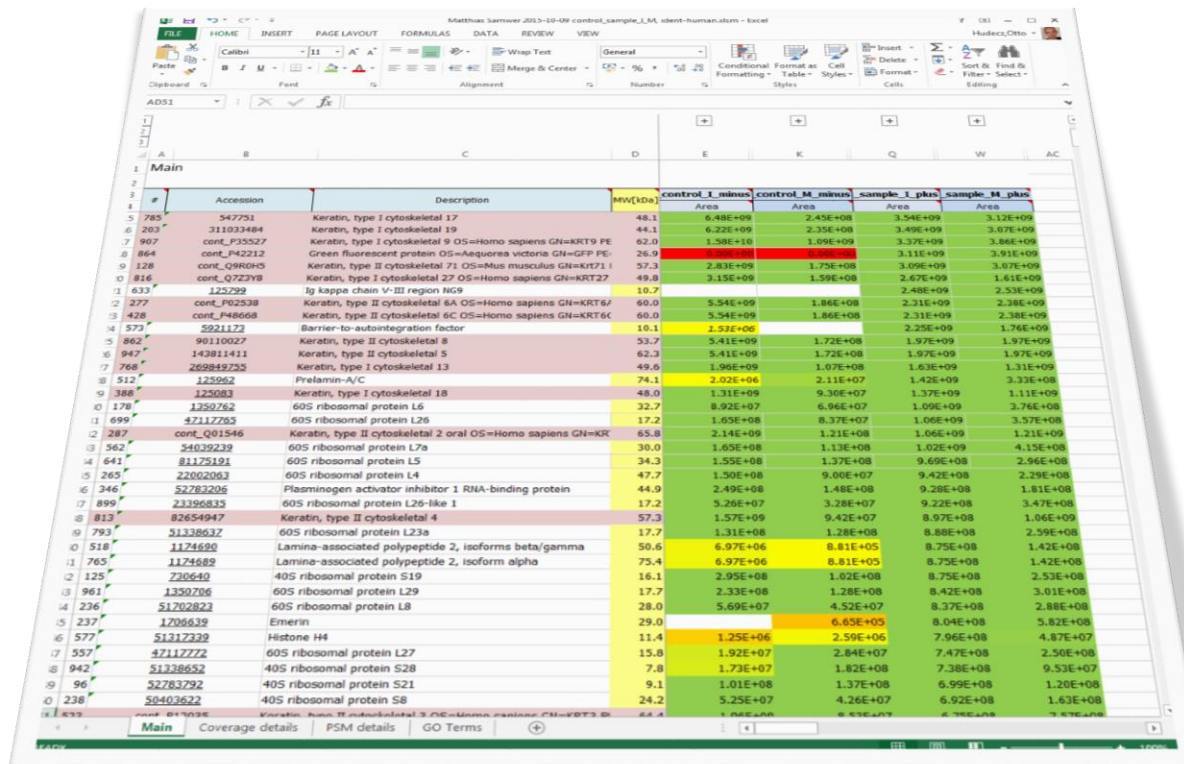


# Mass Spectrometry

## How to read your mass spectrometry result



#	Accession	Description	MW [Da]	control_1_minus Area	control_M_minus Area	sample_1_plus Area	sample_M_plus Area
5	S47751	Keratin, type I cytoskeletal 17	48.1	6.48E+09	2.45E+08	3.54E+09	3.12E+09
6	31103448	Keratin, type I cytoskeletal 19	44.1	6.22E+09	2.35E+08	3.49E+09	3.07E+09
7	cont_F35027	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE	42.0	1.58E+10	1.69E+09	3.37E+09	3.84E+08
8	cont_P42212	Green fluorescent protein OS=Aequorea victoria GN=GFP PE	26.9	1.08E+08	1.49E+08	3.11E+09	3.91E+09
9	cont_Q9R0H5	Keratin, type II cytoskeletal 71 OS=Mus musculus GN=KRT71 I	57.3	2.83E+09	1.75E+08	3.05E+09	3.07E+09
10	cont_Q72Y98	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27	49.8	3.15E+09	1.59E+08	2.67E+09	1.61E+09
11	125299	Ig kappa chain V-III region IG9	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_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
14	5921173	Barrier-to-autointegration factor	10.1	1.53E+06		2.25E+09	1.76E+09
15	90110027	Keratin, type II cytoskeletal 8	33.7	5.41E+09	1.72E+08	1.97E+09	1.97E+09
16	143811411	Keratin, type II cytoskeletal 5	62.3	9.41E+09	1.72E+08	1.97E+09	1.97E+09
17	269849255	Keratin, type I cytoskeletal 13	49.6	1.90E+09	1.07E+08	1.63E+09	1.31E+09
18	125062	Prelamin-A/C	74.1	2.02E+06	2.11E+07	1.42E+09	2.33E+08
19	125083	Keratin, type I cytoskeletal 18	48.0	1.31E+09	9.30E+07	1.37E+09	1.11E+09
20	1350762	60S ribosomal protein L6	22.7	8.92E+07	6.96E+07	1.09E+09	3.76E+08
1	699	60S ribosomal protein L28	17.2	1.65E+08	8.37E+07	1.06E+09	3.37E+08
2	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
3	34039239	60S ribosomal protein L7a	30.0	1.65E+08	1.13E+08	1.02E+09	4.15E+08
4	81175191	60S ribosomal protein L5	34.3	1.55E+08	1.37E+08	9.69E+08	2.96E+08
5	22002063	60S ribosomal protein L4	47.7	1.50E+08	9.00E+07	9.42E+08	2.29E+08
6	52783206	Plasminogen activator inhibitor 1 RNA-binding protein	44.9	2.49E+08	1.48E+08	9.28E+08	1.81E+08
7	23390833	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	51338632	60S ribosomal protein L23a	17.7	1.31E+08	1.28E+08	8.88E+08	2.59E+08
10	1124460	Lamina-associated polypeptide 2, isoforms beta/gamma	50.6	6.97E+06	8.81E+05	8.75E+08	1.42E+08
11	1124689	Lamina-associated polypeptide 2, isoform alpha	75.4	6.97E+06	8.81E+05	8.75E+08	1.42E+08
12	125	40S ribosomal protein S19	16.1	2.95E+08	1.02E+08	8.75E+08	2.53E+08
13	1350706	60S ribosomal protein L29	17.7	2.33E+08	1.28E+08	8.42E+08	3.01E+08
14	51702823	60S ribosomal protein L8	28.0	5.69E+07	4.52E+07	8.37E+08	2.88E+08
