LKPDDSGVNIAEAAAQNVYCLR**
Found in **Q92547**, DNA topoisomerase 2-binding protein 1 - Homo sapiens (Human)
Match to Query 48917: 2573.303from(858.775,3+)
Title: File: SCX238.wiff, Sample: ICAT (sample number 2), Elution: 40.044 min, Period: 1, Cycle(s): 1569 (Experiment 4)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 2573.303
Variable modifications:
C20 :ICAT-C (C)
Ions Score: 39.79 **Expect:** 0.008



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	114.09	57.55					L							22
2	242.19	121.60	225.16	113.08			K	2,461.21	1,231.11	2,444.19	1,222.60	2,443.20	1,222.11	21
3	339.24	170.12	322.21	161.61			P	2,333.12	1,167.06	2,316.09	1,158.55	2,315.11	1,158.06	20
4	454.27	227.64	437.24	219.12	436.26	218.63	D	2,236.07	1,118.54	2,219.04	1,110.02	2,218.06	1,109.53	19
5	569.29	285.15	552.27	276.64	551.28	276.14	D	2,121.04	1,061.02	2,104.01	1,052.51	2,103.03	1,052.02	18
6	**656.32**	328.67	639.30	320.15	638.31	319.66	S	2,006.01	**1,003.51**	1,988.99	995.00	1,988.00	**994.50**	17
7	713.35	357.18	696.32	348.66	695.34	348.17	G	1,918.98	959.99	1,901.95	951.48	1,900.97	950.99	16
8	**812.41**	406.71	795.39	398.20	794.40	397.71	V	1,861.96	931.48	1,844.93	922.97	1,843.95	922.48	15
9	**926.46**	463.73	909.43	**455.22**	908.45	454.73	N	1,762.89	881.95	1,745.86	873.44	1,744.88	872.94	14
10	1,039.54	520.27	1,022.52	511.76	1,021.53	511.27	I	1,648.85	824.93	1,631.82	816.41	1,630.84	815.92	13
11	1,110.58	555.79	1,093.55	547.28	1,092.57	546.79	A	1,535.76	768.39	1,518.74	759.87	1,517.75	759.38	12
12	1,239.62	620.31	1,222.60	611.80	1,221.61	611.31	E	1,464.73	732.87	1,447.70	724.35	1,446.72	723.86	11
13	1,310.66	655.83	1,293.63	647.32	1,292.65	646.83	A	1,335.68	668.35	1,318.66	659.83			10
14	1,381.70	691.35	1,364.67	682.84	1,363.69	682.35	A	**1,264.65**	632.83	1,247.62	624.31			9
15	1,452.73	726.87	1,435.71	718.36	1,434.72	717.86	A	1,193.61	597.31	**1,176.58**	588.80			8
16	1,580.79	790.90	1,563.77	782.39	1,562.78	781.89	Q	**1,122.57**	561.79	1,105.55	553.28			7
17	1,694.83	847.92	1,677.81	839.41	1,676.82	838.92	N	**994.51**	497.76	977.49	489.25			6
18	1,793.90	897.46	1,776.88	888.94	1,775.89	888.45	V	**880.47**	440.74	863.44	432.23			5
19	1,956.97	978.99	1,939.94	970.47	1,938.96	969.98	Y	**781.40**	391.20	764.38	382.69			4
20	2,287.10	1,144.05	2,270.08	1,135.54	2,269.09	1,135.05	C	**618.34**	309.67	601.31	301.16			3
21	2,400.19	1,200.60	2,383.16	1,192.08	2,382.18	1,191.59	L	**288.20**	144.61	271.18	136.09			2
22							R	**175.12**	88.06	158.09	79.55			1

Query 39557 Hit 1

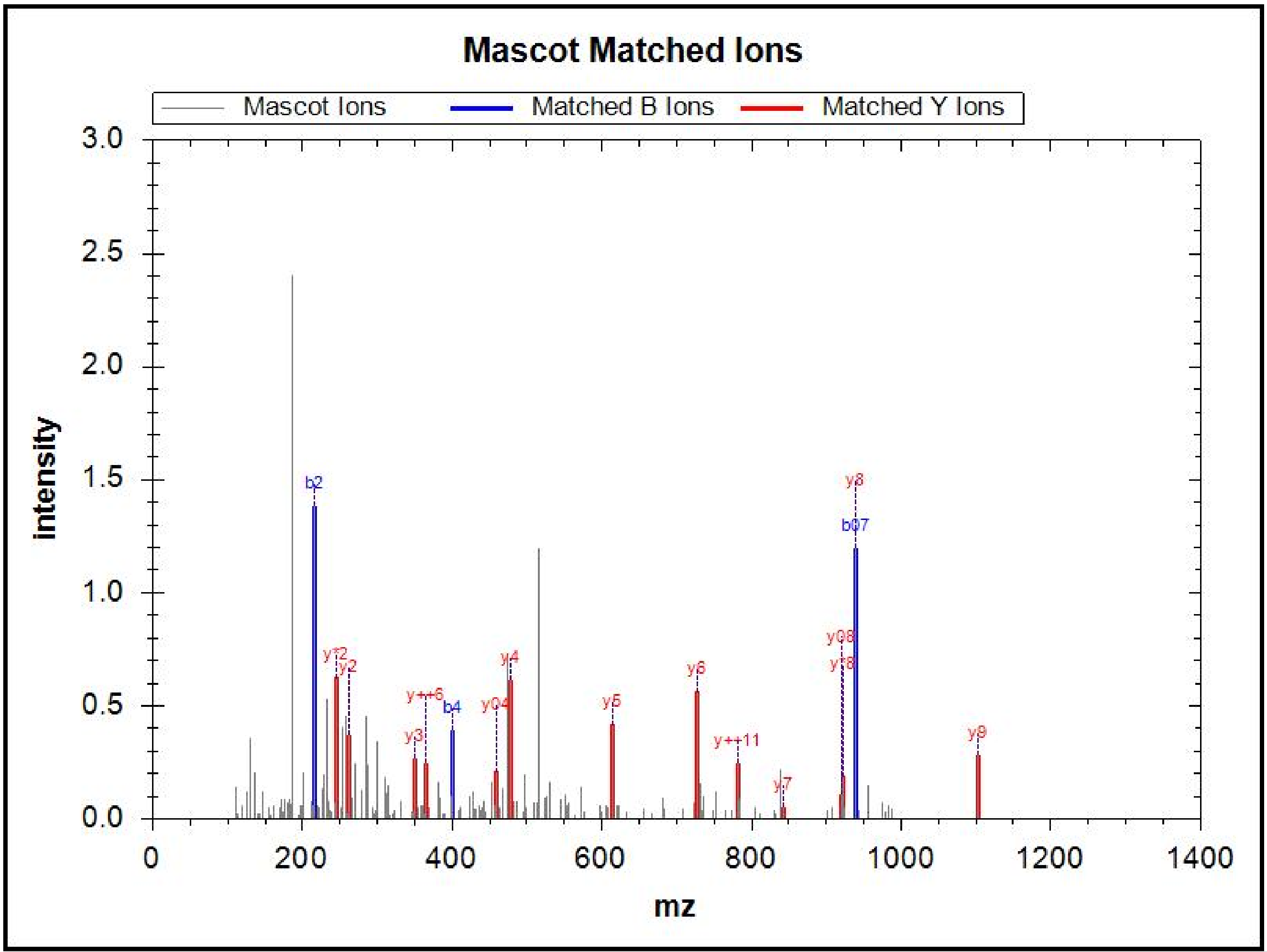
MS/MS Fragmentation of **RPPSAFFLFCSEHRPK**
Found in **P26583**, High mobility group protein B2 - Homo sapiens (Human)
Match to Query 39557: 2145.099from(537.2822,4+)
Title: File: SCX25859.wiff, Sample: ICAT (sample number 1), Elution: 28.769 min, Period: 1, Cycle(s): 1222 (Experiment 2)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 2145.099
Variable modifications:
C10 :ICAT-C (C)
Ions Score: 28.58 **Expect:** 0.110



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	157.11	79.06	140.08	70.54			R							16
2	**254.16**	127.58	237.13	119.07			P	1,990.00	995.50	1,972.97	986.99	1,971.99	986.50	15
3	351.21	176.11	334.19	167.60			P	1,892.95	946.98	1,875.92	938.46	1,874.94	937.97	14
4	**438.25**	219.63	421.22	211.11	420.24	210.62	S	1,795.89	898.45	1,778.87	889.94	1,777.88	889.45	13
5	**509.28**	255.15	492.26	246.63	491.27	246.14	A	1,708.86	854.94	1,691.84	846.42	1,690.85	845.93	12
6	**656.35**	328.68	639.32	320.17	638.34	319.67	F	1,637.83	**819.42**	1,620.80	810.90	1,619.82	810.41	11
7	803.42	**402.21**	786.39	393.70	785.41	393.21	F	1,490.76	**745.88**	1,473.73	737.37	1,472.75	736.88	10
8	**916.50**	458.76	899.48	450.24	898.49	449.75	L	1,343.69	**672.35**	1,326.66	663.83	1,325.68	663.34	9
9	1,063.57	532.29	1,046.55	523.78	1,045.56	523.28	F	1,230.60	**615.81**	1,213.58	**607.29**	1,212.59	606.80	8
10	1,393.71	697.36	1,376.68	688.84	1,375.70	688.35	C	1,083.54	**542.27**	1,066.51	**533.76**	1,065.53	533.27	7
11	1,480.74	740.87	1,463.71	732.36	1,462.73	731.87	S	**753.40**	**377.20**	736.37	368.69	735.39	368.20	6
12	1,609.78	805.40	1,592.76	796.88	1,591.77	796.39	E	666.37	333.69	649.34	325.17	648.36	324.68	5
13	1,746.84	873.92	1,729.82	865.41	1,728.83	864.92	H	537.33	269.17	520.30	260.65			4
14	1,902.94	951.98	1,885.92	943.46	1,884.93	942.97	R	400.27	200.64	383.24	192.12			3
15	2,000.00	1,000.50	1,982.97	991.99	1,981.99	991.50	P	**244.17**	122.59	227.14	114.07			2
16							K	**147.11**	74.06	130.09	65.55			1

