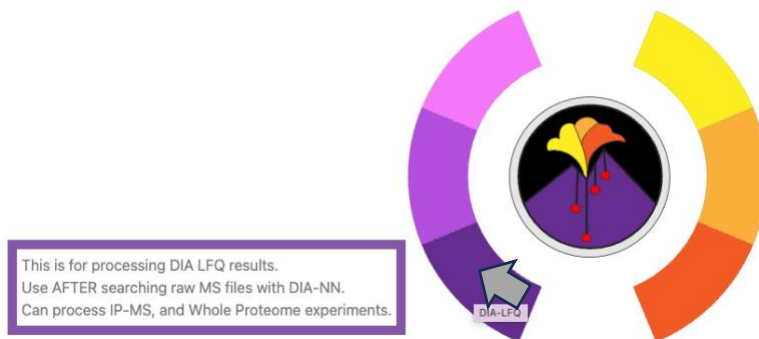# DIA-LFQ (Protein level)

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 DIA LFQ results.
Use AFTER searching raw MS files with DIA-NN.
Can process IP-MS, and Whole Proteome experiments.

DIA-LFQ

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 analysis type (MAGMa LM for a two-sample t-test and MAGMa Limma for a one sample t-test)

Click on the Protein-level arm (highlighted with red arrow in the figure below) to access to workflow.

Analysis Type

For more information: ?

○ Magma (Linear Model)
● Magma (Limma)

Choose the strategy for analysis with two choices:
1. Choose the model type to run the differential expression analysis with (between linear model (two sample) vs limma (one sample))
2. Choose the type of analysis (Whole Proteome - Precursor or Protein level) or IP-DIA-LFQ. Output files from DIA-NN should be used as input after.

NOTE: No default set but recommend setting of Protein level/IP-DIA + Magma (limma model). Check "About" page or manuscript for more details.

Protein-level   Precursor-level   IP-MS DIA-LFQ
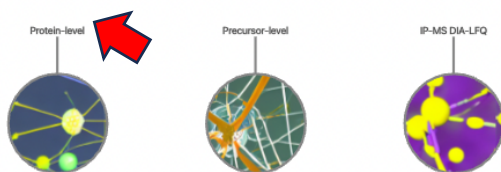
Step 3: Upload the annotation file. This is made using the experimental setup.

An example can be seen below taken from a benchmarking whole proteome (human with yeast spike in) DIA-LFQ experiment. Here each Channel is associated with a separate machine run. So, in the example below, condition "Sample A" (Human: Yeast:: 1:1) was run thrice and thus has three separate files generated which correspond to two columns in the protein level quantification file (highlighted in green). **These are headers of the files that would be input in step 5 below (see second screen shot for corresponding color in column header).**

A	B
Channel	Label
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2524.d	Sample A
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2525.d	Sample A
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2526.d	Sample A
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2531.d	Sample B
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2532.d	Sample B
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2533.d	Sample B
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2535.d	Sample C
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2536.d	Sample C
D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2537.d	Sample C