15	1708639	Emerin	29.0		6.65E+05	8.04E+08	5.82E+08
16	51312339	Histone H4	11.4	1.25E+06	2.59E+06	7.06E+08	4.87E+07
17	557	60S ribosomal protein L27	15.8	1.92E+07	2.84E+07	7.47E+08	2.50E+08
18	51338652	40S ribosomal protein S28	7.8	1.73E+07	1.82E+08	7.38E+08	9.53E+07
19	52783792	40S ribosomal protein S21	9.1	1.01E+08	1.37E+08	6.99E+08	1.20E+08
20	50403622	40S ribosomal protein S8	24.2	5.25E+07	4.26E+07	6.92E+08	1.63E+08





➤ **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 average of the peak area of the top three precursors and is a semi-quantitative value reflecting the protein abundance

contaminants are marked by color and by prefix cont\_

#	Accession	Description	MW[kDa]	control_I_minus Area	control_M_minus Area	sample_I_plus Area	sample_M_plus Area
5	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	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_ENSEMBL:ENSBTAP0000002	(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 125799	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 5921173	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 269849755	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 47117765	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 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 82654947	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 1350706	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

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.

➤ **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

Norm. Area: areas are normalized to protein sequence length

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	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	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_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 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-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		TNAALMNMGRPFQK	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+06		
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+06	M4(Oxidation)	M4(Oxidation): 100
16	189047131	La-related protein 4			X		SSPMVQVDEK	184.8	6E+06	M4(Oxidation)	M4(Oxidation): 100
17	189047131	La-related protein 4			X		HNPTVTGQHQEQTYLQK	402.8	1E+06		
18	189047131	La-related protein 4			X		SSGGSEHSTEGSVSLDGGQLNR	325.6	9E+06		
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+06		
27	189047131	La-related protein 4			X		EIPETTPIEEVK	201.4	8E+06		
28	189047131	La-related protein 4			X		EYEVMYSSSCETTR	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_I_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





future plans:

tab 5

## Quality Control plots

