

Thermo Proteome Discoverer 2.5.0.400

File View Administration Tools Window Help

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Proteome Discoverer 2.5

Start	Recent Studies	Recent Results
New Study/Analysis...	Ryan	TMT11-pm-1077_individual
Open Study...	New Study	TMT11-pm-group_individual
Open Result...	Ricardo	TMT11-pm-1077_mtor_group
	New Study	TMT11-pm-1077_ampk_group
	SeaStar	TMT11-pm-1077_tyms_individual_across
	New Study 1	PM-1081-TMTpro
	New Study 1	PM-1081-TMTpro_WD
	Passion Fruit	ZX_groups
	U Florida Eclipse Oct 2020	TMT11-pm-1077_Vinod_target
	SeaStar	Seastar_Group
	New Study 1	BSA120-2-0213-(1)
	PM952	LM08_1-SILAC_10ppm1Da_Ch
	New Study 1	C1_S1-D2_1_3651_5.3.556
	New Study	Ruchir-20ng-EV1112_CE59deepWH20SPD_S1-B7_1_3321_5.3.556
	BrassicaPolyploids	Ruchir_S1-A3_1_3036_uncalibrated
	HFGDB	PassionFruit_TMTpro_Group
	New Study	PassionFruit_TMTpro_Group

Ready

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File View Administration Tools Window Help

Start Page x TMT11-pm-group_individual x

Proteins Protein Groups Peptide Groups PSMs MS/MS Spectrum Info Quan Spectra Input Files Specialized Traces Study Information Result Statistics

	Checked	Protein	Master	Accession	Description	Exp. q-value	Sum PEP Score	Coverage [%]	Sequence Coverage	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	ca
1	<input type="checkbox"/>	High	✓	A0A024R0K5	Carcinoembryonic antigen-related cell adhesion molecule 5	0.001	5.958	2%		1	3	1	702	76.7	
2	<input type="checkbox"/>	High	✓	Q14571	Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapie	0.000	113.587	13%		29	66	23	2701	307.9	
3	<input type="checkbox"/>	High	✓	Q9NPJ6	Mediator of RNA polymerase II transcription subunit 4 OS=H	0.006	3.556	4%		1	1	1	270	29.7	
4	<input type="checkbox"/>	High	✓	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein	0.000	40.009	40%		8	17	8	326	36.9	
5	<input type="checkbox"/>	High	✓	F5H8H2	Mevalonate kinase OS=Homo sapiens OX=9606 GN=MVK	0.002	4.520	5%		2	6	2	344	37.1	
6	<input type="checkbox"/>	High	✓	A0A3B3IRL5	Inosine-5'-monophosphate dehydrogenase (Fragment) OS=	0.000	7.260	6%		3	3	2	509	54.3	
7	<input type="checkbox"/>	High	✓	Q15042	Rab3 GTPase-activating protein catalytic subunit OS=Homc	0.000	29.858	12%		10	13	10	981	110.5	
8	<input type="checkbox"/>	High	✓	Q6GMV3	Putative peptidyl-HRNA hydrolase PTRHD1 OS=Homo sapie	0.000	12.724	21%		3	10	3	140	15.8	
9	<input type="checkbox"/>	High	✓	Q14657	EKC/KEOPS complex subunit LAGE3 OS=Homo sapiens O	0.000	16.137	31%		3	6	3	143	14.8	
10	<input type="checkbox"/>	High	✓	P51809	Vesicle-associated membrane protein 7 OS=Homo sapiens	0.003	4.250	10%		2	2	2	220	24.9	
11	<input type="checkbox"/>	High	✓	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GI	0.000	214.053	64%		25	417	14	462	50.1	
12	<input type="checkbox"/>	High	✓	B4DDF4	Calponin OS=Homo sapiens OX=9606 GN=CNN2 PE=1 Sv	0.000	10.827	13%		4	16	3	298	32.6	
13	<input type="checkbox"/>	High	✓	A0A3B3ITT1	Ras-related protein Rab-12 OS=Homo sapiens OX=9606 G	0.000	16.491	9%		3	24	2	340	36.3	
14	<input type="checkbox"/>	High	✓	Q9Y2H0	Disks large-associated protein 4 OS=Homo sapiens OX=96i	0.000	44.135	9%		7	21	7	992	107.9	
15	<input type="checkbox"/>	High	✓	P49418	Amphiphysin OS=Homo sapiens OX=9606 GN=AMPH PE=	0.006	3.557	2%		2	5	1	695	76.2	
16	<input type="checkbox"/>	High	✓	A0A7I2V383	BCL2L2-PABPN1 readthrough OS=Homo sapiens OX=960i	0.000	30.799	21%		7	33	1	365	40.5	
17	<input type="checkbox"/>	High	✓	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens i	0.000	8.812	10%		3	6	3	397	41.3	
18	<input type="checkbox"/>	High	✓	Q9NW08	DNA-directed RNA polymerase III subunit RPC2 OS=Homo	0.001	5.950	4%		3	3	3	1133	127.7	
19	<input type="checkbox"/>	High	✓	Q9NWK9	Box C/D snoRNA protein 1 OS=Homo sapiens OX=9606 GI	0.000	16.763	14%		5	9	5	470	53.9	
20	<input type="checkbox"/>	High	✓	Q9NVJ2	ADP-ribosylation factor-like protein 8B OS=Homo sapiens C	0.001	6.283	13%		2	6	2	186	21.5	
21	<input type="checkbox"/>	High	✓	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Homo sapie	0.000	41.356	51%		5	24	5	142	15.6	
22	<input type="checkbox"/>	High	✓	F1DAL9	COUP transcription factor 1 OS=Homo sapiens OX=9606 G	0.000	24.442	17%		6	11	6	398	43.9	
23	<input type="checkbox"/>	High	✓	P62861	40S ribosomal protein S30 OS=Homo sapiens OX=9606 GI	0.001	5.185	31%		3	6	3	59	6.6	1
24	<input type="checkbox"/>	High	✓	Q8NAV1	Pre-mRNA-splicing factor 38A OS=Homo sapiens OX=9606	0.000	7.770	10%		3	4	3	312	37.5	

