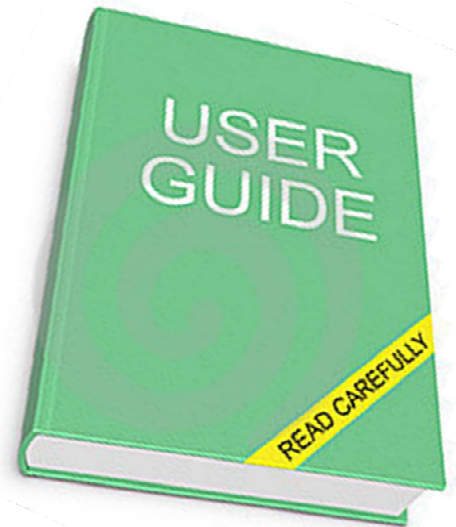


“How to read my .xlsm mass spec result”

#	Accession	Description	Mw(kDa)	control 1 minus Area	control 4 minus Area	sample 1 plus Area	sample 4 plus Area
5	947751	Keratin, type I cytoskeletal 17	48.1	6.48E+09	2.43E+08	3.54E+09	3.12E+09
6	311033484	Keratin, type I cytoskeletal 19	44.1	6.22E+09	2.35E+08	3.49E+09	3.07E+09
7	cont_P33527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE	62.0	1.58E+10	1.09E+09	3.37E+09	3.86E+09
8	cont_P42212	Green fluorescent protein OS=Aequorea victoria GN=GFP PE	26.9	8.39E+08	8.89E+08	3.11E+09	3.91E+09
9	cont_Q99045	Keratin, type II cytoskeletal 71 OS=Mus musculus GN=KIF71	57.3	2.81E+09	1.75E+08	3.09E+09	3.07E+09
10	cont_K12339	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27	49.8	3.13E+09	1.59E+08	2.67E+09	1.61E+09
11	122729	Ig kappa chain V-III region NG9	10.7			2.48E+09	2.53E+09
12	cont_P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A	60.0	5.54E+09	1.86E+08	2.31E+09	2.38E+09
13	cont_P46668	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C	60.0	5.34E+09	1.86E+08	2.31E+09	2.38E+09
14	5221123	Barrier-to-autointegration factor	10.1	1.53E+06		2.25E+09	1.76E+09
15	90110027	Keratin, type II cytoskeletal 8	53.7	5.41E+09	1.72E+08	1.97E+09	1.97E+09
16	143811411	Keratin, type II cytoskeletal 5	62.3	5.41E+09	1.72E+08	1.97E+09	1.97E+09
17	269848753	Keratin, type I cytoskeletal 13	49.6	1.96E+09	1.07E+08	1.63E+09	1.31E+09
18	122592	Prelamin-A/C	74.1	2.02E+06	2.11E+07	1.42E+09	3.33E+08
19	122583	Keratin, type I cytoskeletal 18	48.0	1.31E+09	9.30E+07	1.37E+09	1.11E+09
0	1250762	60S ribosomal protein L6	32.7	8.92E+07	6.94E+07	1.05E+09	3.76E+08
1	42112763	60S ribosomal protein L26	17.2	1.65E+08	8.37E+07	1.06E+09	3.57E+08
2	cont_Q01546	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT2	65.8	2.14E+09	1.21E+08	1.06E+09	1.21E+09
3	54039239	60S ribosomal protein L7a	30.0	1.65E+08	1.13E+08	1.02E+09	4.15E+08
4	81128191	60S ribosomal protein L5	34.3	1.55E+08	1.37E+08	9.69E+08	2.96E+08
5	22602093	60S ribosomal protein L4	47.7	1.59E+08	9.06E+07	9.42E+08	2.29E+08
6	52282206	Fibrinogen activator inhibitor 1 RNA-binding protein	44.9	2.49E+08	1.48E+08	9.28E+08	1.81E+08
7	23396835	60S ribosomal protein L26-like 1	17.2	5.26E+07	3.28E+07	9.22E+08	3.47E+08
8	82654947	Keratin, type II cytoskeletal 4	57.3	1.57E+09	9.42E+07	8.97E+08	1.06E+09
9	51338637	60S ribosomal protein L23a	17.7	1.31E+08	1.28E+08	8.88E+08	2.59E+08
0	1124690	Lamina-associated polypeptide 2, isoforms beta/gamma	50.6	6.97E+06	8.81E+05	8.75E+08	1.42E+08
1	1124689	Lamina-associated polypeptide 2, isoform alpha	75.4	6.97E+06	8.81E+05	8.75E+08	1.42E+08
2	720640	40S ribosomal protein S19	16.1	2.95E+08	1.02E+08	8.75E+08	2.53E+08
3	1350706	60S ribosomal protein L29	17.7	2.33E+08	1.28E+08	8.42E+08	3.01E+08
4	51202823	60S ribosomal protein L8	28.0	5.69E+07	4.52E+07	8.37E+08	2.88E+08
5	1709639	Emerin	29.0		6.65E+05	8.04E+08	5.82E+08
6	51312339	Histone IH	11.4	1.25E+06	2.55E+06	7.96E+08	4.87E+07
7	47112722	60S ribosomal protein L27	15.8	1.92E+07	2.86E+07	7.47E+08	2.50E+08
8	51338652	40S ribosomal protein S28	7.8	1.73E+07	1.82E+08	7.38E+08	9.53E+07
9	52783792	40S ribosomal protein S21	9.1	1.01E+08	1.37E+08	6.99E+08	1.20E+08
0	50402622	40S ribosomal protein S8	24.2	5.25E+07	4.26E+07	6.92E+08	1.63E+08
1	51338652	Keratin, type I cytoskeletal 3 OS=Homo sapiens GN=KRT3	44.4	1.05E+09	8.43E+07	6.75E+08	8.73E+08