Query 40675 Hit 1

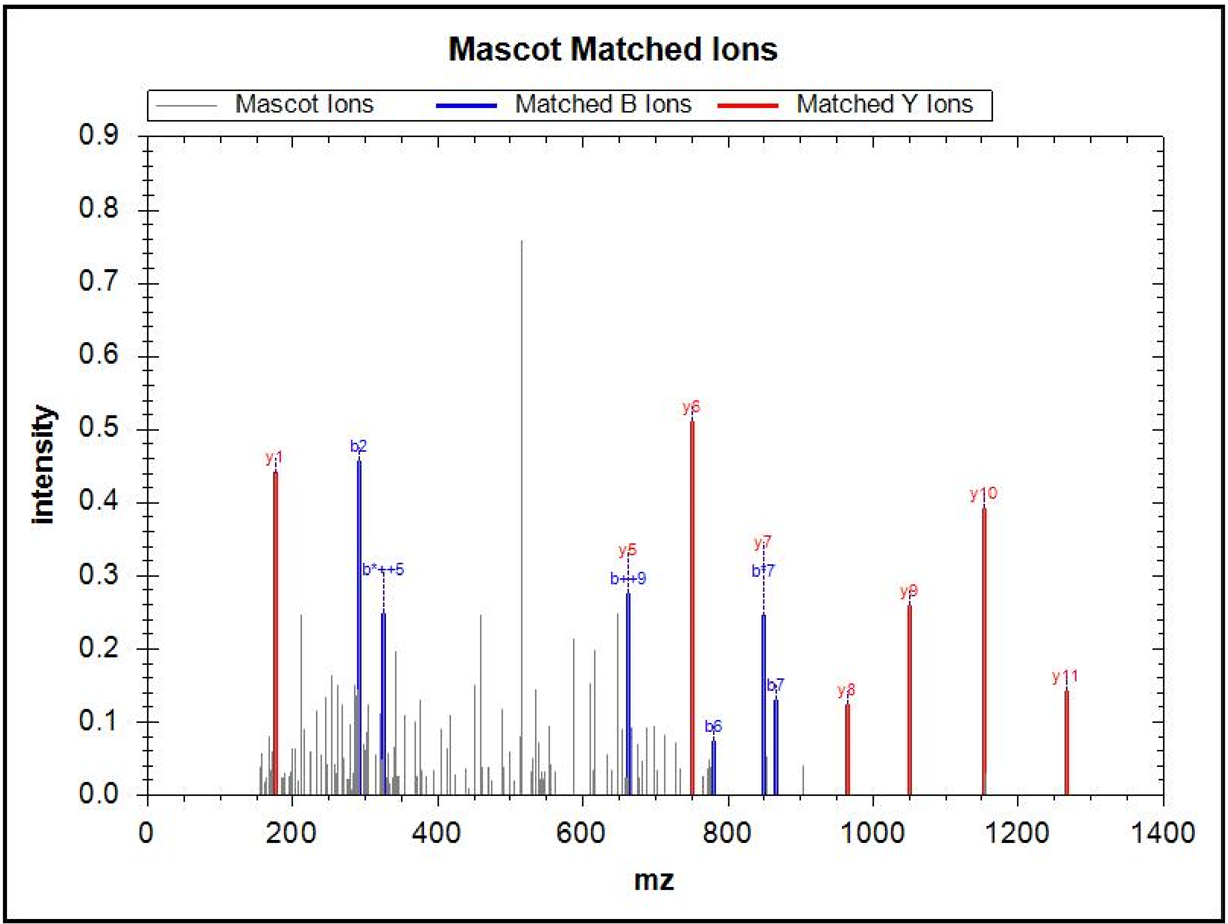
MS/MS Fragmentation of **TLADIICEYPDIHQSSR**
Found in **P56282**, DNA polymerase epsilon subunit 2 - Homo sapiens (Human)
Match to Query 40675: 2187.052from(730.0246,3+)
Title: File: SCX238.wiff, Sample: ICAT (sample number 2), Elution: 34.06 min, Period: 1, Cycle(s): 1512 (Experiment 4)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 2187.052
Variable modifications:
C7 :ICAT-C (C)
Ions Score: 30.38 **Expect:** 0.077



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	102.05	51.53			84.04	42.53	T							17
2	**215.14**	108.07			197.13	99.07	L	2,087.02	1,044.02	2,070.00	1,035.50	2,069.01	1,035.01	16
3	286.18	143.59			268.17	134.59	A	1,973.94	987.47	1,956.91	978.96	1,955.93	978.47	15
4	**401.20**	201.11			383.19	192.10	D	1,902.90	951.95	1,885.88	943.44	1,884.89	942.95	14
5	514.29	257.65			496.28	248.64	I	1,787.87	894.44	1,770.85	885.93	1,769.86	885.44	13
6	627.37	314.19			609.36	305.18	I	1,674.79	837.90	1,657.76	829.39	1,656.78	828.89	12
7	957.51	479.26			**939.50**	470.25	C	1,561.71	**781.36**	1,544.68	772.84	1,543.70	772.35	11
8	1,086.55	543.78			1,068.54	534.77	E	1,231.57	616.29	1,214.54	607.78	1,213.56	607.28	10
9	1,249.61	625.31			1,231.60	616.30	Y	**1,102.53**	551.77	1,085.50	543.25	1,084.52	542.76	9
10	1,346.67	673.84			1,328.66	664.83	P	**939.46**	470.24	**922.44**	461.72	**921.45**	461.23	8
11	1,461.69	731.35			1,443.68	722.34	D	**842.41**	421.71	825.38	413.20	824.40	412.70	7
12	1,574.78	787.89			1,556.77	778.89	I	**727.38**	**364.20**	710.36	355.68	709.37	355.19	6
13	1,711.84	856.42			1,693.83	847.42	H	**614.30**	307.65	597.27	299.14	596.29	298.65	5
14	1,839.89	920.45	1,822.87	911.94	1,821.88	911.45	Q	**477.24**	239.12	460.22	230.61	**459.23**	230.12	4
15	1,926.93	963.97	1,909.90	955.45	1,908.92	954.96	S	**349.18**	175.10	332.16	166.58	331.17	166.09	3
16	2,013.96	1,007.48	1,996.93	998.97	1,995.95	998.48	S	**262.15**	131.58	**245.12**	123.07	244.14	122.57	2
17							R	175.12	88.06	158.09	79.55			1

Query 51316 Hit 1

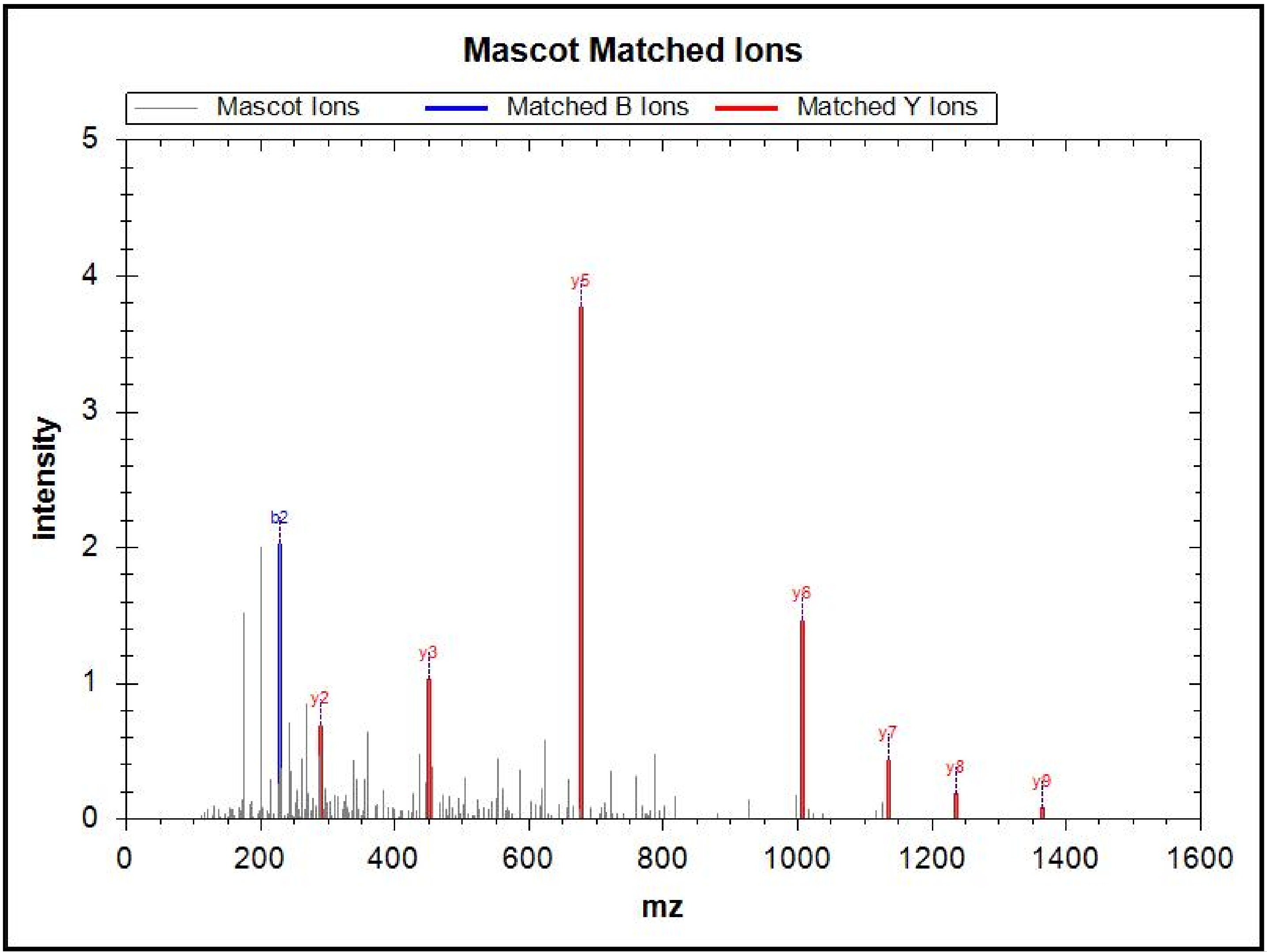
MS/MS Fragmentation of **YKYPNISCELLTSDVSQMNDR**
Found in **Q5H9R7**, SAPS domain family member 3 - Homo sapiens (Human)
Match to Query 51316: 2702.334from(901.7852,3+)
Title: File: SCX40_1.wiff, Sample: hung (sample number 1), Elution: 61.637 min, Period: 1, Cycle(s): 1550 (Experiment 2)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 2702.334
Variable modifications:
C8 :ICAT-C (C)
Ions Score: 39.91 **Expect:** 0.008



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	164.07	82.54					Y							21
2	**292.17**	146.59	275.14	138.07			K	2,540.21	1,270.61	2,523.19	1,262.10	2,522.20	1,261.60	20
3	455.23	228.12	438.20	219.60			Y	2,412.12	1,206.56	2,395.09	1,198.05	2,394.11	1,197.56	19
4	552.28	276.64	535.26	268.13			P	2,249.05	1,125.03	2,232.03	1,116.52	2,231.04	1,116.03	18
5	666.32	333.67	649.30	**325.15**			N	2,152.00	1,076.50	2,134.97	1,067.99	2,133.99	1,067.50	17
6	**779.41**	390.21	762.38	381.69			I	2,037.96	1,019.48	2,020.93	1,010.97	2,019.95	1,010.48	16
7	**866.44**	433.72	**849.41**	425.21	848.43	424.72	S	1,924.87	962.94	1,907.85	954.43	1,906.86	953.94	15
8	1,196.58	598.79	1,179.55	590.28	1,178.57	589.79	C	1,837.84	919.42	1,820.82	910.91	1,819.83	910.42	14
9	1,325.62	**663.31**	1,308.59	654.80	1,307.61	654.31	E	1,507.71	754.36	1,490.68	745.84	1,489.70	745.35	13
10	1,438.70	719.86	1,421.68	711.34	1,420.69	710.85	L	1,378.66	689.84	1,361.64	681.32	1,360.65	680.83	12
11	1,551.79	776.40	1,534.76	767.88	1,533.78	767.39	L	**1,265.58**	633.29	1,248.55	624.78	1,247.57	624.29	11
12	1,652.84	826.92	1,635.81	818.41	1,634.82	817.92	T	**1,152.49**	576.75	1,135.47	568.24	1,134.48	567.75	10
13	1,739.87	870.44	1,722.84	861.92	1,721.86	861.43	S	**1,051.45**	526.23	1,034.42	517.71	1,033.44	517.22	9
14	1,854.89	927.95	1,837.87	919.44	1,836.88	918.95	D	**964.42**	482.71	947.39	474.20	946.40	473.71	8
15	1,953.96	977.49	1,936.94	968.97	1,935.95	968.48	V	**849.39**	425.20	832.36	416.68	831.38	416.19	7
16	2,040.99	1,021.00	2,023.97	1,012.49	2,022.98	1,012.00	S	**750.32**	375.66	733.29	367.15	732.31	366.66	6
17	2,169.05	1,085.03	2,152.03	1,076.52	2,151.04	1,076.03	Q	**663.29**	332.15	646.26	323.63	645.28	323.14	5
18	2,300.09	1,150.55	2,283.07	1,142.04	2,282.08	1,141.55	M	535.23	268.12	518.20	259.61	517.22	259.11	4
19	2,414.14	1,207.57	2,397.11	1,199.06	2,396.13	1,198.57	N	404.19	202.60	387.16	194.08	386.18	193.59	3
20	2,529.16	1,265.09	2,512.14	1,256.57	2,511.15	1,256.08	D	290.15	145.58	273.12	137.06	272.14	136.57	2
21							R	**175.12**	88.06	158.09	79.55			1