Show Associated Tables

Overview of the file from the search

5829/21739 Proteins; 5829 Protein Groups; 39027 Peptide Groups; 126040 PSMs; 1345816 MS/MS Spectrum Info; 677162 Quan Spectra; 39/40 Input Files; 429 Study Information...

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File View Administration Tools Window Help

Start Page x TMT11-pm-group_individual x

Proteins Protein Groups Peptide Groups PSMs MS/MS Spectrum Info Quan Spectra Input Files Specialized Traces Study Information Result Statistics

Right Click in Checked column

Click "Check All"

Click "In This Table"

	les	# AAs	MW [kDa]	ce
1	1	702	76.7	
2	23	2701	307.9	
3	1	270	29.7	
4	8	326	36.9	
5	2	344	37.1	
6	2	509	54.3	
7	10	981	110.5	
8	3	140	15.8	
9	3	143	14.8	
10	2	220	24.9	
11	14	462	50.1	
12	3	298	32.6	
13	2	340	36.3	
14	7	992	107.9	
15	1	695	76.2	
16	1	365	40.5	
17	3	397	41.3	
18	3	1133	127.7	
19	5	470	53.9	
20	2	186	21.5	
21	5	142	15.6	
22	6	398	43.9	
23	3	59	6.6	
24	3	312	37.5	

Show Associated Tables

Ready 5829/21739 Proteins; 5829 Protein Groups; 39027 Peptide Groups; 126040 PSMs; 1345816 MS/MS Spectrum Info; 677162 Quan Spectra; 39/40 Input Files; 429 Study Information...

Thermo Proteome Discoverer 2.5.0.400

File View Administration Tools Window Help

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 Save All Ctrl+Shift+S
 Export
 Recent Studies
 Recent Results
 Exit

Go to File → Export

Peptide Groups PSMs MS/MS Spectrum Info Quan Spectra Input Files Specialized Traces Study Information Result Statistics

