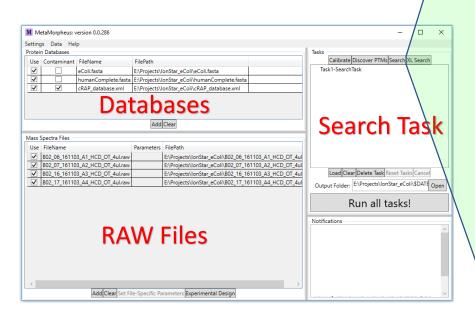
LFQ with FlashLFQ in MetaMorpheus

Modes of Quantification

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

Easy Peptide/Protein LFQ

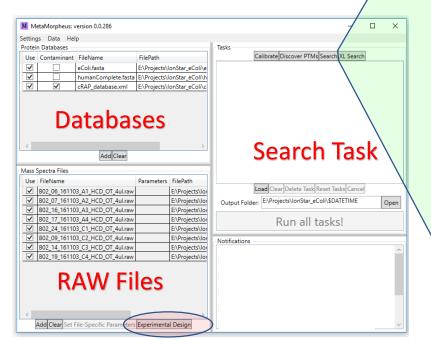
- Add databases and RAW files to MetaMorpheus
- Select 'Search Task'
- Open Post-Search Analysis
- Check 'Quantify peptides/proteins with FlashLFQ'
- Check 'Match between runs' (Optional)
- Click 'Add the Search Task'
- Click 'Run all tasks!'



M Search 1	ask				—	\Box \times
Task Name	SearchTask					1
- File Loading	Parameters					
\odot						
~ '	ectral Data Para	meters				
\odot						
Search Para						
Some s	earch properties					
Modificatio	ns					
\odot						
Post-Search	Analysis					
🔿 Hide						
Protein Pa						
		y and construct prote ptides to identify prote				
		as different peptides				
Quantifica			/			
🖌 Quanti	y peptides/prote	eins with FlashLFQ 🗸				
5 ppr	n peakfinding to	lerance				
	between runs 💙					
🗌 Norma	lize quantificatio	n results				
	rence Histogram					
Constru	uct mass-differer	nce histogram				
Histogram	ı bin width (Da):	0.003				
	tabase Writing					
		bases (Mod and Mod-				
Mod Typ	e	Do not Write	Write if in DB and Obser		Write if Observe	ed
Common	Fixed	۲	•	•		
Common	Variable	۲	0	0	0	
Artifact		۲	•		•	
Biologica		۲	0	0	0	
Crosslink		۲	•			
Detached	1	۲	0	0	0	
fallOffC		۲	•	•		
fallOffN		۲	0	0	0	
N-linked	glycosylation	۲	•	•		
O-linked	glycosylation	۲	0	0	0	
Other gly	cosylation	۲	•	•		
missing		۲	0	0	0	
ProteinTe	rmMod	0	•		۲	
Mod		۲	0	0	0	· · · · · · · · · · · · · · · · · · ·
		Cance	Add the Searc	h Task		

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!'



				- 0
ask Name SearchTask				
ile Loading Parameters				
•				
ssumed Spectral Data Par	ameters			
•				
earch Parameters				
 Some search propertie 	5			
Modifications				
$\overline{\mathbf{v}}$				
ost-Search Analysis				
Hide				
Protein Parsimony				
Apply protein parsimo				
Require at least two per Treat modified peptide				
Quantification		1		
Quantification Quantify peptides/pro	teins with FlachLEO			
5 ppm peakfinding to				
	ole ance			
PP				
Match between runs				
Match between runs	on results			
Match between runs Normalize quantificati	on results m Analysis			
Match between runs Normalize quantificati Mass Difference Histogram Construct mass-differe	on results m Analysis ence histogram			
Match between runs Mormalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da)	m Analysis ence histogram 1: 0.003			
Match between runs March between runs Normalize quantificati Mass Difference Histogra Construct mass-differe Histogram bin width (Da) Pruned Database Writing	on results m Analysis ence histogram 1: 0.003	1+Protein pruned)		
Match between runs Match between runs Normalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data	on results m Analysis ence histogram 1: 0.003	d+Protein pruned) Write if in DB and Obser	Write if in DB	Write if Observed
Match between runs Mormalize quantificatio Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing	on results m Analysis ence histogram 1: 0.003 abases (Mod and Mod		Write if in DB	Write if Observed
Match between runs March between runs Normalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type	on results m Analysis ence histogram bo not Write	Write if in DB and Obser		
Match between runs March between runs Normalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed	on results m Analysis ence histogram i: 0.003 abases (Mod and Mod Do not Write ()	Write if in DB and Obser	0	
Match between runs March between runs Normalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Fixed Common Variable	on results m Analysis ence histogram t: 0.003 abases (Mod and Mod Do not Write	Write if in DB and Obser	0	0
Match between runs Normalize quantificatio Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Fixed Artifact	on results m Analysis ence histogram bit (0.003) abases (Mod and More Do not Write 0 0 0 0 0 0 0 0 0 0 0 0 0	Write if in DB and Obser	0	0
Match between runs Normalize quantificatio Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Variable Artifact Biological	on results	Write if in DB and Obser		0 0 0
Match between runs Normalize quantification Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Variable Artifact Biological Crosslink	on results	Write if in DB and Obser		0 0 0
Match between runs Mormalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Variable Artifact Biological Crosslink Detached	on results	Write if in DB and Obser		
Match between runs Normalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Fixed Common Variable Artifact Biological Crosslink Detached fallOffC	on results	Write if in DB and Obser		
Match between runs March between runs Normalize quantificati Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Fixed Common Variable Artifact Biological Crosslink Detached fallOffC fallOffN	on results	Write if in DB and Obser		
Match between runs Normalize quantificatii Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Fixed Common Variable Artifact Biological Crosslink Detached fallOffC fallOffC fallOffN N-linked glycosylation	on results	Write if in DB and Obser		
Match between runs Normalize quantification Mass Difference Histogram Construct mass-difference Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Variable Artifact Biological Crosslink Detached fallOffC fallOffN N-linked glycosylation O-linked glycosylation	on results	Write if in DB and Obser		
Match between runs Mormalize quantificatii Mass Difference Histogram Construct mass-differe Histogram bin width (Da) Pruned Database Writing Write Two Pruned Data Mod Type Common Fixed Common Fixed Common Variable Artifact Biological Crosslink Detached fallOffN N-linked glycosylation Other glycosylation	on results	Write if in DB and Obser		