Query 21128 Hit 1

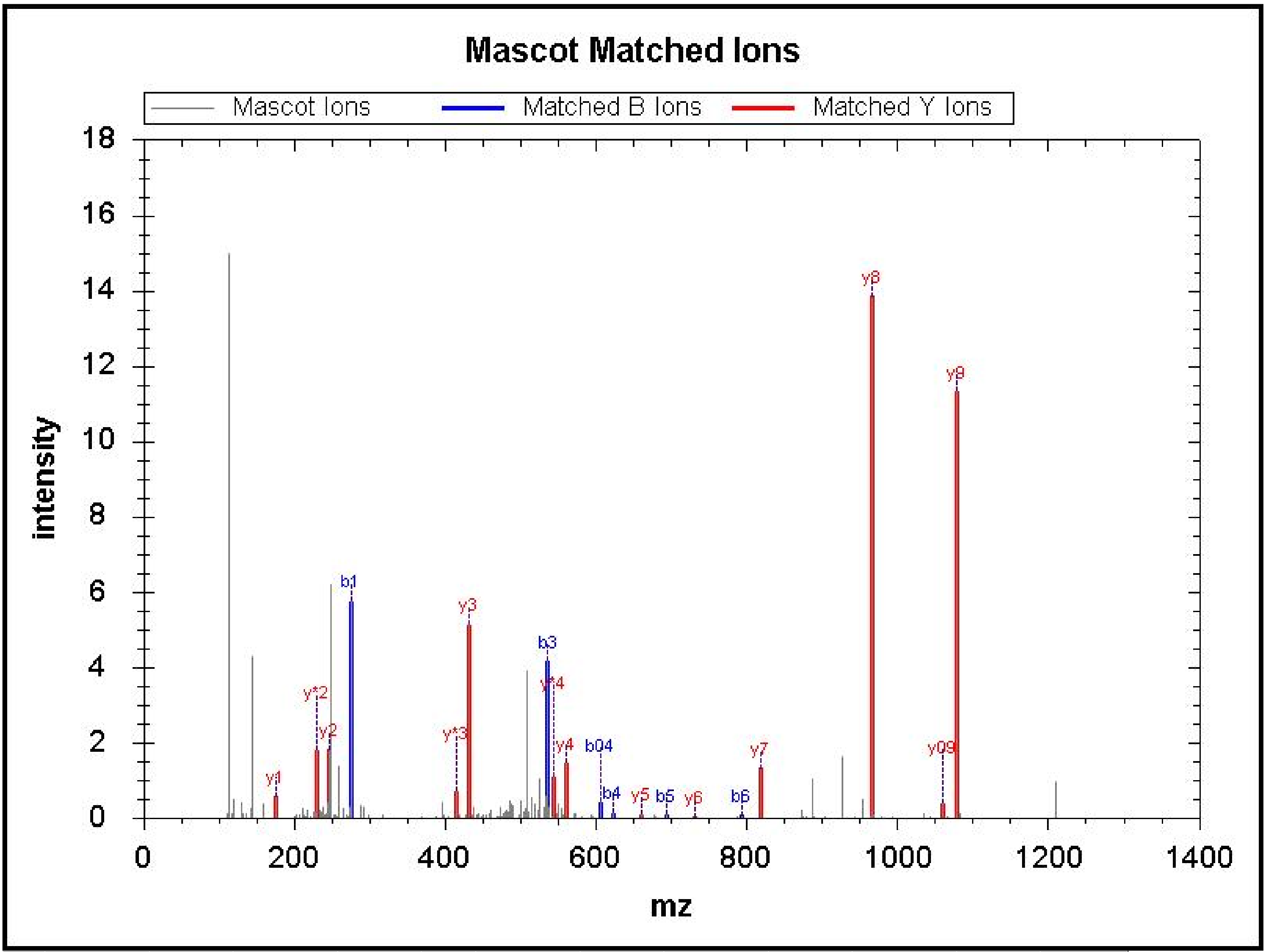
MS/MS Fragmentation of **LLETECPQYIR**
Found in **P05109**, Protein S100-A8 - Homo sapiens (Human)
Match to Query 21128: 1590.776from(796.3953,2+)
Title: File: SCX26_1.wiff, Sample: hung (sample number 1), Elution: 29.297 min, Period: 1, Cycle(s): 1529 (Experiment 2)
Data File:Ku-ICAT_SPROT-RESEARCHED
Monoisotopic mass of neutral peptide Mr(calc): 1590.776
Variable modifications:
C6 :ICAT-C (C)
Ions Score: 31.13 **Expect:** 0.058



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	114.09	57.55					L							11
2	**227.18**	114.09					L	1,478.73	739.87	1,461.70	731.36	1,460.72	730.86	10
3	356.22	178.61			338.21	169.61	E	**1,365.65**	683.33	1,348.62	674.81	1,347.64	674.32	9
4	457.27	229.14			439.26	220.13	T	**1,236.60**	618.81	1,219.58	610.29	1,218.59	609.80	8
5	586.31	293.66			568.30	284.65	E	**1,135.56**	568.28	1,118.53	559.77	1,117.55	559.28	7
6	916.44	458.73			898.43	449.72	C	**1,006.51**	503.76	989.49	495.25			6
7	1,013.50	507.25			995.49	498.25	P	**676.38**	338.69	659.35	330.18			5
8	1,141.56	571.28	1,124.53	562.77	1,123.55	562.28	Q	579.32	290.17	562.30	281.65			4
9	1,304.62	652.81	1,287.59	644.30	1,286.61	643.81	Y	**451.27**	226.14	434.24	217.62			3
10	1,417.70	709.36	1,400.68	700.84	1,399.69	700.35	I	**288.20**	144.61	271.18	136.09			2
11							R	175.12	88.06	158.09	79.55			1

Supplementary Figure 2
Query 33441 Hit 1

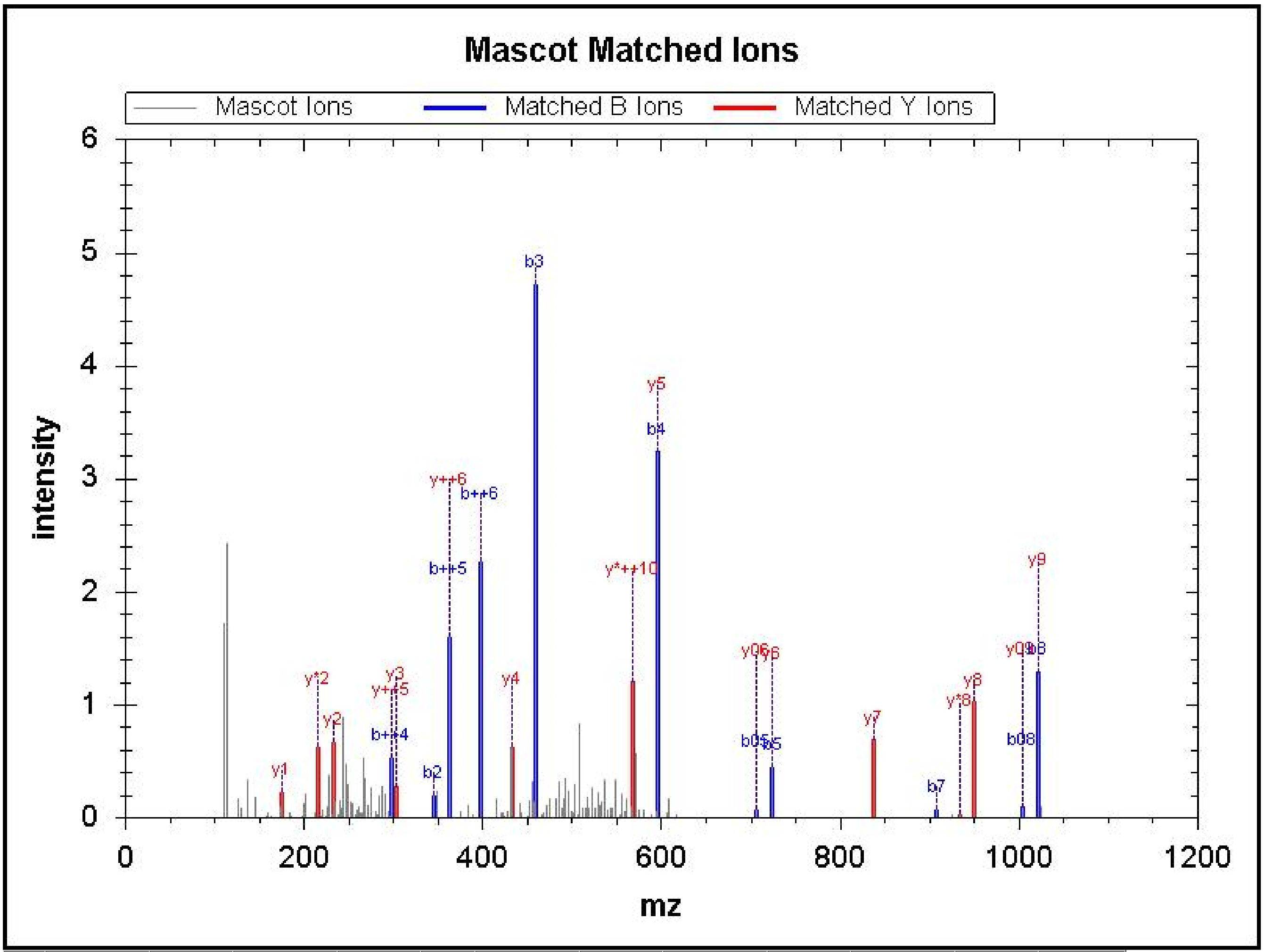
MS/MS Fragmentation of **MLFSAVEWAR**
Found in **P24468**, COUP transcription factor 2 - Homo sapiens (Human)
Match to Query 33441: 1352.709from(677.3616,2+)
Title: File: 080430AP4iTRAQ_31_01.wiff, Sample: Sample (sample number 1), Elution: 54.982 min, Period: 1, Cycle(s): 1675 (Experiment 4)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1352.709
Variable modifications:
Ions Score: 62.75 **Expect:** 0.000



No	b	b++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	**276.15**	138.58			M							10
2	389.23	195.12			L	**1,078.57**	539.79	1,061.54	531.27	**1,060.56**	530.78	9
3	**536.30**	268.65			F	**965.48**	483.25	948.46	474.73	947.47	474.24	8
4	**623.33**	312.17	**605.32**	303.17	S	**818.42**	409.71	801.39	401.20	800.40	400.71	7
5	**694.37**	347.69	676.36	338.68	A	**731.38**	366.20	714.36	357.68	713.37	357.19	6
6	**793.44**	397.22	775.43	388.22	V	**660.35**	330.68	643.32	322.16	642.34	321.67	5
7	922.48	461.74	904.47	452.74	E	**561.28**	281.14	**544.25**	272.63	543.27	272.14	4
8	1,108.56	554.78	1,090.55	545.78	W	**432.24**	216.62	**415.21**	208.11			3
9	1,179.60	590.30	1,161.59	581.30	A	**246.16**	123.58	**229.13**	115.07			2
10					R	**175.12**	88.06	158.09	79.55			1

