ProSightPD 1.1 Quick Start Guide

The ProSightPD[™] application assists you in performing top-down searches in the Thermo Proteome Discoverer[™] application. This quick start guide briefly explains the software required to use the ProSightPD application, ProSightPD nodes, ProSightPD workflows, and ProSightPD-specific information contained in the search results.

This guide assumes that you are familiar with both the $ProSightPC^{TM}$ and Proteome Discoverer applications. For detailed information about these applications, refer to their respective user guides: the *ProSightPC User Guide* or the *Proteome Discoverer User Guide*.

Contents

- System Requirements
- Installing the ProSightPD Nodes
- Searching with ProSightPD
- Performing the Search
- Reviewing ProSightPD Search Results
- References
- Trademarks

The ProSightPD application uses the following terminology:

- High/High—FTMS data with isotopically resolved MS1 and MS2 data.
- Medium/High—Short transient low-resolution FT MS1 data and isotopically resolved MS2 data.
- Low/High—Ion trap resolution MS1 data and isotopically resolved MS2 data.

System Requirements

The Proteome Discoverer and the ProSightPD applications have configuration requirements that your data system must meet before the software operates correctly.

Hardware Requirements

The Proteome Discoverer Release Notes lists the minimum and recommended hardware system requirements.

Table 1. Minimum and recommended hardware requirements for Proteome Discoverer

System	Requirements
Hardware (minimum)	 Data system computer with 2 GHz processor 2 GB RAM DVD-ROM drive Video card and monitor capable of 1280 ×1024 resolution (XGA) Screen resolution of 96 dpi 75 GB available on drive C NTFS format
Hardware (recommended)	 Data system computer with two Intel[™] Xeon[™] 6-core processors, 2.4 GHz 24 GB RAM DVD-ROM drive Video card and monitor capable of 1280×1024 resolution (XGA) Screen resolution of 96 dpi 1 TB available on drive C

Software Requirements	You must insta application.	ll the following software packages to use ProSightPD version 1.1 in the Proteome Discoverer								
·	System	Requirements								
	Software	ProSightPC								
		• Proteome Discoverer (x64 version)								
		ProSight Lite (freeware from prosightlite.northwestern.edu)								
		 Thermo Proteome Discoverer ThirdParty Components installer (also installs the ProSightPD nodes) 								
		 Microsoft[™] Windows[™] 7 x64 Professional (English version) with current service pack 								
Installing the ProSightPD	The Thermo P	roteome Discoverer ThirdParty Components Installer installs the ProSightPD nodes.								
Nodes	Note ProSig Installer are a	htPD nodes that you install with the Thermo Proteome Discoverer ThirdParty Components automatically licensed for 60 days.								
	✤ To install F	roSightPD								
	Select the I	ProSightPD check box in the Select Features dialog box.								
	Contact your le information or	ocal Thermo Fisher Scientific sales representative or email info@proteinaceous.net to obtain how to license ProSightPD and ProSightPD High Mass.								
ProSightPD	Installing the P	roSightPD application adds the following nodes to the Proteome Discoverer application:								
Nodes	 ProSightPD Top-Down High/High cRAWler node—Uses the Xtract algorithm to create experiments from High/High data. 									
	 ProSightPI 	ProSightPD Absolute Mass Search node—Performs a ProSightPC absolute mass search.								
	 ProSightPI) BioMarker Search node—Performs a ProSightPC biomarker search.								
	• ProSightPD Gene-Restricted Absolute Mass Search node—Performs a ProSightPC gene-restricted absolute mass search.									
	 ProSightPI) Gene-Restricted BioMarker Search node—Performs a ProSightPC gene-restricted biomarker search.								
	 ProSightPC 	2 Puf Exporter node—Creates PUF files that you can open in the ProSightPC application.								
Additional	Installing the h	igh-mass version of the ProSightPD application adds these two additional nodes:								
Nodes	 ProSightPI Low/High) Spectrum Selector node—Replaces the default Proteome Discoverer Spectrum Selector node in and Medium/High searches. It collects the profile data that is required to perform these searches.								
	 ProSightPI Low/High) Top-Down Low/High cRAWler node—Uses the ReSpect algorithm to create experiments from and Medium/High data.								
	Parallel Xtr	act—Transforms spectra so that they contain only singly charged ions.								
Searching	To use the Pros	SightPD application in a search, follow these topics:								
with	ProSightPC	C Search Requirements								
ProSightPD	 Downloadi 	Downloading a ProSightPD Database in ProSightPC								
	• Creating a	StudyDefault ProSightPD Templates								
	Setting Up a ProSightPD Database Search									
	Adding File	es to the Study and Selecting Files								
ProSightPC Search	Every ProSight	PD search requires a ProSightPC 4.0 database (PSCW). You can create the ProSightPC database in								
Requirements	1. Download	the database directly from the Proteinaceous web page.								
	2. Download	the ProSightPC database through the ProSightPC application.								
	3. Create a da Database V	tabase using a FASTA file, a UniProtKB XML file, or a UniProtKB flat file with the ProSightPC Vizard.								

