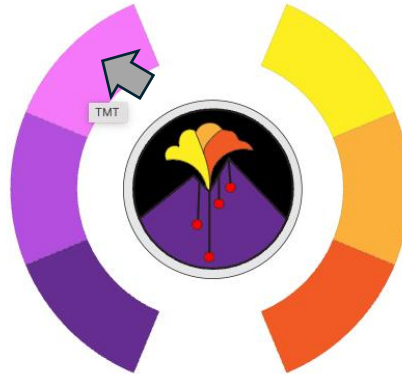


TMT (Phospho Proteome)

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).

This is for processing TMT DDA results.
Use AFTER searching raw MS files.
Can process IP-MS, Fusion-IP-MS,
Whole Proteome, Phospho-proteome experiments.



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 Phospho-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:

Choose the strategy for analysis with two choices:

Magma (Linear Model)

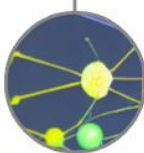
1. Choose the search engine that was used for generating the PSM list.

Magma (Limma)

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.

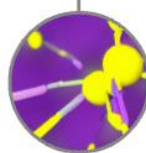
IP-TMT (Mutation or drug treatment)



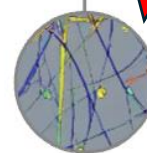
IP-TMT (Fusions)



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 phospho-proteome 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	one
3	127N	four
4	127C	ten
5	128N	one
6	128C	four
7	129N	ten
8	129C	one
9	130N	four
10	130C	ten
11	131	none

1 Upload the 'Annotation file'

For more information: ?

Select a file:

Choose File No file chosen

Submit Reset

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)