MetaMorpheus: v	ersion 0.0.286		
Settings Data Hel	р		
Protein Databases			
Use Contaminant	FileName	FilePath	
	eColi.fasta	E:\Projects\I	onStar_eColi\e
	humanComplete.fasta	E:\Projects\I	onStar_eColi\h
 Image: A start of the start of	cRAP_database.xml	E:\Projects\I	onStar_eColi\c
<			>
	Add Clear		
Mass Spectra Files —			
Use FileName		Parameters	FilePath
B02_06_16110	3_A1_HCD_OT_4ul.raw		E:\Projects\lor
	3_A2_HCD_OT_4ul.raw		E:\Projects\lor
B02_16_16110	3_A3_HCD_OT_4ul.raw		E:\Projects\lor
B02_17_16110	3_A4_HCD_OT_4ul.raw		E:\Projects\lor
B02_24_16110	3_C1_HCD_OT_4ul.raw		E:\Projects\lor
B02_09_16110	3_C2_HCD_OT_4ul.raw		E:\Projects\lo
	3_C3_HCD_OT_4ul.raw		E:\Projects\loi
B02_19_16110	3_C4_HCD_OT_4ul.raw		E:\Projects\lor
	ile-Specific Parameters	Evneriments	> Decise

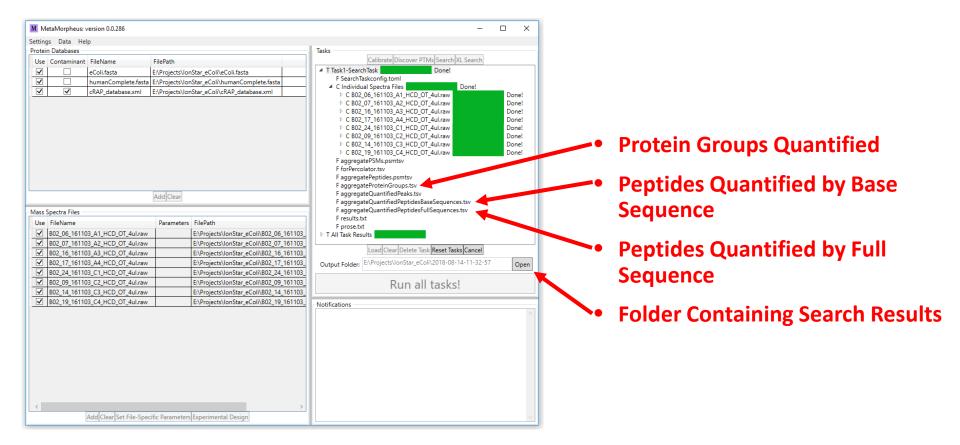
Open 'Experimental Design'

M 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 Exp	periment	tal Design	Cancel		

Set values for Condition, Biorep, Fraction & Techrep

M 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	Α	4	1	1			
B02_24_161103_C1_HCD_OT_4ul	С	1	1	1			
B02_09_161103_C2_HCD_OT_4ul	С	2	1	1			
B02_14_161103_C3_HCD_OT_4ul	С	3	1	1			
B02_19_161103_C4_HCD_OT_4ul	С	4	1	1			
	Save Ex	periment	tal Design	Cancel			

