

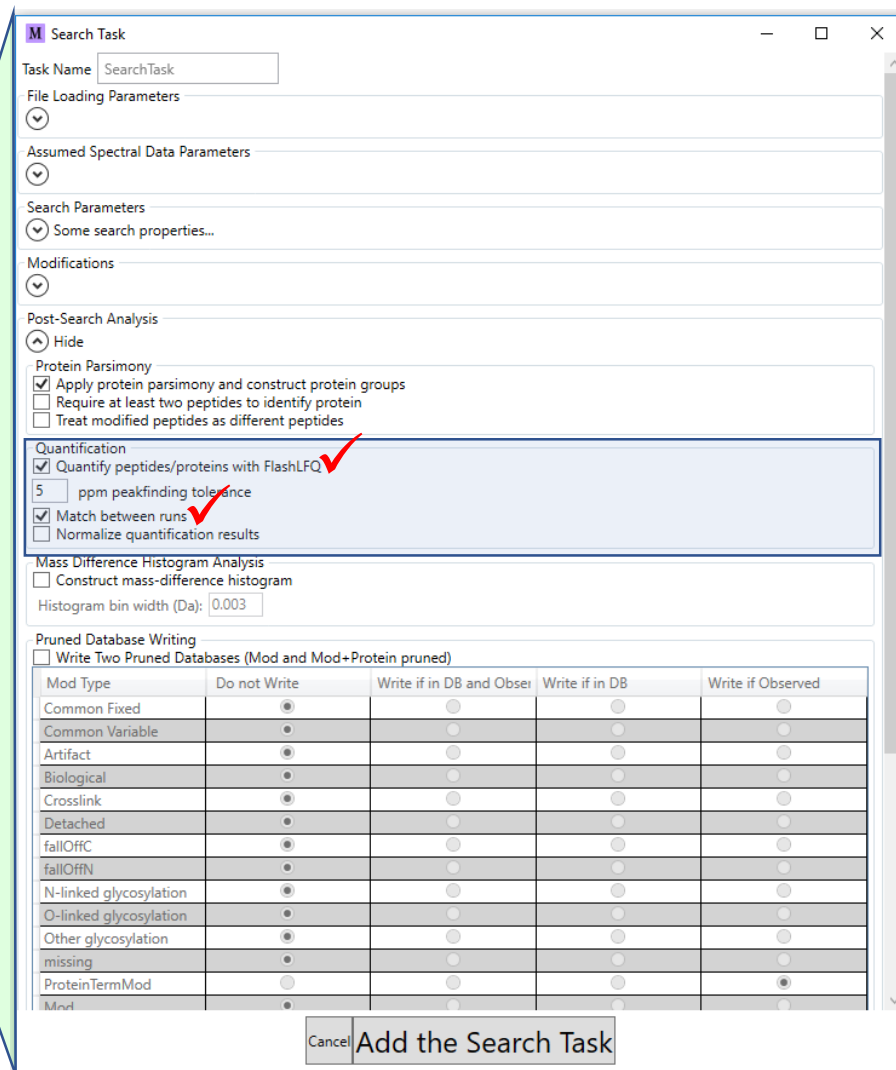
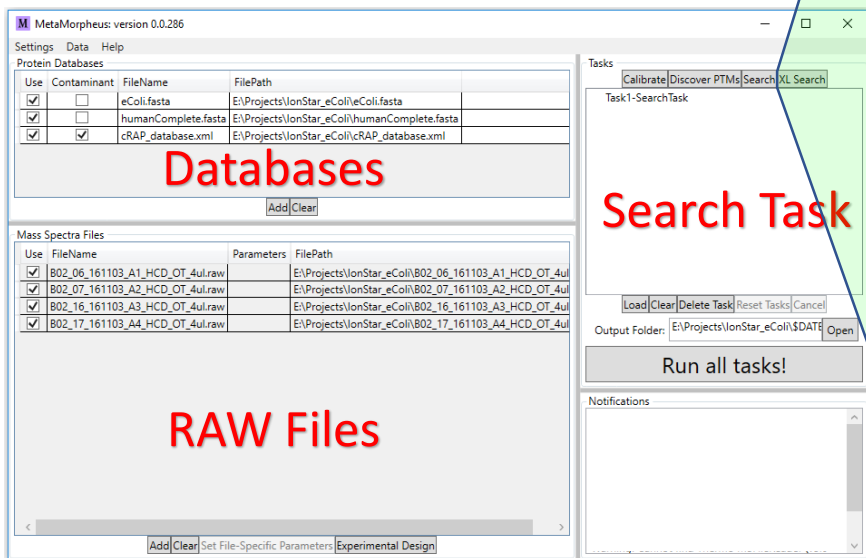
LFQ with FlashLFQ in
MetaMorpheus