Reset

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 phospho-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	T	U
1	Checked	Confidence	Identifying N: PSM Ambiguity	Sequence	Annotated Set Modification	# Proteins	Master Prote	Protein Acce	# Missed Cts	Charge	DeltaScore	DeltaCn	Rank	Search Engin	m/z [Da]	MH+ [Da]	Theo. MH+ [D	DeltaM [ppm	DeltaM		
2	FALSE	High	Sequest HT (Unambiguou	GRAEGEWEL [K]_gRAEGEW N-Term(TMT)		3	Q9NYF8	Q9NYF8-3; Q	1	3	0.1318	0	1	1	928.42222	2783.2521	2783.26019	-2.91	-0.1		
3	FALSE	High	Sequest HT (Unambiguou	LENESLPNLS [K]_LENESLPN N-Term(TMT)		1	Q05024	Q05024	0	2	0.437	0	1	1	741.3585	1481.70973	1481.70862	0.75	0.01		
4	FALSE	High	Sequest HT (Unambiguou	GSELEEIAEG [K]_gSELEEIAE N-Term(TMT)		1	P02400	P02400	0	3	0.5211	0	1	1	578.00106	1731.98862	1731.98929	-0.39	-0.01		
5	FALSE	High	Sequest HT (Unambiguou	DVPPLESETA [K]_dVPPLESET N-Term(TMT)		2	P27816	P27816; P27	0	3	0.3436	0	1	1	744.40428	2231.19627	2231.19764	0.29	0.01		
6	FALSE	High	Sequest HT (Unambiguou	AFGPDQLQGG [K]_fFGPDQLQ N-Term(TMT)		2	P21333	P21333; P21	1	3	-0.084	0	1	1	891.79824	2673.38018	2673.38019	0	0		
7	FALSE	High	Sequest HT (Unambiguou	GGITTDISEI [K]_gGITTDID; N-Term(TMT)		1	Q06704	Q06704	0	3	0.0516	0	1	1	1085.50074	3254.48767	3254.48774	-0.02	-2.00		
8	FALSE	High	Sequest HT (Unambiguou	DNEELQEDID [K]_dNEELQEI N-Term(TMT)		1	P25037	P25037	0	4	0.4519	0	1	1	632.05695	2525.20598	2525.20603	-0.02	-1.00		
9	FALSE	High	Sequest HT (Unambiguou	TQSSSRLYE [K]_tQSSSR; N-Term(TMT)		1	P53885	P53885	1	3	0.0355	0	1	1	875.10173	2623.29064	2623.29043	0.08	7.00		
10	FALSE	High	Sequest HT (Unambiguou	QFSVADTPE [K]_qFSVAD; N-Term(TMT)		3	Q14847	Q14847-2; Q	1	3	0.2827	0	1	1	733.40466	2198.19942	2198.19964	0.35	0.01		
11	FALSE	High	Sequest HT (Unambiguou	CTGGGIIITAI [K]_cTGGGIII; N-Term(TMT)		1	P33401	P33401	0	3	0.0949	0	1	1	972.82841	2916.47067	2916.46908	0.55	0.01		
12	FALSE	High	Sequest HT (Unambiguou	IEEVLSPGFS [K]_iEEVLSP; N-Term(TMT)		2	Q9UEY8	Q9UEY8-2; Q	0	3	0.5768	0	1	1	663.99105	1989.95861	1989.95873	-0.06	-4.00		
13	FALSE	High	Sequest HT (Unambiguou	VQGEAVSNIC [K]_vQGEAVSI N-Term(TMT)		3	Q13765	Q13765; ESP	0	4	0.0284	0	1	1	1100.52038	4399.05967	4399.06016	-0.11	-0.01		
