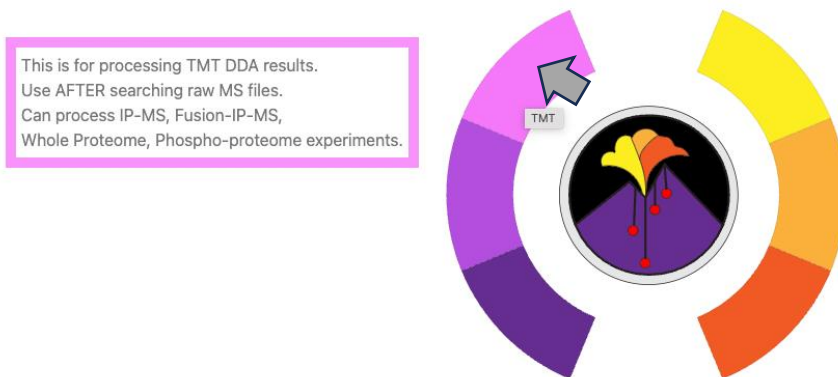


## TMT (Whole Proteome)

**Step 1:** Click on the TMT tab on the home page to access all the TMT workflows (as shown in figure below with the grey arrow).



**Step 2:** Choose the type of analysis to run. You can hover over the question mark to get more details on the different choices and recommended settings (as shown by the grey arrow below). The choices to be made here include:

1. The choice of search engine (SEQUEST in Proteome Discoverer vs COMET)
2. The choice of analysis type (MAGMA LM for a two-sample t-test and MAGMA Limma for a one sample t-test)

Click on the Whole proteome arm (highlighted with red arrow in the figure below) to access to workflow.

### Analysis Type

For more information: ?

Use COMET Search results:

Use SEQUEST Search results:

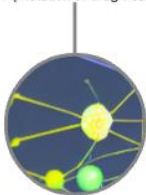
- Magma (Linear Model)
- Magma (Limma)

Choose the strategy for analysis with two choices:

1. Choose the search engine that was used for generating the PSM list.
2. Choose the model type to run the differential expression analysis with (between linear model (two sample) vs limma (one sample))

NOTE: No default set but recommend setting of COMET search + Magma (linea model). Check "About" page or manuscript for more details.

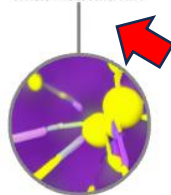
IP-TMT (Mutation or drug treatment)



IP-TMT (Fusions)



Whole Proteome TMT



PhosphoProteome TMT



**Step 3:** Upload the annotation file. This is made using the experimental setup.

An example can be seen below taken from a benchmarking two whole proteome (yeast spiked into human) TMT10 experiment. Here each TMT label is associated with a separate condition. For example, ten implies Human:Yeast of 1:1, four implies Human: Yeast of 1:0.4 and one implied Human: Yeast of 1:0.1. You can also hover over question mark for more details. [Click on the "Sample File" in blue to download this example annotation file.](#)

	A	B
1	Channel	Label
2	126	ten
3	127N	ten
4	127C	four
5	128N	ten
6	128C	four
7	129N	four
8	129C	one
9	130N	none
10	130C	one
11	131	one

1 Upload the 'Annotation file'

For more information: ?

Select a file:

No file chosen

[Sample file](#)

This file is to assign labels to channels according to experimental setup. Columns necessary for the file are Channel and Label. Channel is to specify the TMT tags used in the experiment. Label is to specify the biological condition encoded by the corresponding TMT tag. Important for choosing the conditions to be compared.

NOTE: File name should not have spaces and should be ".csv" format.

NOTE (2): Label column should not have "-" character.

**Step 4:** Choose the conditions you want to compare in a pairwise fashion. And choose the direction of comparison. So, choosing comparison ('four', 'ten') and direction (Condition\_2/Condition\_1) means the following comparison will run – (ten/four).

2 Select the Comparison You Would Like to Perform

Choose a comparison

('one', 'four')

('one', 'ten')

('four', 'ten')

Choose the direction for comparison:

(Condition\_1/Condition\_2)

(Condition\_2/Condition\_1)

**Step 5:** Upload the input files (PSM list) for quantification.

For SEQUEST in Proteome Discoverer search, upload a tab separated file of PSM (filtered at 1% FDR or filter cutoff of choice) and associated reporter ion abundance (per TMT channel). The abundances must be exported as signal-to-noise as well raw reporter intensities. Make sure the

files have the following columns – 'Intensity', 'Annotated Sequence', 'Master Protein Accessions', 'Protein Accessions', 'Isolation Interference [%]', 'Spectrum File', 'Charge', 'RT [min]', '# Protein Groups'.