MetaMorpheus Search Results



aggregateQuantifiedPeptidesBaseSequences.tsv

Base Peptide Peak Intensity by Filename									Method of Quantification									
			Intensity_B02_	Intensity_B02_	Intensity_B02_	Intensity_B02_	Intensity_B02_	Intensity_B02_	Intensity_B02_	Intensity_B02_	Detection	Detection	Detection	Detection	Detection	Detection	Detection	Detection
			06_161103_A1_	07_161103_A2_	16_161103_A3_	17_161103_A4_	24_161103_C1_	09_161103_C2_	14_161103_C3_	19_161103_C4_	Type_B02_06_16110	Type_B02_07_16110	Type_B02_16_16110	Type_B02_17_16110	Type_B02_24_16110	Type_B02_09_16110	Type_802_14_16110	J Type_B02_19_16110
	Gene Names	Organism	HCD_OT_4ul	HCD_OT_4ul	HCD_OT_4ul	HCD_OT_4ul	HCD_OT_4ul	HCD_OT_4ul	HCD_OT_4ul	HCD_OT_4ul	3_A1_HCD_OT_4ul	3_A2_HCD_OT_4ul	3_A3_HCD_OT_4ul	3_A4_HCD_OT_4ul	3_C1_HCD_OT_4ul	3_C2_HCD_OT_4ul	3_C3_HCD_OT_4ul	
ΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑ	SLC12A2	Homo sapiens	2024023	2083710	2133025	1883695	2232650	1693873	1728255	2415002	MSMS	MSMS	MBR	MSMS	MSMS	MSMS	MBR	MSMS
AAAAAAAAAKNGSSGK Q99453	PHOX2B	Homo sapiens	7795307	19317229	17782742	18098788	15668998	18650120	0	7042231	MSMS	MSMS	MBR	MBR	MBR	MBR	NotDetected	MBR
	9 ZFP91-CNTF ZF		1141879	1322240	1812870	1758023	1413848	1500682	1123805	1357574	MBR	MBR	MBR	MSMS	MBR	MBR	MBR	MBR
AAAAAAALQAK P36578	RPL4	Homo sapiens	86925702	96358798	82589209	86896474	77499416	90823230	84114807	75777860	MSMS	MSMS MSMSIdentifiedBut	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAAAADPNAAWAAYY Q92945	KHSRP	Homo sapiens	6294241	0	3881751	7103922	0	5385209	2406010	6614632	MSMS	NotQuantified	MBR	MBR	NotDetected	MSMS	MSMS	MBR
AAAAALSQQQSLQER Q8WUQ7	CACTIN	Homo sapiens	799652	513508	754868	0	680713	573565	0	635732	MBR	MBR	MBR	NotDetected	MBR	MBR	NotDetected	MSMS
AAAAASAAGPGGLVAGIA6NIH7	UNC119B	Homo sapiens	392496	365278	489378	453394	348127	525213	421424	398881	MBR	MBR	MBR	MBR	MBR	MBR	MSMS	MSMS
AAAAAWEEPSSGNGTAI Q9P258	RCC2	Homo sapiens	2476677	2463076	2760996	2606628	2571122	2928982	2822238	2875010	MSMS	MSMS	MBR	MBR	MSMS	MBR	MSMS	MSMS
AAAALGOLFEGMKAFK M0OZP4	BCAT2	Homo sapiens	0	0	0	0	739194	0	1127013	589504	NotDetected	NotDetected	NotDetected	NotDetected	MSMS	NotDetected	MBR	MBR
AAAAPAATTATPPPEGA Q9UPT8	ZC3H4	Homo sapiens	1455951	1747112	1440498	2090075	1594094	1525081	1284833	1271864	MSMS	MSMS	MSMS	MSMS	MBR	MSMS	MSMS	MSMS
																MSMSAmbiguousPe		
AAAAPGASPSPGGDAA\P52701	MSH6	Homo sapiens	1103533	1010521	1178333	1479205	1791254	0	0	1987672	MSMS	MSMS	MSMS	MSMS	MSMS	akfinding	NotDetected	MSMS
AAAASAAEAGIATTGTEL P55036	PSMD4	Homo sapiens	4320679	5667492	4759674	4776653	4189929	4459108	5010230	4059170	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAASAAEAGIATTGTE(Q5VWC4	PSMD4	Homo sapiens	1739704	2144122	1827000	1453355	904921	1650869	1457234	1247950	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
														MSMSIdentifiedBut	MSMSIdentifiedBut			
AAAAVAAAASSCRPLGS Q9NRL3	STRN4	Homo sapiens	891442	1311253	1399247	0	0	1544585	904715	0	MBR	MBR	MSMS	NotQuantified	NotQuantified	MBR	MSMS	NotDetected
AAADEWDER W8SPD7	msyB	Escherichia coli	4824727	4818676	5282501	5375380	10926824	10658485	12200827	11776081	MBR	MBR	MBR	MBR	MBR	MSMS	MBR	MBR
AAADSDPNLDPLMNPHI 095159	ZFPL1	Homo sapiens	5145489	3950973	3581656	4626429	3594316	4281838	4504505	3550408	MBR	MSMS	MSMS	MSMS	MBR	MSMS	MSMS	MSMS
AAADVQLR C3SJT7	dsbA	Escherichia coli	1543271	1425151	1057114	1557705	3521825	1375845	3170113	2218328	MSMS	MBR	MBR	MSMS	MSMS	MBR	MSMS	MSMS