Query 60621 Hit 1

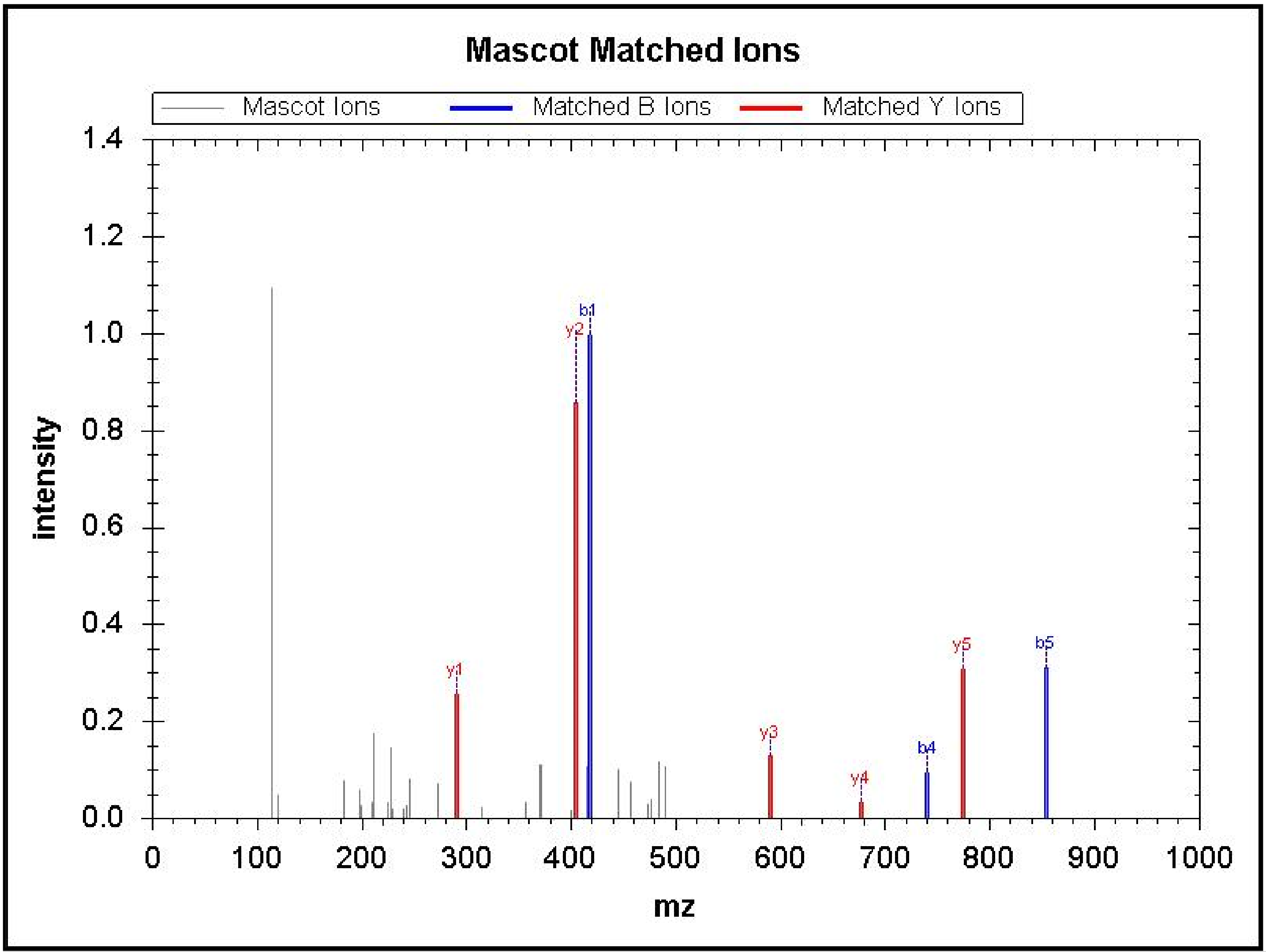
MS/MS Fragmentation of **EALHEALLEYEAGR**
Found in **P11474**, Steroid hormone receptor ERR1 - Homo sapiens (Human)
Match to Query 60621: 1743.984from(582.3354,3+)
Title: File: 080430AP4iTRAQ_40_02.wiff, Sample: Sample (sample number 1), Elution: 35.332 min, Period: 1, Cycle(s): 1438 (Experiment 4)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1743.984
Variable modifications:
Ions Score: 49.72 **Expect:** 0.006



No	b	b++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	274.15	137.58	256.14	128.57	E							14
2	**345.19**	173.10	327.18	164.09	A	1,471.75	736.38	1,454.73	727.87	1,453.74	727.38	13
3	**458.27**	229.64	440.26	220.63	L	1,400.72	700.86	1,383.69	692.35	1,382.71	691.86	12
4	**595.33**	**298.17**	577.32	289.16	H	1,287.63	644.32	1,270.61	635.81	1,269.62	635.31	11
5	**724.37**	**362.69**	**706.36**	353.69	E	1,150.57	575.79	1,133.55	**567.28**	1,132.56	566.79	10
6	795.41	**398.21**	777.40	389.20	A	**1,021.53**	511.27	1,004.50	502.76	**1,003.52**	502.26	9
7	**908.50**	454.75	890.49	445.75	L	**950.49**	475.75	**933.47**	467.24	932.48	466.75	8
8	**1,021.58**	511.29	**1,003.57**	502.29	L	**837.41**	419.21	820.38	410.70	819.40	410.20	7
9	1,150.62	575.81	1,132.61	566.81	E	**724.33**	**362.67**	707.30	354.15	**706.32**	353.66	6
10	1,313.69	657.35	1,295.68	648.34	Y	**595.28**	**298.15**	578.26	289.63	577.27	289.14	5
11	1,442.73	721.87	1,424.72	712.86	E	**432.22**	216.61	415.19	208.10	414.21	207.61	4
12	1,513.77	757.39	1,495.75	748.38	A	**303.18**	152.09	286.15	143.58			3
13	1,570.79	785.90	1,552.78	776.89	G	**232.14**	116.57	**215.11**	108.06			2
14					R	**175.12**	88.06	158.09	79.55			1

Query 53520 Hit 1

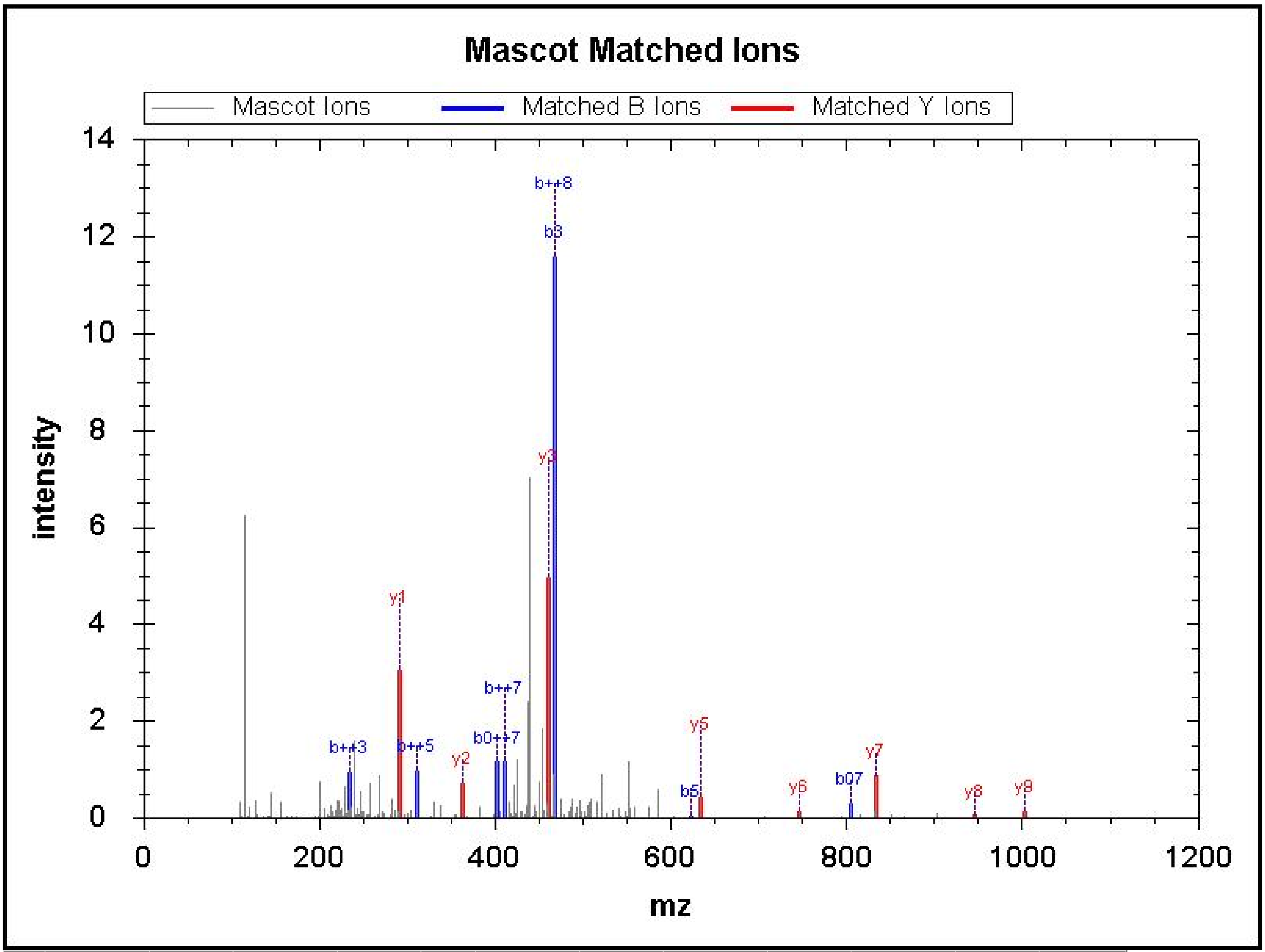
MS/MS Fragmentation of **KPILLPSWIK**
Found in **Q92547**, DNA topoisomerase 2-binding protein 1 - Homo sapiens (Human)
Match to Query 53520: 1626.046from(543.0226,3+)
Title: File: 080430AP4iTRAQ_4647_02.wiff, Sample: Sample (sample number 1), Elution: 51.939 min, Period: 1, Cycle(s): 2084 (Experiment 2)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1626.046
Variable modifications:
K1 :iTRAQ4plex (K)
K10 :iTRAQ4plex (K)
Ions Score: 40.55 **Expect:** 0.047



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	417.31	209.16	400.28	200.64			K							10
2	514.36	257.68	497.33	249.17			P	1,210.77	605.89	1,193.74	597.37	1,192.76	596.88	9
3	627.44	314.23	610.42	305.71			I	1,113.72	557.36	1,096.69	548.85	1,095.70	548.36	8
4	740.53	370.77	723.50	362.25			L	1,000.63	500.82	983.60	492.31	982.62	491.81	7
5	853.61	427.31	836.58	418.80			L	887.55	444.28	870.52	435.76	869.54	435.27	6
6	950.66	475.84	933.64	467.32			P	774.46	387.74	757.44	379.22	756.45	378.73	5
7	1,037.70	519.35	1,020.67	510.84	1,019.69	510.35	S	677.41	339.21	660.38	330.70	659.40	330.20	4
8	1,223.78	612.39	1,206.75	603.88	1,205.76	603.39	W	590.38	295.69	573.35	287.18			3
9	1,336.86	668.93	1,319.83	660.42	1,318.85	659.93	I	404.30	202.65	387.27	194.14			2
10							K	291.21	146.11	274.19	137.60			1