Modes of Quantification

- Easy Peptide/Protein LFQ
- Advanced Protein LFQ with Fraction and Biorep Normalization

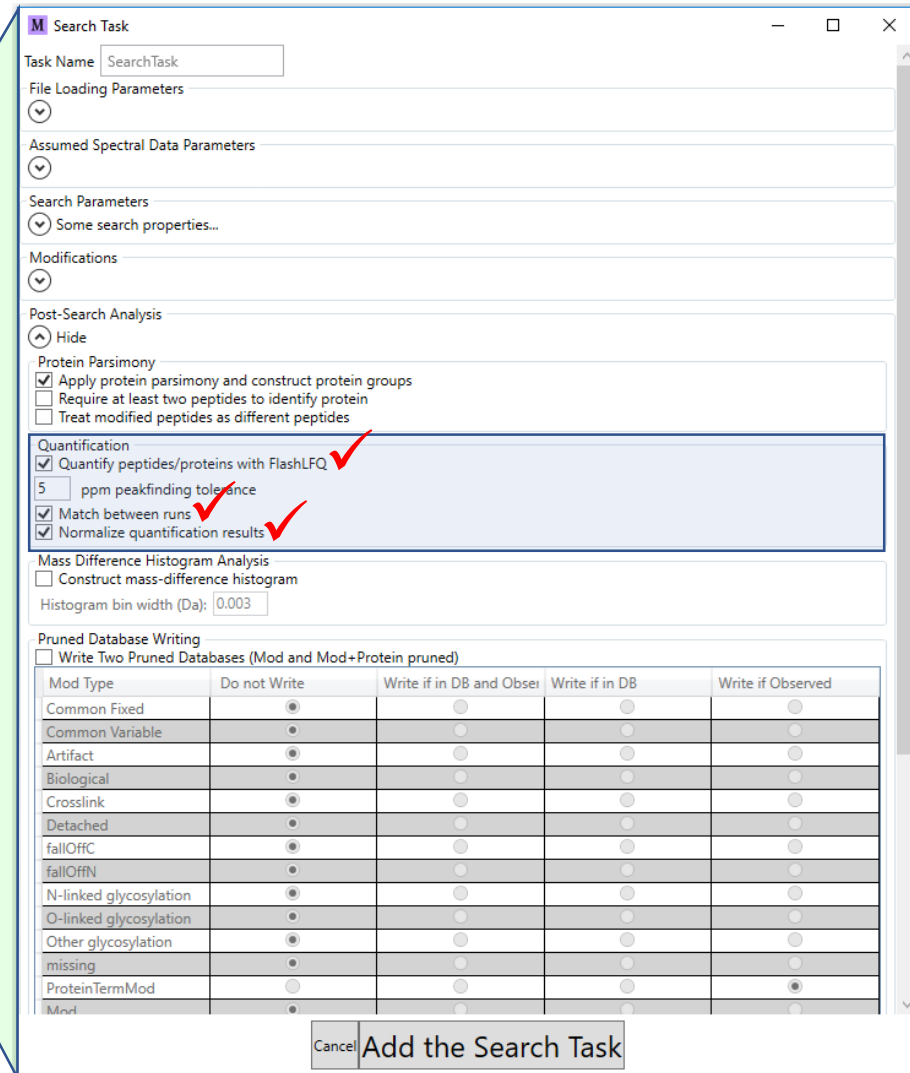
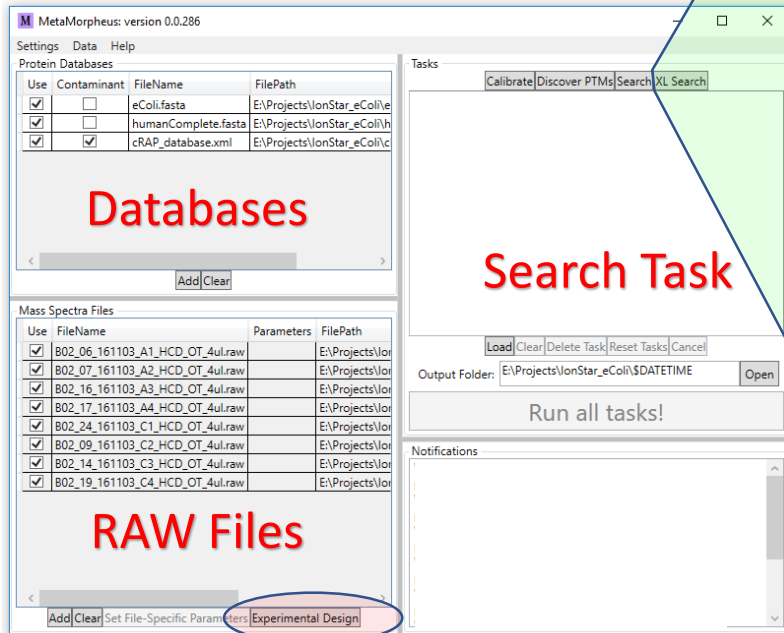
Easy Peptide/Protein Lfq