AAAEAAAEAKAR Q9UNF1	MAGED2	Homo sapiens	753797	813753	0	305020	0	1049800	835788	0	MBR	MBR	NotDetected	MSMS	NotDetected	MBR	MBR	NotDetected
AAAEDVNVTFEDQQK E9PQY2 Q9NQP		Homo sapiens	10032355	12077808	8535651	8419863	7621301	12421266	7707956	7494278	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAEEGHIIPR 095551	TDP2	Homo sapiens	1093415	838005	819711	761524	571278	746590	684111	539234	MSMS	MSMS	MSMS	MBR	MSMS	MBR	MSMS	MSMS
AAAEELLAR 015357	INPPL1	Homo sapiens	1979145	2257325	1854321	2031065	1802034	1842520	1313112	1757490	MBR	MSMS	MBR	MSMS	MSMS	MBR	MSMS	MSMS
AAAEGLMSLLR P30260	CDC27	Homo sapiens	1359355	1155189	1385768	1046756	1473247	1235718	1117962	1838350	MSMS	MSMS	MBR	MBR	MBR	MSMS	MSMS	MSMS
AAAEQAISVR Q01780	EXOSC10	Homo sapiens	1392023	1527150	1396347	1399839	1377022	1742151	1419914	1483432	MBR	MBR	MSMS	MSMS	MBR	MBR	MBR	MBR
AAAEVAGQFVIK P02786	TFRC	Homo sapiens	3158513	2694103	2272499	1865704	1950231	1412561	2329118	2183229	MBR	MSMS	MBR	MBR	MSMS	MSMS MSMS	MBR	MBR
AAAEVNQDYGLDPK P07954	FH	Homo sapiens	13153641	14065641	13218911 5860728	13738388	11464664 3745006	14740526 6247362	15076120 4872461	13015689 4844068		MSMS		MSMS	MSMS		MSMS	MSMS
AAAFEEQENETVVVK Q9Y490	TLN1	Homo sapiens	6727983	7787535		5104404					MSMS MSMS	MSMS MSMS	MSMS MSMS	MSMS	MSMS MSMS	MSMS MSMS	MSMS MSMS	MSMS
AAAFEGELIPASQIDR C3SIB7 AAAFEQLQK 094826	rplJ TOMM70	Escherichia coli	77377561 6502333	75893381 6700626	83640134 6816364	83183428 7774521	158632790 7199886	156536075 6551805	172693740 6686263	157780065 7503903	MSMS	MSMS	MSMS		MSMS	MSMS	MSMS	MSMS MSMS
AAAFPOLOK 094820 AAAFPPGFSISEIK 09H9Y2	RPF1	Homo sapiens	759391	965685	1071079	1114988	1195467	1265656	1227280	937263	MSMS	MBR	MSMS	MBR	MBR	MBR	MBR	MBR
AAAGAAATHLEVAR Q96552	PIGS	Homo sapiens Homo sapiens	1487620	2480576	2156424	2338793	1609517	2288204	2119347	1699779	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAGEDYKADCPPGNP/ P23381	WARS	Homo sapiens	4169190	4515924	3156164	4097474	3664579	3841138	1405438	4360185	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAGEFADDPCSSVK P35221	CTNNA1	Homo sapiens	2266276	4515924	1987778	1780949	1896004	2031455	1944469	4300185	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAGELQEDSGLCVLAR Q96C19	EFHD2	Homo sapiens	7812687	7384101	6722067	6110466	8318407	7320776	6312267	7341077	MSMS	MSMS	MSMS	MSMS	MSMS	MBR	MSMS	MBR
AAAGGLAMLTSMR A0A1W2PNX8	UNC45A	Homo sapiens	5138526	4756166	2912265	3634160	1758823	4643869	3722314	2118940	MSMS	MSMS	MSMS	MBR	MBR	MSMS	MSMS	MSMS
AAAGGLAMLTSMR A0A1W2PNX8	UNC45A	Homo sapiens	3433227	4423831	3627291	5246230	2502620	5525068	5143868	2257693	MSMS	MBR	MBR	MBR	MSMS	MBR	MBR	MBR
AAAGGQGSAVAAEAEPI Q9GZT9	EGLN1	Homo sapiens	1011134	1406539	1155455	1141935	1084773	1291909	1177764	1127368	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
AAAGLMSLLR G5EA36	CDC27	Homo sapiens	918249	770397	0	470368	0	743734	0	0	MSMS	MSMS	NotDetected	MBR	NotDetected	MSMS	NotDetected	NotDetected
AAAGMVWKPK Q9H147	DNTTIP1	Homo sapiens	335208	1116239	1029958	1056234	895554	894132	1170662	592629	MBR	MSMS	MBR	MBR	MBR	MBR	MBR	MBR
AAAGPLDMSLPSTPDIK K7ELQ4		rionio sapiens	1107405	913315	1143690	1065978	1211158	881403	1067428	821425	MBR	MBR	MBR	MSMS	MBR	MBR	MSMS	MBR
AAAGQESEGPAVGPPQI 014497	ARID1A	Homo sapiens	3219455	3070734	2152909	3117065	2492229	3229262	2934383	2973003	MSMS	MSMS	MSMS	MSMS	MSMS	MBR	MSMS	MSMS
	received and	creative supretta	5113400	2012/24	2102005	5227000	2.0.1115	SELFEVE	230,4903	231 3003								