Accession	Description	Exp. q-value	Sum PEP Score	Coverage [%]	Sequence Coverage	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	ca
A0A024R0K5	Carcinoembryonic antigen-related cell adhesion molecule 5	0.001	5.958	2%		1	3	1	702	76.7	
O14671	Inositol 1,4,5-bisphosphate receptor type 2 OS=Homo sapiens	0.000	113.587	13%		29	66	23	2701	307.9	
	RNA polymerase II transcription subunit 4 OS=Homo sapiens	0.006	3.556	4%		1	1	1	270	29.7	
	pre-mRNA domain-containing protein	0.000	40.009	40%		8	17	8	326	36.9	
	OS=Homo sapiens OX=9606 GN=MVK	0.002	4.520	5%		2	6	2	344	37.1	
		0.000	7.260	6%		3	3	2	509	54.3	
		0.000	29.858	12%		10	13	10	981	110.5	
		0.000	12.724	21%		3	10	3	140	15.8	
	transcription subunit LAGE3 OS=Homo sapiens	0.000	16.137	31%		3	6	3	143	14.8	
	membrane protein 7 OS=Homo sapiens	0.003	4.250	10%		2	2	2	220	24.9	
	alpha 1 OS=Homo sapiens OX=9606 GI	0.000	214.053	64%		25	417	14	462	50.1	
	sapiens OX=9606 GN=CNN2 PE=1 Sv	0.000	10.827	13%		4	16	3	298	32.6	
	rib-12 OS=Homo sapiens OX=9606 G	0.000	16.491	9%		3	24	2	340	36.3	
	protein 4 OS=Homo sapiens OX=9606	0.000	44.135	9%		7	21	7	992	107.9	
	OS=Homo sapiens OX=9606 GN=AMPH PE=	0.006	3.557	2%		2	5	1	695	76.2	
	through OS=Homo sapiens OX=9606	0.000	30.799	21%		7	33	1	365	40.5	
	transferase, cytosolic OS=Homo sapiens	0.000	8.812	10%		3	6	3	397	41.3	
	polymerase III subunit RPC2 OS=Homo	0.001	5.950	4%		3	3	3	1133	127.7	
	protein 1 OS=Homo sapiens OX=9606 GI	0.000	16.763	14%		5	9	5	470	53.9	
Q9NVJ2	ADP-ribosylation factor-like protein 8B OS=Homo sapiens	0.001	6.283	13%		2	6	2	186	21.5	
P26885	Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Homo sapiens	0.000	41.356	51%		5	24	5	142	15.6	
F1DAL9	COUP transcription factor 1 OS=Homo sapiens OX=9606 G	0.000	24.442	17%		6	11	6	398	43.9	
P62861	40S ribosomal protein S30 OS=Homo sapiens OX=9606 GI	0.001	5.185	31%		3	6	3	59	6.6	
O8NAV1	Pre-mRNA-splicing factor 38A OS=Homo sapiens OX=9606	0.000	7.770	10%		3	4	3	312	37.5	

Click "To Microsoft Excel"

Study
 Annotated Spectra...
 Spectra...
 To FASTA...
 To Microsoft Excel...
 To mzIdentML...
 To mzTab...
 To PepXML...
 To ProtXML...
 To Text (tab delimited)...
 To xiNET...
 To PyMOL...
 LTQ Orbitrap Mass List...
 Orbitrap Fusion Mass List...
 Q Exactive Mass List...

Show Associated Tables

Ready 5829/21739 Proteins; 5829 Protein Groups; 39027 Peptide Groups; 126040 PSMs; 1345816 MS/MS Spectrum Info; 677162 Quan Spectra; 39/40 Input Files; 429 Study Information...

The screenshot displays the Thermo Proteome Discoverer 2.5.0.400 software interface. The main window shows a table of protein and peptide data. An 'Export To Excel' dialog box is open, allowing the user to select the export path and options for the data to be exported.