Protein	Protein.Ids	Protein.Nam	Genes	First.Protein.	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\2023_May_C
A2RTX5	A2RTX5	SYTC2_HUM	TARS3	Threonine--t	15944.2	16235.8	13334.3	18015.2	14564.8	16957.2	13874.6	13973.4	15230.1
L0R8F8	L0R8F8	MIDUO_HUN	MIEF1	MIEF1 upstre	20306.6	31025.5	26134.2	40500	38305.6	33994.6	27231.9	23019.6	25284
O00257	O00257	CBX4_HUMA	CBX4	E3 SUMO-pr	31290.3	25705.3	31914.9	32556.9	30615.1	32384.1	25321.9	26297.9	27565.1
O00258	O00258	GET1_HUMA	GET1	Guided entry	4101.55	5184.99	4891.59	5610.92	4383.75	4045.87	4969.71	4638.22	4514.36
O00264	O00264	PGRC1_HUM	PGRMC1	Membrane-a	343183	340696	326223	442980	467482	451763	438401	425337	441216
O00469	O00469	PLOD2_HUM	PLOD2	Procollagen-	50505.6	52641.1	51054.5	60625.4	60709.3	60564.4	56156.1	54538.3	56712.9
O14639	O14639	ABLM1_HUN	ABLIM1	Actin-binding	4485.57	15124.2	14480.6	16178.3	19332.8	18881.9	15269.6	13856	15082.2
O14657	O14657	TOR1B_HUN	TOR1B	Torsin-1B	19376.3	18249.9	17701.6	20595.4	23204.8	13031.6	18856.8	17889.5	19488.8
O15126	O15126	SCAM1_HUN	SCAMP1	Secretory car	29889.3	24671.2	30634.5	37534.6	37673.6	42550.1	35807.3	35401.7	32844.4
O15304	O15304	SIVA_HUMA	SIVA1	Apoptosis re	10081.2	7646.25	6616.17	1996.03	5434.4	7202.26	7641.77	7319.09	4708.16
O15321	O15321	TM9S1_HUN	TM9SF1	Transmembr	20380.2	20410.9	18020.2	16311.2	15967	20695.8	19330.4	16006.9	16209.2
O43292	O43292	GPAA1_HUN	GPAA1	Glycosylphos	17202.3	23281.9	15531.9	15748.9	20459.9	17869.3	19818.7	17386.3	18820.7
O43447	O43447	PPIH_HUMAI	PPIH	Peptidyl-prol	419765	468936	396211	450160	431498	413610	442408	406987	415182
O43567	O43567	RNF13_HUN	RNF13	E3 ubiquitin-	7219.94	5406.75	8014.85	8639.45	9969.08	5437.31	10265.9	8413.95	8364.91
O43663	O43663	PRC1_HUMA	PRC1	Protein regul	170001	189163	151910	246849	230180	207287	172238	155032	174000
O43929	O43929	ORC4_HUMA	ORC4	Origin recogi	46247.6	50641.1	52583.5	65225.3	63211.1	62048	53586.3	52464.5	56440.2
O60826	O60826	CCD22_HUM	CCDC22	Coiled-coil d	70250.5	63085	70690.2	72434.8	66947.7	70907.2	69190.9	69623.2	66484.8
O75113	O75113	N4BP1_HUM	N4BP1	NEDD4-bindi	41987.7	41924.5	33715.9	41820.6	44669.1	42690	35225.5	37276.3	40062.3
O75121	O75121	MFA3L_HUN	MFAP3L	Microfibrillar	6653.58	8527.04	9984.36	9157.86	10465	10372.1	6270.57	11724.9	9080.72
O75150	O75150	BRE1B_HUN	RNF40	E3 ubiquitin-	60382.3	65078.3	65609.7	79460.4	73603.8	74264.1	72510.9	69577.8	69485.5
O75417	O75417	DPOLQ_HUM	POLQ	DNA polyme	13776.2	9876.68	13463.9	10645.6	14391.4	11181.3	13195.2	11602.1	10996.7
O75525	O75525	KHDR3_HUM	KHDRBS3	KH domain-c	334471	322770	321972	367780	360167	356982	365355	364374	351086
O94788	O94788	AL1A2_HUM	ALDH1A2	Retinal dehy	99285	98671.8	97095.1	119611	115296	105823	108459	105469	93010.6
O94905	O94905	ERLN2_HUM	ERLIN2	Erlin-2	47687	58778.7	54064.7	67397.6	66855	60591.2	57872.3	59537.2	53766.4
O0E201		SLU7_HUMA SLU7		Pro-mRNA-c	24496.6	17779.7	15361	23070.0	23676.4	18148.5	19560.7	21103.6	17053.7

Benchmark_DIA-LFQ_wholeproteome +

(the pg_matrix file is inputted in step 5)

You can also hover over question mark for more details. Click on the "Sample File" in blue to download this example annotation file.

1 Upload the 'Annotation file'

For more information: ?

Select a file:

This file is to assign labels to channels according to experimental setup. Columns needed in this file are – Channel and Label. Channel are the column header(s) in the DIANN output specifying quantification per row. Important to choose the conditions to be compared.

Choose File | No file cho

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

Submit Reset

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

Sample file

Step 4: Choose the conditions you want to compare in a pairwise fashion. And choose the direction of comparison. So, choosing comparison ('Sample A, 'Sample B') and direction (Condition_1/Condition_2) means the following comparison will run – (Sample A/Sample B).

Step 5: Upload the input files (protein level aggregated) for quantification.