As before hover over question mark for more information. [Click on the “Sample File” in blue to download this example PSM files.](#)

3 Upload a tab separated PD text file with "S/N" values

For more information: ?

Select a file:

- This field is required.

Choose File No file chosen

Reset

Sample file

This file is the output from Proteome Discoverer(PD) search in the form of tab delimited ".txt" file of all PSMs passing 1% FDR threshold. The reporter ion intensities need to be exported as signal-to-noise ratios.

NOTE: File name should not have spaces.

For PD search ensure the following columns are present - 'Intensity', 'Annotated Sequence', 'Master Protein Accessions', 'Protein Accessions', 'Isolation Interference [%]', 'Spectrum File', 'Charge', 'RT [min]', '# Protein Groups' Ensure the column "Intensity" corresponding to precursor ion intensities associated with each PSM is uploaded.

4 Upload a tab separated PD text file with "Intensity" values

For more information: ?

Select a file:

- This field is required.

Choose File No file chosen

Reset

The example has been down sampled to 500 proteins from a real benchmarking whole-proteome experiment and looks like the screenshot below.

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
Checked	Confidence	Identifying N PSM	Ambigu Sequence	Annotated Si	Modification #	Proteins	Master Prote	Protein Acce	# Missed	Cle Charge	DeltaScore	DeltaCn	Rank	Search Engin	m/z [Da]	MH+ [Da]	Theo. MH+	Delta
1	FALSE	High	Sequest HT ( Unambiguou	LINEPTAAIA [R].IINEPTAA	N-Term(TMT)	3	P0DMV9	P17066; POD	0	3	0.7037	0	1	1	639.69289	1917.06411	1917.06429	
2	FALSE	High	Sequest HT ( Unambiguou	DVTFLNDCV [K].dVTFLN	N-Term(TMT)	1	P00560	P00560	0	3	0.642	0	1	1	807.76363	2421.27633	2421.27358	
3	FALSE	High	Sequest HT ( Unambiguou	ELMQQIENFI [K].eL	MQQIE N-Term(TMT)	1	P04807	P04807	0	3	0.4396	0	1	1	623.00582	1867.0029	1867.00356	
4	FALSE	High	Sequest HT ( Unambiguou	TGSQGGCTC [R].tGSQGG	Q N-Term(TMT)	1	P62857	P62857	0	2	0.5774	0	1	1	725.86732	1450.72737	1450.72699	
5	FALSE	High	Sequest HT ( Unambiguou	NLDGQDLDI [R].nLDGQD	N-Term(TMT)	1	Q9Y310	Q9Y310	0	3	0.3244	0	1	1	555.64673	1664.92562	1664.92596	
6	FALSE	High	Sequest HT ( Unambiguou	DFSYLFSDET [R].dFSYL	FS N-Term(TMT)	1	P53090	P53090	0	3	0.5372	0	1	1	598.62285	1793.85399	1793.85436	
7	FALSE	High	Sequest HT ( Unambiguou	FTLLPPTS [R].fTLLPPTS	N-Term(TMT)	2	Q13724	Q13724-2; Q	0	3	0.4871	0	1	1	667.38721	2000.14706	2000.14685	
8	FALSE	High	Sequest HT ( Unambiguou	KTSASSASAS [R].kT	SASSA N-Term(TMT)	1	Q86VM9	Q86VM9	1	3	0.565	0	1	1	600.32722	1798.9671	1798.96592	
9	FALSE	High	Sequest HT ( Unambiguou	FDGVCDSLE [R].fDG	VcD N-Term(TMT)	1	P06280	P06280	0	3	0.6649	0	1	1	829.05208	2485.14169	2485.14158	
10	FALSE	High	Sequest HT ( Unambiguou	QIQIFTTYSD [R].qIQ	IFTTY N-Term(TMT)	3	P0DMV9	P0DMV8-2; F	0	3	0.5167	0	1	1	1005.84729	3015.52731	3015.5261	