- Add databases and RAW files to MetaMorpheus
- Select 'Search Task'
- Open Post-Search Analysis
- Check 'Quantify peptides/proteins with FlashLfq'
- Check 'Match between runs' (Optional)
- Click 'Add the Search Task'
- Click 'Run all tasks!'



Advanced Peptide/Protein Lfq

- Add databases and RAW files to MetaMorpheus
- Select 'Search Task'
- Open Post-Search Analysis
- Check 'Quantify peptides/proteins with FlashLfq'
- Check 'Match between runs' (Optional)
- Check 'Normalize quantification results'
- Click 'Add the Search Task'
- Click 'Experimental Design' (See next slide)
- Click 'Run all tasks!'



MetaMorpheus: version 0.0.286

Settings Data Help

Protein Databases

Use	Contaminant	FileName	FilePath
<input checked="" type="checkbox"/>	<input type="checkbox"/>	eColi.fasta	E:\Projects\IonStar_eColi\...
<input checked="" type="checkbox"/>	<input type="checkbox"/>	humanComplete.fasta	E:\Projects\IonStar_eColi\h...
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	cRAP_database.xml	E:\Projects\IonStar_eColi\c...

Add Clear

Mass Spectra Files

Use	FileName	Parameters	FilePath
<input checked="" type="checkbox"/>	B02_06_161103_A1_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_07_161103_A2_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_16_161103_A3_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_17_161103_A4_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_24_161103_C1_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_09_161103_C2_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_14_161103_C3_HCD_OT_4ul.raw		E:\Projects\lor...
<input checked="" type="checkbox"/>	B02_19_161103_C4_HCD_OT_4ul.raw		E:\Projects\lor...

Add Clear Set File-Specific Parameters Experimental Design

Open 'Experimental Design'

Experimental Design

FileName	Condition	Biorep	Fraction	Techrep
B02_06_161103_A1_HCD_OT_4ul				
B02_07_161103_A2_HCD_OT_4ul				
B02_16_161103_A3_HCD_OT_4ul				
B02_17_161103_A4_HCD_OT_4ul				
B02_24_161103_C1_HCD_OT_4ul				
B02_09_161103_C2_HCD_OT_4ul				
B02_14_161103_C3_HCD_OT_4ul				
B02_19_161103_C4_HCD_OT_4ul				

Save Experimental Design Cancel

Set values for Condition, Biorep, Fraction & Techrep

Experimental Design

FileName	Condition	Biorep	Fraction	Techrep
B02_06_161103_A1_HCD_OT_4ul	A	1	1	1
B02_07_161103_A2_HCD_OT_4ul	A	2	1	1
B02_16_161103_A3_HCD_OT_4ul	A	3	1	1
B02_17_161103_A4_HCD_OT_4ul	A	4	1	1
B02_24_161103_C1_HCD_OT_4ul	C	1	1	1
B02_09_161103_C2_HCD_OT_4ul	C	2	1	1
B02_14_161103_C3_HCD_OT_4ul	C	3	1	1
B02_19_161103_C4_HCD_OT_4ul	C	4	1	1

Save Experimental Design Cancel

MetaMorpheus Search Results

MetaMorpheus: version 0.0.286

Settings Data Help

Protein Databases

Use	Contaminant	FileName	FilePath
<input checked="" type="checkbox"/>	<input type="checkbox"/>	eColi.fasta	E:\Projects\IonStar_eColi\eColi.fasta
<input checked="" type="checkbox"/>	<input type="checkbox"/>	humanComplete.fasta	E:\Projects\IonStar_eColi\humanComplete.fasta
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	cRAP_database.xml	E:\Projects\IonStar_eColi\cRAP_database.xml

Mass Spectra Files

Use	FileName	Parameters	FilePath
<input checked="" type="checkbox"/>	B02_06_161103_A1_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_06_161103_
<input checked="" type="checkbox"/>	B02_07_161103_A2_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_07_161103_
<input checked="" type="checkbox"/>	B02_16_161103_A3_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_16_161103_
<input checked="" type="checkbox"/>	B02_17_161103_A4_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_17_161103_
<input checked="" type="checkbox"/>	B02_24_161103_C1_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_24_161103_
<input checked="" type="checkbox"/>	B02_09_161103_C2_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_09_161103_
<input checked="" type="checkbox"/>	B02_14_161103_C3_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_14_161103_
<input checked="" type="checkbox"/>	B02_19_161103_C4_HCD_OT_4ul.raw		E:\Projects\IonStar_eColi\B02_19_161103_

