



**How to convert *Proteome Discoverer* data to
a *Prophane* compatible Protein Report**

- ① Open *.msf data in *Proteome Discoverer*
- ② Apply your preferred filter and protein grouping criteria
- ③ Open report

Proteins	Peptides	Search Input	Result Filters	Peptide Confidence	Search Summary				
		Accession	Description	Score	Coverage	# Proteins	# UniquePepti		
1	<input type="checkbox"/>	A1BN54	Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=2 SV=...	150.05	32.69 %	1			
2	<input type="checkbox"/>	A2A4H9	Peptidyl-prolyl cis-trans isomeraseFKBP10 OS=Mus musc...	4.35	4.05 %	2			
3	<input type="checkbox"/>	A2A4Q0	60S ribosomal proteinL27 (Fragment) OS=Mus musculus...	4.98	10.34 %	2			
4	<input type="checkbox"/>	A2A4X6	MCG21910 OS=Mus musculus GN=Gm12355 PE=4 SV=1...	18.33	13.50 %	2			
5	<input type="checkbox"/>	A2A4Z1	Ubiquitin-conjugating enzyme E2C OS=Mus musculus GN...	2.27	5.85 %	2			
6	<input type="checkbox"/>	A2A513	Keratin,type Icytoskeletal 10 OS=Mus musculus GN=Krt...	4.21	2.14 %	3			
7	<input type="checkbox"/>	A2A547	60S ribosomal proteinL19 OS=Mus musculus GN=Rpl19...	28.69	13.40 %	2			
8	<input type="checkbox"/>	A2A6G6	LIM and SH3 domain protein 1 (Fragment) OS=Mus musc...	9.06	35.96 %	6			
9	<input type="checkbox"/>	A2A6Q8	Myosin light chain 4(Fragment) OS=Mus musculus GN=M...	90.25	63.02 %	2			
10	<input type="checkbox"/>	A2A813	Protein DJ-1 OS=Mus musculus GN=Park7 PE=2 SV=1 - [...	31.36	53.14 %	2			
11	<input type="checkbox"/>	A2A9X5	5(3')-deoxyribonucleotidase, cytosolic type OS=Mus musc...	2.23	4.12 %	2			
12	<input type="checkbox"/>	A2AAN2	Signal recognition particlesubunit SRP68 OS=Mus muscul...	6.17	5.96 %	2			
13	<input type="checkbox"/>	A2AB60	Formin-like 1, isoform CRA_c OS=Mus musculus GN=Fmn...	2.46	1.01 %	2			
14	<input type="checkbox"/>	A2ABY3	Ethanolamine-phosphate cytidylyltransferase OS=Mus mu...	3.70	4.40 %	2			
15	<input type="checkbox"/>	A2ACG7	Dolichyl-diphosphooligosaccharide-protein glycosyltransfe...	20.19	8.78 %	2			
16	<input type="checkbox"/>	A2ACM0	Regulatory-associated protein of mTOR OS=Mus musculus...	3.57	1.20 %	2			
17	<input type="checkbox"/>	A2ADY9	ProteinDDI1 homolog2 OS=Mus musculus GN=Ddi2PE=...	7.95	8.52 %	1			
18	<input type="checkbox"/>	A2AEF0	Sortilin (Fragment) OS=Mus musculus GN=Sort1 PE=2 SV...	2.84	2.70 %	2			
19	<input type="checkbox"/>	A2AEJ8	Cleavage stimulation factorsubunit 2 (Fragment) OS=Mu...	3.16	5.98 %	3			
20	<input type="checkbox"/>	A2AEX7	Four and a half LIM domains protein 1 OS=Mus musculus...	11.76	15.24 %	6			
21	<input type="checkbox"/>	A2AFI9	Histone-binding protein RBBP7 OS=Mus musculus GN=Rb...	30.52	15.54 %	2			
22	<input type="checkbox"/>	A2AFK7	Eukaryotic initiation factor 4A-III(Fragment) OS=Mus mu...	4.34	4.68 %	3			

④ Export all PSMs to a tab delimited text file

The screenshot shows the Thermo Proteome Discoverer 1.4.1.14 interface. The 'Export' menu is open, and 'To Text (tab delimited)...' is selected. The background shows a table of search results with columns for Score, Coverage, # Proteins, and # Unique Peptides.

