

PMI Byonic™

User Manual

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Overview

Byonic™ is a software package for identifying peptides and proteins by tandem mass spectrometry. Byonic plays the same role as Mascot, SEQUEST, and X!Tandem, but offers greater accuracy, sensitivity, and flexibility. Byonic provides several major features not found in the other search engines:

Modification Fine Control™ enables the user to search for 10s or even 100s of modification types at a time without a combinatorial explosion. For example, a user might allow up to three phosphoserines, S[+80], per peptide, but allow at most one beta elimination, S[-18], and at most one deamidated asparagine, N[+1]. To further reduce the search, the user might allow at most one of *either* S[-18] *or* N[+1], that is, disallowing peptides containing one of each. Modification Fine Control empowers the user to tailor the search to the sample, and thus avoid overly narrow searches that miss interesting peptides and overly broad searches that run for hours or days and produce "noisy" results with many false positives.

Wildcard Search™ enables the user to search for unanticipated, or even unknown, modifications. A wildcard can modify any residue by any mass delta within a user-settable range. Wildcard masses occur at roughly 1.0 Dalton spacing just like molecular masses. There is a limit of one wildcard per peptide.

Glycopeptide search enables the user to search for glycosylated peptides, without prior knowledge of either glycosylation sites or glycan masses. Byonic now offers three ways to specify glycopeptide searches: internal tables, external tables, and modification fine control. Byonic's internal tables contain the most likely N- and O-linked glycan compositions. The other two options allow the user to customize the list of glycans and/or allow more than one glycan per peptide.

Top-down, middle-down, and bottom-up proteomics – Byonic is uniquely capable of top-down, middle-down, and bottom-up searches, but it relies upon isotope-resolved precursors in order to determine precursor ion charges. Without isotope-resolved precursors, the user will need to assign charge and set a large precursor mass tolerance.

Disulfide bonds, trisulfide bonds, and general crosslinking – Byonic has disulfide bond, trisulfide bond, and general crosslink search capability. It is designed to search for all disulfide pairs (both expected and shuffled disulfide bonds) and the user can constrain which protein chains to consider when doing the search.

Requirements

System Requirements

The following systems are recommended:

Recommended PC:

Windows 7 64-bit

16 GB RAM or more

1TB disk space or more

Multi core CPU (E.g. Intel Core i7-5930K @ 3.50GHz)

High performance PC (for 32+ core system):

Windows Server 2012 or higher

64 GB RAM or more

2TB disk space or more

Two Xeon CPUs (recommend 8 to 16 physical cores)

Java Requirement

Java is required to run Byonic. Either Oracle JRE or OpenJDK needs to be installed. Byonic uses the system environmental variable PMI_JAVA_HOME to determine the version of Java to use. If undefined, then the default Oracle Java registered in the system is used.

To load Java:

- Oracle JRE:

Download and install the 64-bit version from https://www.java.com/en/.

- OpenJDK:

1. If it does not already exist, create the subfolder “java” under the “C:\Program Files” folder. This requires Administrator privileges on the machine.