Tasks

Calibrate Discover PTMs Search XL Search

- T Task1-SearchTask: [redacted] Done!
- F SearchTaskconfig.toml
- C Individual Spectra Files: [redacted] Done!
 - C B02_06_161103_A1_HCD_OT_4ul.raw Done!
 - C B02_07_161103_A2_HCD_OT_4ul.raw Done!
 - C B02_16_161103_A3_HCD_OT_4ul.raw Done!
 - C B02_17_161103_A4_HCD_OT_4ul.raw Done!
 - C B02_24_161103_C1_HCD_OT_4ul.raw Done!
 - C B02_09_161103_C2_HCD_OT_4ul.raw Done!
 - C B02_14_161103_C3_HCD_OT_4ul.raw Done!
 - C B02_19_161103_C4_HCD_OT_4ul.raw Done!
- F aggregatePSMs.psmstsv
- F forPercolator.tsv
- F aggregatePeptides.psmstsv
- F aggregateProteinGroups.tsv
- F aggregateQuantifiedPeaks.tsv
- F aggregateQuantifiedPeptidesBaseSequences.tsv
- F aggregateQuantifiedPeptidesFullSequences.tsv
- F results.txt
- F prose.txt
- T All Task Results: [redacted]

Output Folder: E:\Projects\IonStar_eColi\2018-08-14-11-32-57 Open

Run all tasks!

Notifications

- Protein Groups Quantified
- Peptides Quantified by Base Sequence
- Peptides Quantified by Full Sequence
- Folder Containing Search Results

aggregateQuantifiedPeptidesFullSequences.tsv

Note: Modifications

Sequence	Protein Groups	Gene Names	Organism
[UniProt:N-acetylalanine]ASDRPASDQMHWK	UNDEFINED		
[UniProt:N-acetylalanine]ASQNRDPAATVAAAR	000762	UBE2C	Homo sapiens
[UniProt:N-acetylmethionine]M[Common Variable]	UNDEFINED		
[UniProt:N-acetylmethionine]MDC[Common Fixed]	UNDEFINED		
[UniProt:N-acetylmethionine]MVNPTVFFDIAVDG	UNDEFINED		
[UniProt:N-acetyls erine]S[UniProt:Phosphoserine]	P63165	SUMO1	Homo sapiens
[UniProt:N-acetyls erine]SDQELKPTIEDLGGDK	P63165	SUMO1	Homo sapiens
[UniProt:N-acetyls erine]VNIPTVFFDIAVDGPELGR	UNDEFINED		
AAAAAAAAAAAAAAAAAGAGAGAK	P25911	SLC12A2	Homo sapiens
AAAAAAAAAKNGSSGK	C94543	PHOX2B	Homo sapiens
AAAAAAAAAVSR	A0DA6RYC7[Q5ZF93]-CNTF[ZFF]		Homo sapiens
AAAAAAAAAQAK	P36578	RPL4	Homo sapiens
AAAAADPNAAWAAAYSHYQQPPGVPGPAPAPA[Q2945]	KHSRP	Homo sapiens	
AAAAALSQDQSLGER	Q8WUQ7	Homo sapiens	
AAAAAAGGGVLGAKKEK	ABN1H7	UNC119B	Homo sapiens
AAAAAWEPPSNGTAR	Q8P258	RCC2	Homo sapiens
AAAAALGQLFGM[Common Variable:Oxidation of N MQDZP4]	BCAT2	Homo sapiens	
AAAAAATATTAPPPEGAPGPPGVNHLVPVTLFGTVK	OSUPT8	Homo sapiens	
AAAAAGASPSRGGDAAVSEAPGPR	P52701	MSH6	Homo sapiens
AAAAASAEAGIAITGTEDSDALK	P5M04	Homo sapiens	
AAAAASAEAGIATGTEGERSDDALK	Q5VWC4	Homo sapiens	
AAAAVAAAASSC[Common Fixed:Carbamidomethyl Q9NRL3]	STRN4	Homo sapiens	
AAADEWDER	WISSP07	msyB	Escherichia coli
AAADSDNLDPLMNPHIR	Q95159	ZFP11	Homo sapiens
AAADVQLR	C3S177	dsbA	Escherichia coli
AAAAEAAEKAR	Q0UNF1	MAGED2	Homo sapiens
AAAEEDVNFIFDQK	ESPQY2[Q5NQP]-PFDN4[PFDN4]	Homo sapiens	
AAAEHIIIPR	Q55511	TD2	Homo sapiens
AAAEELLAR	Q15357	INPPL1	Homo sapiens
AAAEGLMSLLR	P30260	CDC27	Homo sapiens
AAAEQASVR	Q01780	EXD5C10	Homo sapiens
AAAEVAGQVYK	P92786	TRFC	Homo sapiens
AAAEVNDQGLDQK	P07954	FIH	Homo sapiens
AAAEFEGENETVIVVK	C8Y490	TLN1	Homo sapiens
AAAFEGULPASQIDR	C3S187	rplJ	Escherichia coli
AAAFELQIK	Q94826	TOMM70	Homo sapiens
AAAFPPGFSIEK	Q9HY92	RPF1	Homo sapiens
AAAGAAATHLEVAR	Q96552	PIGS	Homo sapiens
AAAGEDYKAD[Common Fixed:Carbamidomethyl P23381]	WARS	Homo sapiens	
AAAGFADDDC[Common Fixed:Carbamidomethyl P35221]	CTNNA1	Homo sapiens	