Downloading a ProSightPD Database in ProSightPC

To download a ProSightPC database through the ProSightPC application

1. Start the ProSightPC application.

2. Choose Databases > Download ProSightPC Databases.

From proteinaceous.net, you can access top-down and bottom-up databases.

- 3. Click the date of the database that you are interested in, for example, July 2016.
- 4. Click Archaebacteria, Eukaryotes, Prokaryotes, or Custom, as appropriate.

You must know the taxonomy of the species of the database that you want to download.

You can choose from one of the following types of databases:

- TD Complex PSCW—Includes N-terminal acetylation and initial methionine cleavage. This database contains 12 to 15 modifications per entry.
- TD Simple PSCW—Includes N-terminal acetylation and initial methionine cleavage. This database contains up to three modifications per entry.
- Bottom Up PSCW—Includes trypsin digestion using two missed cleavages.
- UniProt XML File—Recreates a PSCW database in the Database Manager.

The website automatically downloads the database once you select it. The downloaded database (a PSCW or an XML file) appears in the Downloads folder in the following directory:

C:\Users > your_name_folder > Downloads

- 5. Choose **Databases > Database Manager**, or click the **View Database Info** icon, **1**, to open the Database Manager window.
- 6. Click 🧰 Open Folder in the toolbar of the Database Manager window.
- 7. Browse to the Downloads folder at the location just given.
- 8. Copy the downloaded database to the database folder.
- 9. In the Database Manager, click Refresh Lists.

The downloaded database now appears in the list of searchable databases.

Database Manager								- 0
Create Search Databa	ase Open F	older 😰 Refr	esh Li:	sts				
Search Databases	High Throughput	Repositories						
Name	Description	Proteome	Strain	Annotated By	Basic Sequences	Proteoforms	Size (MB)	Date
allergens	allergens	cow	n/a	n/a	45	37,200	13.09	7/21/2016
demo	Demo Databas	Human and pheATE	none	Proteinaceous, Inc.	47	102	0.04	8/29/2016
gallus_gallus_2016_07_top_dow	n_simple Gallus gallus ((Gallus gallus (Chicken)		Proteomics Center of Excellenc	23,383	88,833	70.81	2/15/2017

Downloaded database

Creating a Study

Start your data analysis by creating a ProSightPD study in the Proteome Discoverer application. For more information on Proteome Discoverer studies, refer to the *Proteome Discoverer User Guide*.

To create a study

- 1. Start the Proteome Discoverer application.
- 2. Do one of the following:
 - On the Start Page, click New Study/Analysis.
 - Choose File > New Study/Analysis.
 - Click the Create New Study/Analysis icon,

- 3. In the New Study and Analysis dialog box, do the following:
 - a. In the Study Name box type the name of the new study.
 - b. In the Study Root Directory box, browse to or type the location of the study root directory.
 - c. In the Processing Workflow list, select the processing template to use (see the next topic).
 - d. In the Consensus Workflow list, select the consensus template to use (see the next topic).
 - e. Click OK.