- One intensity is reported for each base sequence for each file.
- This intensity is the sum of <u>all</u> forms (modified and unmodified) 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/MSIdentifedButNotQuantified: A peptide with that base sequence was found but no peak could be identified in the MS1 spectra.

aggregateQuantifiedPeptidesFullSequences.tsv

Note:			ſ																
Note:				I	Base Pe	eptide	Peak Ir	ntensit	v by Fil	lename				Met	thod of Q	uantifica	tion		
Modifications										Intensity B02		Detection							
wouncations				06_161103_A1_	07_161103_A2_	16_161103_A3_	17_161103_A4_	24_161103_C1_	09_161103_C2	14_161103_C3_	19_161103_C4_	Type_B02_06_16110	Type_B02_07_16110	Type_B02_16_16110	Type_B02_17_16110	Type_B02_24_16110	Type_B02_09_16110	Type_B02_14_16110	Type_B02_19_16110
Sequence	Protein Groups	Gene Names	Organism	HCD_OT_4ul	3_A1_HCD_OT_4ul	3_A2_HCD_OT_4ul	3_A3_HCD_OT_4ul	3_A4_HCD_OT_4ul	3_C1_HCD_OT_4ul	3_C2_HCD_OT_4ul	3_C3_HCD_OT_4ul	3_C4_HCD_OT_4ul							
[UniProt:N-acetylalanine]ADSRDPASDQMQHWK	UNDEFINED			2998436	3357256	3060362	3031378	3056672	2876728	2702817	3051927	MSMS							
[UniProt:N-acetylalanine]ASQNRDPAATSVAAAR	O00762	UBE2C	Homo sapiens	5049784	5180823	5428400	5181106	5067962	4688841	5203300	4431331	MSMS	MSMS	MSMS	MSMS	MBR	MSMS	MSMS	MSMS
[UniProt:N-acetyImethionine]M[Common Variabl				1312574	798689	1891729	2390753	1118747	2742391	1497020	1590447	MSMS	MBR	MSMS	MSMS	MSMS	MSMS	MSMS	MSMS
[UniProt:N-acetylmethionine]MDC[Common Fixe				476762	0	672927	0	700986	0	769758	0	MBR	NotDetected	MBR	NotDetected	MBR	NotDetected	MSMS	NotDetected
[UniProt:N-acetylmethionine]MVNPTVFFDIAVDG	UNDEFINED			4817699	5078744	6163723	8840746	5789679	8040549	7162674	6089070	MSMS							
[UniProt:N-acetylserine]S[UniProt:Phosphoserine]		SUM01	Homo sapiens	3377474	3539174	3699109	3748185	3598145	3072051	3060495	3593864	MSMS							
[UniProt:N-acetylserine]SDQEAKPSTEDLGDKK		SUMO1	Homo sapiens	3160655	2363532	3480506	2851716	2651231	3061158	3333656	2273607	MBR	MBR	MSMS	MBR	MBR	MSMS	MSMS	MBR
[UniProt:N-acetylvaline]VNPTVFFDIAVDGEPLGR	UNDEFINED			2238133	2746306	3384751	3720439	3010366	4124573	3599864	3562692	MSMS							
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	P55011	SLC12A2	Homo sapiens	2024023	2083710	2133025	1883695	2232650	1693873	1728255	2415002	MSMS	MSMS	MBR	MSMS	MSMS	MSMS	MBR	MSMS
AAAAAAAAKNGSSGK		PHOX2B	Homo sapiens	7795307	19317229	17782742	18098788	15668998	18650120	0	7042231	MSMS	MSMS	MBR	MBR	MBR	MBR	NotDetected	MBR
AAAAAAAAVSR			F Homo sapiens	1141879	1322240	1812870	1758023	1413848	1500682	1123805	1357574	MBR	MBR	MBR	MSMS	MBR	MBR	MBR	MBR
AAAAAAAQAK	P36578	RPL4	Homo sapiens	86925702	96358798	82589209	86896474	77499416	90823230	84114807	75777860	MSMS							
													MSMSIdentifiedBut						
AAAAAADPNAAWAAYYSHYYQQPPGPVPGPAPAPA		KHSRP	Homo sapiens	6294241	0	3881751	7103922	0	5385209	2406010	6614632	MSMS	NotQuantified	MBR	MBR	NotDetected	MSMS	MSMS	MBR
AAAAALSQQQSLQER		CACTIN	Homo sapiens	799652	513508	754868	0	680713	573565	0	635732	MBR	MBR	MBR	NotDetected	MBR	MBR	NotDetected	MSMS
AAAAASAAGPGGLVAGKEEK		UNC1198	Homo sapiens	392496	365278	489378	453394	348127	525213	421424	398881	MBR	MBR	MBR	MBR	MBR	MBR	MSMS	MSMS
AAAAAWEEPSSGNGTAR		RCC2	Homo sapiens	2476677	2463076	2760996	2606628	2571122	2928982	2822238	2875010	MSMS	MSMS	MBR	MBR	MSMS	MBR	MSMS	MSMS