	Score	Coverage	# Proteins	# Unique Peptides
PE=2 SV=...	150.05	32.69 %	1	
=Mus musc...	4.35	4.05 %	2	
s musculus...	4.98	10.34 %	2	
E=4 SV=1...	18.33	13.50 %	2	
usculus GN...	2.27	5.85 %	2	
s GN=Krt...	4.21	2.14 %	3	
GN=Rpl19...	28.69	13.40 %	2	
Mus musc...	9.06	35.96 %	6	
ulus GN=M...	90.25	63.02 %	2	
=2 SV=1 - [...]	31.36	53.14 %	2	
5(3')-deoxyribonucleotidase, cytosolic type OS=Mus musc...	2.23	4.12 %	2	
Signal recognition partidesubunit SRP68 OS=Mus muscul...	6.17	5.96 %	2	
Formin-like 1, isoform CRA_c OS=Mus musculus GN=Fmn...	2.46	1.01 %	2	
Ethanolamine-phosphate cytidylyltransferase OS=Mus mu...	3.70	4.40 %	2	
Dolichyl-diphosphooligosaccharide-protein glycosyltranse...	20.19	8.78 %	2	
Regulatory-associated protein of mTOR OS=Mus muscalu...	3.57	1.20 %	2	
ProteinDDI1 homolog2 OS=Mus musculus GN=Ddi2PE=...	7.95	8.52 %	1	
Sortilin (Fragment) OS=Mus musculus GN=Sort1 PE=2SV...	2.84	2.70 %	2	
Cleavage stimulation factor subunit 2 (Fragment) OS=Mu...	3.16	5.98 %	3	
Four and a half LIM domains protein 1 OS=Mus musculus...	11.76	15.24 %	6	
Histone-binding protein RBBP7 OS=Mus musculus GN=Rb...	30.52	15.54 %	2	
A2AFK7 Eukaryotic initiation factor 4A-III (Fragment) OS=Mus mu...	4.34	4.68 %	3	

The dialog box 'To Text (tab delimited)...' is shown. The destination is set to 'X:\VAG_Hecker\GM\MMS Standard\Standard_A_test\V3\131'. The 'Criteria' section has 'Peptides' selected. Under 'With peptide grouping disabled', 'All PSMs' is selected. Under 'With peptide grouping enabled', 'All PSMs of checked peptide groups' is selected. The 'Export' button is highlighted.



5 Export all protein groups to ProtXML

The screenshot shows the Thermo Proteome Discoverer 1.4.1.14 interface. The 'Export' menu is open, and 'To ProtXML...' is selected. The background shows a table of search results with columns for Score, Coverage, # Proteins, and # Unique Peptides.

	Score	Coverage	# Proteins	# Unique Peptides
PE=2 SV=...	150.05	32.69 %	1	
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=2 SV=1 - [...]	31.36	53.14 %	2	
5(3')-deoxyribonucleotidase, cytosolic type OS=Mus musc...	2.23	4.12 %	2	
Signal recognition partidesubunit SRP68 OS=Mus muscul...	6.17	5.96 %	2	
Formin-like 1, isoform CRA_c OS=Mus musculus GN=Fmn...	2.46	1.01 %	2	
Ethanolamine-phosphate cytidylyltransferase OS=Mus mu...	3.70	4.40 %	2	
Dolichyl-diphosphooligosaccharide-protein glycosyltranse...	20.19	8.78 %	2	
Regulatory-associated protein of mTOR OS=Mus muscalu...	3.57	1.20 %	2	
ProteinDD11 homolog 2 OS=Mus musculus GN=Ddi2PE=...	7.95	8.52 %	1	
Sortilin (Fragment) OS=Mus musculus GN=Sort1 PE=2SV...	2.84	2.70 %	2	
Cleavage stimulation factor subunit 2 (Fragment) OS=Mu...	3.16	5.98 %	3	
Four and a half LIM domains protein 1 OS=Mus musculus...	11.76	15.24 %	6	
Histone-binding protein RBBP7 OS=Mus musculus GN=Rb...	30.52	15.54 %	2	
Eukaryotic initiation factor 4A-III (Fragment) OS=Mus mu...	4.34	4.68 %	3	

The 'Export to ProtXML' dialog box is shown. The 'Destination' field is set to 'C:\Users\vnslab\Desktop\SF\131102_V3_PM2_SK_GM_Star'. The 'Criteria' section has 'Checked protein groups' unchecked. The 'Export' and 'Close' buttons are visible.



do not activate
checked protein groups

⑥ Open Prophane's PDconverter via

<http://prophane.de/index.php?p=pdwiz>

Proteome Discoverer output converter

Prophane accepts only Scaffold Protein Reports so far. However, you can use this wizard to generate an artificial Protein Report accepted by Prophane from your Proteome Discoverer data. To consider all relevant data you have to provide different files (see [this manual](#) how to export them):

protXML export Kein...hit

all PSMs export Kein...hit

target database Kein...hit

Dependent on the size of the submitted files processing will take some time. Thus, please be patient after submission and do not close the window.

submit

7 Submit all needed files exported files

Proteome Discoverer output converter

Prophane accepts only Scaffold Protein Reports so far. However, you can use this wizard to generate an artificial Protein Report accepted by Prophane from your Proteome Discoverer data. To consider all relevant data you have to provide different files (see [this manual](#) how to export them):

protXML export

all PSMs export

target database

Dependent on the size of the submitted files processing will take some time. Thus, please be patient after submission and do not close the window.

Load the exported ProtXML file

Load the exported PSMs file

Load a FASTA file containing all accessions with the original accession tags*

* e.g. **gi|** for GI numbers
tr| for GI TrEMBL accessions

- ⑧ Follow the instructions
- ⑨ Download the generated Protein Report
- ⑩ Start the *Prophane* Workflow via

<http://www.prophane.de/index.php?p=new>