New Study and Analysis	
Study Name: Top Down Example	Add Files Add Fractions Kernove Treat as Replicates
Study Root Directory: C:\Program Files\Proteome Discoverer source files \studies\Top Down Example	
Processing Workflow: 2 4.0 Templates \ ProSightPD MED HI.pdProcessingWF	
Consensus Workflow:	
(empty workflow) PMI-Byonic Template.pdConsensusWF ConsensusWF \ CWF_Basic.pdConsensusWF	
ConsensusWF \ CWF_Basic_Annotation.pdConsensusWF ConsensusWF \ CWF_Comprehensive_Enhanced Annotation.pdCor ConsensusWF \ CWF_Comprehensive_Enhanced Annotation_Quan	nsensusWF adConsensusWF
ConsensusWF \ CWF_Comprehensive_Enhanced Annotation_Quan ProSightPD 1.1 for PD 2.2 and PSPC 4.0 Templates \ ProSightPD Bc	_Results export.pdConsensusWF ottom Up.pdConsensusWF
ProSightPD 1.1 for PD 2.2 and PSPC 4.0 Templates \ ProSightPD HJ ProSightPD 1.1 for PD 2.2 and PSPC 4.0 Templates \ ProSightPD LC ProSightPD 1.1 for PD 2.2 and PSPC 4.0 Templates \ ProSightPD M	I HLpdConsensusWF O HLpdConsensusWF IED HLpdConsensusWF
	OK Cancel

Default ProSightPD Templates

You can find the default ProSightPD templates in Libraries > Documents > Thermo > Proteome Discoverer 2.2 > Common Templates > ProSightPD 1.1 for PD 2.2 and PSPC 4.0 Templates.

These are the default ProSightPD processing workflows:

- ProSighPD Bottom Up Absolute Mass.pdProcessingWF—Performs a peptide analysis.
- ProSightPD HI HI Absolute Mass.pdProcessingWF—Performs a basic top-down proteomic search, using a narrow precursor and product ion mass tolerance.
- ProSightPD HI HI Two Tier.pdProcessingWF—Performs a basic top-down proteomic search, followed by a biomarker search using a narrow precursor and product ion mass tolerance.
- ProSight Hi HI Three Tier Search.pdProcessingWF—Performs a basic two-tier proteomic search, followed by an error-tolerant search as a third step.
- ProSightPD HI HI GRAM.pdProcessingWF—Performs a sequence tag search, followed by a gene-restricted absolute mass search of only those proteins found in the sequence tag search.
- ProSightPD HI HI GRBM.pdProcessingWF—Performs a sequence tag search, followed by a gene-restricted biomarker search of only those proteins found in the sequence tag search.

(For the high-mass version of ProSightPD 1.1 only) These are the available processing workflows:

- ProSightPD LO HI.pdProcessingWF—Performs a search similar to the absolute mass search performed by the ProSightPD HI HI Absolute Mass.pdProcessingWF workflow but uses ReSpect deconvolution for precursor mass determination. It is intended for ion trap MS precursor detection. Because MS/MS is still a high-resolution type of mass spectrometry, a narrow mass tolerance is used for the fragment ions.
- ProSight MED HI.pdProcessingWF—Performs a search similar to absolute mass search performed by the ProSightPD HI HI Absolute Mass.pdProcessingWF workflow but uses ReSpect deconvolution for precursor mass determination. It is intended for low-resolution (for example, 17.5k) Orbitrap[™] MS precursor detection. Because MS/MS is still a high-resolution type of mass spectrometry, a narrow mass tolerance is used for the fragment ions.

These are the default ProSightPD consensus workflows:

- ProSightPD Bottom Up.pdConsensusWF—Intended for use with the ProSightPD Bottom Up Absolute Mass.pdProcessingWF processing workflow.
- ProSightPD HI HI.pdConsensusWF—Intended for use with the ProSightPD HI HI Two Tier.pdProcessingWF and ProSight Hi HI Three Tier Search.pdProcessingWF processing workflows.
- ProSightPD LO HI.pdConsensusWF—Intended for use with the ProSightPD LO HI.pdProcessingWF (high-mass version of ProSightPD only) processing workflow.
- ProSightPD MED Hi.pdConsensusWF—Intended for use with the ProSight MED HI.pdProcessingWF (high-mass version of ProSightPD only) processing workflow.