Query 49776 Hit 1

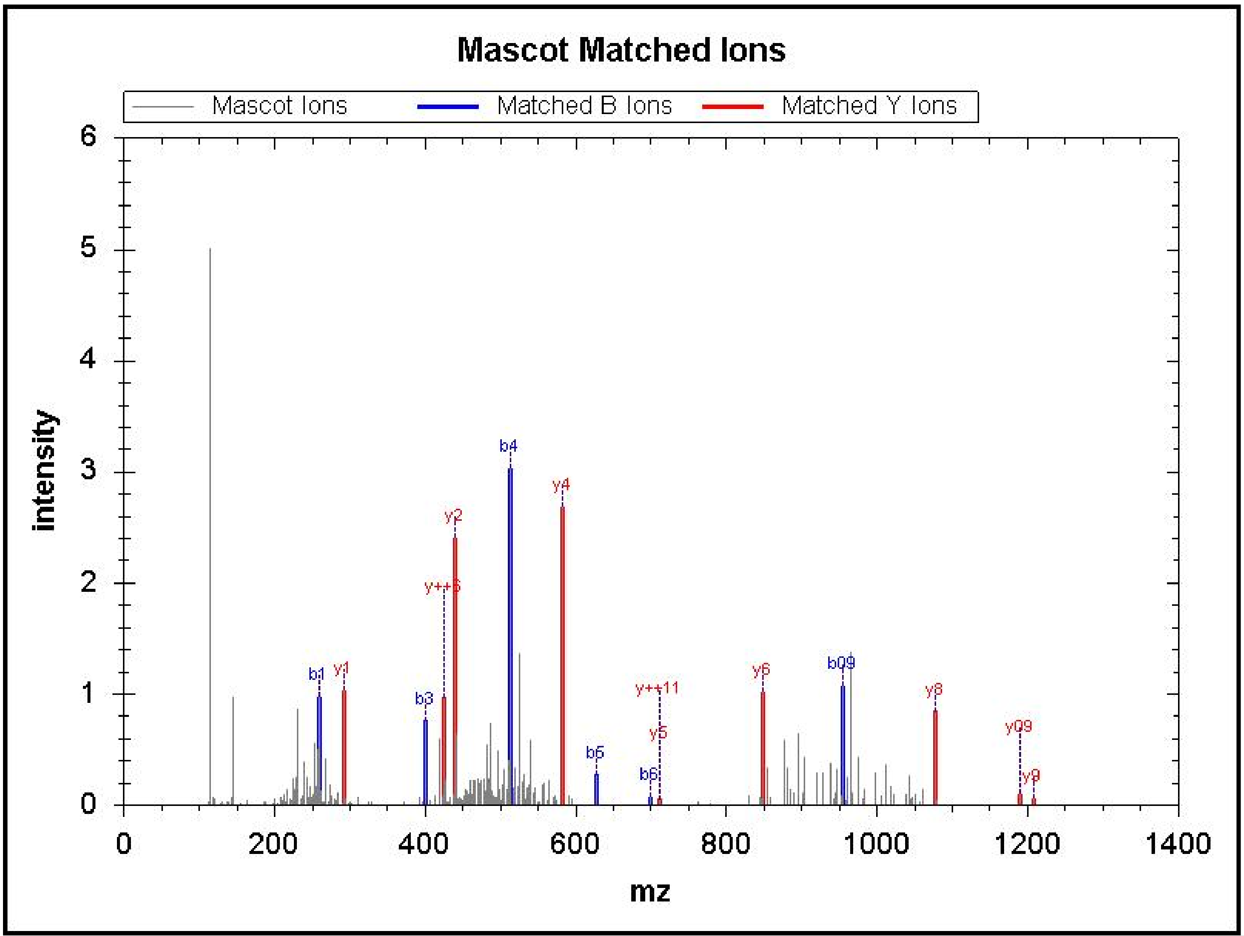
MS/MS Fragmentation of **GEHPGLSIGDVAK**
Found in **Q9UGV6**, High mobility group protein 1-like 10 - Homo sapiens (Human)
Match to Query 49776: 1566.908from(523.3099,3+)
Title: File: 080430AP4iTRAQ_4243_01.wiff, Sample: Sample (sample number 1), Elution: 33.12 min, Period: 1, Cycle(s): 1940 (Experiment 4)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1566.908
Variable modifications:
K13 :iTRAQ4plex (K)
Ions Score: 47.54 **Expect:** 0.009



No	b	b++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	202.13	101.57			G							13
2	331.17	166.09	313.16	157.09	E	1,366.74	683.88	1,349.72	675.36	1,348.73	674.87	12
3	**468.23**	**234.62**	450.22	225.61	H	1,237.70	619.35	1,220.68	610.84	1,219.69	610.35	11
4	565.29	283.15	547.27	274.14	P	1,100.64	550.83	1,083.62	542.31	1,082.63	541.82	10
5	**622.31**	**311.66**	604.30	302.65	G	**1,003.59**	502.30	986.56	493.79	985.58	493.29	9
6	735.39	368.20	717.38	359.19	L	**946.57**	473.79	929.54	465.27	928.56	464.78	8
7	822.42	**411.71**	**804.41**	**402.71**	S	**833.48**	417.25	816.46	408.73	815.47	408.24	7
8	935.51	**468.26**	917.50	459.25	I	**746.45**	373.73	729.43	365.22	728.44	364.72	6
9	992.53	496.77	974.52	487.76	G	**633.37**	317.19	616.34	308.67	615.36	308.18	5
10	1,107.56	554.28	1,089.54	545.28	D	576.35	288.68	559.32	280.16	558.34	279.67	4
11	1,206.62	603.82	1,188.61	594.81	V	**461.32**	231.16	444.29	222.65			3
12	1,277.66	639.33	1,259.65	630.33	A	**362.25**	181.63	345.23	173.12			2
13					K	**291.21**	146.11	274.19	137.60			1

Query 85508 Hit 1

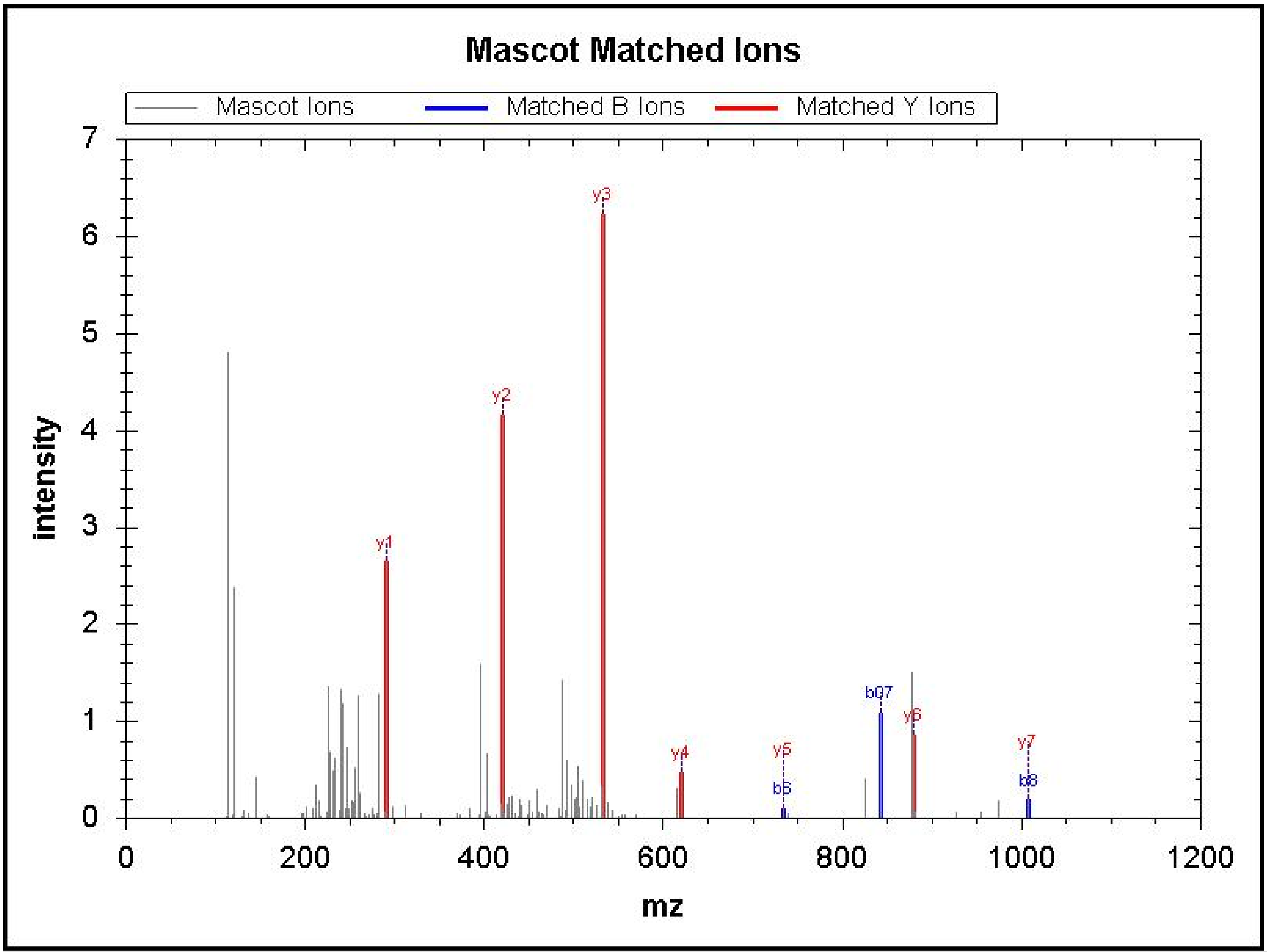
MS/MS Fragmentation of **IAALNASSTIEDDHEGSFK**
Found in **Q9Y6J0**, Calcineurin-binding protein Cabin 1 - Homo sapiens (Human)
Match to Query 85508: 2292.211from(765.0775,3+)
Title: File: 080430AP4iTRAQ_39_01.wiff, Sample: Sample (sample number 1), Elution: 34.373 min, Period: 1, Cycle(s): 1490 (Experiment 3)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 2292.211
Variable modifications:
K19 :iTRAQ4plex (K)
Ions Score: 51.37 **Expect:** 0.005