AAAALGQLFEGM[Common Variable:Oxidation of I		BCAT2	Homo sapiens	0	0	0	0	739194	0	1127013	589504	NotDetected	NotDetected	NotDetected	NotDetected	MSMS	NotDetected	MBR	MBR
AAAAPAATTATPPPEGAPPQPGVHNLPVPTLFGTVK	Q9UPT8	ZC3H4	Homo sapiens	1455951	1747112	1440498	2090075	1594094	1525081	1284833	1271864	MSMS	MSMS	MSMS	MSMS	MBR	MSMS	MSMS	MSMS
																	MSMSAmbiguousPe		
AAAAPGASPSPGGDAAWSEAGPGPR		MSH6	Homo sapiens	1103533	1010521	1178333	1479205	1791254	0	0	1987672	MSMS	MSMS	MSMS	MSMS	MSMS	akfinding	NotDetected	MSMS
AAAASAAEAGIATTGTEDSDDALLK		PSMD4	Homo sapiens	4320679	5667492	4759674	4776653	4189929	4459108	5010230	4059170	MSMS							
AAAASAAEAGIATTGTEGERDSDDALLK	Q5VWC4	PSMD4	Homo sapiens	1739704	2144122	1827000	1453355	904921	1650869	1457234	1247950	MSMS							
																MSMSIdentifiedBut			
AAAAVAAAASSC[Common Fixed:Carbamidometh		STRN4	Homo sapiens	891442	1311253	1399247	0	0	1544585	904715	0	MBR	MBR	MSMS	NotQuantified	NotQuantified	MBR	MSMS	NotDetected
AAADEWDER		msyB	Escherichia coli	4824727	4818676	5282501	5375380	10926824	10658485	12200827	11776081	MBR	MBR	MBR	MBR	MBR	MSMS	MBR	MBR
AAADSDPNLDPLMNPHIR		ZFPL1	Homo sapiens	5145489	3950973	3581656	4626429	3594316	4281838	4504505	3550408	MBR	MSMS	MSMS	MSMS	MBR	MSMS	MSMS	MSMS
AAADVQLR		dsbA	Escherichia coli	1543271	1425151	1057114	1557705	3521825	1375845	3170113	2218328	MSMS	MBR	MBR	MSMS	MSMS	MBR	MSMS	MSMS
AAAEAAAEAKAR		MAGED2	Homo sapiens	753797	813753	0	305020	0	1049800	835788	0	MBR	MBR	NotDetected	MSMS	NotDetected	MBR	MBR	NotDetected
AAAEDVNVTFEDQQK	E9PQY2 Q9NQP		Homo sapiens	10032355	12077808	8535651	8419863	7621301	12421266	7707956	7494278	MSMS							
AAAEEGHIIPR		TDP2	Homo sapiens	1093415	838005	819711	761524	571278	746590	684111	539234	MSMS	MSMS	MSMS	MBR	MSMS	MBR	MSMS	MSMS
AAAEELLAR		INPPL1	Homo sapiens	1979145	2257325	1854321	2031065	1802034	1842520	1313112	1757490	MBR	MSMS	MBR	MSMS	MSMS	MBR	MSMS	MSMS
AAAEGLMSLLR		CDC27	Homo sapiens	1359355	1155189	1385768	1046756	1473247	1235718	1117962	1838350	MSMS	MSMS	MBR	MBR	MBR	MSMS	MSMS	MSMS
AAAEQAISVR		EXOSC10	Homo sapiens	1392023	1527150	1396347	1399839	1377022	1742151	1419914	1483432	MBR	MBR	MSMS	MSMS	MBR	MBR	MBR	MBR
AAAEVAGQFVIK		TFRC	Homo sapiens	3158513	2694103	2272499	1865704	1950231	1412561	2329118	2183229	MBR	MSMS	MBR	MBR	MSMS	MSMS	MBR	MBR
AAAEVNQDYGLDPK		FH	Homo sapiens	13153641	14065641	13218911	13738388	11464664	14740526	15076120	13015689	MSMS							
AAAFEEQENETVVVK		TLN1	Homo sapiens	6727983	7787535	5860728	5104404	3745006	6247362	4872461	4844068	MSMS							
AAAFEGELIPASQIDR		rplJ	Escherichia coli	77377561	75893381	83640134	83183428	158632790	156536075	172693740	157780065	MSMS							
AAAFEQLQK		TOMM70	Homo sapiens	6502333	6700626	6816364	7774521	7199886	6551805	6686263	7503903	MSMS	MSMS	MSMS	MBR	MSMS	MSMS	MSMS	MSMS
AAAFPPGFSISEIK		RPF1	Homo sapiens	759391	965685	1071079	1114988	1195467	1265656	1227280	937263	MSMS	MBR	MSMS	MBR	MBR	MBR	MBR	MBR
AAAGAAATHLEVAR		PIGS	Homo sapiens	1487620	2480576	2156424	2338793	1609517	2288204	2119347	1699779	MSMS							
AAAGEDYKADC[Common Fixed:Carbamidomethyl AAAGEFADDPC[Common Fixed:Carbamidomethyl		WARS CTNNA1	Homo sapiens	4169190 2266276	4515924 1843670	3156164 1987778	4097474 1780949	3664579 1896004	3841138 2031455	1405438 1944469	4360185 1755770	MSMS							
AAAGERADDPC[common Pixed:carbamidomethyl	P33221	CINDAL	Homo sapiens	2200270	1843670	1987778	1/80949	1830004	2031455	1944409	1/55//0	MoMo	M5M5	M2M2	MSM2	Mama	MSMS	MOMO	M3M3