Checked	Protein	Master	Accession	Description	Exp. q-value	Sum PEP Score	Coverage [%]	Sequence Coverage	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	ca
<input checked="" type="checkbox"/>	High	✓	A0A024R0K5	Carcinoembryonic antigen-related cell adhesion molecule 5	0.001	5.958	2%		1	3	1	702	76.7	
<input checked="" type="checkbox"/>	High	✓	Q14571	Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapie	0.000	113.587	13%		29	66	23	2701	307.9	
<input checked="" type="checkbox"/>	High	✓	Q9NPJ6	Mediator of RNA polymerase II transcription subunit 4 OS=H	0.006	3.556	4%		1	1	1	270	29.7	
<input checked="" type="checkbox"/>	High	✓	Q9NQG5	Regulation of nu					8	17	8	326	36.9	
<input checked="" type="checkbox"/>	High	✓	F5H8H2	Mevalonate kina					2	6	2	344	37.1	
<input checked="" type="checkbox"/>	High	✓	A0A3B3IRL5	Inosine-5'-mono					3	3	2	509	54.3	
<input checked="" type="checkbox"/>	High	✓	Q15042	Rab3 GTPase-a					10	13	10	981	110.5	
<input checked="" type="checkbox"/>	High	✓	Q6GMV3	Putative peptidyl					3	10	3	140	15.8	
<input checked="" type="checkbox"/>	High	✓	Q14657	EKC/KEOPS cor					3	6	3	143	14.8	
<input checked="" type="checkbox"/>	High	✓	P51809	Vesicle-associat					2	2	2	220	24.9	
<input checked="" type="checkbox"/>	High	✓	P68104	Elongation factor					25	417	14	462	50.1	
<input checked="" type="checkbox"/>	High	✓	B4DDF4	Calponin OS=Hc					4	16	3	298	32.6	
<input checked="" type="checkbox"/>	High	✓	A0A3B3ITT1	Ras-related prot					3	24	2	340	36.3	
<input checked="" type="checkbox"/>	High	✓	Q9Y2H0	Disks large-asso					7	21	7	992	107.9	
<input checked="" type="checkbox"/>	High	✓	P49418	Amphiphysin OS					2	5	1	695	76.2	
<input checked="" type="checkbox"/>	High	✓	A0A7I2V383	BCL2L2-PABPN					7	33	1	365	40.5	
<input checked="" type="checkbox"/>	High	✓	Q9BWD1	Acetyl-CoA acet					3	6	3	397	41.3	
<input checked="" type="checkbox"/>	High	✓	Q9NW08	DNA-directed RI					3	3	3	1133	127.7	
<input checked="" type="checkbox"/>	High	✓	Q9NWK9	Box C/D snoRNA					5	9	5	470	53.9	
<input checked="" type="checkbox"/>	High	✓	Q9NVJ2	ADP-ribosylator					2	6	2	186	21.5	
<input checked="" type="checkbox"/>	High	✓	P26885	Peptidyl-prolyl ci					5	24	5	142	15.6	
<input checked="" type="checkbox"/>	High	✓	F1DAL9	COUP transcript					6	11	6	398	43.9	
<input checked="" type="checkbox"/>	High	✓	P62861	40S ribosomal protein					3	6	3	59	6.6	
<input checked="" type="checkbox"/>	High	✓	Q8NAV1	Pre-mRNA-splicing factor 38A OS=Homo sapiens OX=9606	0.000	7.770	10%		3	4	3	312	37.5	

You can export Proteins, peptides, and other options together using different levels of excel format. You can open the result via excel.

Export To Excel dialog box details:
Path: F:\Customer\TMT11-pm-group_individual.xlsx
Items and Associated Tables to be exported:
Level 1: Proteins (checked)
Level 2: Protein Groups (unchecked)
Level 3: Proteins (unchecked)
Options:
Checked Items Only (checked)
Excluded Items Only (unchecked)
Open File After Export (unchecked)

Status bar: Ready 5829/21739 Proteins; 5829 Protein Groups; 39027 Peptide Groups; 126040 PSMs; 1345816 MS/MS Spectrum Info; 677162 Quan Spectra; 39/40 Input Files; 429 Study Information.