11	FALSE	High	Sequest HT ( Unambiguou	AEDNADTLAI [R].aED	NAD N-Term(TMT)	1	P12004	P12004	0	3	0.7182	0	1	1	845.11126	2533.31922	2533.31862	
12	FALSE	High	Sequest HT ( Unambiguou	VLENTEIGDS [K].vLE	TEIG N-Term(TMT)	1	P00560	P00560	0	3	0.4925	0	1	1	680.04149	2038.10992	2038.11086	
13	FALSE	High	Sequest HT ( Unambiguou	ESGDFLAIDU [K].eS	DFLA N-Term(TMT)	1	P04807	P04807	0	2	0.6717	0	1	1	954.00715	1907.00702	1907.00717	
14	FALSE	High	Sequest HT ( Unambiguou	GTNVLMA [K].gTNVLM	N-Term(TMT)	1	P17255	P17255	0	3	0.4637	0	1	1	941.15431	2821.44837	2821.4476	
15	FALSE	High	Sequest HT ( Unambiguou	SGVAVADES [R].sG	VAVAI N-Term(TMT)	1	Q03048	Q03048	0	3	0.5804	0	1	1	732.40384	2195.19696	2195.19598	
16	FALSE	High	Sequest HT ( Unambiguou	GGYFDEF [R].gGYF	DEF N-Term(TMT)	3	P11413	P11413; P11	0	2	0.5077	0	1	1	751.89583	1502.78439	1502.7841	
17	FALSE	High	Sequest HT ( Unambiguou	TSYVYFEQ [R].tSYV	YFEQ N-Term(TMT)	1	P61247	P61247	0	3	0.5152	0	1	1	482.9266	1446.76524	1446.76509	
18	FALSE	High	Sequest HT ( Unambiguou	WVVIQDQ [R].wVVIQ	D N-Term(TMT)	1	P19414	P19414	0	3	0.6983	0	1	1	627.64985	1880.93498	1880.93401	
19	FALSE	High	Sequest HT ( Unambiguou	KTSYVYFEQ [R].kT	SYVYFEQ N-Term(TMT)	1	P61247	P61247	1	4	0.5556	0	1	1	451.76112	1804.02264	1804.02299	
20	FALSE	High	Sequest HT ( Unambiguou	LYVYFEGDE [R].lYV	YFEEC N-Term(TMT)	2	P40825	P40825; P40	0	3	0.5566	0	1	1	607.99409	1821.96771	1821.96749	
21	FALSE	High	Sequest HT ( Unambiguou	TLSSVQNEV [K].tL	SSVQN N-Term(TMT)	1	P12270	P12270	0	3	0.2779	0	1	1	644.35089	1931.03811	1931.03953	
22	FALSE	High	Sequest HT ( Unambiguou	CPLGNPANY [R].cPL	GNPA N-Term(TMT)	1	P38219	P38219	0	3	0.6788	0	1	1	821.07264	2461.20338	2461.20193	
23	FALSE	High	Sequest HT ( Unambiguou	AIEEGIPAF [K].aIEE	GIPA N-Term(TMT)	2	Q9Y2L1	Q9Y2L1; Q9Y	0	3	0.5507	0	1	1	772.0723	2314.20338	2314.20411	
24	FALSE	High	Sequest HT ( Unambiguou	GHGFEVYTH [K].gH	GFEV N-Term(TMT)	1	P14126	P14126	0	3	0.6348	0	1	1	442.56858	1325.69118	1325.6912	
25	FALSE	High	Sequest HT ( Unambiguou	FTFPIVFFK [K].fT	FPIV N-Term(TMT)	1	P41940	P41940	0	3	0.4781	0	1	1	554.99527	1662.97175	1662.97185	

For COMET search after Peptide-Prophet and Libra, upload a tab separated file of PSM (filtered at 0.9 probability or the probability associated with FDR cutoff choice) and associated reporter ion abundance (per TMT channel). Make sure the files have the following columns – "spectrum", "precursor\_intensity", "peptide", "assumed\_charge", "retention\_time\_sec". The second screenshot is of the down-sampled version of the COMET search for the same benchmarking dataset.

As before hover over question mark for more information. [Click on the “Sample File” in blue to download this example PSM files.](#)

## Upload a tab separated COMET search output text file after libra quantification

For more information: ?

Select a COMET output file:

- This field is required.