For DIA-NN search, upload a tab separated file of quantification file (aggregated to protein level). The file usually has "pg_matrix.tsv" in the name. **Set the column name as "Protein" that you want to use as the unique identifier** (every point on your volcano plot would be associated with a unique value in that column). Make sure the files have the following columns – 'Protein', 'Genes'.

As before hover over question mark for more information. Click on the "Sample File" in blue to download this example protein level aggregated file.

The example is taken from a down-sampling of real benchmarking DIA-LFQ experiment run on Bruker timsTOF HT and looks like the screenshot below.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Protein	Protein.Ids	Protein.Nam	Genes	First.Protein	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\202	D:\Data\2023_May_	
2	A2RTX5	A2RTX5	SYTC2_HUM	TARS3	Threonine--t	15944.2	16235.8	13334.3	18015.2	14564.8	16957.2	13874.6	13973.4	15230.1	
3	L0R8F8	L0R8F8	MIDUO_HUN	MIEF1	MIEF1 upstre	20306.6	31025.5	26134.2	40500	38305.6	33994.6	27231.9	23019.6	25284	
4	O00257	O00257	CBX4_HUMA	CBX4	E3 SUMO-pr	31290.3	25705.3	31914.9	32556.9	30615.1	32384.1	25321.9	26297.9	27565.1	
5	O00258	O00258	GET1_HUMA	GET1	Guided entry	4101.55	5184.99	4891.59	5610.92	4383.75	4045.87	4969.71	4638.22	4514.36	
6	O00264	O00264	PGRC1_HUM	PGRMC1	Membrane-a	343183	340696	326223	442980	467482	451763	438401	425337	441216	
7	O00469	O00469	PLOD2_HUM	PLOD2	Procollagen-	50505.6	52641.1	51054.5	60625.4	60709.3	60564.4	56156.1	54538.3	56712.9	
8	O14639	O14639	ABLM1_HUN	ABLIM1	Actin-binding	4485.57	15124.2	14480.6	16178.3	19332.8	18881.9	15269.6	13856	15082.2	
9	O14657	O14657	TOR1B_HUN	TOR1B	Torsin-1B	19376.3	18249.9	17701.6	20595.4	23204.8	13031.6	18856.8	17889.5	19488.8	
10	O15126	O15126	SCAM1_HUN	SCAMP1	Secretory car	29889.3	24671.2	30634.5	37534.6	37673.6	42550.1	35807.3	35401.7	32844.4	
11	O15304	O15304	SIVA_HUMA	SIVA1	Apoptosis re;	10081.2	7646.25	6616.17	1996.03	5434.4	7202.26	7641.77	7319.09	4708.16	
12	O15321	O15321	TM9S1_HUN	TM9SF1	Transmembr	20380.2	20410.9	18020.2	16311.2	15967	20695.8	19330.4	16006.9	16209.2	
13	O43292	O43292	GPAA1_HUN	GPAA1	Glycosylphos	17202.3	23281.9	15531.9	15748.9	20459.9	17869.3	19818.7	17386.3	18820.7	
14	O43447	O43447	PPIH_HUMAI	PPIH	Peptidyl-prol	419765	468936	396211	450160	431498	413610	442408	406987	415182	
15	O43567	O43567	RNF13_HUM	RNF13	E3 ubiquitin-	7219.94	5406.75	8014.85	8639.45	9969.08	5437.31	10265.9	8413.95	8364.91	
16	O43663	O43663	PRC1_HUMA	PRC1	Protein regul	170001	189163	151910	246849	230180	207287	172238	155032	174000	
17	O43929	O43929	ORC4_HUMA	ORC4	Origin recogi	46247.6	50641.1	52583.5	65225.3	63211.1	62048	53586.3	52464.5	56440.2	
18	O60826	O60826	CCD22_HUM	CCDC22	Coiled-coil d	70250.5	63085	70690.2	72434.8	66947.7	70907.2	69190.9	69623.2	66484.8	
19	O75113	O75113	N4BP1_HUM	N4BP1	NEDD4-bindi	41987.7	41924.5	33715.9	41820.6	44669.1	42690	35225.5	37276.3	40062.3	
20	O75121	O75121	MFA3L_HUN	MFAP3L	Microfibrillar	6653.58	8527.04	9984.36	9157.86	10465	10372.1	6270.57	11724.9	9080.72	
21	O75150	O75150	BRE1B_HUM	RNF40	E3 ubiquitin-	60382.3	65078.3	65609.7	79460.4	73603.8	74264.1	72510.9	69577.8	69485.5	
22	O75417	O75417	DPOLQ_HUN	POLQ	DNA polyme	13776.2	9876.68	13463.9	10645.6	14391.4	11181.3	13195.2	11602.1	10996.7	
23	O75525	O75525	KHDR3_HUN	KHDRBS3	KH domain-c	334471	322770	321972	367780	360167	356982	365355	364374	351086	
24	O94788	O94788	AL1A2_HUM	ALDH1A2	Retinal dehy	99285	98671.8	97095.1	119611	115296	105823	108459	105469	93010.6	
25	O94905	O94905	ERLN2_HUM	ERLIN2	Erlin-2	47687	58778.7	54064.7	67397.6	66855	60591.2	57872.3	59537.2	53766.4	