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	**258.19**	129.60					I							19
2	329.23	165.12					A	2,035.97	1,018.49	2,018.94	1,009.97	2,017.96	1,009.48	18
3	**400.27**	200.64					A	1,964.93	982.97	1,947.91	974.46	1,946.92	973.96	17
4	**513.35**	257.18					L	1,893.89	947.45	1,876.87	938.94	1,875.88	938.45	16
5	**627.39**	314.20	610.37	305.69			N	1,780.81	890.91	1,763.78	882.40	1,762.80	881.90	15
6	**698.43**	349.72	681.41	341.21			A	1,666.77	833.89	1,649.74	825.37	1,648.76	824.88	14
7	785.46	393.24	768.44	384.72	767.45	384.23	S	1,595.73	798.37	1,578.70	789.86	1,577.72	789.36	13
8	872.50	436.75	855.47	428.24	854.49	427.75	S	1,508.70	754.85	1,491.67	746.34	1,490.69	745.85	12
9	973.54	487.28	956.52	478.76	**955.53**	478.27	T	1,421.67	**711.34**	1,404.64	702.82	1,403.66	702.33	11
10	1,086.63	543.82	1,069.60	535.30	1,068.62	534.81	I	1,320.62	660.81	1,303.59	652.30	1,302.61	651.81	10
11	1,215.67	608.34	1,198.64	599.83	1,197.66	599.33	E	**1,207.53**	604.27	1,190.51	595.76	**1,189.52**	595.27	9
12	1,330.70	665.85	1,313.67	657.34	1,312.69	656.85	D	**1,078.49**	539.75	1,061.47	531.24	1,060.48	530.74	8
13	1,445.72	723.37	1,428.70	714.85	1,427.71	714.36	D	963.47	482.24	946.44	473.72	945.45	473.23	7
14	1,582.78	791.90	1,565.76	783.38	1,564.77	782.89	H	**848.44**	**424.72**	831.41	416.21	830.43	415.72	6
15	1,711.83	856.42	1,694.80	847.90	1,693.82	847.41	E	**711.38**	356.19	694.35	347.68	693.37	347.19	5
16	1,768.85	884.93	1,751.82	876.41	1,750.84	875.92	G	**582.34**	291.67	565.31	283.16	564.33	282.67	4
17	1,855.88	928.44	1,838.85	919.93	1,837.87	919.44	S	525.32	263.16	508.29	254.65	507.30	254.16	3
18	2,002.95	1,001.98	1,985.92	993.46	1,984.94	992.97	F	**438.28**	219.65	421.26	211.13			2
19							K	**291.21**	146.11	274.19	137.60			1

Query 60397 Hit 1

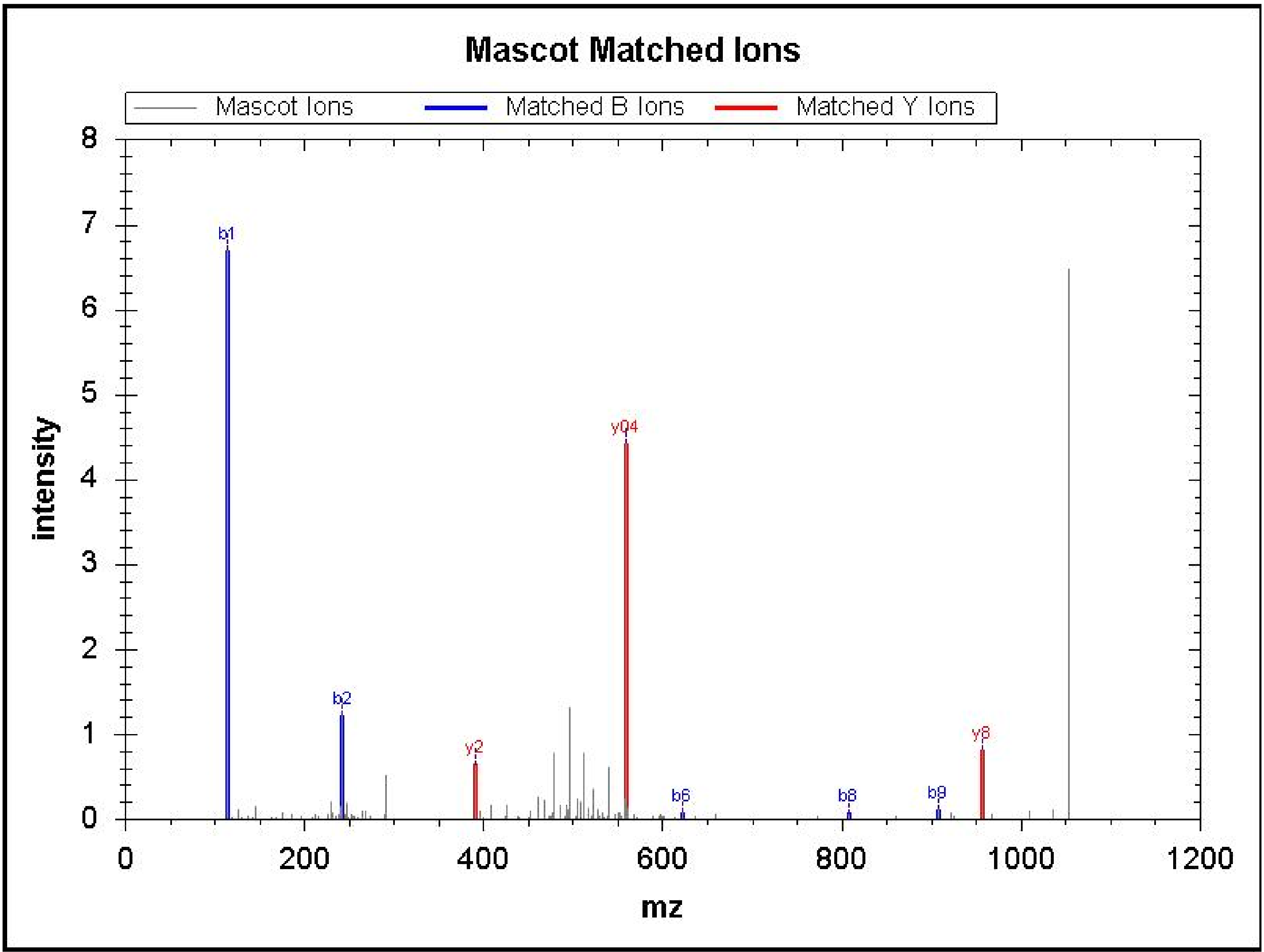
MS/MS Fragmentation of **KMSRTEQMISIQK**
Found in **Q8N5V2**, Ephexin-1 - Homo sapiens (Human)
Match to Query 60397: 1740.046from(581.0227,3+)
Title: File: 080430AP4iTRAQ_4243_01.wiff, Sample: Sample (sample number 1), Elution: 58.294 min, Period: 1, Cycle(s): 2364 (Experiment 4)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1740.046
Variable modifications:
M8 :Oxidation (M), with neutral losses 63.99828
Q12 :Deamidated (NQ)
K13 :iTRAQ4plex (K)
Ions Score: 40.5 **Expect:** 0.049



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	129.10	65.05	112.08	56.54			K							13
2	260.14	130.57	243.12	122.06			M	1,612.82	806.91	1,595.79	798.40	1,594.80	797.91	12
3	347.17	174.09	330.15	165.58	329.16	165.09	S	1,481.77	741.39	1,464.75	732.88	1,463.76	732.39	11
4	503.28	252.14	486.25	243.63	485.27	243.14	R	1,394.74	697.88	1,377.72	689.36	1,376.73	688.87	10
5	604.32	302.67	587.30	294.15	586.31	293.66	T	1,238.64	619.82	1,221.62	611.31	1,220.63	610.82	9
6	**733.37**	367.19	716.34	358.67	715.36	358.18	E	1,137.59	569.30	1,120.57	560.79	1,119.58	560.30	8
7	861.42	431.22	844.40	422.70	**843.41**	422.21	Q	**1,008.55**	504.78	991.53	496.27	990.54	495.77	7
8	**1,008.46**	504.73	991.43	496.22	990.45	495.73	M	**880.49**	440.75	863.47	432.24	862.48	431.74	6
9	1,121.54	561.28	1,104.52	552.76	1,103.53	552.27	I	**733.46**	367.23	716.43	358.72	715.45	358.23	5
10	1,208.58	604.79	1,191.55	596.28	1,190.57	595.79	S	**620.37**	310.69	603.35	302.18	602.36	301.69	4
11	1,321.66	661.33	1,304.63	652.82	1,303.65	652.33	I	**533.34**	267.17	516.31	258.66			3
12	1,450.70	725.86	1,433.68	717.34	1,432.69	716.85	Q	**420.26**	210.63	403.23	202.12			2
13							K	**291.21**	146.11	274.19	137.60			1

Query 20476 Hit 1

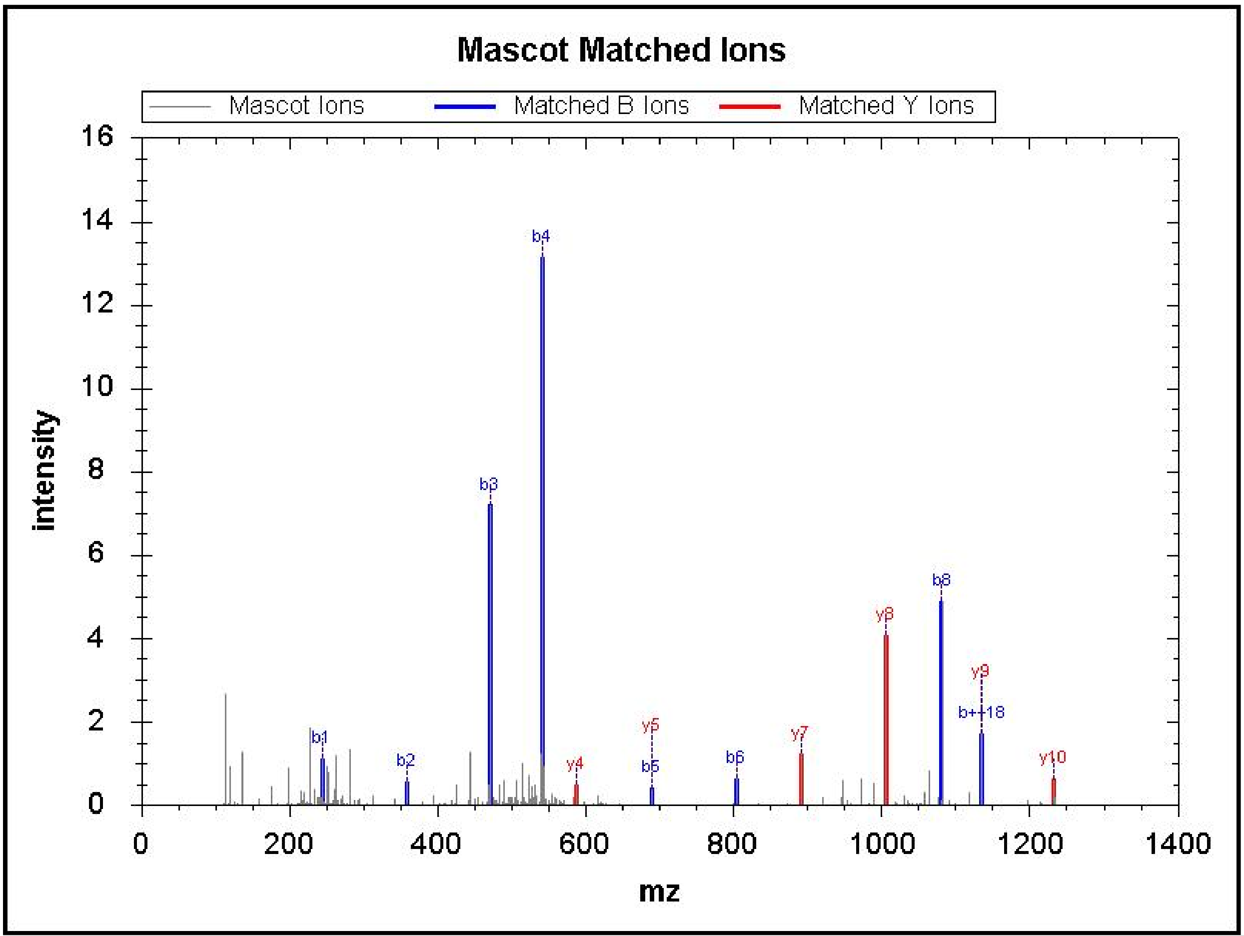
MS/MS Fragmentation of **LKPPVSEGVK**
Found in **Q8IVL0**, Neuron navigator 3 - Homo sapiens (Human)
Match to Query 20476: 1196.763from(599.3889,2+)
Title: File: 080430AP4iTRAQ_37_02.wiff, Sample: Sample (sample number 1), Elution: 21.692 min, Period: 1, Cycle(s): 1264 (Experiment 2)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1196.763
Variable modifications:
K10 :iTRAQ4plex (K)
Ions Score: 40.38 **Expect:** 0.034