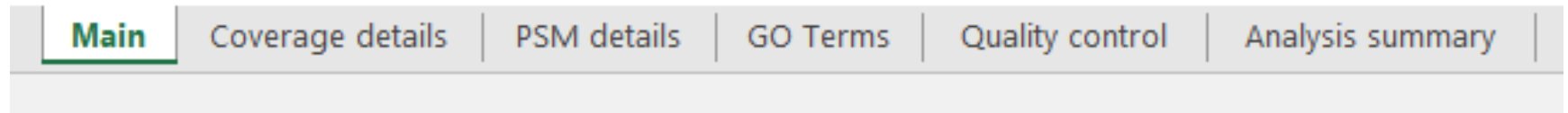


Please also visit our online compilation of FAQs

<http://cores.imp.ac.at/protein-chemistry/faqs/>

The xlsx file is structured in 6 tabs:

- **Main:** containing the list of all identified proteins
- **Coverage Details** showing the detailed sequence coverage of each identified protein
- **PSM Details** containing the list of all identified peptide spectrum matches (PSMs)
- **GO Terms** Gene Ontology analysis
- **Quality Control** containing quality control graphs
- **Analysis Summary** containing parameters used for database search



➤ **tab1 Main:**

containing the list of all identified *proteins* and their according accession number, description, molecular weight and precursor area

each accession is hyperlinked to an online database e.g. NCBI entry

protein description from used database

molecular weight

area is calculated by iBAQ method; The sum of all peptide intensities is divided by the number of observable peptides of a protein; it is a semi-quantitative value reflecting the protein abundance

contaminants are marked by color and by prefix cont_

Some proteins may appear with a red area and a value of 'zero'. This is due to the fact, that the protein in this sample consists only of shared peptides, but no "unique peptides".

Some proteins may appear in italic. They are usually rather weak and they are not identified, but their mass traces have been found by a method called "match between runs". This approach takes the mass traces of identified peptides and compares them to other samples, where the corresponding protein has not been identified.