Base Peptide Peak Intensity by Filename										Method of Quantification									
Intensity_B02_06_161010_A1	Intensity_B02_07_161010_A2	Intensity_B02_16_161010_A3	Intensity_B02_17_161010_A4	Intensity_B02_24_161010_C1	Intensity_B02_09_161010_C2	Intensity_B02_14_161010_C3	Intensity_B02_19_161010_C4	Intensity_B02_06_161010_3_A1_HCD_OT_Aul	Intensity_B02_07_161010_3_A2_HCD_OT_Aul	Intensity_B02_16_161010_3_A3_HCD_OT_Aul	Intensity_B02_17_161010_3_A4_HCD_OT_Aul	Intensity_B02_24_161010_3_C1_HCD_OT_Aul	Intensity_B02_09_161010_3_C2_HCD_OT_Aul	Intensity_B02_14_161010_3_C3_HCD_OT_Aul	Intensity_B02_19_161010_3_C4_HCD_OT_Aul				
2958436	3357256	300362	3031378	3056672	2876728	2702817	3051927	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
5049784	5180823	5428400	5118106	5067962	4688841	5203300	4431331	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1312574	798689	1891279	2390753	1118747	2742391	1497020	1590447	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
476762	0	672927	0	700886	0	769758	0	MS/MS	NotDetected	MS/MS	NotDetected	MS/MS	NotDetected	MS/MS	NotDetected				
4817699	5078744	6163723	8840746	5789679	8040549	7162674	6089070	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
3377474	3539174	3699109	3748185	3598145	3072051	3060495	3593864	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
2160655	2363532	3480506	2851716	2851231	3061158	3333656	2273607	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
2232133	2746906	3384751	3729439	3010966	4124579	3599964	3564692	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
2024023	2083710	2133025	1883695	2232450	1693873	1728255	2415023	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
7955307	19317229	17782742	18098788	15668958	18650120	0	7042231	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1141879	132240	1812870	1758023	1413948	1500982	1123805	1515794	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
86925702	96358798	82589209	86896474	77499416	90822320	84114807	7577860	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
6294241	0	3881751	7103922	0	5385209	2406010	6614632	MS/MS	MSMSIdentifiedButNotQuantified	MS/MS	MS/MS	NotDetected	MS/MS	MS/MS	MS/MS				
799652	513508	754868	0	680713	573945	0	635732	MS/MS	MS/MS	MS/MS	MS/MS	NotDetected	MS/MS	MS/MS	NotDetected				
392496	365278	489378	453394	348127	525213	412424	398881	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
2476677	2463076	2760996	2606628	2571122	2928982	2822238	2875010	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1455951	1747112	1440458	2090075	1594094	1525081	1127013	589504	NotDetected	NotDetected	NotDetected	NotDetected	MS/MS	NotDetected	MS/MS	MS/MS				
1103533	1010521	1178333	1479205	1791254	0	0	1887672	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
4320079	5667492	4759674	4780553	4189923	4459108	5010230	4059170	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1739704	2144122	1827000	1453355	904921	1650869	1457234	1247950	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
891442	1311253	1399247	0	0	1544585	904715	0	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
4824727	4818676	5282501	5375380	10926824	10658485	12200827	11776081	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
5145489	3950973	3581656	4626429	3594316	4281838	4504505	3550408	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1543271	1425151	1057114	1557705	3521825	1375845	3170113	2218328	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
735797	813753	0	305020	0	1049000	835788	0	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
10032355	12077808	8535651	8419863	7621301	12421266	7707956	7494278	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1939415	838005	819711	761524	571278	746390	684111	539234	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1979145	2257325	1854321	2031065	1802034	1842520	1313112	1757490	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1359355	1155189	1385768	1046796	1473247	1235718	1117982	1838350	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1392023	1527150	1396347	1399839	1377022	1742151	1419914	1483432	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
335813	2694403	2272499	1865704	1592021	1412561	2329118	2183229	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
13132641	14065641	13218911	13738388	11464664	14705236	15076120	12015689	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
6727983	7787355	5860728	5104404	3745006	6247362	4873461	4844068	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
7737561	7589381	83640134	831183428	158632790	156536075	172693740	157780065	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
6502333	6700626	6816364	7774521	7199886	6551805	6686263	7503903	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
7509351	950685	1071079	1114988	1159467	1265656	1227280	937263	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
1487620	2084076	2156424	2338793	1609517	2288204	2119347	1699779	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
4169190	4515924	3156184	4097474	3864579	3841138	1405438	4380185	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				
2266276	1843670	1987778	1780949	1896004	2031455	1944469	1755770	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS	MS/MS				