14	FALSE	High	Sequest HT (Unambiguou	VQISPDGGI [K]_vQISPD; N-Term(TMT)		1	Q92945	Q92945	1	4	0.0028	0	1	1	794.92112	3176.66263	3176.66044	0.69	0.01		
15	FALSE	High	Sequest HT (Unambiguou	DIDSEDEQD [K]_dIDSEDE; N-Term(TMT)		1	P40498	P40498	0	3	0.3711	0	1	1	1015.12651	3043.36497	3043.36103	1.3	0.01		
16	FALSE	High	Sequest HT (Unambiguou	SPASDTYWF [K]_sPASDTY; N-Term(TMT)		3	Q13765	Q13765; ESP	0	3	0.3956	0	1	1	648.35564	1943.05236	1943.05261	-0.13	-8.00		
17	FALSE	High	Sequest HT (Unambiguou	VQGEAVSNIC [K]_vQGEAVSI N-Term(TMT)		3	Q13765	Q13765; ESP	0	4	0.0678	0	1	1	1100.52135	4399.06358	4399.06016	0.78	0.01		
18	FALSE	High	Sequest HT (Unambiguou	NPDDEFILN [K]_nPDDEF; N-Term(TMT)		1	Q08412	Q08412	0	3	0.5033	0	1	1	703.28043	2107.82874	2107.82524	0.71	0.1		
19	FALSE	High	Sequest HT (Unambiguou	SEADPEGLSN [K]_sEADPEGI N-Term(TMT)		1	Q06685	Q06685	0	3	0.0627	0	1	1	1047.84009	3141.50553	3141.49892	2.1	0.1		
20	FALSE	High	Sequest HT (Unambiguou	DFSEDLSFI [K]_dFSEDLS; N-Term(TMT)		1	Q04773	Q04773	0	3	0.4485	0	1	1	618.95693	1854.85625	1854.8563	-0.03	-2.00		
21	FALSE	High	Sequest HT (Unambiguou	RQSSPSAPE [K]_rQSSPSA; N-Term(TMT)		4	Q93100-2	Q93100-2; Q	1	4	0.0019	0	1	1	773.89313	3092.55068	3092.54541	1.7	0.01		
22	FALSE	High	Sequest HT (Unambiguou	ALGVSNFNF [K]_aLGVSNF; N-Term(TMT)		2	Q94876	Q94876-2; Q	0	3	0.0322	0	1	1	629.34419	1886.01801	1886.01889	-0.46	0.01		
23	FALSE	High	Sequest HT (Unambiguou	LFESDEEEN [K]_lFESDEE; N-Term(TMT)		1	Q04500	Q04500	0	3	0.1309	0	1	1	883.08927	2647.25326	2647.25404	-0.3	-0.01		
24	FALSE	High	Sequest HT (Unambiguou	IENQGVN [K]_iENQGV; N-Term(TMT)		1	P00549	P00549	0	3	0.509	0	1	1	740.00721	2219.20708	2219.20722	-0.06	-5.00		
25	FALSE	High	Sequest HT (Unambiguou	IGPFVEVGI [K]_iGPFVEV; N-Term(TMT)		1	P39954	P39954	0	3	0.6026	0	1	1	640.02466	1918.05941	1918.06036	-0.49	-0.01		
26	FALSE	High	Sequest HT (Unambiguou	YSDVEVP [K]_ySDVEVP; N-Term(TMT)		6	P35611	P35611-2; P3	1	4	0.0528	0	1	1	1023.22873	4089.89309	4089.89416	-0.26	-0.01		
27	FALSE	High	Sequest HT (Unambiguou	VQGEAVSNIC [K]_vQGEAVSI N-Term(TMT)		3	Q13765	Q13765; ESP	0	4	0.0603	0	1	1	1100.51964	4399.05674	4399.06016	-0.78	-0.01		