Benchmark_DIA-LFQ_wholeproteome   +

Step 6: Enter the full file generated after DIA-NN search. This is used to compute the number of precursors identified per label type (specified in the annotation file in step 3). **Here also, set the column name as 'Protein' for the column to be used for unique identifiers (like step 5).** Usually, this file is very large so you can remove extra columns to reduce size. Just make sure the file have the following columns – 'File.Name', 'Run', 'Protein', 'Protein.Ids', 'Protein.Names', 'Genes'.

As before hover over question mark for more information. Click on the "Sample File" in blue to download this example file for this example (screenshot of what the file looks like where Protein.Groups set to Protein).

4

Upload a tab separated Bruker+DIANN text file with ALL information.

For more information: ?

• This field is require   This file is the output from DIA-NN search in the form of tab delimited ".tsv" file of all information NOT aggregated. Used for finding # Precursors etc per protein. Potential way to filter out noise.

Choose File No file ch   NOTE: After running DIA-NN the output file that is the name of the run in ".tsv" format.

Reset   NOTE (2): IMPORTANT!! Set column name as "Protein" for the column to be used as unique protein ID's.

Sample file

	A	B	C	D	E	F
1	File.Name	Run	Protein	Protein.Ids	Protein.Names	Genes
2	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2524.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
3	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2525.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
4	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2526.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
5	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2531.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
6	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2532.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
7	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2533.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
8	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2536.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
9	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2537.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
10	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2524.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
11	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2525.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
12	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2526.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
13	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2531.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
14	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2532.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
15	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2533.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
16	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2535.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
17	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2536.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
18	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2537.d	20230509_S:	Q12118	Q12118	SGT2_YEAST	SGT2
19	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2524.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
20	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2525.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
21	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleA_500ng_dia-PASEF_30min_Slot1-2_1_2526.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
22	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2531.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
23	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2532.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
24	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleB_500ng_dia-PASEF_30min_Slot1-3_1_2533.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
25	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2535.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
26	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2536.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G
27	D:\Data\2023_May_Cornell_YU\Data_Cornell_HT\500_ng\20230509_SampleC_500ng_dia-PASEF_30min_Slot1-4_1_2537.d	20230509_S:	P26641	P26641	EF1G_HUMAN	EEF1G

Benchmark_DIA-LFQ_wholeproteome   +

Step 7: Choose whether to do imputation on your data or not. Recommended to not penalize proteins that are not going to be identified/quantified in the Control. In certain situations, this is a given (for example, viral bait would never be endogenously expressed and hence might be completely missing in Control runs depending on type of control being compared to).

A successful start of run with look like this –

Run the Analysis

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

ᴄ Loading...

The output page (given a successful run) looks like the screenshot below. You can download the protein level differential expression analysis results as well as the pdf of resulting volcano plot (set at 5 PSM cutoff – **where # PSMs is set as the # of Precursors of the numerator condition. So, if comparison is Sample A vs Sample B then #PSMs is #Precursors for Sample A**). 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
Click Here to Download the baseline Volcano plot (PDF)

FC cutoff choice: Drag the slider to display the current value.
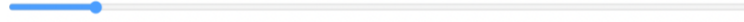
Value: 2

