

With a .group file open use the side bar menu Export> mzIdentML or from the File menu File> Export>mzIdentML to export the results in mzIdentML format.

ProteinPilot™ Software - [Result - C:\Getting Started Examples\8plex\_8 Grad2 1\_6ug A\_EXAMPLE.group]

File Configure Window Help

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
  - Peptide Summary...
  - Distinct Peptide Summary...
  - Protein Summary...
  - Spectrum Summary...
  - MGF Peaklist(s)...
  - mzIdentML...**
  - Features...

Protein ID		Features	Spectra			Summary Statistics			
Results are 'Auto' bias corrected Denominator: IT113									
Accessio...	Name	Species	Peptides(95%)	114:113	115:113	116:113	117:113	118:113	119:113
9 sp P2566...	5-methyltetrahydropteroyltriglutamate-homoocyst...	ECOLI	138	0.6486	0.6607	1.0765	1.0375	0.8954	
3 sp P0CE...	Elongation factor Tu 1 OS=Escherichia coli (strai...	ECOLI	175	0.6607	0.6668	1.1272	0.8472	0.9036	
3 sp P0983...	Glutamate synthase [NADPH] large chain OS=E...	ECOLI	65	0.9817	0.9727	1.0000	0.9727	0.9908	
8 sp P0A8...	DNA-directed RNA polymerase subunit beta OS...	ECOLI	63	0.8630	1.2023	0.8790	0.7047	0.8091	
9 sp P0A9...	Aldehyde-alcohol dehydrogenase OS=Escherich...	ECOLI	67	1.0093	0.9462	0.9550	1.0666	1.0965	
3 sp P0820...	Isocitrate dehydrogenase [NADP] OS=Escherich...	ECOLI	92	0.5649	1.0568	0.9036	0.9462	1.0280	
6 sp P0AF...	Pyruvate dehydrogenase E1 component OS=Es...	ECOLI	69	0.8318	0.6081	0.8954	0.7727	0.8872	
3 sp P0A8...	DNA-directed RNA polymerase subunit beta' OS...	ECOLI	54	1.0471	1.0765	0.9638	1.1912	1.0864	

Remove Redundancy

Conf	Sequence	Modifications	Protein Modifications	Cleavages	ΔMass	Theor m/z	Theor z	Spectrum
99	AALANMVQAAQNLR	iTRAQ8plex@N-term			0.0045	592.3348	3	1.1.1.2054.4
99	ANVYEVR	iTRAQ8plex@N-term			-0.0007	577.8272	2	1.1.1.1309.8
99	APTGEPAAAAEMTK	iTRAQ8plex@N-term iTRAQ8plex(K)@14			0.0008	489.0197	4	1.1.1.1421.5
99	AQESYWAGNSTR	iTRAQ8plex@N-term			0.0029	558.6110	3	1.1.1.1358.12
98.1	CVKPPIVIGDISRPITVEWAK	iTRAQ8plex@N-term Methylthio(C)@1 iTRAQ8plex(K)@3 iTRAQ8plex(K)@23			0.0071	690.4056	5	1.1.1.2092.7
99	DALNSGDTAALAEWSA PIQAR	iTRAQ8plex@N-term			0.0015	821.0923	3	1.1.1.1982.13
99	DDVAELHK	iTRAQ8plex@N-term iTRAQ8plex(K)@6			0.0002	512.2944	3	1.1.1.1315.9
99	DGSVDI DTLFR	iTRAQ8plex@N-term			-0.0001	514.6086	3	1.1.1.1933.3
99	DLWVAS SCSLLHSP IDLSVETR	iTRAQ8plex@N-term Methylthio(C)@8			-0.0007	926.8084	3	1.1.1.2513.15
99	EELLAVGR	iTRAQ8plex@N-term			0.0241	595.8560	2	1.1.1.1608.10
99	EGLPLR	iTRAQ8plex@N-term			-0.0039	494.8083	2	1.1.1.1382.10
99	FKLPAPPTTTIGSFPQTTEIR	iTRAQ8plex@N-term iTRAQ8plex(K)@2		missed K-L...	0.0056	750.6758	4	1.1.1.2191.8

If your data file(s) used in the ProteinPilot search was WIFF use the side bar menu Export MGF Peaklist(s) or the File>Export>MGF Peaklist(s) option to export MGF files.

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Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

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Export

Peptide Summary...

Distinct Peptide Summary...

Protein Summary...

Spectrum Summary...

MGF Peaklist(s)...

Export a recalibrated MGF

Features...

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	99	FKLPAPWPTTITIGSFQITTEIR	iTRAQ8plex@N-term iTRAQ8plex(K)@2		missed K-L...	0.0056	750.6758	4	1.1.1.2191.8
	37.2	GNLDANNYR	iTRAQ8plex@N-term			-0.0009	447.5669	3	1.1.1.1260.4
	99	HQNKDGSVDITLFR	iTRAQ8plex@N-term iTRAQ8plex(K)@4		missed K-D...	-0.0122	589.0735	4	1.1.1.1656.9
	99	HWQQK	iTRAQ8plex@N-term iTRAQ8plex(K)@6			-0.0018	483.9401	3	1.1.1.1231.3
	99	TNDAVAK	iTRAQ8plex@N-term			-0.0068	432.2816	3	1.1.1.1369.4

- **Note: MGF files resulting from TOFTOF data will not contain the necessary information to associate TOFTOF peak list information to identifications in mzIdentML files. Thus it is not necessary to provide TOFTOF MGF files to PRIDE for the purpose of linking spectra to identifications in mzIdentML. Only Partial submission is supported for TOFTOF data.**