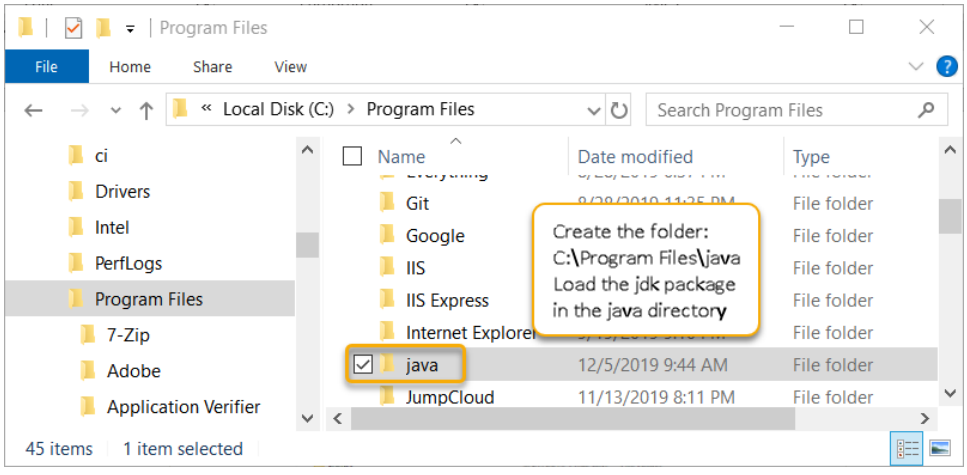


Figure 1: Create a “java” folder

2. Go to https://jdk.java.net/archive/ and download the latest Windows/x64 version. **Note**: OpenJDK version 13.0.1 is the current general-availability release when this manual was written. The older versions 11.0.2 and 12.0.2 are also supported.
3. Unzip and copy the content of the downloaded package to “C:\Program Files\java”.
4. Create the system environmental variable ‘PMI_JAVA_HOME’ and set the value to the OpenJDK installation directory: *e.g:* PMI_JAVA_HOME=C:\Program Files\java\jdk-13.0.1. In older versions of Windows, open **Control Panel -> System Properties -> Advanced -> Environmental Variables**. In Windows 10, open **Control Panel -> System and Security -> System** and click **Advanced system settings**.