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 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	0.9448	20171106_LL	0.00218	#####	K{n(230.17)S} sp P07910		6	1154.46	894.737	1873.646	0	540.61	973.885	2007.639	2164.386	966.096	700.427	2017.693	241	3509
3	0.9973	20171106_LL	4.43E-05	8/1/40:0:0	K{n(230.17)R} sp P32583		1	1827.8882	606.615	3567.901	7890.538	367.212	3441.394	9494.182	709.602	3618.04	10079.5	4901.669	329	4020
4	0.9288	20171106_LL	1.98	#####	K{n(230.17)C} sp Q07959		1	1650.6702	0	2339.931	5174.733	374.255	2234.98	5097.731	721.809	3206.368	6765.972	3335.423	614	5088
5	0.9318	20171106_LL	2.84E-05	8/1/52:0:0	K{n(230.17)S} sp Q8N9E0		1	2046.9149	527.193	869.353	634.643	0	640.67	530.584	515.841	434.694	0	2003.515	734	5459
6	0.9252	20171106_LL	0.00982	7/1/68:0:0	K{n(230.17)E} sp P07910		4	2167.8464	1242.638	1757.752	958.127	1025.828	713.48	2203.318	994.757	2371.54	2410.963	1787.136	812	5685
7	0.9999	20171106_LL	3.37E-09	1/7/76	K{n(230.17)N} sp P0C590		1	2578.1646	0	3084.811	5687.127	795.453	1757.946	5859.067	833.061	3719.576	5333.3	3760.386	831	5738
8	0.9994	20171106_LL	1.12E-05	#####	K{n(230.17)E} sp P07910		4	2247.8128	2777.11	2476.832	1878.312	2344.268	1773.368	2326.991	2859.389	3294.599	2273.282	2199.865	893	5905
9	0.9963	20171106_LL	0.00121	7/1/44:0:0	K{n(230.17)Q} sp Q12263		1	1875.8882	0	784.955	3472.387	485.781	684.094	4534.069	575.893	1874.227	3461.249	1204.583	916	5963
10	0.9985	20171106_LL	0.014	#####	K{n(230.17)N} sp P25567		1	1350.7426	2886.854	12392.292	23682.845	5090.873	10375.126	29239.514	4806.313	11313.255	31869.045	16375.791	1030	6254
11	0.9679	20171106_LL	0.381	#####	K{n(230.17)R} sp P42858		1	1452.7856	4799.673	6137.46	4794.658	4784.563	5137.077	4386.058	6006.882	6327.818	4765.245	5223.074	1317	6933
12	0.9998	20171106_LL	2.03E-06	#####	K{n(230.17)R} sp P27692		1	2514.2684	583.999	3556.573	6732.023	576.838	3124.037	6679.552	484.08	3646.806	8308.1	3071.261	1464	7305
13	0.9994	20171106_LL	3.80E-05	#####	K{n(230.17)D} sp Q14677		3	2491.0576	2840.491	5004.462	4244.52	3223.557	4013.432	2890.394	4868.918	4973.296	6487.802	3556.639	1552	7510
14	0.9961	20171106_LL	4.05E-06	#####	K{n(230.17)D} sp P32589		1	1240.4968	1171.698	3975.021	8591.494	840.521	3133.367	10542.872	924.285	4353.14	9289.967	6015.17	1697	7842
15	0.9818	20171106_LL	0.0561	#####	K{n(230.17)M} sp Q8NCN4		1	2389.1463	2865.514	2964.107	958.54	1862.116	1945.602	3020.06	2857.021	2417.775	3466.249	3018.857	1955	8414
16	0.9955	20171106_LL	0.00583	16/36	K{n(230.17)R} sp Q9BUQ8		1	1581.8758	26800.726	22588.623	16872.066	22052.515	21504.468	19129.949	24265.474	24374.337	21128.106	24258.921	1984	8477
17	0.9993	20171106_LL	0.000347	#####	K{n(230.17)D} sp Q14677		3	2571.0239	7342.345	9793.976	9070.667	11349.497	9095.361	11914.112	11098.983	9975.032	14651.612	6995.473	2005	8523
18	0.9899	20171106_LL	0.228	#####	L{n(230.17)S} sp Q3E752		1	1252.6016	2382.26	7215.687	12857.378	663.53	4871.407	14052.246	2384.258	5877.363	13911.279	8550.365	2037	8591
19	0.9824	20171106_LL	0.494	8/1/68:0:0	K{n(230.17)G} sp P06244		1	2450.1216	0	2165.501	3262.26	411.376	2714.325	3902.23	706.376	2114.491	4122.036	2741.554	2083	8697
20	0.9994	20171106_LL	6.66E-06	8/1/56:0:0	K{n(230.17)G} sp Q96572		2	2123.989	474.057	678.243	1081.948	614.169	440.089	588.535	1032.679	528.552	0	1004.292	2148	8844
21	0.9881	20171106_LL	0.15	#####	K{n(230.17)E} sp Q08945		1	1735.8184	9287.77	7995.223	5586.897	8677.217	7642.418	8795.873	6531.998	7002.826	8494.435	7710.223	2317	9211
22	1	20171106_LL	2.85E-10	20/56	K{n(230.17)R} sp Q8I211		3	2121.0621	9042.338	8505.839	6018.296	6497.321	7865.883	10052.73	7781.25	8204.754	8274.896	9691.027	2465	9529
23	1	20171106_LL	6.91E-06	17/20	K{n(230.17)S} sp P07910		4	1733.8126	71392.832	76003.483	52282.546	77067.242	64354.653	67517.836	83798.642	75329.49	68417.097	72084.462	2547	9710
24	0.9927	20171106_LL	1.31E-15	36/84	K{n(230.17)S} sp Q9BKW9		2	2914.2005	5723.859	6238.138	5279.221	5361.244	5437.253	5679.013	6227.484	5283.838	6036.792	5149.322	2612	9847
25	0.9967	20171106_LL	0.00012	23/78	K{n(230.17)R} sp Q9BUQ3		2	2170.1778	12358.819	11809.062	10859.01	13252.456	15319.129	13949.562	15464.081	13786.604	12469.788	14788.901	2615	9854
26	0.9978	20171106_LL	0.00959	14/54	K{n(230.17)R} sp Q9BUQ8		1	1661.8421	7213.05	7880.069	4485.204	8016.051	7591.575	6629.109	6917.283	8740.404	6507.02	7925.385	2666	9963
27	0.9992	20171106_LL	0.000181	#####	K{n(230.17)D} sp P07910		4	1733.8126	17237.624	17617.994	10477.832	18613.461	19426.668	17192.68	20460.922	18501.651	19978.661	17830.915	2816	10282
28	0.9892	20171106_LL	0.238	#####	K{n(230.17)D} sp ADINW5		2	1487.7539	5850.828	5625.154	4855.103	5982.384	5413.331	6389.735	6269.209	7346.68	6031.455	6294.122	2833	10316