#	Accession	Description	MW[kDa]	control_I_minus Area	control_M_minus Area	sample_I_plus Area	sample_M_plus Area	
5	250	cont_P00761	Trypsin OS=Sus scrofa PE=1 SV=1	24.4	1.34E+10	2.05E+10	3.75E+10	4.23E+10
6	774	cont_P15636	Protease 1 OS=Achromobacter lyticus PE=1 SV=1	68.1	3.24E+10	1.75E+10	1.99E+10	6.94E+09
7	414	<i>ENSEMBL:ENSBTAP0000002</i>	(Bos taurus) 47 kDa protein	46.5	6.02E+07	3.78E+07	1.34E+10	1.10E+10
8	249	269849769	Keratin, type I cytoskeletal 10	58.8	2.88E+10	2.47E+10	1.18E+10	1.05E+10
9	264	238054406	Keratin, type II cytoskeletal 1	66.0	2.05E+10	1.36E+09	6.23E+09	4.56E+09
10	153	cont_P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14	51.5	7.68E+09	3.26E+08	5.64E+09	4.43E+09
11	908	cont_P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16	51.2	7.68E+09	3.26E+08	5.64E+09	4.43E+09
12	50	cont_Q72794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77	61.9	8.01E+09	4.66E+08	4.76E+09	4.12E+09
13	276	cont_P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B	60.0	1.08E+10	4.52E+08	3.92E+09	3.27E+09
14	121	cont_P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens G	65.4	6.15E+09	2.42E+08	3.54E+09	3.62E+09
15	785	547751	Keratin, type I cytoskeletal 17	48.1	6.48E+09	2.45E+08	3.54E+09	3.12E+09
16	203	311033484	Keratin, type I cytoskeletal 19	44.1	6.22E+09	2.35E+08	3.49E+09	3.07E+09
17	907	cont_P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE	62.0	1.58E+10	1.09E+09	3.37E+09	3.86E+09
18	864	cont_P42212	Green fluorescent protein OS=Aequorea victoria GN=GFP PE-	26.9	0.00E+00	0.00E+00	3.11E+09	3.91E+09
19	128	cont_Q9R0H5	Keratin, type II cytoskeletal 71 OS=Mus musculus GN=Krt71 I	57.3	2.83E+09	1.75E+08	3.09E+09	3.07E+09
20	816	cont_Q723Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27	49.8	3.15E+09	1.59E+08	2.67E+09	1.61E+09
21	633	<i>125799</i>	Ig kappa chain V-III region NG9	10.7			2.48E+09	2.53E+09
22	277	cont_P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A	60.0	5.54E+09	1.86E+08	2.31E+09	2.38E+09
23	428	cont_P48668	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C	60.0	5.54E+09	1.86E+08	2.31E+09	2.38E+09
24	573	<i>5921173</i>	Barrier-to-autointegration factor	10.1	1.53E+06		2.25E+09	1.76E+09
25	862	90110027	Keratin, type II cytoskeletal 8	53.7	5.41E+09	1.72E+08	1.97E+09	1.97E+09
26	947	143811411	Keratin, type II cytoskeletal 5	62.3	5.41E+09	1.72E+08	1.97E+09	1.97E+09
27	768	<i>269849755</i>	Keratin, type I cytoskeletal 13	49.6	1.96E+09	1.07E+08	1.63E+09	1.31E+09
28	512	<i>125962</i>	Prelamin-A/C	74.1	2.02E+06	2.11E+07	1.42E+09	3.33E+08
29	388	<i>125083</i>	Keratin, type I cytoskeletal 18	48.0	1.31E+09	9.30E+07	1.37E+09	1.11E+09
30	178	<i>1350762</i>	60S ribosomal protein L6	32.7	8.92E+07	6.96E+07	1.09E+09	3.76E+08
31	699	<i>47117765</i>	60S ribosomal protein L26	17.2	1.65E+08	8.37E+07	1.06E+09	3.57E+08
32	287	cont_Q01546	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KR	65.8	2.14E+09	1.21E+08	1.06E+09	1.21E+09
33	562	<i>54039239</i>	60S ribosomal protein L7a	30.0	1.65E+08	1.13E+08	1.02E+09	4.15E+08
34	641	<i>81175191</i>	60S ribosomal protein L5	34.3	1.55E+08	1.37E+08	9.69E+08	2.96E+08
35	265	<i>22002063</i>	60S ribosomal protein L4	47.7	1.50E+08	9.00E+07	9.42E+08	2.29E+08
36	346	<i>52783206</i>	Plasminogen activator inhibitor 1 RNA-binding protein	44.9	2.49E+08	1.48E+08	9.28E+08	1.81E+08
37	899	<i>23396835</i>	60S ribosomal protein L26-like 1	17.2	5.26E+07	3.28E+07	9.22E+08	3.47E+08
38	813	<i>82654947</i>	Keratin, type II cytoskeletal 4	57.3	1.57E+09	9.42E+07	8.97E+08	1.06E+09
39	793	<i>51338637</i>	60S ribosomal protein L23a	17.7	1.31E+08	1.28E+08	8.88E+08	2.59E+08
40	518	<i>1174690</i>	Lamina-associated polypeptide 2, isoforms beta/gamma	50.6	6.97E+06	8.81E+05	8.75E+08	1.42E+08
41	765	<i>1174689</i>	Lamina-associated polypeptide 2, isoform alpha	75.4	6.97E+06	8.81E+05	8.75E+08	1.42E+08
42	125	<i>730640</i>	40S ribosomal protein S19	16.1	2.95E+08	1.02E+08	8.75E+08	2.53E+08
43	961	<i>1350706</i>	60S ribosomal protein L29	17.7	2.33E+08	1.28E+08	8.42E+08	3.01E+08
44	236	<i>51702823</i>	60S ribosomal protein L8	28.0	5.69E+07	4.52E+07	8.37E+08	2.88E+08