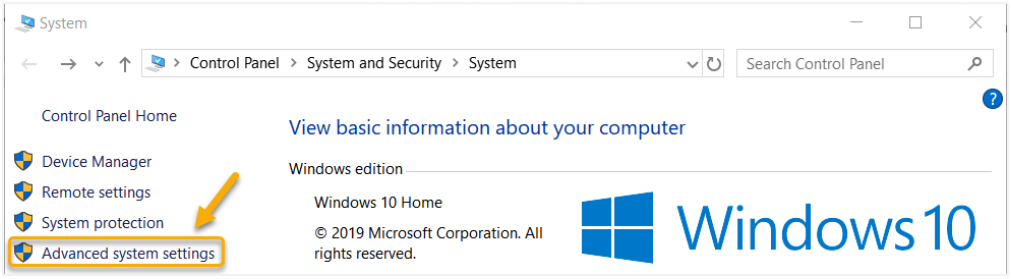


Figure 2: Windows 10 System settings

5. In the Advanced tab, click **Environment Variables**.

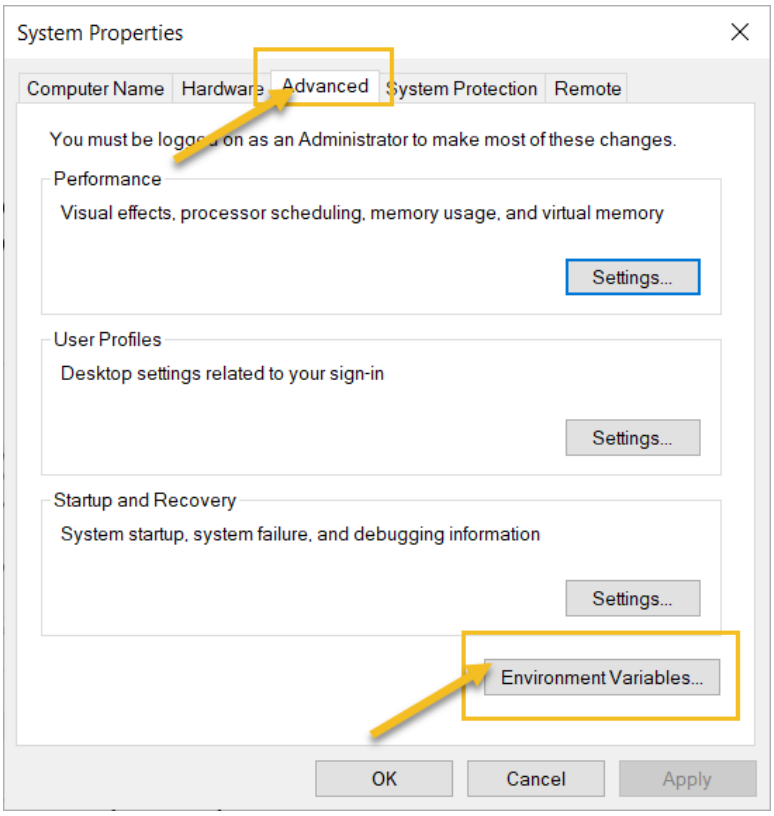


Figure 3: Advanced System Properties from the Control Panel

6. In the Environmental Variables dialog, click **New**.

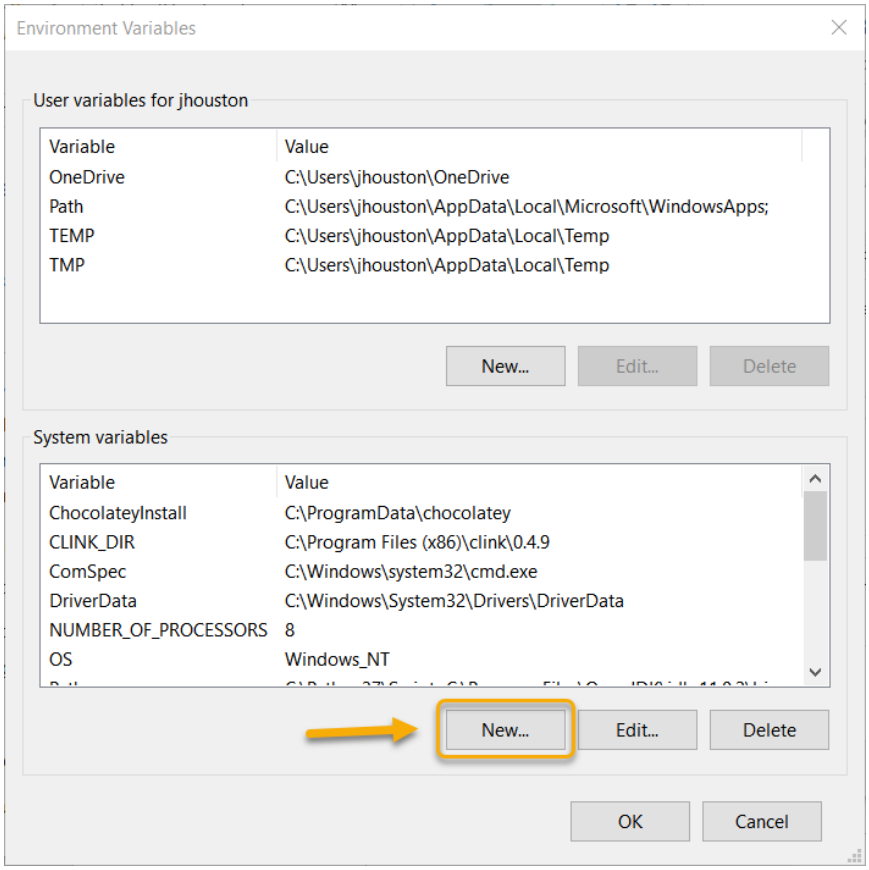


Figure 4: Environmental Variables dialog

7. In the Edit System Variable dialog, enter Variable name “PMI_JAVA_HOME”. Click **Browse Directory** and navigate to the jdk folder (C:\Program Files\java\jdk-XX.X.X) and click **Open**.

