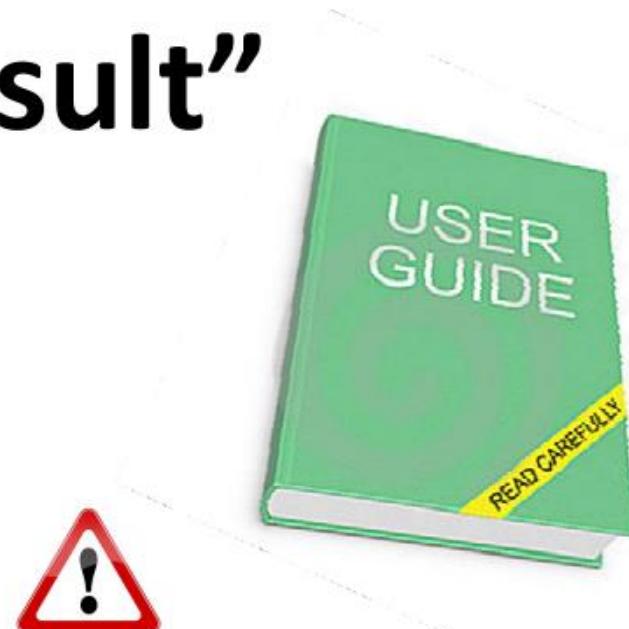
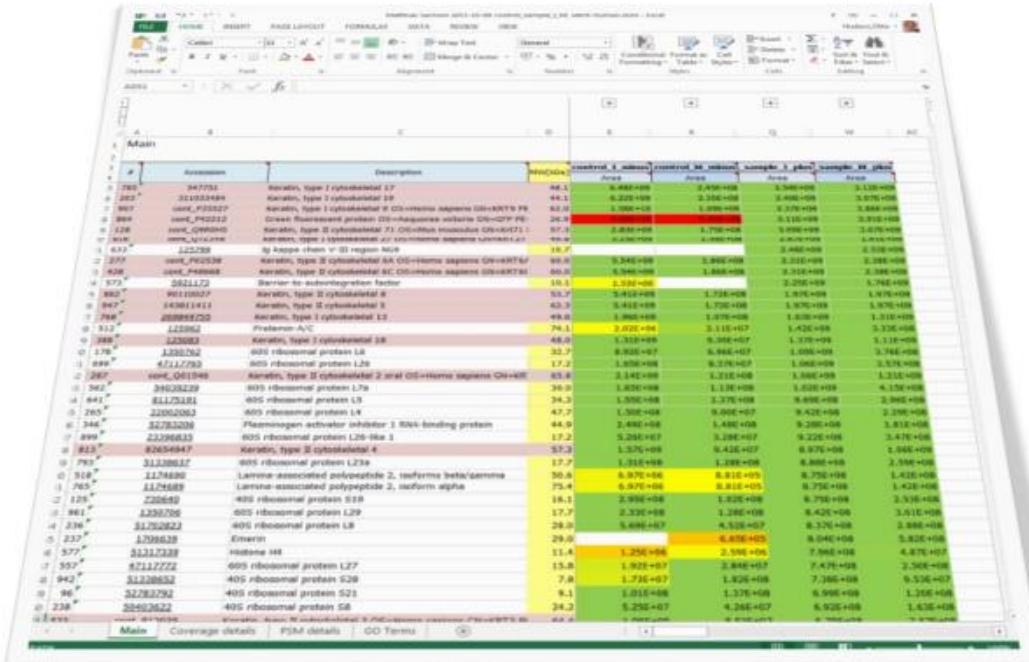


“How to read my .xlsm mass spec result”

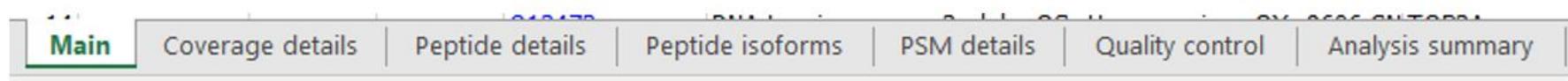


Please also visit our online compilation of FAQs.