➤ **tab1 Main:**

containing the list of all identified *proteins* and their according accession number, gene name, description, molecular weight, sequence coverage, number of peptides, number of PSMs and precursor area

by clicking on '+' symbol hidden information can be made visible by expanding the columns

Raw sample areas are normalized to account for different sample amounts loaded onto the MS. This allows comparison of protein amounts over different samples. Therefore, samples with high total sum are divided by a factor, whereas samples with low total area are multiplied by a linear factor such that all samples finally have the same total area sum after normalization.

each protein sequence coverage is hyperlinked to the according Detailed Coverage region in tab2

each # PSM is hyperlinked to the according Detailed PSM region in tab3

#	Accession	Description	MW[kDa]	Area	Norm. Area	Coverage	# Peptides	Unique Peptides	# PSMs	Area	Area	Area	
				20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_control_I_minus			control_M_minus			sample_I_plus			
				control_M_plus			sample_I_minus			sample_M_plus			
5	250	cont_P00761	Trypsin OS=Sus scrofa PE=1 SV=1	24.4	1.34E+10	5.80E+07	29.44%	14	145	2.05E+10	3.75E+10	4.23E+10	
6	774	cont_P15636	Protease 1 OS=Achromobacter lyticus PE=1 SV=1	68.1	3.24E+10	4.96E+07	17.92%	30	398	1.75E+10	1.99E+10	6.94E+09	
7	414	ENSEMBL:ENSBTAP0000002	(Bos taurus) 47 kDa protein	46.5	6.02E+07	1.44E+05	18.38%	9	16	3.78E+07	1.34E+10	1.10E+10	
8	249	269849769	Keratin, type I cytoskeletal 10	58.8	2.88E+10	4.93E+07	62.84%	69	352	2.47E+10	1.18E+10	1.05E+10	
9	264	238054406	Keratin, type II cytoskeletal 1	66.0	2.05E+10	3.18E+07	67.86%	99	84	1143	1.36E+09	6.23E+09	4.56E+09
10	153	cont_P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14	51.5	7.68E+09	1.63E+07	68.86%	51	14	262	3.26E+08	5.64E+09	4.43E+09
11	908	cont_P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16	51.2	7.68E+09	1.62E+07	63.85%	47	21	226	3.26E+08	5.64E+09	4.43E+09
12	50	cont_Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77	61.9	8.01E+09	1.39E+07	14.36%	16	7	128	4.66E+08	4.76E+09	4.12E+09
13	276	cont_P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B	60.0	1.08E+10	1.91E+07	54.08%	50	2	283	4.52E+08	3.92E+09	3.27E+09
14	121	cont_P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens G	65.4	6.15E+09	9.63E+06	74.65%	63	38	352	2.42E+08	3.54E+09	3.62E+09
15	785	547751	Keratin, type I cytoskeletal 17	48.1	6.48E+09	1.50E+07	40.51%	28	8	107	2.45E+08	3.54E+09	3.12E+09
16	203	311033484	Keratin, type I cytoskeletal 19	44.1	6.22E+09	1.55E+07	14.00%	7	0	27	2.35E+08	3.49E+09	3.07E+09
17	907	cont_P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE	62.0	1.58E+10	2.54E+07	80.42%	86	85	934	1.09E+09	3.37E+09	3.86E+09
18	864	cont_P42212	Green fluorescent protein OS=Aequorea victoria GN=GFP PE:	26.9	0.00E+00	0.00E+00	16.39%	3	0	5	0.00E+00	3.11E+09	3.91E+09
19	128	cont_Q9R0H5	Keratin, type I cytoskeletal 71 OS=Mus musculus GN=Krt71 I	57.3	2.83E+09	5.40E+06	4.01%	8	0	109	1.75E+08	3.09E+09	3.07E+09