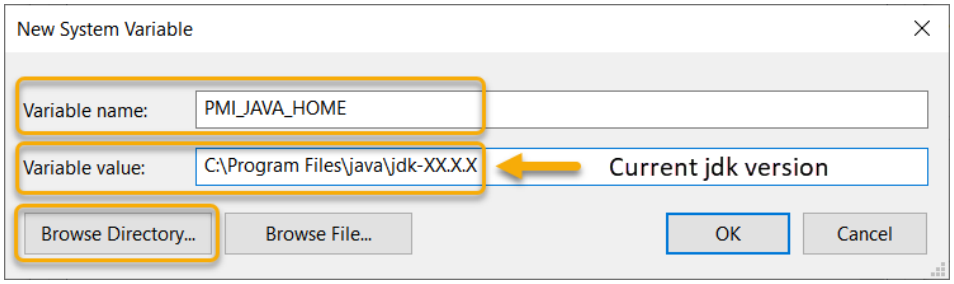


Figure 5: New System Variable creation

Click **OK** to create the variable.
Note: If the PMI_JAVA_HOME variable name already exists with an older version of jdk that was replaced, select the variable name, click **Edit**, click **Browse Directory**, navigate to the jdk folder, click Open, and then click OK to save the edited variable value.

Byonic Search Screen

An example of the Byonic search screen is shown in Figure 6:

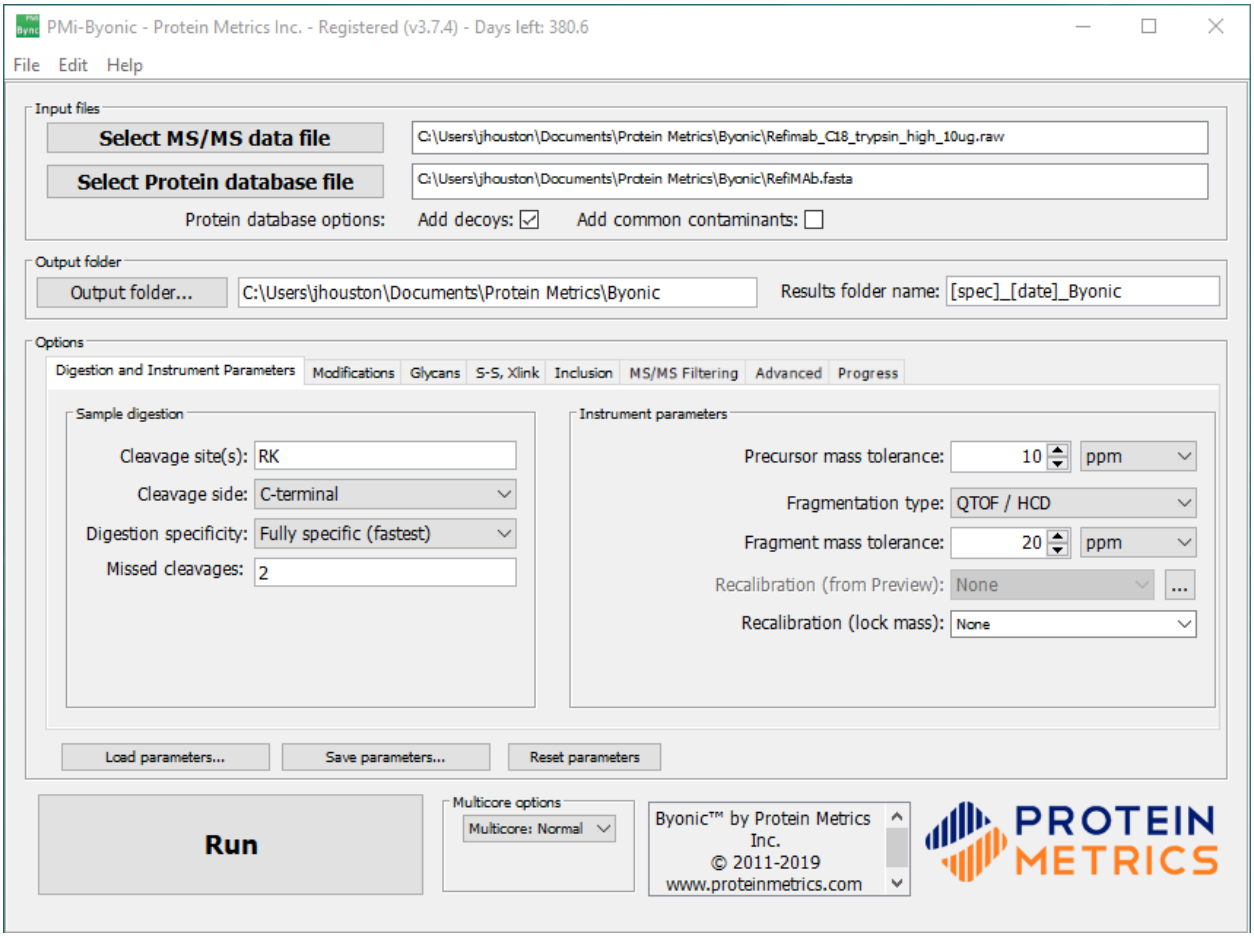


Figure 6: Byonic search screen

The search screen includes input file management, output file management, several tabs for setting search options or parameters, and finally, search management actions.

Input and Output sections

The **Input files** section at the top locates the spectrum data file and protein database file, along with database search options:

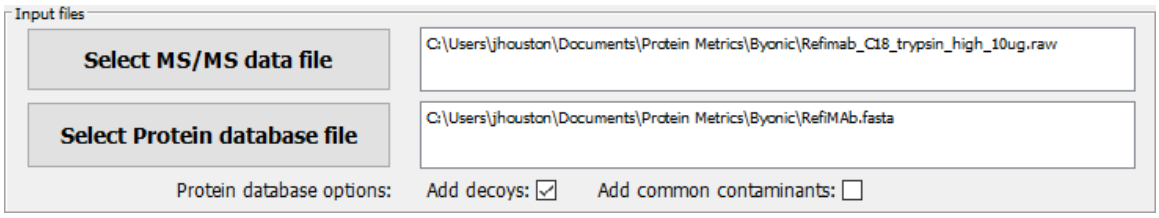


Figure 7: Input files section

To load a mass spectrum data file, click **Select MS/MS data file**, navigate to the desired file, and click **Open**. The spectrum data file can be one of a number of standard formats: *.MGF, *.mzML, *.mzXML, Thermo *.raw, Waters *.raw, Sciex *.wiff, Bruker *.d, Agilent *.d, and Shimadzu *.lcd, etc.

To load a protein database, click **Select Protein database file**, navigate to the desired FASTA file, and click **Open.** The protein database should contain both targets and decoys (recognized by protein names beginning >Reverse or >Decoy) for false discovery rate (FDR) estimation. Byonic will automatically add decoys if the **Add decoys** box is checked and contaminant proteins (e.g., trypsin, bovine serum albumin, and human keratins) if the **Add common contaminants** box is checked. Typical folders to store input files are: C:\data_input\Mass_Spectra and C:\data_input\Protein_Databases.

In the **Output folder** section, appearing next, the user selects the directory under which a results folder will be created and chooses the naming convention for that folder and the results files:

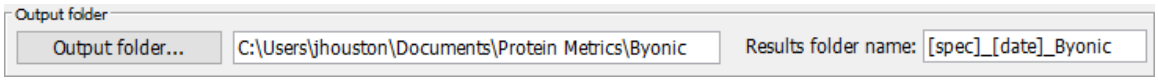


Figure 8: Output folder section

To select the directory where the Byonic search output folder will be created, click **Output folder**, navigate to the target folder, and click **Open**. (Due to a Windows DOS limitation, the total folder path name must be less than 256 characters; please note long .raw file names may 256-character limit) The standard output folder is C:\data_results. In the **Results folder name** cell, the user can choose the format for naming the search output folder and the search result files saved to that folder. Free text will appear in folder and file names as written. The items in square brackets represent supported objects that can become part of these names. The supported objects are:

- [spec] the name of the mass spectrum data file,
- [fasta] the name of the FASTA file,
- [date] the current date (year, month, day)
- [time] the current time (hour, minute)

In the example in Figure 8, if the mass spectrum data file was named “project123.d” and the search was run on 02/15/2020, the output folder name would be “project123.d_20200215_Byonic”.