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

The xlsm file is structured in 7 tabs

- **Main:** containing the list of all identified proteins
- **Coverage Details** showing the detailed sequence coverage of each identified protein
- **Peptide Details** displaying all identified peptides
- **Peptide Isoforms** showing isoforms of peptides
- **PSM Details** containing the list of all identified peptide spectrum matches (PSMs)
- **Quality Control** containing quality control graphs
- **Analysis Summary** containing parameters used for database search



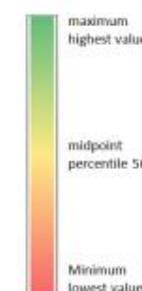
➤ tab1 Main: containing the list of all identified *proteins*
and their according accession number, description, molecular weight and precursor area

#	Accession	Description	MW[kDa]	control_I_minus				control_M_minus				sample_I_plus				sample_M_plus			
				Area	Area	Area	Area	Area	Area	Area	Area	Area	Area	Area	Area				
5	250	Trypsin OS=Sus scrofa PE=1 SV=1	24.4	1.34E+10	2.05E+10	3.75E+10	4.23E+10												
6	774	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_ENSEMBL:ENSTAP0000002	(Bos taurus) 47 kDa protein	46.5	6.02E+07	3.78E+07	1.34E+10	1.10E+10												
8	249	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	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	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	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	Keratin, type II cytoskeletal 68 OS=Homo sapiens GN=KRT68	60.0	1.08E+10	4.52E+08	3.92E+09	3.27E+09												
14	121	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	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_P42312 Green fluorescent protein OS=Aequorea victoria CN=CFP PE	36.9	0.000E+00	0.000E+00	0.000E+00	0.000E+00												
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_Q7Z3Y8 Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27	49.8	3.15E+09	1.59E+08	2.87E+09	1.61E+09												
21	633	125799 Ig kappa chain V-III region NG9	10.7			2.48E+09	2.43E+09												
22	277	cont_P02538 Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6F	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	5921173 Barrier-to-autointegration factor	10.1	1.52E+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	238849755 Keratin, type I cytoskeletal 13	49.6	1.96E+09	1.07E+08	1.63E+09	1.31E+09												
28	512	125962 Prelamin-A/C	74.1	2.02E+06	2.11E+07	1.42E+09	3.33E+08												
29	388	125083 Keratin, type I cytoskeletal 18	48.0	1.31E+09	9.30E+07	1.37E+09	1.11E+09												
30	178	1350762 60S ribosomal protein L6	32.7	8.92E+07	6.96E+07	1.09E+09	3.76E+08												
31	699	47117265 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=KRT2	65.8	2.14E+09	1.21E+08	1.06E+09	1.21E+09												
33	562	54039239 60S ribosomal protein L7a	30.0	1.65E+08	1.13E+08	1.02E+09	4.15E+08												
34	641	81175191 60S ribosomal protein L5	34.3	1.55E+08	1.37E+08	9.69E+08	2.96E+08												
35	265	22002063 60S ribosomal protein L4	47.7	1.50E+08	9.00E+07	9.42E+08	2.29E+08												
36	346	52783206 Plasminogen activator inhibitor 1 RNA-binding protein	44.9	2.49E+08	1.48E+08	9.28E+08	1.81E+08												
37	899	23396835 60S ribosomal protein L26-like 1	17.2	5.26E+07	3.28E+07	9.22E+08	3.47E+08												
38	813	02654947 Keratin, type II cytoskeletal 4	57.3	1.57E+09	9.42E+07	8.97E+08	1.06E+09												
39	793	51338637 60S ribosomal protein L23a	17.7	1.31E+08	1.28E+08	8.88E+08	2.59E+08												
40	518	1174690 Lamina-associated polypeptide 2, isoforms beta/gamma	50.6	6.97E+06	8.81E+05	8.75E+08	1.42E+08												
41	765	1174689 Lamina-associated polypeptide 2, isoform alpha	75.4	6.97E+06	8.81E+05	8.75E+08	1.42E+08												
42	125	730640 40S ribosomal protein S19	16.1	2.95E+08	1.02E+08	8.75E+08	2.53E+08												
43	961	1350206 60S ribosomal protein L29	17.7	2.33E+08	1.28E+08	8.42E+08	3.01E+08												
44	236	51702823 60S ribosomal protein L8	28.0	5.69E+07	4.52E+07	8.37E+08	2.88E+08												