You can open the result via excel.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
1	Checked	Protein FC	Master	Accession	Descripti	Exp. q-val	Sum PEP S	Coverage	# Peptide:	# PSMs	# Unique I	# AAs	MW [kDa]	calc. pI	Score Seq	# Peptide:	# Razor Pe	Abundanc	Abundanc	Abundanc	Abundanc
2	TRUE	High	Master Pri	A0A024R0	Carcinoen	0.001	5.958	2	1	3	1	702	76.7	5.69	8.71	1	0				
3	TRUE	High	Master Pri	Q14571	Inositol 1,	0	113.587	13	29	66	23	2701	307.9	6.43	211.77	29	3	0.993	1.045		0.998579
4	TRUE	High	Master Pri	Q9NPJ6	Mediator	0.006	3.556	4	1	1	1	270	29.7	5.1	2.77	1	0				
5	TRUE	High	Master Pri	Q9NQG5	Regulatio	0	40.009	40	8	17	8	326	36.9	5.97	56.24	8	0	0.897	1.519		0.797516
6	TRUE	High	Master Pri	F5H8H2	Mevalona	0.002	4.52	5	2	6	2	344	37.1	7.08	13.38	2	0	1.363	1.135		0.800009
7	TRUE	High	Master Pri	A0A3B3IR	Inosine-5'	0	7.26	6	3	3	2	509	54.3	6.8	7.61	3	0				
8	TRUE	High	Master Pri	Q15042	Rab3 GTPa	0	29.858	12	10	13	10	981	110.5	5.55	38.38	10	0	0.898	0.931		0.943625
9	TRUE	High	Master Pri	Q6GMV3	Putative p	0	12.724	21	3	10	3	140	15.8	9.1	31.39	3	0	0.993	0.815		0.817011
10	TRUE	High	Master Pri	Q14657	EKC/KEOP	0	16.137	31	3	6	3	143	14.8	8.63	19.87	3	0	1.19	0.873		0.797516
11	TRUE	High	Master Pri	P51809	Vesicle-as	0.003	4.25	10	2	2	2	220	24.9	8.6	6.14	2	0				
12	TRUE	High	Master Pri	P68104	Elongatio	0	214.053	64	25	417	14	462	50.1	9.01	1235.49	25	18	0.921	1		0.912963
13	TRUE	High	Master Pri	B4DDF4	Calponin (0	10.827	13	4	16	3	298	32.6	6.98	48.21	4	1	1.327	1.242		0.772138
14	TRUE	High	Master Pri	A0A3B3IT	Ras-relate	0	16.491	9	3	24	2	340	36.3	8.43	65.48	3	0				
15	TRUE	High	Master Pri	Q9Y2H0	Disks large	0	44.135	9	7	21	7	992	107.9	7.08	66.79	7	0	1.139	0.916		0.943519
16	TRUE	High	Master Pri	P49418	Amphiphy	0.006	3.557	2	2	5	1	695	76.2	4.64	11.14	2	0	1.442	0.937		0.980929
17	TRUE	High	Master Pri	A0A7I2V3	BCL2L2-PA	0	30.799	21	7	33	1	365	40.5	5.78	98.42	7	5	0.868	0.951		0.797516
18	TRUE	High	Master Pri	Q9BWD1	Acetyl-Co	0	8.812	10	3	6	3	397	41.3	6.92	14.68	3	0	1.068	1.015		0.983002
19	TRUE	High	Master Pri	Q9NWX8	DNA-direc	0.001	5.95	4	3	3	3	1133	127.7	8.5	8.48	3	0	0.963	0.98		0.831226
20	TRUE	High	Master Pri	Q9NWX9	Box C/D sr	0	16.763	14	5	9	5	470	53.9	5.8	24.58	5	0	0.599	0.905		0.981318
21	TRUE	High	Master Pri	Q9NVJ2	ADP-ribos	0.001	6.283	13	2	6	2	186	21.5	8.43	16.71	2	0	0.93	0.907		0.99293
22	TRUE	High	Master Pri	P26885	Peptidyl-p	0	41.356	51	5	24	5	142	15.6	9.13	72.13	5	0	1.307	1.06		0.976125
23	TRUE	High	Master Pri	F1DAL9	COUP tran	0	24.442	17	6	11	6	398	43.9	8.25	31.54	6	0	1.846	0.873		0.813804
24	TRUE	High	Master Pri	P62861	40S ribosc	0.001	5.185	31	3	6	3	59	6.6	12.15	9.97	3	0	4.061	0.923		0.940812
25	TRUE	High	Master Pri	Q8NAV1	Pre-mRNA	0	7.77	10	3	4	3	312	37.5	9.96	10.39	3	0				
26	TRUE	High	Master Pri	Q8WY22	BRI3-bind	0	16.667	12	3	11	3	251	27.8	9.44	42.54	3	0	1.197	0.922		0.875233
27	TRUE	High	Master Pri	Q7Z3C6	Autophag	0	13.242	5	3	9	3	839	94.4	6.67	25.87	3	0	0.968	0.863		0.98496
28	TRUE	High	Master Pri	P33993	DNA repli	0	87.668	36	25	55	25	719	81.3	6.46	157.5	25	0	0.806	1.148		0.922905
29	TRUE	High	Master Pri	Q16204	Coiled-co	0	37.213	23	10	17	10	474	53.3	7.34	53.74	10	0	1.241	1.339		0.797516
30	TRUE	High	Master Pri	Q9UGM6	Tryptopha	0.001	6.352	6	2	4	2	360	40.1	9.28	10.3	2	0				
31	TRUE	High	Master Pri	Q95478	Ribosome	0	10.21	17	4	9	4	260	20	10.27	22.78	4	0	0.407	1.185		0.987540

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File View Administration Tools Window Help

Start Page x TMT11-pm-group_individual x

Proteins Protein Groups Peptide Groups PSMs MS/MS Spectrum Info Quan Spectra Input Files

Click "Summary page" to see the search parameters.