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

Value: 0.05

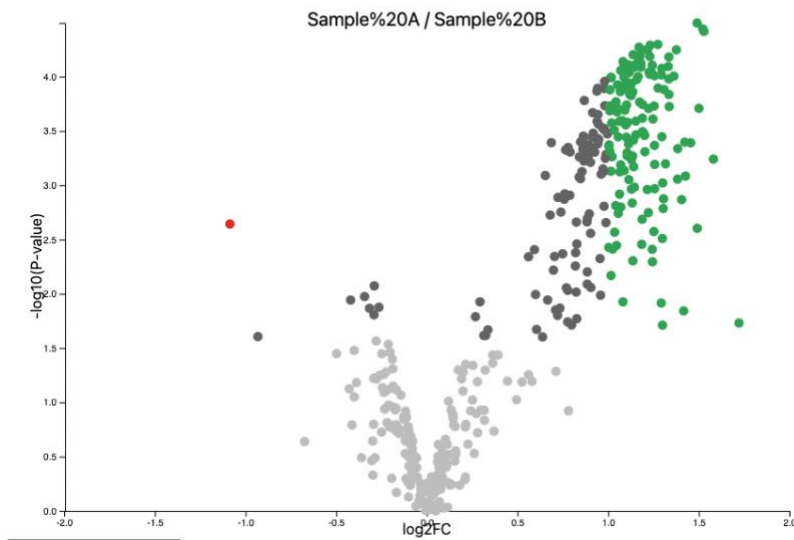PSM cutoff choice: Drag the slider to display the current value.

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]

Download Volcano Plot

The output file looks like this –

	A	B	C	D	E	F	G	H	I	J
1	Protein	log2FC	pval	adjpval	#Precursors-	#Precursors-	#Precursors-	# PSMs	PSM Cutoff	Gene Symbol
2	P39966	1.10159864	0.00018238	0.00131265	37	29	38	37	5	PTC2
3	P00445	1.52273032	3.64E-05	0.00117586	47	45	44	47	5	SOD1
4	P25635	0.97145326	0.00070753	0.00233014	33	16	31	33	5	PWP2
5	P13186	0.82488338	0.00218761	0.00559936	23	7	18	23	5	KIN2
6	P53110	1.05599636	0.00181425	0.00481849	8	1	4	8	5	YGL159W
7	P13861	0.03717888	0.59514466	0.65479168	77	81	81	77	5	PRKAR2A
8	Q12502	1.13465163	0.00053816	0.00198398	14	6	13	14	5	LDB19
9	P36104	0.77748475	0.00929662	0.02005472	17	3	16	17	5	SWD2
10	Q9Y5X4	-1.1916566	0.00150702	0.00415904	3	3	3	3	5	NR2E3
11	Q9NYL9	0.14576137	0.14016324	0.20855615	47	59	52	47	5	TMOD3
12	Q9NQL2	-0.6744407	0.22962786	0.31163781	8	12	12	8	5	RRAGD
13	P28791	0.81897296	0.0055468	0.01239873	6	0	4	6	5	SEC20
14	P40357	0.84109681	0.00054833	0.00198547	33	17	34	33	5	SEC9
15	Q9Y597	-0.1153102	0.50408832	0.58592854	12	18	12	12	5	KCTD3
16	Q96MY7	0.26524255	0.0217614	0.04103104	3	3	3	3	5	FAM161B
17	P37838	1.20147305	0.00034735	0.00170026	36	23	36	36	5	NOP4
18	Q2V2M9	-0.2856924	0.32382714	0.41123549	5	6	4	5	5	FHOD3
19	Q96KQ4	-0.2925342	0.06000278	0.10221164	19	21	20	19	5	PPP1R13B
20	P03872	1.08172197	0.01186634	0.02452709	7	2	7	7	5	REP2
21	Q9BXW7	-0.0346588	0.56008565	0.63025584	77	87	91	77	5	HDHD5
22	Q8TF01	0.13667344	0.57201054	0.64075557	9	12	12	9	5	PNISR
23	P40040	1.13585458	0.00013806	0.00117586	15	13	15	15	5	THO1
24	P19880	1.37645951	5.67E-05	0.00117586	25	14	22	25	5	YAP1
25	P35180	1.12828748	0.0005825	0.00203529	17	10	18	17	5	TOM20
26	Q91080	1.12853771	0.00108764	0.00331733	51	29	46	51	5	BDA40

Sample A-vs-Sample B_FC_and_pva