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.

5c 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 IDs 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 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 \(Peptide level\)](#)

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

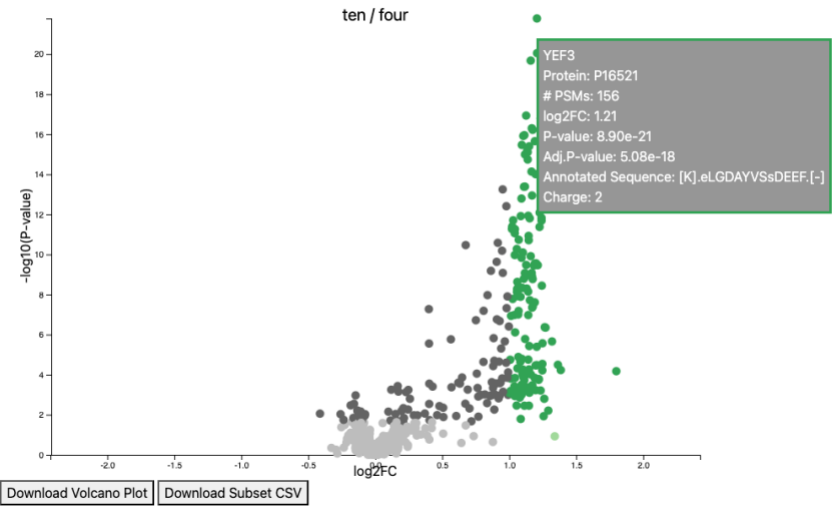
Size of scatter point: Drag the slider to display the current value.