If you want to make any changes to the templates to set up a search, follow these instructions. For example, you might want to choose different search parameters.

To set up a ProSightPD database search

- 1. In the study, click the Workflows tab.
- 2. Click the **Show Workflow** icon, , on the Processing Step toolbar in the Analysis pane for a processing workflow.

The processing workflow appears in the Workflow Tree pane.

- 3. In the workflow, click a search node, for example, the ProSightPD Absolute Mass Search node.
- 4. Select a different setting for a parameter of this node. For example, you might want to select a different database (PSCW file) from the list of databases given by the Proteome Warehouse parameter.
- 5. For any other search nodes in the workflow, follow step 3 and step 4 for each one.

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4. Output Data Event Parente to Per Texe		Result File: Enter result file name.	
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Please select the Proteome Warehouse (pscw) to search against.			
	★		
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Workflow Nodes Parameters of 'ProSightPD Abachida	4	T A A A A A A A A A A A A A A A A A A A	

Adding Files to the Study and Selecting Files

If a raw data file is not defined in the creation of a study, follow these steps.

✤ To add files to the study or select files for the search

- 1. On the Study_name page of the Proteome Discoverer application, click 🚅 Add Files .
- 2. In the Add Files dialog box, select the file and click **Open**.
- 3. Click the **Input Files** tab.

Setting Up a ProSightPD Database Search

4. Drag the input file or files to the Processing Step area of the Analysis pane.

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		Workflow: ProSightPD MED HI	
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		▼ Child Steps: (1)	Add
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Ac	d Files icon	Show Workflow icon F	un icon

Performing the Search

Reviewing ProSightPD Search Results

✤ To perform a search

In the Analysis pane, click 🔐 Run .

To open the .pdResults report

• In the job queue on the Administration page, select the consensus file, and click 👸 Open Results ·

-or-

• In the study, click the Analysis Results tab, and double-click the name of the .pdResults file.

The .pdResults file opens.