- One intensity is reported for each base sequence for each file.
- This intensity is the sum of **individual** modified 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/MSIdentifedButNotQuantified: A peptide with that base sequence was found but no peak could be identified in the MS1 spectra.

aggregateProteinGroups.tsv

Protein Intensity by Filename

																											Best
					Number of				Number of			Sequence	Intensity_B02_0 I	ntensity_B02_0	Intensity_B02_1	Intensity_B02_1	Intensity_B02_2	Intensity_B02_0	Intensity_B02_1	Intensity_B02_1		Protein	Protein	Protein		Best Pe	eptide
					Proteins in		Shared Nun		Unique	Sequence							4_161103_C1_H					coy/Conta C					Notch
Protein Accession			Protein Full Name		Group		Peptides Pep		Peptides				CD_OT_4ul	CD_OT_4ul	CD_OT_4ul	CD_OT_4ul	CD_OT_4ul	CD_OT_4ul	CD_OT_4ul	CD_OT_4ul	of PSMs mi	hant/Target	Target	Decoy			Walue
A0A0C4DGQ5 P046			Calpain small subu 3		2		.GFEEFK Y	10	0 5			mFLVNSFLKGGGGGGGGGGG	114526099	115978189.6	102458196				105888860.5	101794394.5	116 T		1	0		3.23475	0
Q92945	KHSRP		Far upstream elem	73070.02404	1		ISVGVVIG	32	0			o msdystggpppgppppagggg	62033250	64136978.9	60391517.49		59535532.02	67781103.66	63678260.93	64415339.92	428 T		2	0		3.34086	0
P22059	OSBP		Oxysterol-binding	89364.55131		WVTALEU L		14	12			v maatelrGVVGPGPAAIAAL	14525913.64	16069035.47	17356159.91	18891500.27	14455830.12	16371631.01	16821576.39	15225469.28	64 T		3	0		2.38942	0
P13639	EEF2		Elongation factor 2	95276.94909		TILMMGR 0		61	59			MVNFTVDQIRaimdkkanirf	532852902	531395706.9	530941819	549727485.3	439523495.3	491780651.2	536335914.7	506473977.3	1057 T		4	0		2.36091	0
P35527	KRT9		Keratin, type I cytc	62026.81469		TLLDIDNTIL		21	9			: mscrqfsssylsr\$6666666	31137986.54	32719107.34	32085559.62	33239234.14	31700984.11	32362239.84	33308309.26	31698473.79	186 T		5	0		2.34005	0
Q08J23	NSUN2		tRNA (cytosine(34)	86415.80241		QLYMVSK L		40	32			CmgrrsrgrRLQQQQRPEDAE	41277243.94	43167394.28	41496089.19	41113313.2	45968497.29	43015107.1	39478311.24		400 T		6	0		1.43396	0
Q9NZM1	MYOF	Homo sapiens		234560.6019		DVILDEK 19		124	57			5 mlrVIVESASNIPKtkFGKPD	149521088.3	148554503.6	145454655.4	147626168	125062271.3	142775273.9	141194632.8	132225119.6	1610 T		7	0		1.34246	0
Q9BR76	CORO1B	Homo sapiens	Coronin-1B	54200.24774	1	DADPILISL A	AIFLADGK	15	7	28%	msfrkvvrqs	k msfrkvvrqskfrHVFGQPVKI	70411342.75	67033962.68	70123757.51	68030296.41	72206186.23	65729508.37	68592748.94	69404882.76	193 T		8	0	0 31	1.34118	0
P04264	KRT1	Homo sapiens	Keratin, type II cyb	65999.00087	1	SISISVAR I	EISELNR Y	38	32	60%	msrqfssrsg	r msrqfssrsgyrSGGGFSSGSA	82698044.88	83868630.67	76801224.21	86987526.47	92853382.34	83524073.23	77086402.25	82396892.82	343 T		9	0	0 31	1.32602	0
QST1J5 Q9Y6H1	CHCHD2P9 CHCH	CHomo sapiens	Putative coiled-coil	5479.7128356854 1:	2		QFLECAQN	3	0 3			r mprgsrsrtsrmappasrapqm	25777885.91	28140942.32	31788100.97	29989101.59		29179777.2	29996117.43	28795473.31	63 T		10	0	0 31	1.30815	0
P14866	HNRNPL	Homo sapiens	Heterogeneous nu	64092.36373	1	TDNAGDCL	NVCVSK I	27	4	51%	msrrllpraek	u msrrllpraekrrrlegrggpde	131988829.3	131968138.4	130202482.6	131867845.9	115234022	121983516.5	125098373.5	122641595.8	516 T		11	0	0 3	31.1951	0
Q9H4A4	RNPEP	Homo sapiens	Aminopeptidase B	72549.46049	1	· · · ·	NGQIVLK	27	0	45%	masgehspg	s masgehspgsgaarRPLHSAQ	59412438.9	55786019.55	60117457.42	58940734.81	56889609.32	53660656.12	59071011.72	56853965.23	244 T		12	0	0 31	1.16256	0
Q96LD4	TRIM47	Homo sapiens	Tripartite motif-co	69487.87354	1	ALAFYAVER	RLEESLCPR	20	14	41%	mdgsgpfscp	o mdgsgpfscpicleplrepvtlpc	15909262.34	17794476.6	13823118.34	13084520.53	12510832.98	14580661.67	13175949.15	12503769.58	128 T		13	0	0 30	0.36011	0
P02545	LMNA	Homo sapiens	Prelamin-A/C	74094.70819	1	SVTVVEDEL	QLELSK U	65	1	74%	metpsqrrat	r metpsgrratrSGAQASSTPLS	B 334399744.5	318249960.1	279710925.9	276152697.9	286550736.5	288481751.4	271972013.2	287434588	1110 T		14	0	0 3	30.3509	0
A0A0D9SE54	SPTAN1	Homo sapiens	Spectrin alpha chai	282662.363	1	QEQIDNO 0	DLAALEDK	135	1	58%	i mdpsgvkVL	EmdpsgvkVLETAEDIQERrqq	22478753.47	22733433.42	21887476	22801341.31	23075651.28	22658385.17	23034306.53	21347906	1109 T		15	0	0 30	0.34658	0
Q13813	SPTAN1	Homo sapiens	Spectrin alpha chai	284364.2098	1	LQTASDES	DLAALEDK	136	1	58%	i mdpsgvkVL	EmdpsgvkVLETAEDIQERrqq	22478753.47	22733433.42	21887476	22801341.31	23075651.28	22658385.17	23034306.53	21347906	1118 T		16	0	0 30	0.34658	0
P29966	MARCKS	Homo sapiens	Myristoylated alan	31535.86474	1	VNGDASPA	AAESGAK	11	11	83%	i mgaqfsktaa	i mgaqfsktaakGEAAAERPGE	41045492.47	40886801.65	48374570.4	46732025.34	46590615.07	42539510.84	44954812.45	44877045.22	148 T		17	0	0 30	0.33373	0
Q96D17	SNRNP40	Homo sapiens	U5 small nuclear ri	39285.70841	1	KGPELPLV (SWSPDGS	16	10	53%	mieggkrKG	FmieggkrKGPELPLVPVKRQ	16716101.13	16447535.61	17762931.47	19142253.18	16061385.17	17853921.68	17835557.72	16557836	132 T		18	0	0 30	0.33138	0
P63244	RACK1	Homo sapiens	Receptor of activat	35054.55796	1		IVDELK IV	19	0	70%	mteqmtirgt	I mteqmtirgtikGHNGWVTQ	268211867	270565805.6	269068636	263986234.5	330338918.3	236500713.1	262908347.7	312637075.6	359 T		19	0	0 30	0.31634	0