20	816	cont_Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27	49.8	3.15E+09	6.87E+06	3.92%	8	0	102	1.59E+08	2.67E+09	1.61E+09
21	633	125799	Ig kappa chain V-III region NG9	10.7				0	0	0	2.48E+09	2.53E+09	
22	277	cont_P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A	60.0	5.54E+09	9.83E+06	56.03%	53	2	248	1.86E+08	2.31E+09	2.38E+09
23	428	cont_P48668	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C	60.0	5.54E+09	9.83E+06	54.26%	52	1	243	1.86E+08	2.31E+09	2.38E+09
24	573	5921173	Barrier-to-autointegration factor	10.1	1.53E+06	1.72E+04		0	0	0	2.25E+09	1.76E+09	
25	862	90110027	Keratin, type II cytoskeletal 8	53.7	5.41E+09	1.12E+07	13.66%	13	1	124	1.72E+08	1.97E+09	1.97E+09
26	947	143811411	Keratin, type II cytoskeletal 5	62.3	5.41E+09	9.17E+06	55.93%	56	33	282	1.72E+08	1.97E+09	1.97E+09
27	768	269849755	Keratin, type I cytoskeletal 13	49.6	1.96E+09	4.28E+06	9.17%	12	0	38	1.07E+08	1.63E+09	1.31E+09
28	512	125962	Prelamin-A/C	74.1	2.02E+06	3.04E+03	4.67%	2	2	2	2.11E+07	1.42E+09	3.33E+08
29	388	125083	Keratin, type I cytoskeletal 18	48.0	1.31E+09	3.05E+06	1.63%	1	0	4	9.30E+07	1.37E+09	1.11E+09
30	178	1350762	60S ribosomal protein L6	32.7	8.92E+07	3.10E+05	21.18%	6	6	10	6.96E+07	1.09E+09	3.76E+08
31	699	47117765	60S ribosomal protein L26	17.2	1.65E+08	1.14E+06	27.59%	5	1	12	8.37E+07	1.06E+09	3.57E+08
32	287	cont_Q01546	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KR	65.8	2.14E+09	3.36E+06	11.91%	17	0	64	1.21E+08	1.06E+09	1.21E+09
33	562	54039239	60S ribosomal protein L7a	30.0	1.65E+08	6.19E+05	18.80%	6	6	10	1.13E+08	1.02E+09	4.15E+08
34	641	81175191	60S ribosomal protein L5	34.3	1.55E+08	5.23E+05	23.57%	9	9	19	1.37E+08	9.69E+08	2.96E+08
35	265	22002063	60S ribosomal protein L4	47.7	1.50E+08	3.50E+05	12.88%	5	5	11	9.00E+07	9.42E+08	2.29E+08
36	346	52783206	Plasminogen activator inhibitor 1 RNA-binding protein	44.9	2.49E+08	6.10E+05	49.75%	22	22	46	1.48E+08	9.28E+08	1.81E+08
37	899	23396835	60S ribosomal protein L26-like 1	17.2	5.26E+07	3.63E+05	27.59%	5	1	10	3.28E+07	9.22E+08	3.47E+08
38	813	82654947	Keratin, type II cytoskeletal 4	57.3	1.57E+09	2.94E+06	11.42%	9	2	36	9.42E+07	8.97E+08	1.06E+09
39	793	51338637	60S ribosomal protein L23a	17.7	1.31E+08	8.40E+05	35.26%	6	6	17	1.28E+08	8.88E+08	2.59E+08
40	518	1174690	Lamina-associated polypeptide 2, isoforms beta/gamma	50.6	6.97E+06	1.53E+04	12.56%	4	0	4	8.81E+05	8.75E+08	1.42E+08
41	765	1174689	Lamina-associated polypeptide 2, isoform alpha	75.4	6.97E+06	1.00E+04	9.94%	5	1	5	8.81E+05	8.75E+08	1.42E+08
42	125	730640	40S ribosomal protein S19	16.1	2.95E+08	2.03E+06	22.76%	3	3	5	1.02E+08	8.75E+08	2.53E+08
43	961	1350706	60S ribosomal protein L29	17.7	2.33E+08	1.47E+06	9.43%	3	3	9	1.28E+08	8.42E+08	3.01E+08
44	236	51702823	60S ribosomal protein L8	28.0	5.69E+07	2.21E+05	13.23%	3	3	7	4.52E+07	8.37E+08	2.88E+08

this column shows the total number of peptides including peptides shared with homologue proteins

this column shows the total number of distinct peptides uniquely assigned to the according protein

➤ tab3 PSM Details

containing the list of all identified *PSMs (peptide spectrum matches)* and their related values