Choose File No file chosen

Reset

### Sample file

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	
1	probability	spectrum	expect	ions	peptide	protein	num_prots	calc_neutral	libra1	libra2	libra3	libra4	libra5	libra6	libra7	libra8	libra9	libra10	index	start_scan
2	0.9973	R_TMT_who	2.25	15/16	R.n[230.17]C sp Q15056		2	1013.5205	2658.578	1996.662	1205.419	1779.85	1268.423	2304.24	919.248	0	1219.511	1262.328	911	5572
3	1	R_TMT_who	0.00148	29/32	R.n[230.17]F sp Q14103		2	1198.6257	46913.817	39150.931	25729.469	38213.792	29825.273	43323.339	40178.805	882.797	27355.422	32722.026	1351	6684
4	0.9997	R_TMT_who	0.235	23/28	R.n[230.17]F sp Q9UBV2		1	1195.6261	16022.308	13417.121	14385.506	12223.949	12416.482	15747.328	15723.023	249.863	19622.387	15091.735	1554	7120
5	1	R_TMT_who	2.91E-08	34/56	A.n[230.17]C sp P3489V7		3	1840.8979	2166.382	1541.334	1425.058	1550.252	2044.142	3459.879	2443.281	0	2081.542	3355.161	1612	7242
6	0.9979	R_TMT_who	0.655	14/14	K.n[230.17]C sp P16861		1	948.5191	57086.023	45440.74	14036.377	44536.528	19946.75	23937.951	6368.725	0	5646.629	6336.316	1633	7287
7	0.9975	R_TMT_who	0.763	14/14	K.n[230.17]H sp P02293		2	1084.5828	52914.859	54193.044	18290.995	75239.524	54073.757	62195.122	63842.744	0	21211.305	54943.984	1731	7491
8	0.9962	R_TMT_who	1.84	16/16	R.n[230.17]F sp Q9Y6D9		1	891.4977	6884.009	7120.072	7066.058	5871.214	3900.529	8271.583	9028.243	0	7041.006	6153.501	1749	7532
9	1	R_TMT_who	0.000223	16/16	R.n[230.17]C sp P16861		1	1111.5937	11747.896	6320.618	4541.432	6872.677	2197.08	4013.847	0	0	923.721	1869	7809	
10	0.9247	R_TMT_who	0.599	21/24	K.n[230.17]K sp P49368		2	1262.6985	80456.755	77832.259	57609.413	76163.861	69252.131	88779.839	100258.097	0	86785.331	82815.5	2000	8089
11	0.9979	R_TMT_who	0.0593	14/16	R.n[230.17]E sp Q06505		1	1135.5672	2684.161	2193.952	717.692	2056.611	0	876.104	0	0	0	2068	8230	
12	0.9993	R_TMT_who	0.0111	20/24	R.n[230.17]C sp O75475		1	1312.7141	19125.786	18077.969	24373.386	18180.737	19677.454	20561.532	27909.893	0	27997.887	19649.664	2094	8286
13	0.9718	R_TMT_who	0.185	16/18	K.n[230.17]E sp P36542		2	1323.6469	0	0	0	0	0	0	0	0	0	2099	8295	
14	0.9889	R_TMT_who	0.242	24/24	R.n[230.17]R sp Q13813		3	1375.7461	16408.627	17272.188	17391.268	16035.534	16867.636	18797.392	20180.521	10.581	20223.603	15656.796	2211	8550
15	1	R_TMT_who	1.75E-05	19/20	N.n[230.17]F sp P34897		3	1374.7054	1251.386	1301.89	2129.427	2281.447	1635.196	2395.034	2541.981	0	3100.044	2358.115	2220	8569
16	0.9999	R_TMT_who	0.00138	26/28	R.n[230.17]A sp P80967		1	1427.7774	260291.359	243746.559	85600.452	221962.015	70889.797	101361.155	17022.976	0	18955.51	14850.995	2262	8655
17	0.9999	R_TMT_who	0.00101	30/36	K.n[230.17]A sp Q16831		1	1412.667	6710.196	5477.483	6385.944	5782.308	4439.501	5596.537	7479.873	0	7712.871	6087.428	2269	8671
18	0.9989	R_TMT_who	0.216	14/14	R.n[230.17]H sp P38205		1	1073.5668	13238.392	19555.599	2110.122	18043.275	5682.343	9585.556	520.494	0	676.302	1796.761	2418	8982
19	0.9346	R_TMT_who	0.0347	29/56	R.n[230.17]H sp Q92804		2	2090.9061	2980.106	4627.007	726.203	3828.628	4085.367	5275.674	5182.056	375.319	989.836	5885.661	2458	9063
20	1	R_TMT_who	0.00706	18/18	R.n[230.17]S sp Q92804		2	1170.5468	7220.386	8147.471	3784.446	8627.999	5500.215	9934.274	9993.403	0	6692.612	9003.918	2555	9263
21	0.9837	R_TMT_who	4.69	18/18	K.n[272.18]S sp P17098		1	1076.6232	16237.864	15545.34	11487.484	14731.979	14259.547	18282.277	19268.547	0	13486.848	14597.368	2603	9364
22	0.9987	R_TMT_who	0.093	16/16	R.n[230.17]S sp Q92804		2	1053.5042	81971.488	74895.901	38077.627	69587.085	71880.857	95650.78	108985.562	0	42830.101	84792.734	2626	9411
23	1	R_TMT_who	0.00479	16/16	K.n[230.17]G sp P52893		1	1177.5713	5774.009	5413.42	1644.857	5795.336	2354.862	3782.601	1975.867	0	1796.947	2041.66	2666	9505
24	0.9989	R_TMT_who	0.155	14/14	R.n[230.17]C sp Q92804		4	966.4722	27940.301	24064.286	29443.23	22456.842	27023.244	33441.342	41180.378	640.735	32651.28	28006.886	2718	9611
25	0.9992	R_TMT_who	0.0816	15/20	K.n[230.17]N sp P51858		3	1316.6523	2601.85	3059.973	0	1955.304	2565.296	1751.545	2498.999	0	0	2291.626	2721	9616
26	0.9807	R_TMT_who	14.1	16/16	K.n[230.17]V sp P07342		1	960.5191	232090.812	239461.235	40403.982	237075.329	76958.565	94930.668	31162.505	0	19172.526	22919.26	2779	9745
27	0.9977	R_TMT_who	1.77	16/16	K.n[230.17]C sp P23254		1	947.5239	702013.799	715121.712	173012.595	657745.062	232622.736	309021.461	79515.147	0	54745.132	51522.242	2834	9865