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	**114.09**	57.55					L							10
2	**242.19**	121.60	225.16	113.08			K	1,084.65	542.83	1,067.62	534.31	1,066.64	533.82	9
3	339.24	170.12	322.21	161.61			P	**956.55**	478.78	939.53	470.27	938.54	469.77	8
4	436.29	218.65	419.27	210.14			P	859.50	430.25	842.47	421.74	841.49	421.25	7
5	535.36	268.18	518.33	259.67			V	762.45	381.73	745.42	373.21	744.44	372.72	6
6	**622.39**	311.70	605.37	303.19	604.38	302.69	S	663.38	332.19	646.35	323.68	645.37	323.19	5
7	751.43	376.22	734.41	367.71	733.42	367.22	E	576.35	288.68	559.32	280.16	**558.34**	279.67	4
8	**808.46**	404.73	791.43	396.22	790.45	395.73	G	447.30	224.16	430.28	215.64			3
9	**907.52**	454.27	890.50	445.75	889.51	445.26	V	**390.28**	195.65	373.26	187.13			2
10							K	291.21	146.11	274.19	137.60			1

Query 89482 Hit 1

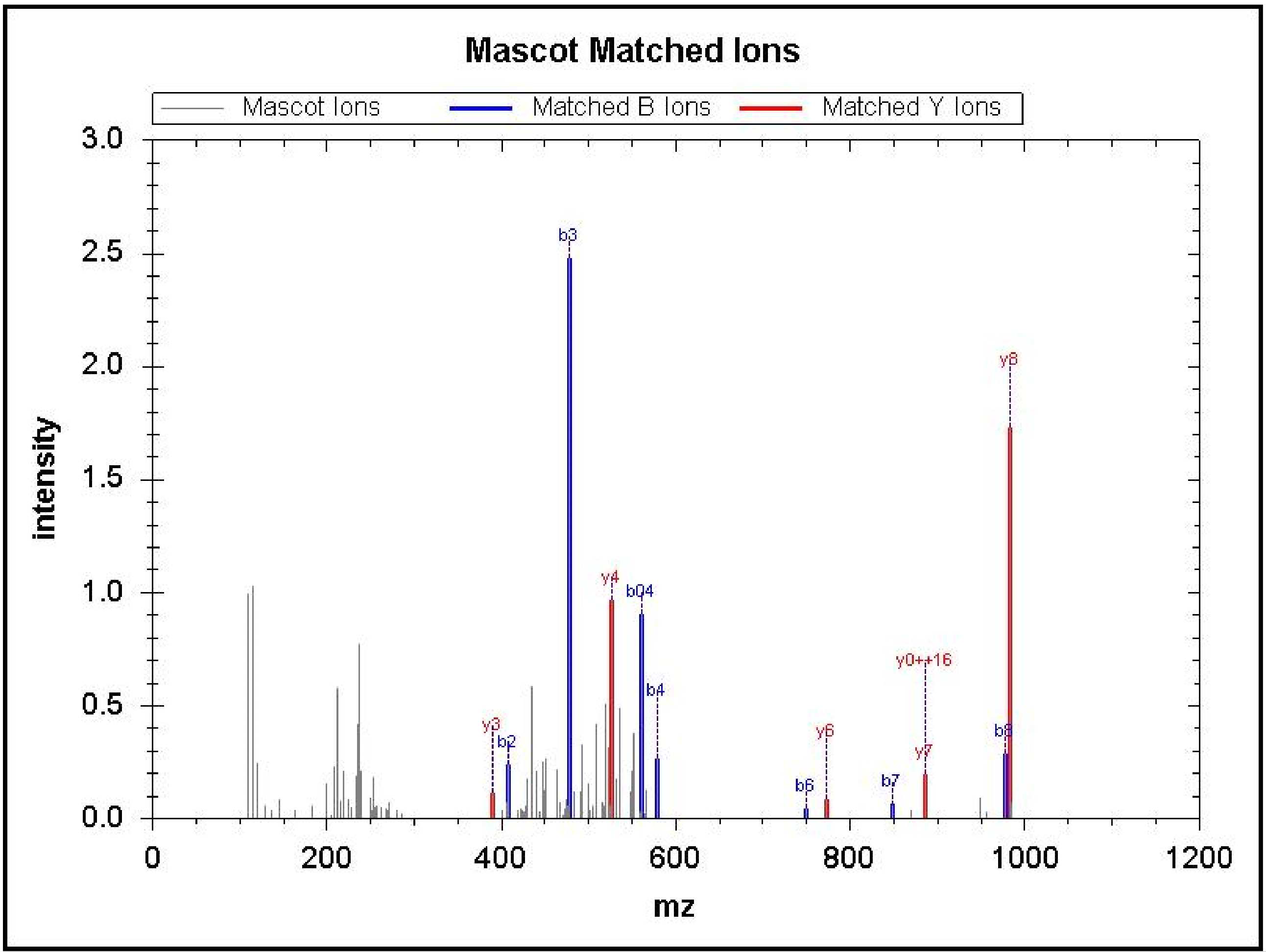
MS/MS Fragmentation of **VNIAFNYDMPEDSDTYLHR**
Found in **Q13838**, Spliceosome RNA helicase BAT1 - Homo sapiens (Human)
Match to Query 89482: 2443.24from(815.4205,3+)
Title: File: 080430AP4iTRAQ_36_02.wiff, Sample: Sample (sample number 1), Elution: 48.602 min, Period: 1, Cycle(s): 3240 (Experiment 2)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 2443.24
Variable modifications:
Ions Score: 57.4 **Expect:** 0.001



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	**244.18**	122.59					V							19
2	**358.22**	179.61	341.19	171.10			N	2,200.96	1,100.98	2,183.93	1,092.47	2,182.95	1,091.98	18
3	**471.30**	236.16	454.28	227.64			I	2,086.92	1,043.96	2,069.89	1,035.45	2,068.91	1,034.96	17
4	**542.34**	271.67	525.32	263.16			A	1,973.83	987.42	1,956.81	978.91	1,955.82	978.42	16
5	**689.41**	345.21	672.38	336.70			F	1,902.80	951.90	1,885.77	943.39	1,884.79	942.90	15
6	**803.45**	402.23	786.43	393.72			N	1,755.73	878.37	1,738.70	869.85	1,737.72	869.36	14
7	966.52	483.76	949.49	475.25			Y	1,641.68	821.35	1,624.66	812.83	1,623.67	812.34	13
8	**1,081.54**	541.28	1,064.52	532.76	1,063.53	532.27	D	1,478.62	739.81	1,461.60	731.30	1,460.61	730.81	12
9	1,212.58	606.80	1,195.56	598.28	1,194.57	597.79	M	1,363.59	682.30	1,346.57	673.79	1,345.58	673.30	11
10	1,309.64	655.32	1,292.61	646.81	1,291.63	646.32	P	**1,232.55**	616.78	1,215.53	608.27	1,214.54	607.78	10
11	1,438.68	719.84	1,421.65	711.33	1,420.67	710.84	E	**1,135.50**	568.25	1,118.47	559.74	1,117.49	559.25	9
12	1,553.71	777.36	1,536.68	768.84	1,535.70	768.35	D	**1,006.46**	503.73	989.43	495.22	988.45	494.73	8
13	1,640.74	820.87	1,623.71	812.36	1,622.73	811.87	S	**891.43**	446.22	874.41	437.71	873.42	437.21	7
14	1,755.77	878.39	1,738.74	869.87	1,737.75	869.38	D	804.40	402.70	787.37	394.19	786.39	393.70	6
15	1,856.81	928.91	1,839.79	920.40	1,838.80	919.90	T	**689.37**	345.19	672.35	336.68	671.36	336.18	5
16	2,019.88	1,010.44	2,002.85	1,001.93	2,001.87	1,001.44	Y	**588.33**	294.67	571.30	286.15			4
17	2,132.96	1,066.98	2,115.93	1,058.47	2,114.95	1,057.98	L	425.26	213.13	408.24	204.62			3
18	2,270.02	**1,135.51**	2,252.99	1,127.00	2,252.01	1,126.51	H	312.18	156.59	295.15	148.08			2
19							R	175.12	88.06	158.09	79.55			1

Query 82251 Hit 1

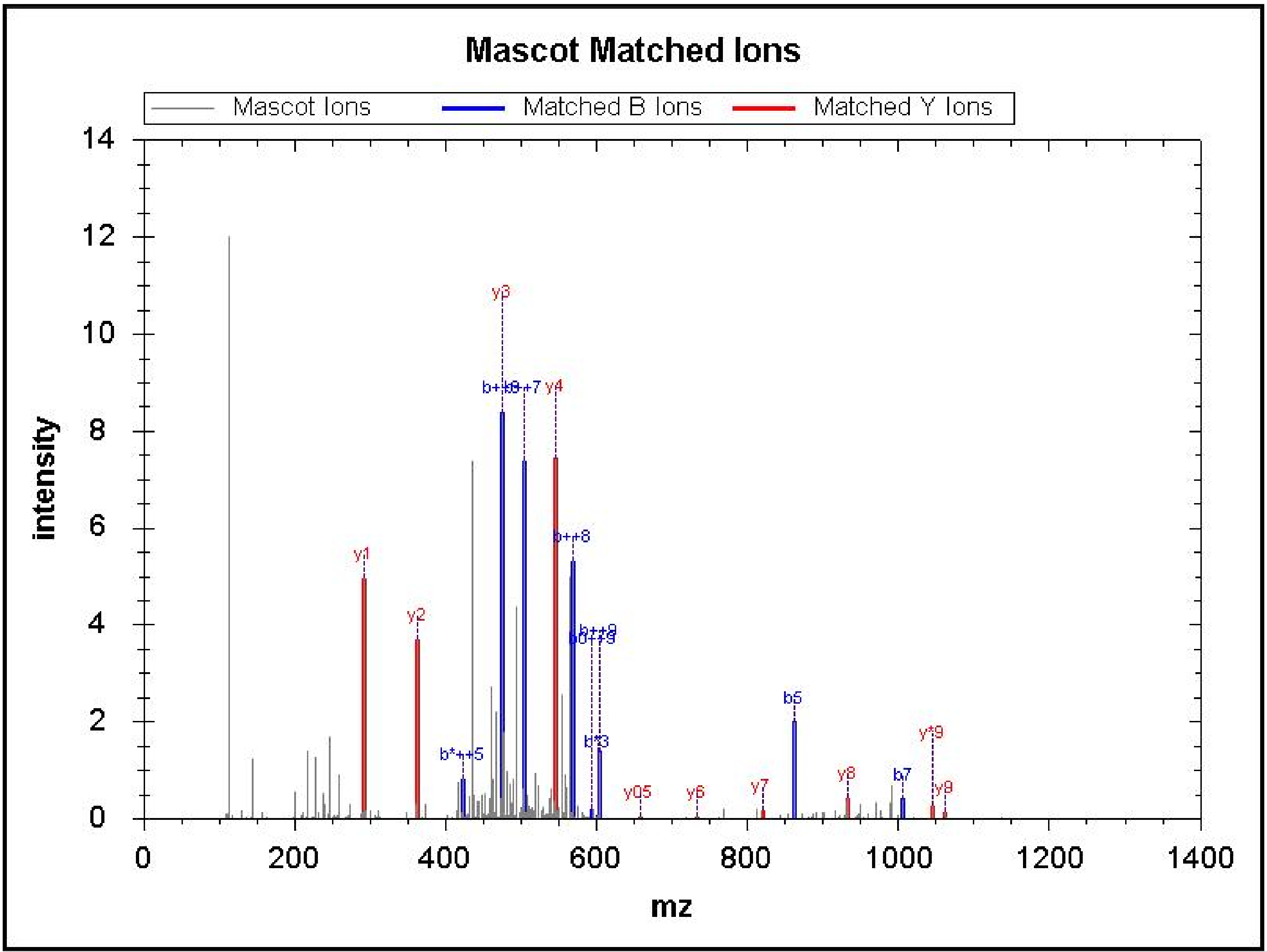
MS/MS Fragmentation of **YVATLGVEVHPLVFHTNR**
Found in **P62826**, GTP-binding nuclear protein Ran - Homo sapiens (Human)
Match to Query 82251: 2195.291from(549.83,4+)
Title: File: 080430AP4iTRAQ_4849_02.wiff, Sample: Sample (sample number 1), Elution: 54.639 min, Period: 1, Cycle(s): 2390 (Experiment 2)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 2195.291
Variable modifications:
Ions Score: 45.32 **Expect:** 0.019