D3DQV9 P78344	EIF4G2 EIF4G2	Homo sapiens	Eukaryotic translat 1	02264.840893747 1	2	1	/IILSLDR A	43	0 5	52% 52%	vesalaegga	s vesaiaeggasrfsassggggsrg	136864616	79020712.49	76543722.65	77512697.3	74611243.86	71782072.2	76064855.17	81662578.74	493 T		20	0	0 30	0.30552	0
P62263	RPS14	Homo sapiens	405 ribosomal prot	16262.53281	1	IEDVTPIPS T	PGPGAQS	12	3	47%	maprkgkek	k maprkgkekkeeqvislgpqva	201816010	202574281.9	216584905.3	213620892.4	214235416	212210464.9	206230867.2	213590686.7	167 T		21	0	0 30	0.28724	0
Q15149	PLEC	Homo sapiens	Plectin	531465.9865	1	VAQUER P	ISETLR LL	292	237	58%	mVAGMLM	FmVAGMLMPRdqIrAIYEVLF	214845666.3	217856777.2	239079743.6	236479175	241848602.4	215580521.7	236882770.3	242151258.9	3292 T		22	0	0 30	0.27388	0
C3TRK2	dnaK_1	Escherichia col	i Chaperone proteir	69072.4863	1	IAGLEVK D	QGIDLR K	44	44	74%	mgkIIGIDLO	mgkliGIDLGTTNSCVAIMDO	181577792.2	174861210	202120860.3	213278322.8	416252589.7	385014431.7	387113801.4	433891458.8	643 T		23	0	0 30	.26179	0
Q9Y6C9	MTCH2	Homo sapiens	Mitochondrial carr	33308.864	1	GNSLFFR 0	SLFTGLTPR	13	3	44%	madaasqvll	s madaasqvllgsgltilsqplmyv	20613846.19	24920899.95	25396407.56	24986579.5	23092195.64	24256637.82	22862741.63	23345827.92	176 T		24	0	0 30	.24961	0
P62937	PPIA	Homo sapiens	Peptidyl-prolyl cis-	18000.88528	1	ITIADCGQ T	TEWLDGK]	15	5			MVNPTVFFDIAVDGEPLGR	2160687528	2096201913	2097596125	2077439299	2388762069	2033692394	2006697544	2177272238	1208 T		25	0	0 30	.24714	0
000267	SUPTSH		Transcription elone	120924-5129	1	VILGEDR	ATAISLMR	45	38	45%	msdsedsnf	s msdsedsnfseeedserssdge	59801442.81	63554575.21	67312683.58	70997700.57	73445268.79	66695273.98	69695711.31	74766257.06	402 T		26	0	0 30	0.23798	0
P35579	MYH9	Homo sapiens	Myosin-9	226391.5913		GALALEEK T		172	125			1 maggaadkYLYVDKNFINNP	434569523	447409919.8	425240413.2	438626502.4	429952656.8	411714282.8	428369628.8	419252594.2	2781 T		27	0	0 30	0.21924	0
P14618	PKM		Pyruvate kinase PF	57900.02336	1		APIIAVTR	50	0			t mskphseagtafigtgglhaam	798331501.3	774764623.7	758747527.6	718336213.2	747850822.1	736975002.7	724786893.6	699432570.7	1442 T		28	0		0.21663	0
H3BTN5	PKM		Pyruvate kinase (F	53011.21951	1		APIIAVTR	40	0			t mskphseagtafigtgglhaam	754585813.3	757573607.4	758747527.6	718336213.2	724817761.4	725113827.9	724786893.6	699110536.2	1204 T		29	0		0.21663	0
P04083	ANXA1	Homo sapiens		38689.97913	1	CLTAIVKIII		28	15			mamyseflkQAWFIENEEQE	205879001.5	472337724.9	252548669.3	240992370.3	257690738.2	209915140.8	239601027.1	242270554.8	400 T		30	0		.49801	0
P10768	ESD		S-formylglutathior	31442.45797		CFGGLQK		11	2			C malkgissnkCFGGLQKVFEH	91247295.5	102221031.9	100988639.5	100379729.6	102625312.4	90321514.44	92504014.81	104080846.6	146 T		31	0		0.43478	0
015511	ARPC5		Actin-related prote	16310.29922		ALAAGGV N		10	1			f mskntvssarfrKVDVDEYDE	67010531.56	63960847.02	82357173.38	85547988.16	81419055.05	79596026.36	82917175.49	88637425.92	93 T		32	0		0.41475	0
P07355	ANXA2	Homo sapiens		38579.81475	1		MVALAK	45	0			mstyheilckLSLEGDHSTPPS	1741822608	1851794295	1683479586	1709139942	1636408389	1494992322	1564897027	1817933154	1260 T		33	0		.40855	0
015942	ZYX	Homo sapiens		61238.16688			SPVTPK[F	21	0			I maaprPSPAISVSVSAPAFYA	50578514.35	51928364.82	53567235.8		57001817.14	54379869.5	54344785.54		333 T		34	0		29.3924	0
P18206	VCL	Homo sapiens		123721.8125		NLGPGMT		76	27			s mpvfhtrtiesilepvaggishlv	265278904.3	255131726.6	268689949.3	284629743.3	274917633	240569507.8	294705392.7	277210929.9	1049 T		35	0		.38368	0
Q9H3P7	ACBD3		Golgi resident prot	60555.9794		EDAMVEFV		13	13			Empirina cresine praggistine empirina cresine praggistic empirina cresine cresin	14675163.63	14219650.28	13547745.78		11976034.96	13548017.07	12465251.7	12918783.64	153 T		36			9.37306	0
Q9Y5S9	RBM8A		RNA-binding prote	19876.73069		MREDYDS'F		6	2			a madvidiheaggedfamdedg	32772252.19	33369727.98	30891973.07	30647121.11	30635230.14	29446616.08	31132875.37	28938800.89	84 T		37	0		9.36559	0
P13489	RNH1		Ribonuclease inhit	49941.08721		DSPCQLEAV		25	ŝ			msldigsldigceelsdarWAEL	193141783.8	195021934.4	207904417.2	204999584.3	222226415.4	194641806.2	210422513.7	211771314.3	322 T		38			9.34363	0
E9PMN0	RNH1		Ribonuclease inhit	18093.84282		LPAASPW (6	1			msldigsldigceelsdarWAEL	121127176.5	116385962	121122918.9	122195466.1	119655862	116508478.5	111914450.1	125547021.3	69 T		39			9.34363	0
A0A1L7AWT6	BUE82_15155	Escherichia col		37441.73261		LIGGMVWR		15	10			a mkktalalavalagfatvaqaapi	258275779	249210629.9	240745806.6	245423573.5	463173971.5	486605826.3	474865133.6	461026775.6	219 T		40			9.33582	ŏ
P14625	HSP90B1	Homo sapiens		92411.34412		KTLDMIK] E		51	23			c mralwylglccylltfgsyraddey		350070808.1	353371089.6			348622140.1	341934064.3	368866180.9	755 T		41	~		0.31688	0
124023	Haraval	nomo sapiens	encopresmin	52411.54412	1	KING MINI D	romas 1	51	23	51%	manwvigici	e interwygrocyntigsyraddey	370909035	550070808.1	555571089.0	555462280.5	551/49207.2	546022140.1	341334004.3	300000100.3	/55 1		41	0	0 23	1.31005	2

- One intensity is reported for protein group for each file.
- This intensity is the sum of all <u>individual</u> modified and unmodified forms of peptides from that protein group.
- Intensities are summed from both MS/MS and MBR.
 - 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.