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

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



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.

In order to be able to calculate some kind of ratio ('fold change') we perform imputation to empty values. This is also indicated by 'italic' expression of the value.

➤ **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]	20151009_QexHF2_RSLC8_Samwer_Gerlich_IMBA_onbead_try_dig_control_I_minus												control_M_minus			sample_I_plus		
				Area	Norm. Area	Coverage	# Peptides	Unique Peptides	# PSMs	Area	Area	Area	Area	Area	Area	Area	Area	Area	Area		
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	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	51	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_F42212	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 II 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-II region NG9	10.7				0	0	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	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+07	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	51338632	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	Lamine-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	Lamine-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

➤ **tab2 Coverage details:** showing the detailed **sequence coverage** of each protein
covered regions are highlighted in green
modified amino acids are highlighted in red

➤ Tab3 peptide details

Peptide details										
#	Contaminant	Unique	Master protein accessions	Master protein descriptions	Sequence	Modifications	Start in protein(s)	# Protein groups	# Proteins	# PSMs
1		✓	P36578	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=1	AAAAAAALQAK		00354	1	1	2
2		✓	Q14498	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1	AAAMANNLQK		00235	1	1	2
3		✓	P06753	Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1	AADAAEAVASLNR		00079	1	1	3
4		✓	Q9H922	Protein lin-28 homolog A OS=Homo sapiens OX=9606 GN=LIN28A PE=1	AADEPQLHAGAGICK	1×Methylthio [C14]	00031	1	1	1
5		✓	Q01995	Transgelin OS=Homo sapiens OX=9606 GN=TAGLN PE=1 SV=4	AAEDYGVIK		00100	1	1	1
6		✓	Q9H922	Protein lin-28 homolog A OS=Homo sapiens OX=9606 GN=LIN28A PE=1	AAEEAPEAPEDAAR		00016	1	1	2
7		✓	O95425	Supervillin OS=Homo sapiens OX=9606 GN=SIVL PE=1 SV=2	AAEFGEPTSEQTGTAAKG		01055	1	1	1
8		✓	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606	AAEVLNK		00128	1	1	1
9		✓	O75369	Filamin-B OS=Homo sapiens OX=9606 GN=FLNB PE=1 SV=2	AAAGSGELGVTMK	1×Oxidation [M11]	00481	1	1	3
10		✓	Q69YQ0	Cytospin-A OS=Homo sapiens OX=9606 GN=SPECCL1 PE=1 SV=2	AALAAATLEEYK		00556	1	1	1
11		✓	Q9H1K1	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial OS=Homo sapien	AAALADYK		00148	1	1	5
12		✓	P35637	RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS PE=1 SV=1	AAIDWFDFKK		00349	1	1	2
13		✓	Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606	GN=AALLELWLR		00450	1	1	1
14		✓	P62851	40S ribosomal protein S25 OS=Homo sapiens OX=9606 GN=RPS25 PE=1	AAALQELLSK		00086	1	1	3
15		✓	Q9P0K7	Ankyrin OS=Homo sapiens OX=9606 GN=RA114 PE=1 SV=2	AAAMTDAMVPR	2×Oxidation [M3; M7]	00777	1	1	1
16			P0D0Y2; A0M8Q6	Immunoglobulin lambda constant 2 OS=Homo sapiens OX=9606 GN=IGLAAAPSVLTEFPSSSEELQANK			00005; 00005	2	2	4
17		✓	P62910	60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1	AAQLAIR		00115	1	1	1
18		✓	Q6WCQ1	Myosin phosphatase Rho-interacting protein OS=Homo sapiens OX=9606	AAATEALGEK		00968	1	1	1
19		✓	P63316	Tropomodulin C, slow skeletal and cardiac muscles OS=Homo sapiens OX=96	AAVEQLTEEQK		00007	1	1	1
20		✓	Q01844	RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1	AAAEWFDFKK		00425	1	1	1
21	✓	✓	P01024; cont_Q2UVX4	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2 Comp	ACEPGVDDYYK	1×Methylthio [C2]	01536; 01534	2	2	6
22		✓	Q6WCQ1	Myosin phosphatase Rho-interacting protein OS=Homo sapiens OX=9606 ADCCDISR		1×Methylthio [C3]	00955	1	1	1
23			P35579; P35580	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4 Myosin-1ADEWLMK			00581; 00588	2	2	1
24			P35580; P35579	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3 Myosin ADEWLMK		1×Oxidation [M6]	00588; 00581	2	2	12
25			P35579; P35580	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4 Myosin-1ADFCIIHYAKG		1×Methylthio [C4]	00566; 00573	2	2	2