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	308.17	154.59					Y							18
2	**407.24**	204.12					V	1,889.04	945.02	1,872.01	936.51	1,871.03	936.02	17
3	**478.28**	239.64					A	1,789.97	895.49	1,772.94	886.98	1,771.96	**886.48**	16
4	**579.33**	290.17			**561.32**	281.16	T	1,718.93	859.97	1,701.91	851.46	1,700.92	850.97	15
5	692.41	346.71			674.40	337.70	L	1,617.89	809.45	1,600.86	800.93	1,599.88	800.44	14
6	**749.43**	375.22			731.42	366.21	G	1,504.80	752.90	1,487.78	744.39	1,486.79	743.90	13
7	**848.50**	424.75			830.49	415.75	V	1,447.78	724.39	1,430.75	715.88	1,429.77	715.39	12
8	**977.54**	489.27			959.53	480.27	E	1,348.71	674.86	1,331.69	666.35	1,330.70	665.85	11
9	1,076.61	538.81			1,058.60	529.80	V	1,219.67	610.34	1,202.64	601.83	1,201.66	601.33	10
10	1,213.67	607.34			1,195.66	598.33	H	1,120.60	560.80	1,103.57	552.29	1,102.59	551.80	9
11	1,310.72	655.86			1,292.71	646.86	P	**983.54**	492.27	966.52	483.76	965.53	483.27	8
12	1,423.81	712.41			1,405.80	703.40	L	**886.49**	443.75	869.46	435.24	868.48	434.74	7
13	1,522.88	761.94			1,504.86	752.94	V	**773.41**	387.21	756.38	378.69	755.39	378.20	6
14	1,669.94	835.48			1,651.93	826.47	F	674.34	337.67	657.31	329.16	656.33	328.67	5
15	1,807.00	904.00			1,788.99	895.00	H	**527.27**	264.14	510.24	255.62	509.26	255.13	4
16	1,908.05	954.53			1,890.04	945.52	T	**390.21**	195.61	373.18	187.10	372.20	186.60	3
17	2,022.09	1,011.55	2,005.07	1,003.04	2,004.08	1,002.54	N	289.16	145.08	272.14	136.57			2
18							R	175.12	88.06	158.09	79.55			1

Query 56952 Hit 1

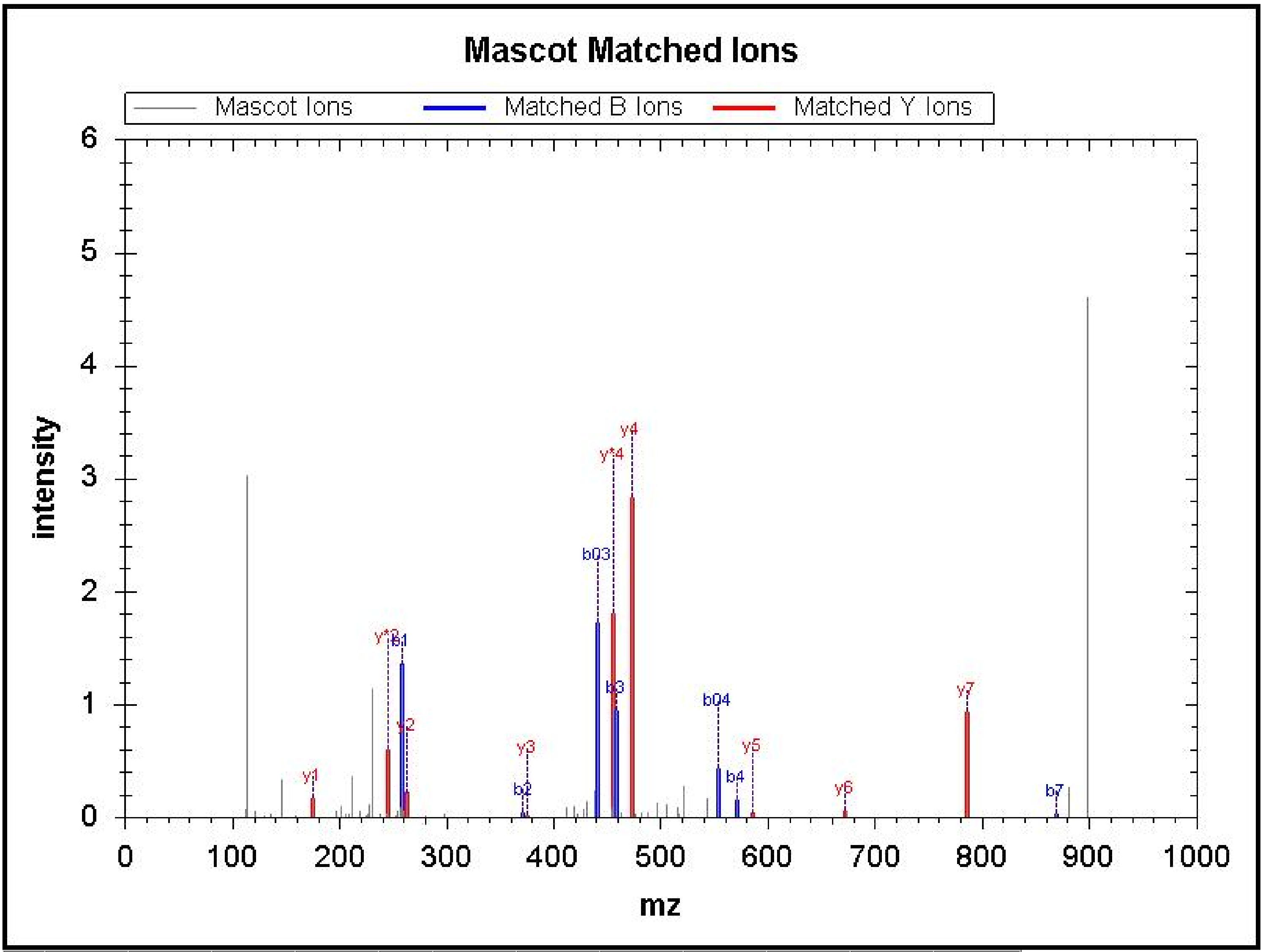
MS/MS Fragmentation of **TKTENSGEALAK**
Found in **Q9P016**, Thymocyte nuclear protein 1 - Homo sapiens (Human)
Match to Query 56952: 1679.97from(560.9972,3+)
Title: File: 080430AP4iTRAQ_4647_01.wiff, Sample: Sample (sample number 1), Elution: 23.097 min, Period: 1, Cycle(s): 1612 (Experiment 3)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1679.97
Variable modifications:
K2 :iTRAQ4plex (K)
K12 :iTRAQ4plex (K)
Ions Score: 41.8 **Expect:** 0.036



No	b	b++	b*	b*++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	246.16	123.58			228.15	114.58	T							12
2	518.35	259.68	501.33	251.17	500.34	250.68	K	1,435.80	718.40	1,418.77	709.89	1,417.79	709.40	11
3	619.40	310.20	**602.38**	301.69	601.39	301.20	T	1,163.60	582.30	1,146.58	573.79	1,145.59	573.30	10
4	748.44	374.73	731.42	366.21	730.43	365.72	E	**1,062.55**	531.78	**1,045.53**	523.27	1,044.54	522.78	9
5	**862.49**	431.75	845.46	**423.23**	844.48	422.74	N	**933.51**	467.26	916.49	458.75	915.50	458.25	8
6	949.52	**475.26**	932.49	466.75	931.51	466.26	S	**819.47**	410.24	802.44	401.72	801.46	401.23	7
7	**1,006.54**	**503.77**	989.51	495.26	988.53	494.77	G	**732.44**	366.72	715.41	358.21	714.43	357.72	6
8	1,135.58	**568.30**	1,118.56	559.78	1,117.57	559.29	E	675.42	338.21	658.39	329.70	**657.41**	329.21	5
9	1,206.62	**603.81**	1,189.59	595.30	1,188.61	**594.81**	A	**546.37**	273.69	529.35	265.18			4
10	1,319.70	660.36	1,302.68	651.84	1,301.69	651.35	L	**475.34**	238.17	458.31	229.66			3
11	1,390.74	695.87	1,373.72	687.36	1,372.73	686.87	A	**362.25**	181.63	345.23	173.12			2
12							K	**291.21**	146.11	274.19	137.60			1

Query 10073 Hit 1

MS/MS Fragmentation of **LISLPLSR**
Found in **Q9NRG0**, Chromatin accessibility complex protein 1 - Homo sapiens (Human)
Match to Query 10073: 1041.688from(521.8515,2+)
Title: File: 080430AP4iTRAQ_27_01.wiff, Sample: Ku (sample number 1), Elution: 43.939 min, Period: 1, Cycle(s): 1577 (Experiment 3)
Data File:iTRAQ_080430_combined Search
Monoisotopic mass of neutral peptide Mr(calc): 1041.688
Variable modifications:
Ions Score: 47.04 **Expect:** 0.006



No	b	b++	b0	b0++	Seq	y	y++	y*	y*++	y0	y0++	RevNo
1	**258.19**	129.60			L							8
2	**371.28**	186.14			I	**785.49**	393.25	768.46	384.73	767.48	384.24	7
3	**458.31**	229.66	**440.30**	220.65	S	**672.40**	336.71	655.38	328.19	654.39	327.70	6
4	**571.39**	286.20	**553.38**	277.20	L	**585.37**	293.19	568.35	284.68	567.36	284.18	5
5	668.45	334.73	650.44	325.72	P	**472.29**	236.65	**455.26**	228.13	454.28	227.64	4
6	781.53	391.27	763.52	382.26	L	**375.24**	188.12	358.21	179.61	357.22	179.12	3
7	**868.56**	434.78	850.55	425.78	S	**262.15**	131.58	**245.12**	123.07	244.14	122.57	2
8					R	**175.12**	88.06	158.09	79.55			1