- One intensity is reported for each base sequence for each file.
- This intensity is the sum of **individual** quantified forms with that base sequence.
- There are three methods of quantification
 - MS/MS: The peak intensity reported is from a file where that base peptide was identified by MS/MS
 - MBR: The peak intensity reported is found in a file where that base peptide was NOT identified by MS/MS. Instead, the peak was detected by matching the mass and elution time to others found in other files.
 - MS/MSIdentifiedButNotQuantified: A peptide with that base sequence was found but no peak could be identified in the MS1 spectra.

aggregateProteinGroups.tsv

Protein Intensity by Filename

Protein Accession	Gene	Organism	Protein Full Name	Protein Unmodified Mass	Number of Proteins in Group	Unique Peptides	Shared Peptides	Number of Peptides	Sequence Coverage %	Sequence Coverage with Mods	Sequence Modification	Intensity_002_0_CD_01_A01	Intensity_002_0_CD_01_A02	Intensity_002_1_CD_01_A01	Intensity_002_1_CD_01_A02	Intensity_002_2_CD_01_C01	Intensity_002_2_CD_01_C02	Intensity_002_2_CD_01_C03	Intensity_002_2_CD_01_C04	Intensity_002_2_CD_01_C05	Number of PSMs	Protein Decoy/Conta	Protein Cumulative Target	Protein Cumulative	Protein QValue	Best Peptide Score	Best Peptide Notch	Best Peptide QValue
AD04CAG025 P0683 CAPNS1 CAPNS1	Capns1	Homo sapiens	Capain small subu	33764.046400529142	2	1	1	2	0.51%	0.1%	mLVNSFLU	114526099	115701839.6	102485196	101401510.3	9922328.19	9525219.97	10588860.5	101794394.5	116	T	1	0	0	0	43.23475	0	
Q22945	HISR9	Homo sapiens	Far upstream elem	73070.02004	1	1	0	1	62%	50%	mdspgvdq	6032320	64313078.9	60335157.49	59949559.92	5953532.02	6781103.66	6367820.93	64415339.92	428	T	2	0	0	0	33.34066	0	
Q529P	OSBP	Homo sapiens	Oxysterol-binding	45936.53141	1	1	0	1	25%	100%	maelrvvqv	145299134	16069005.47	17366159.91	18891500.27	1445880.12	1671831.01	1682125.01	15229468.28	64	T	3	0	0	0	32.89842	0	
P13639	EEF2	Homo sapiens	Elongation factor 2	95276.94909	1	1	0	1	65%	65%	MVNFVTQD	532852902	531195706.9	530941819	549727485.3	439523495.3	491780851.2	536335914.7	506473977.3	1057	T	4	0	0	0	32.86091	0	
P35527	KRT9	Homo sapiens	Keratin, type I cytc	62026.81469	1	1	0	1	44%	44%	mscrgfssyrl	31137888.34	32719134.24	32085559.62	33239234.14	31700984.11	32362239.84	33308309.26	31688473.79	188	T	5	0	0	0	32.34005	0	
Q08123	NSUN2	Homo sapiens	tRNA (cytosine)34	86415.80241	1	1	0	1	64%	64%	mrgsrslrc	41727243.94	43167934.28	41496089.19	41113313.2	45968497.29	43015107.1	39478311.24	42549148.72	400	T	6	0	0	0	31.43396	0	
Q9NZM1	MYOF	Homo sapiens	Myofibrin	234560.6703	1	1	0	1	61%	61%	mrvvvesas	149521088.3	148554503.6	14545465.4	147626168	125062721.3	142775273.9	141194632.8	132225118.6	1610	T	7	0	0	0	31.34246	0	
Q9BR76	CDR318	Homo sapiens	Coronin-1B	54200.24774	1	1	0	1	28%	28%	mrfvrvvsg	70411342.75	6703962.68	70123757.51	68020296.41	72205186.23	65729508.37	685927488.94	6804882.76	193	T	8	0	0	0	31.34118	0	