File View Administration Tools Window Help																					
Start Page 🗴 Study: Top Down Example 🗴 Administration X 20160901_PierceProteinMix_MabPac_150x15_CD_water_water_60C_200mg_01 x																					
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k m/z [Da]	MH+ [Da]	Theo. MH+ [Da]	ΔM [ppm]	∆m/z [Da]	Activation Type	MS Order	Isolation Interferen	nce [%] Ion	Inject Time [ms]	RT [min]	First Scan Spectru	um File		File ID	-Log P-Score -	Log E-Value 🔻	C Score	Corrected Delta Mass (Da)	Corrected Delta Mass (ppm)	Fragment Map	^
1 989.76106	11866.05264	11859.05120	590.39	0.58345	CID	MS2		55	174.370	7.9986	689 201609	01_PierceProt	einMix_MabPac_	F1	74.09	72.34	118	-0.579	-48.83	View	
I 913.70307	11866.05264	11859.05120	590.39	0.53857	CID	MS2		50	143.422	7.9327	686 201605	01_PierceProt	einMix_MabPac_	F1	69.16	67.41	121	-0.579	-48.83	View	
1 913.68993	11865.88174	11859.05120	575.98	0.52543	CID	MS2		56	67.497	7.4312	662 201609	01_PierceProt	einMix_MabPac_	F1	66.00	64.25	137	-0.750	-63.23	View	
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1 913.65455	11865.42178	11859.05120	537.19	0.49004	CID	MS2		49	128.647	11.5631	856 201605	01_PierceProt	einMix_MabPac_	F1	63.58	61.83	146	-1.210	-102.00	View	
1 989.74682	11865.88174	11859.05120	575.98	0.56921	CID	MS2		61	95.720	7.4515	663 201605	01_PierceProt	einMix_MabPac_	F1	63.04	61.30	173	-0.750	-63.23	View	
1 1187.52871	11866.22158	11859.05120	604.63	0.71704	CID	MS2		0	0.323	7.5744	669 201605	01_PierceProt	einMix_MabPac_	F1	60.73	58.98	109		-34.59	View	
1 989.83845	11866.98135	11859.05120	668.70	0.66085	CID	MS2		29	2.256	6.9469	638 201605	01_PierceProt	einMix_MabPac_	F1	60.54	58.79	126	0.349	29.44	View	
1 848.70353	11868.75479	11859.05120	818.24	0.69311	CID	MS2		70	107.656	7.4736	664 201605	301_PierceProt	einMix_MabPac_	F1	57.81	56.07	115	2.123	178.90	View	
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1 11864.82075	11865.82803	11859.05120	5/1.45	6.77683	CID	MS2		38	187.349	10.0487	788 201605	01_PierceProt	einMix_MabPac_	F1	56.93	55.18	91	-0.804	-67.76	View	_
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1 848.57685	11866.98135	11859.05120	668.70	0.56644	CID	MS2		66	4,495	6.9662	639 201605	JUI_PierceProt	einmix_mabPac_	F1	47.60	45.90	52	0.349	29.44	View	-
1 1187.60468	11866.98135	11859.05120	668.70	0.79301	CID	MS2		54	12,010	7.0104	641 201605	01_PierceProt	einmix_mabPac_	F1	40.83	39.08	166	0.349	29.44	View	-
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1 20002 12010	20304.14340	20304.03337	671.44	10.43007	CID	MS2 MC2		74	7.3.473	0.5750	717 201603	01_PierceProt	einMix_MabPac_	F1	27.62	26.97	100	1.529	52.75	View	-