#	Accessions	Protein descriptions	20151009_QexHF2	20151009_QexHF2	20151009_QexHF2	20151009_QexHF2	Sequence	Amanda Score	Peakjuggler Area	Modifications	ptmRS: Best Site Probabilities
1	116241284	Chromobox protein homolog 3			X		KVEEAEPEEFVVEK	438.4	2E+06		
2	116241284	Chromobox protein homolog 3			X		VEEAEPEEFVVEK	266.6	7E+05		
3	116241284	Chromobox protein homolog 3			X		VEEAEPEEFVVEK	299.8	5E+05		
4	116241284	Chromobox protein homolog 3				X	KVEEAEPEEFVVEK	423.4	1E+06		
5	116241284	Chromobox protein homolog 3	X				VEEAEPEEFVVEK	211.9	7E+05		
6	116241284	Chromobox protein homolog 3		X			KVEEAEPEEFVVEK	493.2	2E+06		
7	116241284	Chromobox protein homolog 3		X			VEEAEPEEFVVEK	327.2	1E+06		
8	189047131	La-related protein 4			X		TNAALMNGRPFQK	292.4	7E+05	M6(Oxidation); M8(Oxidation)	M6(Oxidation): 100; M8(Oxidation): 100
9	189047131	La-related protein 4			X		SSGGSEHSTEGSVSLDGGQLNR	349.4	1E+06		
10	189047131	La-related protein 4			X		ETSTLQVEQNGDYGR	375.9	1E+06		
11	189047131	La-related protein 4			X		DLIEDSSVQK	180.1	1E+06		
12	189047131	La-related protein 4			X		ISRPHPSTAESK	161.0	7E+05		
13	189047131	La-related protein 4			X		ISRPHPSTAESK	239.0	3E+06		
14	189047131	La-related protein 4			X		NEDNGAPENSVEKPEKPEAR	434.9	2E+06		
15	189047131	La-related protein 4			X		SSPMVQVDEK	190.5	6E+05	M4(Oxidation)	M4(Oxidation): 100
16	189047131	La-related protein 4			X		SSPMVQVDEK	184.8	6E+05	M4(Oxidation)	M4(Oxidation): 100
17	189047131	La-related protein 4			X		HNPTVTGHQEQTYLQK	402.8	1E+06		
18	189047131	La-related protein 4			X		SSGGSEHSTEGSVSLDGGQLNR	325.6	9E+05		
19	189047131	La-related protein 4			X		SSGGSEHSTEGSVSLDGGQLNR	403.3	2E+06		
20	189047131	La-related protein 4			X		ETSTLQVEQNGDYGR	348.0	3E+06		
21	189047131	La-related protein 4			X		ETSTLQVEQNGDYGR	384.2	4E+06	N10(Deamidated)	N10(Deamidated): 99.59
22	189047131	La-related protein 4			X		MPGELVLENR	254.3	1E+07	M1(Oxidation)	M1(Oxidation): 100
23	189047131	La-related protein 4			X		DLIEDSSVQK	203.3	2E+07		
24	189047131	La-related protein 4			X		DGLNQTTIPVSPPTTKPSR	285.4	3E+06		
25	189047131	La-related protein 4			X		EPSSVLVQPLR	184.5	2E+07		
26	189047131	La-related protein 4			X		EIPETTPIEEVK	229.8	8E+05		
27	189047131	La-related protein 4			X		EIPETTPIEEVK	201.4	8E+05		
28	189047131	La-related protein 4			X		EYEVMYSSSCETIR	369.5	9E+05	M5(Oxidation); C10(Methylthio)	M5(Oxidation): 100
29	189047131	La-related protein 4			X		ASTASPCNNNINAATAVALQEPR	314.5	3E+06	C7(Methylthio)	
30	189047131	La-related protein 4			X		ASTASPCNNNINAATAVALQEPR	381.7	9E+05	C7(Methylthio)	
31	189047131	La-related protein 4			X		LTIDPDLILEVLR	264.9	1E+06		
32	189047131	La-related protein 4			X		SSGGSEHSTEGSVSLDGGQLNR	278.5	1E+06		
33	189047131	La-related protein 4			X		MPGELVLENR	262.6	2E+06	M1(Oxidation)	M1(Oxidation): 100

protein accession from used database

protein description from used database

'x' marks the identification

sequence of identified peptide
red highlighted amino acid indicates modification

probabilistic search engine identification score

precursor area

chemical or post-translational modification

site probability of modified residue (localization probability)