	Checked	Protein FDI	Master	Accession	Description	Exp. q-value	Sum PEP Score	Coverage [%]	Sequence Coverage	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	ca
1	<input checked="" type="checkbox"/>	High	✓	P10645	Chromogranin-A OS=Homo sapiens OX=9606 GN=CHGA F	0.000	894.698	76%		39	2596	9	457	50.7	
2	<input checked="" type="checkbox"/>	High	✓	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens OX=9606 (0.000	795.505	83%		51	1542	40	483	53.7	
3	<input checked="" type="checkbox"/>	High	✓	P13521	Secretogranin-2 OS=Homo sapiens OX=9606 GN=SCG2 P	0.000	739.615	79%		51	898	51	617	70.9	
4	<input checked="" type="checkbox"/>	High	✓	Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens OX=9606 G	0.000	698.479	70%		87	923	87	1410	152.4	
5	<input checked="" type="checkbox"/>	High	✓	P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapien	0.000	676.560	74%		37	1128	37	573	61.0	
6	<input checked="" type="checkbox"/>	High	✓	P08670	Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4	0.000	668.439	87%		53	1370	48	466	53.6	
7	<input checked="" type="checkbox"/>	High	✓	Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens	0.000	658.673	47%		118	500	2	2472	284.4	
8	<input checked="" type="checkbox"/>	High	✓	A0A0D9SGF6	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens	0.000	653.931	47%		117	495	1	2498	287.4	
9	<input checked="" type="checkbox"/>	High	✓	P11021	Endoplasmic reticulum chaperone BiP OS=Homo sapiens C	0.000	648.819	61%		43	1056	40	654	72.3	
10	<input checked="" type="checkbox"/>	High	✓	P05783	Keratin, type I cytoskeletal 18 OS=Homo sapiens OX=9606	0.000	627.886	89%		47	1100	45	430	48.0	
11	<input checked="" type="checkbox"/>	High	✓	Q01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens C	0.000	614.713	47%		101	396	97	2364	274.4	
12	<input checked="" type="checkbox"/>	High	✓	P35579	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV	0.000	593.400	50%		92	407	76	1960	226.4	
13	<input checked="" type="checkbox"/>	High	✓	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=	0.000	593.069	77%		42	819	26	646	70.9	
14	<input checked="" type="checkbox"/>	High	✓	P05060	Secretogranin-1 OS=Homo sapiens OX=9606 GN=CHGB P	0.000	560.417	61%		44	617	44	677	78.2	
15	<input checked="" type="checkbox"/>	High	✓	P14625	Endoplasmic reticulum chaperone BiP OS=Homo sapiens C	0.000	548.789	73%		61	904	59	803	92.4	
16	<input checked="" type="checkbox"/>	High	✓	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens OX=96	0.000	548.021	73%		49	854	30	724	83.2	
17	<input checked="" type="checkbox"/>	High	✓	P13667	Protein disulfide-isomerase A4 OS=Homo sapiens OX=960	0.000	545.979	69%		46	612	1	645	72.9	
18	<input checked="" type="checkbox"/>	High	✓	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9	0.000	545.362	71%		48	886	28	732	84.6	
19	<input checked="" type="checkbox"/>	High	✓	G5E968	Chromogranin A (Parathyroid secretory protein 1), isoform C	0.000	532.144	71%		31	1515	1	306	34.2	
20	<input checked="" type="checkbox"/>	High	✓	P60709	Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACT	0.000	522.301	80%		26	1148	6	375	41.7	
21	<input checked="" type="checkbox"/>	High	✓	A0A499F148	Protein disulfide-isomerase OS=Homo sapiens OX=9606 G	0.000	513.964	69%		46	577	1	646	73.0	
22	<input checked="" type="checkbox"/>	High	✓	P38646	Stress-70 protein, mitochondrial OS=Homo sapiens OX=96	0.000	508.842	66%		46	569	45	679	73.6	
23	<input checked="" type="checkbox"/>	High	✓	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens OX=9606	0.000	497.386	88%		41	747	32	400	44.1	
24	<input checked="" type="checkbox"/>	High	✓	A0A804HL40	Leucine-rich PPP motif-containing protein, mitochondrial OS	0.000	490.425	54%		66	392	36	1393	157.7	

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