Value: 5

Enter Uniprot IDs separated by @
Example: Q08945@Q9UQE7

Update Volcano Plot



The output file (peptide) looks like this –

Unipeptide	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	
1 Unipeptide	log2FC	FC	pval	adjpval	126	127C	127N	128C	128N	129C	129N	130C	130N	131C	131N	132C	132N	133C	133N	134C	134N
2 K.n[230.17]SLEGGDSTPPS	-0.0151519	0.98955245	0.69418808	0.80714298	0.00011983	0.00011551	0.00011527	0.00010307	0.00010537	0.00010954	0.00011165	0.00010969	0.00011538	K.n[230.17]L	3	AGNMY6	AGNMY6	ANKX2P2	10		
3 K.n[230.17]EEVLSPEGS167	-0.0276467	0.98101919	0.54547607	0.73871733	0.00011551	0.00010303	0.00010802	0.00011066	0.00011826	0.00012398	0.00010458	0.00010597	0.00011383	K.n[230.17]E	3	Q9UEY8	Q9UEY8	ADD3	10		
4 K.n[230.17]REAAVPPVS167	0.140054817	1.10232388	0.23399348	0.53573267	0.00010754	0.00011873	0.00010699	0.00010075	0.00011147	0.00010726	0.00011561	0.00011935	0.00011374	K.n[230.17]R	3	Q04637	Q04637	EIF4G1	23		
5 K.n[230.17]YQDEFM167.00J	-0.0434905	0.97030453	0.62491922	0.76892609	0.00011827	0.00011291	0.00011557	0.00011518	0.00010627	0.00011171	0.00010461	0.00011176	0.00010948	K.n[230.17]Y	3	Q6P6C2	Q6P6C2	ALKBH5	5		
6 K.n[230.17]EELQANGSAPAA	-0.1694464	0.88918384	0.12082854	0.36471159	0.00011191	0.00010225	0.00010568	0.00011457	0.00011934	0.00013032	0.00012029	9.40E-05	0.0001166	K.n[230.17]E	4	P29966	P29966	MARCKS	76		
7 K.n[230.17]SPREVS167.00C	0.0150592	1.01049291	0.28903308	0.59380895	0.00013482	0.00012502	0.00011304	0.00010345	0.00010447	0.00011433	0.00010447	0.00011433	0.00010653	0.00011227	K.n[230.17]S	3	Q9Y6X9	Q9Y6X9	MORC2	5	
8 K.n[230.17]RINPPSSGTS167.00I	-0.0629627	0.95729618	0.39463211	0.6695844	0.00011628	0.00010756	0.00011286	0.00011597	0.00011579	0.00011216	0.00010819	0.00010337	0.00011259	K.n[230.17]R	3	P14859	P14859	POU2F1	2		
9 K.n[230.17]M147.00QJG	0.79180724	1.73124181	0.0013531	0.00866213	7.02E-05	0.00017683	9.81E-05	0.00010761	6.65E-05	7.09E-05	0.00015901	0.00016382	9.67E-05	K.n[230.17]M	4	Q12888	Q12888	TP53BP1	38		
10 K.n[230.17]ADAPS167.00S	0.12345104	1.08933753	0.29377747	0.59979566	0.00010828	0.00010986	0.00010476	0.00011199	0.00011537	0.00010173	0.00011858	0.00012237	0.00010854	K.n[230.17]A	3	P60502	P60502	ST13	30		
11 K.n[230.17]QPCVQAQAW	-0.0069792	0.99517406	0.36111872	0.97112073	0.00011687	0.00010907	0.00010953	0.00010589	0.0001217	9.69E-05	0.00010475	0.0001203	0.00012088	K.n[230.17]G	5	O60264	O60264	SHARCA5	8		
12 K.n[230.17]SS167.00JLDV	0.05615117	1.03968837	0.87647841	0.91527139	0.00010455	9.72E-05	0.00012023	0.00010679	0.00011451	0.00010641	0.00012501	0.00011877	0.00010801	K.n[230.17]S	2	P24534	P24534	EEF1B2	93		
13 K.n[230.17]LAVPAAGPASAC	1.22743626	2.34150523	0.00070191	0.0050669	1.96E-05	0.00018328	7.83E-05	0.00010454	4.61E-05	3.48E-05	0.00022331	0.00022871	9.42E-05	K.n[230.17]J	5	P05319	P05319	RPP2A	163		
14 K.n[230.17]RSEDES167.00L	-0.1969911	0.98644392	0.80075168	0.86763131	0.00011448	0.00010848	0.00010882	0.00011028	0.00011476	0.00012179	0.00010563	0.00011021	0.00010997	K.n[230.17]R	3	P25205	P25205	MCM3	22		
15 K.n[230.17]DRITFFLNS16	-0.1387506	0.90830564	0.22924211	0.53129099	0.00012241	0.00010261	0.00011009	0.00010939	0.00012828	0.00011843	9.86E-05	0.00010871	0.00010992	K.n[230.17]D	3	Q8WYF5	Q8WYF5	AHCTF1	20		
16 K.n[230.17]GLAADS167.00	0.16076055	1.1178763	0.406407	0.67535989	0.00011302	9.69E-05	0.00010921	0.00011621	0.00010138	0.00011058	0.00012888	0.00011943	0.00011481	K.n[230.17]G	2	P04075	P04075	ALDOA	7		