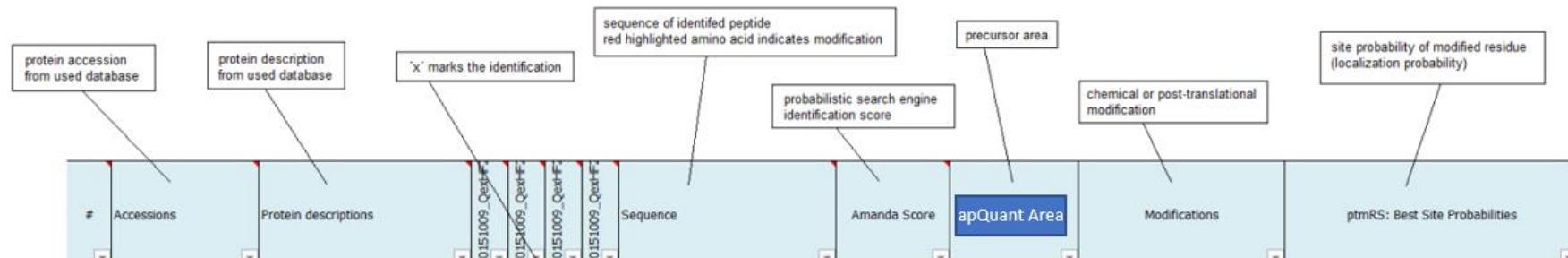
➤ Tab4 peptide isoforms

Peptide isoforms											
#	Contaminant	Unique	Master protein accessions	Master protein descriptions	Sequence	Modifications	Start in protein(s)	# Protein groups	# Proteins	# PSMs	Score
1		✓	P36578	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=1	AAAAAAALQAK		00354	1	1	1	411,3
2		✓	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing	AAADCGGPGQGASVGCTTEDGGVGCHR	1×Acetyl [N-Term]	00002	1	1	2	624,1
3		✓	O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapien	AAAEELLAR		00029	1	1	3	291,1
4		✓	P30260	Cell division cycle protein 27 homolog OS=Homo sapiens OX=9606 GN=CAAEGLMSLLR		1×Oxidation [M7(100)]	00457	1	1	1	406,2
5		✓	Q01780	Exosome component 10 OS=Homo sapiens OX=9606 GN=EXOSC10 PE=1	AAAQQAISVR		00759	1	1	4	370,3
6		✓	Q13523	Serine/threonine-protein kinase PRF4 homolog OS=Homo sapiens OX=9606 QTQSLR		1×Acetyl [N-Term]	00002	1	1	2	303,3
7		✓	Q96T51	RUN and FYVE domain-containing protein 1 OS=Homo sapiens OX=9606 AAAGLGGGSDGDTAR			00087	1	1	1	354,0
8		✓	Q14498	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1	AAAMNNLQK		00235	1	1	1	326,3
9		✓	Q15042	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens OX=9606	AAAMTPPEEELKR	1×Oxidation [M4(100)]	00904	1	1	2	267,2
10		✓	P31350	Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens OX=9606	AAAPGVDEPLL		00062	1	1	1	335,9
11		✓	Q99733	Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606	AAATAEPPDK		00147	1	1	4	331,0
12		✓	Q9NVG6	Mediator of RNA polymerase II transcription subunit 17 OS=Homo sapien	AAATIDSLASR		00444	1	1	2	331,6
13		✓	Q7KZF4	Staphylococcal nuclelease domain-containing protein 1 OS=Homo sapiens	AAATQPDAKDTPDEPWAFPAR		00063	1	1	1	303,4
14		✓	Q8N201	Integrator complex subunit 1 OS=Homo sapiens OX=9606 INTS1 PE=1	AAAVQADDVEVLK		00683	1	1	1	367,4
15		✓	Q9UBF2	Coatomer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1	AAAVSALAK		00489	1	1	1	259,3
16		✓	P55060	Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3	AAACDLVR	1×Methylthio [C3]	00385	1	1	6	201,0
17		✓	P13796	Plastin-2 OS=Homo sapiens OX=9606 GN=LCP1 PE=1 SV=6	AACLPLPGYR	1×Methylthio [C3]	00040	1	1	1	183,8
18		✓	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUIAADALEEQQR			00725	1	1	1	339,9
19		✓	P55060	Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3	AAADEFAFDENSEEYIRR		00356	1	1	6	380,2
20		✓	P49916	DNA ligase 3 OS=Homo sapiens OX=9606 GN=LIG3 PE=1 SV=2	AAADETCQTK	1×Methylthio [C7]	00923	1	1	1	262,3
21		✓	Q6P1J9	Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1	AADEVIAEAK		00127	1	1	5	323,8