**Step 6:** You can modify settings (using fractions, doing row normalization and type of column normalization) for your specific analysis. Recommendation is to use the default settings. Hover over question mark for more information.

**For the example dataset choose "Protein-list Normalization" for type of column type normalization. Put "Human" in the text box.**

### Choose type of column-type normalization:

For more information: ?

- Global Normalization Choose global normalization if you can assume that most proteins in your experiment are NOT going to be differentially up or down regulated for the conditions being compared.
- Protein-list Normalization Choose protein list normalization and provide a list of uniprot in case you know of specific proteins that can be assumed to be unchanging between the conditions compared as a result of experimental setup.
- No Column Normalization Choose no column normalization in case none of the situations discussed are applicable.

Input the uniprot ID's comma separated.

Example: P16140,P39107,P04806.

Enter - "human" or "yeast" or "ecoli" for whole proteome

human

Reset

**Step 8:** Choose whether to do imputation on your data or not. Recommendation is to not to not introduce biases.

A successful start of run with look like this –

Run the Analysis

Your job has been successfully submitted, you will be redirected to the result page once the analysis is complete

⌂ Loading...

The output page (given a successful run) looks like the screenshots below. You can download the protein level and peptide level differential expression analysis results as well as the pdf of resulting volcano plot (set at 5 PSM cutoff). You can highlight specific proteins on the volcano plot by entering the associated Uniprot IDs. You can dynamically set the thresholds and download the resulting file, as well as subset the result file with user-defined thresholds. –

### Success!

[Click Here to Download the Result File \(Protein level\)](#)

[Click Here to Download the Result File \(Peptide level\)](#)

[Click Here to Download the baseline Volcano plot \(PDF\)](#)

FC cutoff choice: Drag the slider to display the current value.



Value: 2

Adjusted P-value cutoff choice: Drag the slider to display the current value.



Value: 0.05

PSM cutoff choice: Drag the slider to display the current value.