➤ **tab3 PSM Details**

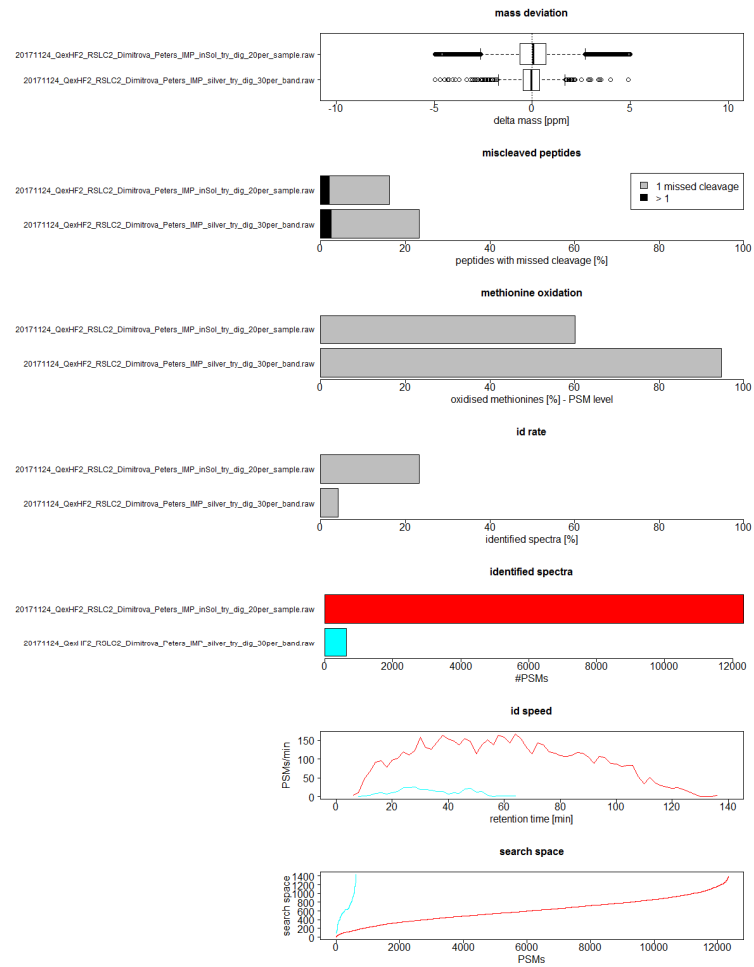
containing the list of all identified *PSMs (peptide spectrum matches)* and their related values

# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	ΔM [ppm]	Isolation Interference [%]	RT [min]	First Scan	Spectrum File
1	2	831.4165	1,661.8257	-0.68	47	80.49	14339	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	767.3683	1,533.7293	-1.70	19	97.59	16792	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	767.3696	1,533.7319	-0.02		97.67	18937	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_M_plus_50per_LysC.raw
1	2	831.4171	1,661.8270	0.06	32	80.73	15884	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_M_plus_50per_LysC.raw
	2	767.3691	1,533.7309	-0.66		99.12	20083	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_control_I_minus_50per_LysC.raw
1	2	831.4167	1,661.8262	-0.38	39	81.18	16598	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_control_M_minus_50per_LysC.raw
	2	767.3702	1,533.7332	0.85	7	98.00	19638	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_control_M_minus_50per_LysC.raw
1	2	784.8682	1,568.7292	-1.04		31.23	7167	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_glycine.raw
	3	720.9965	2,160.9748	-0.18	13	63.46	12398	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_glycine.raw
	2	848.8940	1,696.7807	2.01		70.96	13784	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_glycine.raw
	2	567.2877	1,133.5682	-0.26	38	71.56	13875	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_glycine.raw
1	3	437.2330	1,309.6845	-1.03	61	17.11	4152	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
1	2	655.3463	1,309.6854	-0.41	4	17.20	4172	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
2	3	783.0349	2,347.0902	-0.31		29.23	6334	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	568.2695	1,135.5318	1.60	27	39.16	7932	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	568.2687	1,135.5302	0.21	18	38.51	7829	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	940.9673	1,880.9273	1.25		43.05	8538	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	3	720.9964	2,160.9746	-0.26	24	63.19	11668	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	1,080.9910	2,160.9747	-0.25	11	63.28	11680	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	848.8918	1,696.7763	-0.58	2	70.55	12812	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	849.3848	1,697.7624	0.64		74.61	13497	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	587.3000	1,173.5927	-0.46	9	76.76	13822	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	567.2878	1,133.5683	-0.15	28	71.15	12899	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
1	3	699.3716	2,096.1002	0.94	29	87.01	15264	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	612.8507	1,224.6941	-0.43	28	94.29	16352	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	692.8666	1,384.7259	3.81	39	90.71	15830	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	692.8658	1,384.7244	2.75	22	91.26	15910	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	873.8385	1,746.6697	2.39		91.56	15959	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	3	787.0425	2,359.1131	0.07		125.41	20885	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw
	2	1,180.0599	2,359.1126	-0.13		125.45	20891	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_sample_I_plus_50per_LysC.raw