P04264	KRT1	Homo sapiens	Keratin, type II cytc	65999.00087	1	1	0	1	60%	60%	msrgfssyrl	82698044.48	8686036.67	76801234.21	86987526.47	92853382.34	83524079.23	77084602.25	832948892.82	343	T	9	0	0	0	31.32602	0	
Q5T1J1 Q9Y6H1	CHCHD2P9 CHCHC	Homo sapiens	Putative colled-co	15479.71263568541	3	0	27%	127%	27%	27%	mrgsrstrs	2577885.91	28140942.37	31788100.97	29989101.59	27567309.43	29179777.2	29996117.43	28795474.31	63	T	10	0	0	0	31.30815	0	
P14866	HNRNP1	Homo sapiens	Heterogeneous nu	64092.36373	1	1	0	1	51%	51%	mrrflrflpe	131888283.3	131968138.4	130202482.6	131867845.9	115234022	121983516.5	125093973.5	122641558.6	516	T	11	0	0	0	31.1551	0	
Q9H4A4	RNPBP	Homo sapiens	Aminopeptidase B	72549.46049	1	1	0	1	45%	45%	masghepss	5941248.9	55786019.55	60117457.42	58940734.81	56889609.32	56690656.12	59071701.12	56859952.23	244	T	12	0	0	0	31.16226	0	
Q96LD4	TRIM47	Homo sapiens	Tripartite motif-c	69487.87354	1	1	0	1	41%	41%	mdgspgsc	19509262.34	17794476.61	13823118.34	13084520.53	12510832.58	14580661.67	13175949.15	12503769.58	118	T	13	0	0	0	30.36011	0	
P02545	LMNA	Homo sapiens	Prelamin A/C	74094.70819	1	1	0	1	74%	74%	metpqrnt	33439744.5	31824960.1	27971925.5	276152697.9	286550736.5	284841751.4	271972013.2	287434088	120	T	14	0	0	0	30.3509	0	
A0A009SF54	SPTAN1	Homo sapiens	Spectrin alpha cha	78262.361	1	1	0	1	58%	58%	mdspgvvlv	22487753.47	22733433.42	21887476	22801341.31	23075651.28	2268385.17	23034306.53	21347900	119	T	15	0	0	0	30.34658	0	
Q13813	SPTAN1	Homo sapiens	Spectrin alpha cha	294394.2798	1	1	0	1	58%	58%	mdspgvvlv	22487753.47	22733433.42	21887476	22801341.31	23075651.28	2268385.17	23034306.53	21347900	119	T	16	0	0	0	30.34658	0	
P29966	MARCKS	Homo sapiens	Myristoylated alan	31535.86474	1	1	0	1	83%	83%	mgqfssyrl	41054892.47	40888601.65	48371570.4	4671205.34	46590615.07	42339110.94	44954812.45	44877045.27	148	T	17	0	0	0	30.33373	0	
Q96D17	SNRNP40	Homo sapiens	U5 small nuclear ri	93825.70841	1	1	0	1	53%	53%	mseqmqrqg	16716101.13	16447535.61	17762931.47	19142253.18	16061385.17	17853921.68	17855557.72	1657838	132	T	18	0	0	0	30.31318	0	
P63264	RACK1	Homo sapiens	Receptor of activat	35054.55796	1	1	0	1	70%	70%	meqtmtigt	388211867	37505805.6	269068636	265986234.5	30338918.3	278590713.1	262980470.7	312637075.6	359	T	19	0	0	0	30.31604	0	
D3DQV9 P78344	E1F4G2 E1F4G2	Homo sapiens	Eukaryotic transtat	102264.840893171	2	0	52%	52%	52%	52%	vesaiaegag	136864616	79002741.49	76543722.65	77512697.3	7461124.86	7172027.2	76064855.17	81662578.74	493	T	20	0	0	0	30.30552	0	
P32623	RPS14	Homo sapiens	40S ribosomal prot	16262.53281	1	1	0	1	47%	47%	maprteqik	20181601	202574281.9	216584905.3	213620899.2	21423561.4	212210464.9	206230867.2	211590688.7	167	T	21	0	0	0	30.28704	0	
Q15149	PLEC	Homo sapiens	Plectin	531465.9865	1	1	0	1	58%	58%	mvaagmlm	214848666.3	217856772.2	239079743.6	2364791.75	241848602.4	215880521.7	236882770.3	242151258.9	3292	T	22	0	0	0	30.27888	0	