Value: 5

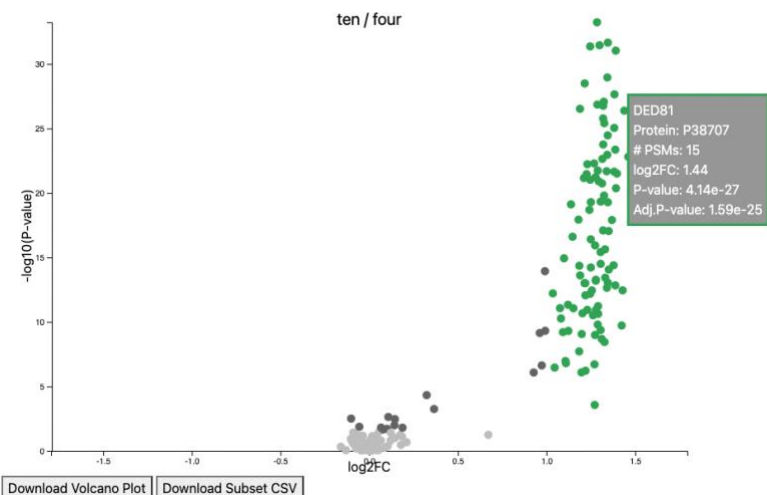
Size of scatter point: Drag the slider to display the current value.



Value: 5

Enter Uniprot IDs separated by @  
Example: Q08945@Q9UQE7

Update Volcano Plot





### The output file (protein) looks like this –

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Protein	log2FC	pval	adjpval	Proteinnoiso	Gene Symbo	# PSMs	log2_127C	log2_129N	log2_128N	log2_127N	log2_128C	log2_126	PSM Cutoff
2	P26784	1.38134962	2.23E-22	4.11E-21	P26784	RPL16A	12	-11.726424	-11.768642	-10.474821	-10.422956	-11.861789	-10.440364	5
3	Q96F63	0.34030288	0.06213941	0.10918158	Q96F63	CCDC97	2	-11.408906	-11.50002	-11.205176	-11.038491	-11.745837	-10.928838	
4	P06280	-0.0384584	0.90470072	0.91944126	P06280	GLA	5	-11.667265	-11.250148	-11.502813	-11.65461	-11.614298	-11.353603	
5	Q3E792	1.21820791	9.91E-14	7.75E-13	Q3E792	RPS25A	5	-11.50257	-11.801045	-10.503787	-10.442304	-11.89155	-10.44524	
6	Q12207	1.35761863	0.02973173	0.05577494	Q12207	NCE102	2	-12.775087	-12.264278	-11.417469	-10.79947	-11.709065	-10.554678	
7	O43747	0.01812818	0.45050281	0.57056066	O43747	AP1G1	5	-11.197248	-11.623892	-11.539199	-11.481668	-11.659592	-11.425964	
8	Q05506	1.28455969	5.85E-34	2.92E-31	Q05506	YDR341C	28	-11.761494	-11.793693	-10.552705	-10.48513	-11.818836	-10.499439	
9	P13861	0.02960514	0.48693274	0.60292664	P13861	PRKAR2A	15	-11.474795	-11.56569	-11.449339	-11.573047	-11.477439	-11.490748	
10	P53090	1.29083586	2.38E-11	1.47E-10	P53090	ARO8	8	-11.587725	-11.835221	-10.628664	-10.525632	-11.852603	-10.486275	
11	P46109	0.02998512	0.12793197	0.2033059	P46109	CRKL	8	-11.602967	-11.429439	-11.372418	-11.478999	-11.412675	-11.362643	
12	PODMV9	-0.0457134	0.91229316	0.92339612	PODMV9	HSPA1B	76	-11.520141	-11.519697	-11.498504	-11.506837	-11.440221	-11.558125	
13	O76095	-0.1619452	0.30064374	0.41214623	O76095	JTB	1	-11.518074	-11.376478	-11.68002	-11.377997	-11.396209	-11.588197	