> tab5 PSM Details

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

#	Accessions	Protein descriptions	20151009_QexA	20151009_QexA	20151009_QexA	20151009_QexA	Sequence	Amanda Score	apQuant Area	Modifications	ptmRS: Best Site Probabilities
1	116241284	Chromobox protein homolog 3		X	KVEEAEPPEEVVKEK			438.4	2E+06		
2	116241284	Chromobox protein homolog 3		X	VKEEAEPPEEVVKEK			266.6	7E+05		
3	116241284	Chromobox protein homolog 3		X	VKEEAEPPEEVVKEK			299.8	5E+05		
4	116241284	Chromobox protein homolog 3		X	VKEEAEPPEEVVKEK			423.4	1E+06		
5	116241284	Chromobox protein homolog 3	X		VKEEAEPPEEVVKEK			211.9	7E+05		
6	116241284	Chromobox protein homolog 3	X		VKEEAEPPEEVVKEK			493.2	2E+06		
7	116241284	Chromobox protein homolog 3	X		VKEEAEPPEEVVKEK			327.2	1E+06		
8	189047131	La-related protein 4		X	TNAAAANMGRFFQK			292.4	7E+05	M6(Oxidation); M8(Oxidation)	M6(Oxidation): 100; M8(Oxidation): 100
9	189047131	La-related protein 4		X	SSGGSEHSTEGSVSLGDGQLNR			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	ISRPHPDSTAESK			161.0	7E+06		
13	189047131	La-related protein 4		X	ISRPHPDSTAESK			239.0	3E+06		
14	189047131	La-related protein 4		X	NEDNGAPENSVKPKHEKPEAR			434.9	2E+06		
15	189047131	La-related protein 4		X	SSP M VQVDEK			190.5	6E+06	M4(Oxidation)	M4(Oxidation): 100
16	189047131	La-related protein 4		X	SSP M VQVDEK			184.8	6E+06	M4(Oxidation)	M4(Oxidation): 100
17	189047131	La-related protein 4		X	HNPVTIGHQETTYLQK			402.8	1E+06		
18	189047131	La-related protein 4		X	SSGGSEHSTEGSVSLGDGQLNR			325.6	9E+06		
19	189047131	La-related protein 4		X	SSGGSERHSSTEGSVSLGDGQLNR			403.3	2E+06		
20	189047131	La-related protein 4		X	ETSTLQVEQNGDYGR			348.0	3E+06		
21	189047131	La-related protein 4		X	ETSTLQVEQ N GDYGR			384.2	4E+06	N10(Deamidated)	N10(Deamidated): 99.59
22	189047131	La-related protein 4		X	M PGEVLLENR			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	DGLNQTIIIFVSPPPSTIKPSR			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+06		
27	189047131	La-related protein 4		X	EIPETTPIEEVK			201.4	8E+06		
28	189047131	La-related protein 4		X	EYEV M YSSCETTR			369.5	9E+05	M5(Oxidation); C10(Methylthio)	M5(Oxidation): 100
29	189047131	La-related protein 4		X	ASTASP C NNNNINAATAVALQEPR			314.5	3E+06	C7(Methylthio)	
30	189047131	La-related protein 4		X	ASTASP C NNNNINAATAVALQEPR			381.7	9E+05	C7(Methylthio)	
31	189047131	La-related protein 4		X	LTTDDDLILEVLN			264.9	1E+06		
32	189047131	La-related protein 4		X	SSGGSEHSTEGSVSLGDGQLNR			278.5	1E+06		
33	189047131	La-related protein 4		X	M PGEVLLENR			262.6	2E+06	M1(Oxidation)	M1(Oxidation): 100