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1 11865 79927	11866 80655	11859.05120	653.96	7 75534	CID	MS2		68	58 841	6.9157	636 201605	01 PierceProt	einMix_MabPac	F1	34.14	32.39	3	0.174	14.71	View	_
1 21442 76900	21443 77627	21430 76642	607.06	13,00985	CID	MS2		42	200.000	5 3272	558 201605	01 PierceProt	einMix MabPac	F1	32.19	30.45	153	-0.067	-3.14	View	_
1 21442.66743	21443.67471	21430.76642	602.32	12.90829	CID	MS2		0	48.172	5.4567	564 201605	01 PierceProt	einMix MabPac	F1	31.03	29.29	125	-0.169	-7.87	View	_
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1 11865.79927	11866.80655	11859.05120	653.96	7,75534	CID	MS2		44	68,110	6.8494	633 201609	01 PierceProt	einMix MabPac	F1	25.53	23.78	291	0.174	14.71	View	-
1 68001.01509	68002.02237	67960.43243	611.97	41.58994	CID	MS2		87	148.630	9.7461	774 201605	- 01_PierceProt	einMix_MabPac_	F1	18.20	16.45	104	-0.817	-12.02	View	-
1 50422.72993	50423.73721	50430.85368	-141.11	-7.11647	CID	MS2		37	23.636	5.9588	588 201605	01_PierceProt	einMix_MabPac_	F1	17.10	15.35	186	-37.535	-743.85	View	
1 21442.76900	21443.77627	21341.73650	4781.23	102.03977	CID	MS2		39	200.000	5.2776	556 201605	01_PierceProt	einMix_MabPac_	F1	16.39	14.64	0	89.085	4,171.89	View	
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1 853.45246	28984.14346	28964.69537	671.44	0.57200	CID	MS2		70	7.894	8.6192	719 201605	01_PierceProt	einMix_MabPac_	F1	15.69	13.94	88	1.529	52.75	View	
1 11865.79927	11866.80655	11859.05120	653.96	7.75534	CID	MS2		66	119.224	6.8715	634 201605	01_PierceProt	einMix_MabPac_	F1	14.66	12.91	102	0.174	14.71	View	
1 11865.79927	11866.80655	11859.05120	653.96	7.75534	CID	MS2		57	80.244	6.8288	632 201605	01_PierceProt	einMix_MabPac_	F1	13.90	12.15	194	0.174	14.71	View	
1 11865.33931	11866.34658	11859.05120	615.17	7.29538	CID	MS2		74	200.000	10.8442	824 201605	01_PierceProt	einMix_MabPac_	F1	13.75	12.00	111	-0.285	-24.06	View	
1 68003.77290	68004.78018	67960.43243	652.55	44.34775	CID	MS2		65	52.642	9.0399	740 201609	01_PierceProt	einMix_MabPac_	F1	12.59	10.84	44		28.53	View	
1 28996.05610	28997.06338	28964.69537	1117.50	32.36801	CID	MS2		24	200.000	8.2684	702 201605	01_PierceProt	einMix_MabPac_	F1	11.14	9.39	92	14.449	498.55	View	
1 29013.46821	29014.47549	28964.69537	1718.65	49.78012	CID	MS2		24	200.000	8.2684	702 201605	01_PierceProt	einMix_MabPac_	F1	11.14	9.39	89	31.861	1,099.35	View	
1 68003.77290	68004.78018	67960.43243	652.55	44.34775	CID	MS2		82	31.352	9.0821	742 201605	01_PierceProt	einMix_MabPac_	F1	11.05	9.30	82	1.940	28.53	View	
4																					Þ
Show Asso	ciated Tables																				
Ready	eshy 6 Proteins, 6																				