14	Q9BUJ2	-0.1597208	0.47721427	0.5953248	Q9BUJ2	HNRNPULL1	6	-11.439283	-11.49517	-11.732362	-11.656188	-11.525864	-11.626989	
15	Q8TEQ6	0.31017975	0.23309433	0.34009963	Q8TEQ6	GEMIN5	2	-11.382307	-11.885992	-11.050817	-11.340174	-11.586252	-11.575813	
16	P36018	0.90554353	6.35E-07	2.60E-06	P36018	YPT52	4	-11.648322	-11.606236	-10.749002	-10.723762	-11.868766	-10.721091	
17	P38791	0.99104217	1.16E-14	1.02E-13	P38791	DYS1	13	-11.632256	-11.647798	-10.60166	-10.764521	-11.772198	-10.84641	
18	Q9UNH5	0.09600367	0.35627739	0.4715714	Q9UNH5	CDC14A	1	-11.497843			-11.399855	-11.381747	-11.287731	
19	P45973	0.06565392	0.6568898	0.74666973	P45973	CBX5	3	-11.580473	-11.565569	-11.490778	-11.477054	-11.478546	-11.498655	
20	Q02878	0.00560888	0.68024662	0.76279341	Q02878	RPL6	17	-11.570794	-11.506728	-11.481798	-11.490027	-11.482545	-11.550941	
21	Q969Q5	-0.012839	0.81862909	0.86362772	Q969Q5	RAB24	1	-11.398085	-11.588733	-11.53585	-11.410924	-11.465611	-11.558748	
22	P13674	-0.1468863	0.58969541	0.68912883	P13674	P4HA1	1	-11.296898	-11.362917	-11.510518	-11.443784	-11.710561	-11.670512	
23	P40926	-0.0105211	0.53037069	0.63926322	P40926	MDH2	22	-11.395903	-11.465077	-11.494215	-11.462558	-11.498413	-11.482076	
24	Q16204	-0.0936251	0.47355475	0.59224016	Q16204	CCDC6	2	-11.269886	-11.574696	-11.510263	-11.732625	-11.432712	-11.363511	
25	Q12287	1.32409542	0.00204293	0.00476366	Q12287	COX17	1	-11.375748	-11.838521	-10.514425	-10.407758	-11.901406	-10.541281	
26	P15703	1.16134159	8.73E-12	5.75E-11	P15703	BGL2	4	-11.648393	-11.712628	-10.556376	-10.590355	-11.843102	-10.50546	
27	Q8IY81	0.3241989	4.75E-05	0.00015283	Q8IY81	FTSJ3	6	-11.666386	-11.626663	-11.280481	-11.185315	-11.59718	-11.421914	
28	P38986	1.38802544	3.15E-05	0.00010708	P38986	ASP1	1	-11.866326	-11.752365	-10.547192	-10.46865	-11.873223	-10.36434	
29	P35178	0.80046002	0.00029336	0.00082704	P35178	RRP1	1	-11.547308	-11.632503	-10.829477	-10.92925	-11.687103	-10.746848	