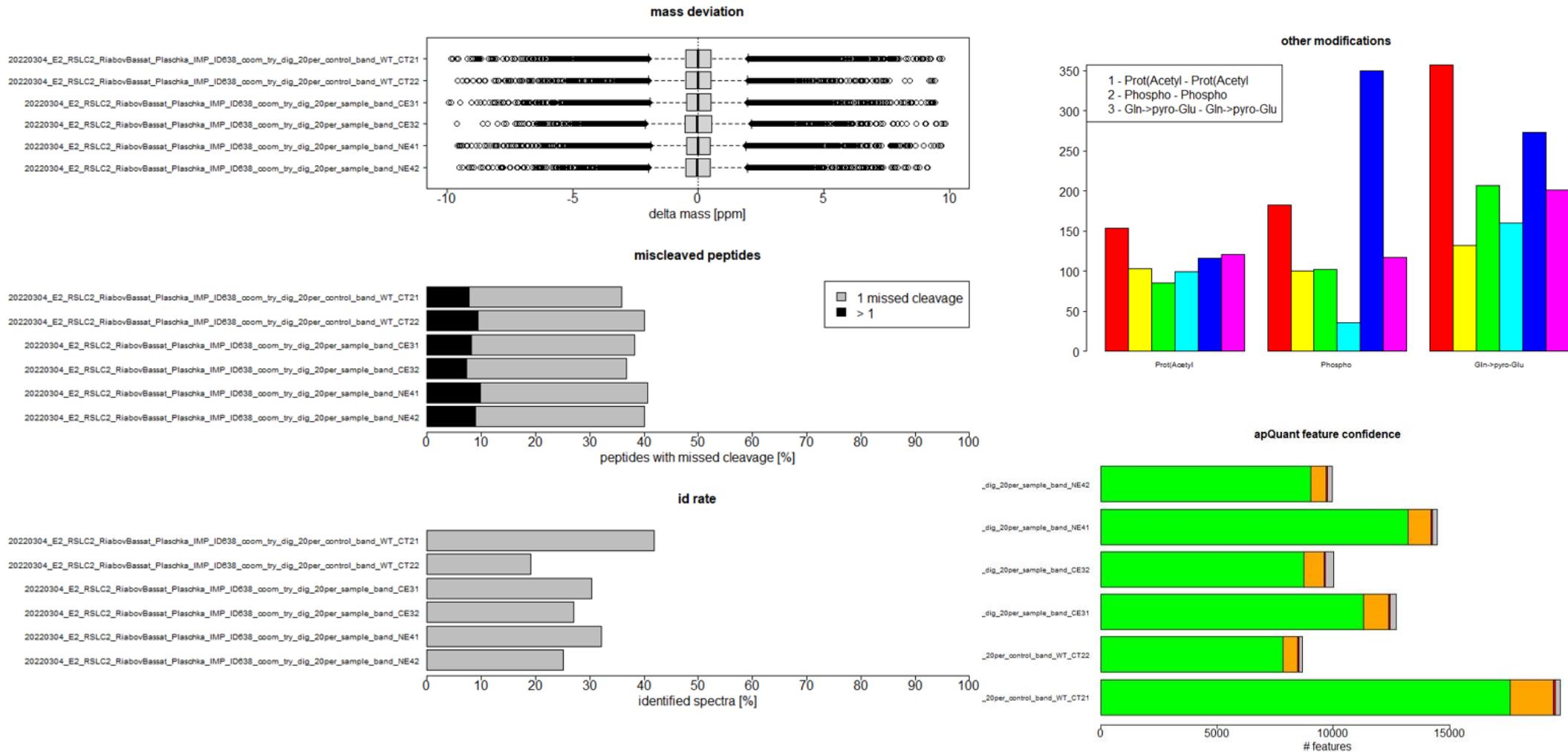


➤ tab5 PSM Details

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	720.0965	2,160.0718	-0.18	13	63.16	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	720.0964	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 6 Quality Control



➤ Analysis Summary

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

Analysis summary

For peptide identification, the RAW-files were loaded into Proteome Discoverer (version 2.5.0.400, Thermo Scientific).

All hereby created MS/MS spectra were searched using MS Amanda v2.0.0.16129 (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 databases ID635_GFP.fasta (1 sequences; 247 residues), ID635_SART3.fasta (1 sequences; 963 residues), uniprot_reference_human_2021-11-19.fasta (20 521 sequences; 11 394 277 residues) and PD_Contaminants_2014_11_updated_w_IGGs_and_TAGS_v17_tagsremoved.fasta , using following search parameters:

The peptide mass tolerance was set to ± 10 ppm and the fragment mass tolerance to ± 10 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-databases called ID635_GFP.fasta (1 sequences; 247 residues), ID635_SART3.fasta (1 sequences; 963 residues), subdb_20220301_E2_RSLC2_Rothe_Plasczka_IMP_ID635_2bands_inclwashes_step1.fasta (411 sequences; 285 594 residues).

The following search parameters were used:

Beta-methylthiolation on cysteine was set as a fixed modification, oxidation on methionine, phosphorylation on serine, threonine and tyrosine, deamidation on asparagine and glutamine, pyro-glu from q on peptide N-terminal glutamine, acetylation on protein N-Terminus were set as variable modifications.

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

The peptide mass tolerance was set to ± 10 ppm and the fragment mass tolerance to ± 10 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.

Additional high quality filtering by setting a minimum MS Amanda Score of 150 on PSM level was applied.

Proteins were filtered to be identified by a minimum of 2 PSMs in at least 1 sample.

The corresponding sample submission form is located here:

<https://ms-submission.imp.ac.at>Status?projectId=635>

This result file and the associated PD files are located here:

\\storage.imp.ac.at\groups\massspec\masarchive\Projects\projects 2022\IMP\Plasczka\Rothe\2022-03-02_ID635