➤ tab 5

Quality Control plots:

- mass deviation
- missed cleavages
- methionine oxidation
- ID rate
- identified spectra
- ID speed
- search space
- correlation plots



➤ tab 6 Analysis summary

containing parameters used for database search
useful for materials & methods section of a manuscript

For peptide identification, the RAW-files were loaded into Proteome Discoverer (version 2.1.0.81, Thermo Scientific).

All hereby created MS/MS spectra were searched using MS Amanda v2.0.0.9849 (Dorfer V. et al., J. Proteome Res. 2014 Aug 1;13(8):3679-84).

For the 1st step search the RAW-files were searched against the human swissprot database, using following search parameters:

The peptide mass tolerance was set to ± 5 ppm and the fragment mass tolerance to 15 ppm.

The maximal number of missed cleavages was set to 2.

The result was filtered to 1% FDR on protein level using Percolator algorithm integrated in Thermo Proteome Discoverer.

A sub-database was generated for further processing.

For the 2nd step the RAW-files were searched against the created sub-database called subdb_20171124_QexHF2_RSLC2_Dimitrova_Peters_IMP_inSol_try_dig_20per_sample_and_band_hsSorrerin_Sf9_Ecoli_conta_step1.fasta (1,057 sequences; 782,301 residues).

The following search parameters were used:

Beta-methylthiolation on cysteine was set as a fixed modification, oxidation on methionine, deamidation on asparagine and glutamine, acetylation on lysine, phosphorylation on serine, threonine and tyrosine, methylation on lysine and arginine, di-methylation on lysine and arginine, tri-methylation on lysine, ubiquitinylation residue on lysine were set as variable modifications.

Monoisotopic masses were searched within unrestricted protein masses for tryptic enzymatic specificity.

The peptide mass tolerance was set to ± 5 ppm and the fragment mass tolerance to ± 15 ppm.

The maximal number of missed cleavages was set to 2.

The result was filtered to 1% FDR on peptide level using Percolator algorithm integrated in Thermo Proteome Discoverer.

The localization of the post-translational modification sites within the peptides was performed with the tool ptmRS (Taus T. et al., J. Proteome Res. 2011, 10, 5354-62).

Peptide areas have been quantified using PeakJuggler.

We also would like to draw attention to our online compilation of FAQs, which has proven helpful in better understanding of the mass spec result:

<http://cores.imp.ac.at/protein-chemistry/faqs/>

Please Notice This



Home > Protein Chemistry > FAQs

FAQs

- What is LC/MSMS?
- What is shotgun proteomics?
- What is # peptides?
- What is a protein group?
- What is Protein Inference?
- What is # unique peptides?
- What is # PSMs?
- What is a missed cleavage?
- What is MS Amanda Score?
- Which modifications can be identified?
- What are the concerns about mapping PTM sites?
- What can I do to increase the sequence coverage of my protein(s) of interest for mapping PTMs?
- What is ptmRS?
- How is the False-Discovery-Rate (FDR) calculated?
- What is the protein area?
- How is the normalization of the protein areas performed?
- What is m/z?
- What is MH+?
- What is search space?
- What is Isolation Interference [%]?
- What are GO terms?
- What is sequence coverage?
- Why are some protein areas written in bold and some not?
- What is match-between-runs (MBR)?
- I expected one single protein in the band we cut from the gel, but the result shows one hundred proteins. How come?
- I see quite a lot of keratins in my result list of identified proteins. Where do they come from?
- What is the detection limit and how many proteins can be detected in a typical proteomics analysis?
- Is it possible to distinguish between modifications that differ in decimal region of mass?
- I cannot find my protein of interest in the list of identified proteins. Does this mean it is not in the sample?
- I found some interesting and promising candidates (potential members of my protein complex or binding partners of my protein of interest) in the mass spec result. What can I do next as follow-up to confirm those proteins?
- How can I evaluate the quality of my data?
- What can I do if I cannot find the mass spec result files you sent me anymore?
- Can the raw data be accessed too?