### The output file (peptide) looks like this -

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	PeakID	AnnotatedSe	Charge	Fraction	Protein	126	127C	127N	128C	128N	129C	129N	130C	131
2	[K].IKGDDLQ	[K].IKGDDLQ	3	HPH7.raw	P07910	0.00033327	0.0003802	0.00033692	0.00032673	0.00034862	0.00036727	0.00033562	0.00038573	0.00033549
3	[K].dNQIYAI	[K].dNQIYAI	3	HPH5.raw	P38879	0.00074752	0.00026469	0.00075403	0.00024236	0.00075802	5.00E-05	0.00027379	3.55E-05	4.08E-05
4	[R].dSGYGV	[R].dSGYGV	2	HPH2.raw	P13663	0.00070923	0.00030735	0.00066538	0.00022826	0.0006035	0.00010463	0.00032957	0.00010376	0.00010806
5	[K].VEEQEQ	[K].VEEQEQ	3	HPH3.raw	P38701	0.00071763	0.00026167	0.00068688	0.00026264	0.00070311	7.07E-05	0.00031346	9.23E-05	4.98E-05
6	[K].IYDLGV	[K].IYDLGV	3	HPH5.raw	P25294	0.00048221	0.00018885	0.00053643	0.00014272	0.00054058		0.00022006		
7	[R].eAGEVK	[R].eAGEVK	3	HPH3.raw	P41805	0.00067574	0.00032078	0.00072417	0.00025971	0.00070877	4.73E-05	0.00032821	6.05E-05	4.64E-05
8	[R].gKLEEEY	[R].gKLEEEY	3	HPH3.raw	P32589	0.00074303	0.00037201	0.0006442	0.0002381	0.00067626	5.02E-05	0.00032111	8.03E-05	5.33E-05
9	[K].aGAHLQ	[K].aGAHLQ	3	HPH7.raw	P04406	0.00032877	0.00041784	0.00034462	0.00035303	0.00034255	0.0003306	0.00035312	0.00037582	0.00031547
10	[R].gFLSDLPI	[R].gFLSDLPI	3	HPH6.raw	P05317	0.00069354	0.00037472	0.00071906	0.00025598	0.00069285	5.74E-05	0.00028641	5.68E-05	4.88E-05
11	[R].ILNTFLER	[R].ILNTFLER	2	HPH8.raw	Q14204	0.00033171	0.00032232	0.00034876	0.00039399	0.0003956	0.00041236	0.00036113	0.00029225	0.00029544
12	[R].gGYDFEF	[R].gGYDFEF	2	HPH5.raw	P11413	0.00028778	0.00044996	0.00036879	0.00027447	0.00034816	0.00037051	0.00033086	0.00040549	0.00032448
13	[R].gWDDLFI	[R].gWDDLFI	2	HPH7.raw	Q14204	0.00035529	0.00041456	0.0003319	0.00031538	0.00033567	0.00033693	0.00033518	0.00041115	0.00032618
14	[R].dNQLSEV	[R].dNQLSEV	2	HPH3.raw	Q14978	0.00034719	0.00029993	0.00036285	0.00038731	0.00035562	0.00036434	0.00036569	0.00031091	0.00033842
15	[K].hLEDNTLI	[K].hLEDNTLI	3	HPH6.raw	P05739	0.00073257	0.00024626	0.00075546	0.0002609	0.00072149	4.87E-05	0.0003024	4.62E-05	4.75E-05
16	[K].tLDVVER	[K].tLDVVER	2	HPH3.raw	P00942	0.00071685	0.00025749	0.00072301	0.00027892	0.00076609	6.17E-05	0.00029212	2.97E-05	3.49E-05
17	[R].eLDLYDN	[R].eLDLYDN	3	HPH3.raw	Q15435	0.00033634	0.00042543	0.00037834	0.00030226	0.00041087	0.00029255	0.00037885	0.00037224	0.00026275
18	[R].aEVSQPR	[R].aEVSQPR	2	HPH7.raw	P22314	0.00022849	0.00041725	0.00023279	0.00053172	0.00025502	0.00040786	0.00029357	0.00038406	0.00042454
19	[-].mGSGAG	[-].mGSGAG	2	HPH1.raw	Q9Y5G0	0.00038931	0.000332	0.00061138	0.00032747	0.00052097	0.00022755	0.00029517	0.00028301	0.00017976
20	[K].IEGVATP	[K].IEGVATP	3	HPH6.raw	P41056	0.00069567	0.00027261	0.00069091	0.00027398	0.00072077	7.28E-05	0.0003124	5.97E-05	6.19E-05
21	[K].thIGDGF	[K].thIGDGF	3	HPH8.raw	Q12074	0.00071313	0.00019546	0.00077785	0.00028266	0.00073519	6.00E-05	0.00029518	3.66E-05	5.77E-05
22	[K].sVDELITE	[K].sVDELITE	3	HPH2.raw	P05319	0.00075717	0.00032846	0.0007171	0.0002409	0.00070871	5.14E-05	0.0002749	4.88E-05	5.09E-05
23	[K].INTAISNL	[K].INTAISNL	2	HPH5.raw	P07806	0.00038151	0.00031786	0.00046773	0.00036292	0.00041521		0.0002059		
24	[K].aTGDETG	[K].aTGDETG	2	HPH2.raw	P61247	0.00033086	0.00039852	0.00031653	0.00032255	0.00031704	0.00035513	0.00032157	0.00044364	0.00035643
25	[R].IHVLEAQ	[R].IHVLEAQ	3	HPH6.raw	Q9B5J8	0.0003478	0.00034907	0.00032907	0.00036826	0.00035332	0.00035113	0.00034791	0.00034868	0.00035292
26	[K].eIHFFGD	[K].eIHFFGD	3	HPH5.raw	P07283	0.00069107	0.00037161	0.00071913	0.00024916	0.00067682	5.42E-05	0.0003102	5.96E-05	4.97E-05
27	[R].kQFDAE	[R].kQFDAE	3	HPH5.raw	P07263	0.0006758	0.00034609	0.00072885	0.0002552	0.00069311	6.18E-05	0.00030948	5.28E-05	5.30E-05
28	[R].dMYEQFI	[R].dMYEQFI	3	HPH6.raw	P61011	0.00048423	0.00029595	0.00040941	0.00028214	0.00044429	0.00023958	0.00038542	0.000303	0.00030104
29	[K].tLQNISL	[K].tLQNISL	3	HPH8.raw	Q14204	0.00056728	0.00040193	0.00025426	0.00025606	0.00040678	0.00029987	0.00036162	0.00030783	0.00029106