The *Proteome Discoverer User Guide* explains in detail how to review search results. Each proteoform identified by the ProSightPD application is stored in the Proteome Discoverer application as a PSM. The results of a ProSightPD search include the following features on the PSMs page:

- Three scoring columns (-Log P-Score, -Log E-Value, and C Score)
- Two Corrected Delta Mass columns (Da and ppm)
- One Fragment Map column

By clicking View in the Fragment Map column, you can view the fragment map associated with the hit in ProSight Lite (see the next figure). If ProSight Lite is not already installed, download and install it from the prosightlite.northwestern.edu website.

File View Administration Tools Window Help										
Ast Date, V Sudo Ton Down Formale, V (definitivities, V) 20160001 Enceptorbandler Mobber 150-15 (D) water water 60 (200n; 01 V)										
💷 Proteins Protein Groups Peptide Groups PSMs MS/MS Spectrum Info Input Files 😵 Specialized Traces										
k m/z (Da) MH+ [Da] Theo. MH+ [Da] ΔM (ppm) Δm/z (Da) Δctivation Type MS Order isolation interference [12] ion inject Time [ms] RT (min) First Scan Spectrum File File ID -Log P-Score -Log E-Value + [C Score Corrected Delta Mass (Dan) Corrected Delta Mass (Dan) Fragment Mag										
989.76106 11866.05264 11859.05120 590.39 0.58345 CID MS2 55 174.370 7.9986 689 20160901_PierceProteinMix_MabPac_F1	74.09 72.34 118	-0.579	-48.83	View						
1 913.70307 11866.05264 11859.05120 590.39 0.53857 CID MS2 50 143.422 7.9327 686 20160901_PierceProteinMix_MabPac_ F1	69.16 67.41 121	-0.579	-48.83	- Men						
1 913.68993 11865.88174 11859.05120 575.98 0.52543 CID MS2 56 67.497 7.4312 662 20160901_PierceProteinMix_MabPac_ F1	66.00 64.25 137	-0.750	-63.23	View						
1 913.84791 11867 93545 11859 05120 749.15 0.68340 B Declinite Lite		1.303	109.85	View						
1 913.65455 11865.42178 11859.05120 537.19 0.49004		-1.210	-102.00	View						
1 989.74682 11865.88174 11859.05120 575.98 0.56921 BEILE Modify Experimental Data Modify Candidate Sequence Expert	Help	-0.750	-63.23	View						
1 1187.52871 11866.22158 11859.05120 604.63 0.71704	About		-34.59	View						
I 989.83845 11866.98135 11859.05120 668.70 0.66085	Des evenes Mars	0.349	29.44	View						
I 848.70353 11868.75479 11859.05120 818.24 0.69311 N T T F N I Q D G P D F Q D R V V N S E T P V V V D 25	Precursor Mass	2.123	178.90	View						
848.51352 11866.09463 11859.05120 593.93 0.50310	Type: Average	-0.537	-45.29	View						
11854 22075 11855 22003 11859 05120 57145 6.77683 26 FHAQW GP KILGPRLEKMVAKQHG 50	Observed: 11,865.05	-0.804	-67.76	View						
	Theoretical: 11,865.63	1.529	52.75	View						
	Mass Diff. (Da): -0.587	0.349	29.44	View						
	Mass Diff. (ppm): -49.49	0.349	29.44	View						
1 744 JOE 1 2004 JUL 1006 30135 11033 U012U 1006./U 0.32006		1.520	23.44	View						
1 29909 19919 29909 19349 20194 00330 07144 0 43009 101 FLLKKLIGC	Scores	1.525	52.75	View						
2 2030-3 Jol 6 2 2030+1-3-96 2 2030+03J37 011+4 13-44602	PCS: 867.97	0.906	21.26	View						
2 11967 7977 11962 R0457 1 2000 10057 4 2000 10053 10 100200	P-Score: 8.1e-75	-1.846	-155.51	View						
11865/7927 11866.80655 1185/05120 653.96 7.75534	% Fragments Expl 27 %	0.174	14 71	View						
1 21442 70200 21443 77627 21430 76642 607.06 13.00885	% Residue Cleava 39 %	-0.067	-3.14	View						
21442.66743 21443.67471 21430.76642 602.32 12.90829		-0.169	-7.87	View						
1 28982.51314 28983.52041 28964.69537 649.93 18.82505	Modification (T1)	0.906	31.26	View						
1 28982 51314 28983 52041 28964 69537 649.93 18.82505		0.906	31.26	View						
28983.13618 28984.14346 28964.69537 671.44 19.44809	No Modification	1.529	52.75	View						
1 11865.79927 11866.80655 11859.05120 653.96 7.75534	Custom	0.174	14.71	View						
1 68001.01509 68002.02237 67960.43243 611.97 41.58994	Commun	-0.817	-12.02	View						
1 50422.72993 50423.73721 50430.85368 -141.11 -7.11647	Common	-37.535	-743.85	View						
1 21442.76900 21443.77627 21341.73650 4781.23 102.03977	Phosphorylation	89.085	4,171.89	View						
2 21442.76900 21443.77627 21430.76642 607.06 13.00985	Uncommon	-0.067	-3.14	View						
1 853.45246 28984.14346 28964.69537 671.44 0.57200	Monomethylation	1.529	52.75	View						
11865.79927 11866.80655 11859.05120 653.96 7.76534	Acetylation	0.174	14.71	View						
1 1185b./992/ 1186b.8065b 11859.00120 603.96 /.79634		0.174	14.71	View						
1 11855.3331 11855.49058 11853.05120 615.17 7.29538		-0.285	-24.06	View						
8 8003.//280 88004./8018 6 /980.43243 6 bb.25 44.34/75		11.00	28.53	View						
1 2395 U391 2337 U3538 2397 U5538 23954 53537 1117.39 22.39001 23012 2402 2012 2014 2451 23924 62923 1219 2451 2451 2451 2451 2451 2451 2451 2451		14.449	498.55	View						
1 C0002 T2010 C0004 C2011474/2492 C0204-05242 (1/10.50) 49.7/01/2 ⊗ Matching Fragments (Count: 53)		31.861	1,039.35	View						
00003/1/30 00004/0010 0/30043649 002.30 44.347/0 101241007 0112 0/1007 0112 0/1007 0112 0/2007		0.116	28.03	View						
1 796 7527 2911 1028 29687 2015 00000 Neutral Masses, CID, 10ppm		58.420	2 015 74	View						
		30,420	2,013.74							
Chan Associated Tables				,						

References

The following references are useful in understanding the searches in the ProSightPD application. You can direct additional questions to info@proteinaceous.net.

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