C3TRK2	dnak_1	Escherichia coli	Chaperone protein	69072.4863	1	1	0	1	74%	74%	mgkigildl	181577992.2	174861120	202120860.3	213278322.8	416252589.7	385014311.7	387113801.4	41891458.8	84	T	23	0	0	0	30.26179	0	
Q9Y6C9	MTC2	Homo sapiens	Mitochondrial carr	33308.864	1	1	0	1	44%	44%	madaevayl	20613846.19	24920899.55	25396407.56	24986579.5	23092195.64	24256637.82	22862741.63	23454827.92	176	T	24	0	0	0	30.24961	0	
P9194	PR1A	Homo sapiens	Prolyl-4-hydroxylase	18006.88528	1	1	0	1	82%	82%	MVNFVTQD	21466879.98	2096281913	209596125	2078439299	2388762069	2033829394	2006697544	21772722.66	24	T	25	0	0	0	30.24784	0	
Q00287	SUPT5H	Homo sapiens	Transcription elonq	120934.5129	1	1	0	1	58%	58%	mdafsdofas	598014621	6354575.21	67312683.58	70997700.57	74452657.98	66695273.98	69695171.31	747862527.08	402	T	26	0	0	0	30.23798	0	
P35579	MYH9	Homo sapiens	Myosin-9	22831.2913	1	1	0	1	65%	65%	maeqaagtl	43459523	447402919.8	425204913.2	438626502.4	429952656.8	41744282.8	428396928.8	42522594.2	2741	T	27	0	0	0	30.21924	0	
P14618	PKM	Homo sapiens	Pyruvate kinase P	57900.02316	1	1	0	1	76%	76%	mkpshaeag	798331501.3	774796623.7	758747527.6	718336213.2	74785001.2	739970002.7	724789806.6	699425270.7	1482	T	28	0	0	0	30.21663	0	
H8B7N5	PKM	Homo sapiens	Pyruvate kinase P	57901.21951	1	1	0	1	67%	67%	mkpshaeag	754858813.3	757579007.4	758747527.6	718336213.2	724817761.4	712718827.9	724789806.6	699110582.6	1204	T	29	0	0	0	30.21663	0	
P04083	ANXA1	Homo sapiens	Annexin A1	38889.97913	1	1	0	1	74%	74%	mamvsefkk	205879001.5	472337724.9	252548669.3	240992170.3	257690738.2	20915140.8	23961027.1	242220554.8	400	T	30	0	0	0	30.19801	0	
P10768	ESD	Homo sapiens	S-formylglutathio	31442.45797	1	1	0	1	41%	41%	malikssnkk	51427295.5	102221031.9	100988639.5	100379729.6	102625121.4	90321514.44	92540041.81	104008046.6	146	T	31	0	0	0	30.19478	0	
Q13511	ARPC5	Homo sapiens	Actin-related pro	16310.29922	1	1	0	1	72%	72%	mkntbsarf	670103131.56	63960847.02	623517173.38	6547988.16	81419055.05	79396020.6	82917175.49	88637425.92	93	T	32	0	0	0	30.14475	0	
P07355	ANXA2	Homo sapiens	Annexin A2	38579.81475	1	1	0	1	64%	64%	mstvhelckl	174182208	1851794295	1683479586	1709139942	1636408389	164972322	1564897027	161733134	1260	T	33	0	0	0	30.14055	0	
P29537	ZTK	Homo sapiens	Zyxin	61238.18688	1	1	0	1	55%	55%	mapspfsrl	58578314.35	5182804.82	53567235.8	54474655.91	57001817.14	5437868.5	54344785.54	58888661.31	333	T	34	0	0	0	30.13924	0	
P13206	VCL	Homo sapiens	Vinculin	123731.8125	1	1	0	1	64%	64%	movftrtes	265278904.3	253111728.6	268889949.3	284629741.3	274817613	240569507.8	294703982.7	28721929.9	1049	T	35	0	0	0	30.13838	0	
Q9H3P7	ACBD3	Homo sapiens	Golgi resident pro	60555.9794	1	1	0	1	38%	38%	maavnrlae	14875183.63	14219650.28	13547745.78	12558344.09	11978094.96	13548017.07	12465251.7	12918784.84	153	T	36	0	0	0	30.13706	0	
Q9Y559	RBM8A	Homo sapiens	RNA-binding prot	19876.73069	1	1	0	1	27%	27%	madvldlea	32772551.9	33369727															