17 K.n[230.17]ENDTVIS167.00	0.02285288	1.01596653	0.77373086	0.85403598	0.00012185	9.55E-05	0.00010771	0.00011167	0.00011859	0.00011933	0.00011731	0.00011295	9.40E-05	K.n[230.17]S	2	Q8UGU0	Q8UGU0	TCF20	10		
18 K.n[230.17]S167.00FEDRV	0.15087983	1.11024558	0.16888043	0.44780843	0.00011214	0.00011882	0.00010462	0.00010586	0.00010665	0.00010802	0.00012002	0.00012021	0.00010886	K.n[230.17]S	3	O43399	O43399	TPD52L2	5		
19 K.n[230.17]K357.26EQ11E	-0.1821911	0.88136338	0.45457262	0.69996832	8.92E-05	0.00011549	0.00013247	0.00015566	0.0001167	8.72E-05	8.16E-05	0.00013971	9.26E-05	K.n[230.17]K	4	O76021	O76021	RSL1D1	31		
20 K.n[230.17]YERRGGGSG	0.03475782	1.02438485	0.53821326	0.73629977	0.00011867	0.00011627	0.00011677	8.49E-05	0.00011015	0.00010637	0.00011375	0.00011424	0.00011541	K.n[230.17]L	3	Q96QR8	Q96QR8	PURB	8		
21 K.n[230.17]ERAT181.01PS	-0.0122774	0.99152004	0.71488649	0.81789868	0.00011143	0.00010857	0.00011288	0.00010774	0.00011132	0.00010906	0.00011201	0.00010979	0.00011296	K.n[230.17]E	3	Q641Q2	Q641Q2	WASHC2A	14		
22 K.n[230.17]AM147.00AJDEI	-0.1129583	0.92469003	0.31689754	0.6171968	0.00010332	0.00010432	0.00011647	0.00011353	0.00011925	0.00011689	0.00010418	0.00011291	0.00011266	K.n[230.17]A	2	Q03135	Q03135	CAVI1	14		
23 K.n[230.17]MGAGS167.00	0.11963848	2.28253737	0.00011176	0.00166639	3.13E-05	0.00021281	9.81E-05	9.88E-05	2.69E-05	2.87E-05	0.00022908	0.00020556	8.64E-05	K.n[230.17]G	3	P32578	P32578	SIP1	2		
24 K.n[230.17]RSEERTAEAE	0.13739597	1.09989009	0.55016194	0.74003225	7.50E-05	9.68E-05	7.47E-05	0.0001626	6.38E-05	0.00020068	0.00017884	7.57E-05	7.30E-05	K.n[230.17]D	4	P26038	P26038	MSN	6		
25 K.n[230.17]RSYS167.00SI	0.52165869	1.43560484	0.00151251	0.0094971	7.62E-05	0.00015401	0.00010044	0.00010228	8.92E-05	8.22E-05	0.0001442	0.00051219	0.00010956	K.n[230.17]R	3	Q9P0V3	Q9P0V3	SH3BP4	30		
26 K.n[230.17]MSQPGS167.00C	-0.0385329	0.97364455	0.7076951	0.82709014	0.00011952	0.00010514	0.00011508	0.00010492	0.0001232	0.00011808	0.00010739	0.00011064	0.0001103	K.n[230.17]M	2	Q14839	Q14839	CHD4	6		
27 K.n[230.17]DS167.00ASEE	0.31947955	1.2478803	0.26363329	0.56804221	9.72E-05	0.00013755	9.75E-05	0.00010741	0.00010541	0.00010657	0.00012124	0.00012865	0.00010552	K.n[230.17]D	3	Q9NX58	Q9NX58	LYAR	9		
28 K.n[230.17]DIDVVGAPL1	-0.0924194	0.93794848	0.25238634	0.55501758	0.00011566	9.87E-05	0.0001091	0.00011159	0.00011625	0.00010449	0.00011868	0.00011229	0.00011103	K.n[230.17]D	4	Q9NFF5	Q9NFF5	DMAP1	6		
29 K.n[230.17]HEADTFANM14	0.21857751	1.16358573	0.55035635	0.74003225	7.81E-05	0.00022662	8.70E-05	0.00011978	0.00014237	6.54E-05	0.00014322	0.00012203	0.0001116	K.n[230.17]E	3	Q9BX9	Q9BX9	NAAT15	6		
30 K.n[230.17]FELRVNVDIP	1.17870877	2.26374679	0.00012371	0.00168501	2.99E-05	0.00020668	8.95E-05	9.94E-05	3.12E-05	2.87E-05	0.00021792	0.00021416	9.38E-05	K.n[230.17]H	4	P52468	P52468	CDC12	3		
31 K.n[230.17]FAC160.03D	1.21549885	2.32221065	3.74E-05	0.00144962	2.97E-05	0.00021267	9.16E-05	9.08E-05	3.15E-05	2.76E-05	0.00021649	0.00021538	9.80E-05	K.n[230.17]F	3	P08105	P08105	SCP160	11		
32 K.n[230.17]GYS167.00PPE	-0.0964048	0.93636103	0.7009148	0.52616152	0.00017883	0.00011444	0.00011273	0.00011275	0.00011085	9.97E-05	9.84E-05	0.00010667	0.00011405	K.n[230.17]K	3	O14669.3	O14669	TRIP12	1		