Digestion and Instrument Parameters tab

The first tab in the **Options** section is the **Digestion and Instrument Parameters** tab:

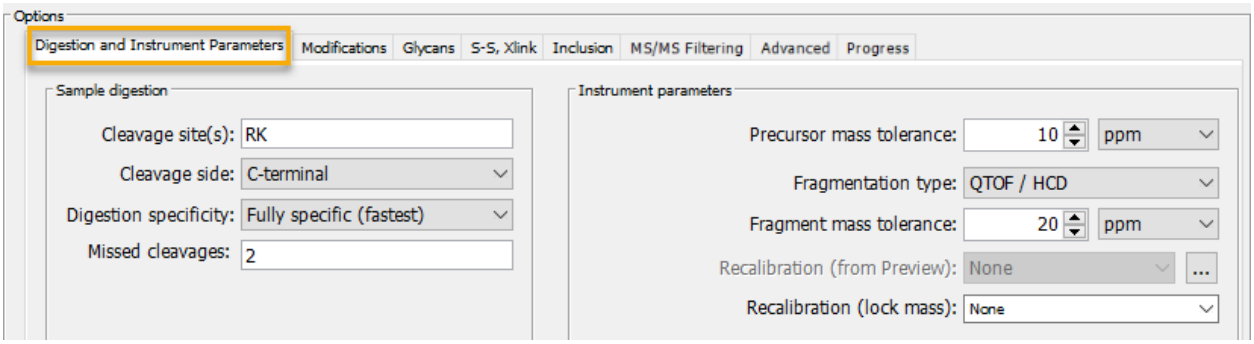


Figure 9: Digestion and Instrument Parameters tab

Sample digestion

The **Sample digestion** section allows the user to set the residues recognized by the digestion enzyme as shown. For example, in Figure 9 the enzyme is trypsin, so the user entered RK for arginine and lysine and chose C-terminal for the cleavage side.

- **Cleavage site(s)** identifies specific cleavage sites. When the Cleavage site(s) box is blank, specific cleavage sites are limited to protein termini.
- **Cleavage side** designates the C-, N- or both termini for the cleavage side. For example, RK; DE for Cleavage site(s) along with C-terminal; N-terminal for Cleavage side would be appropriate for digestion by a combination of trypsin and Asp-N.

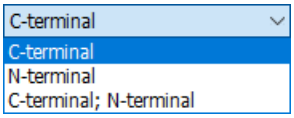


Figure 10: Cleavage side options

- **Digestion specificity** balances search specificity and performance. For example, the “Fully specific (fastest)” search selected in Figure 11, requires that both the N- and C-terminal cleavages be C-terminal to R or K. Nonspecific cleavage at either or both endpoints is supported.

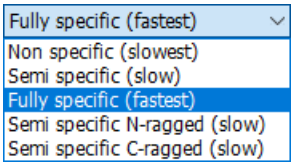


Figure 11: Digestion specificity

A nonspecific search will search all peptides but favors specified digestions. In Figure 9, Cleavage Site(s) is set to RK which searches all peptides but favors tryptic peptides. For a true no-enzyme search, leave the Cleavage Site(s) box blank.

- **Missed cleavages** limits the maximum number of missed cleavages. In Figure 9, a setting of two missed cleavages limits internal R’s and K’s not followed by P to 2. The default value for Missed cleavages is -1, which allows any number of internal R’s and K’s.

Instrument parameters

The **Instrument parameters** section sets values controlling precursor mass, fragmentation and recalibration. Both Dalton and ppm mass tolerances for precursors and fragments are supported, along with several fragmentation types

- **Precursor mass tolerance** sets the maximum mass difference between observed and theoretical (calculated) peptide mass.
- **Fragmentation type** sets the model(s) used to scan and score fragment peaks.

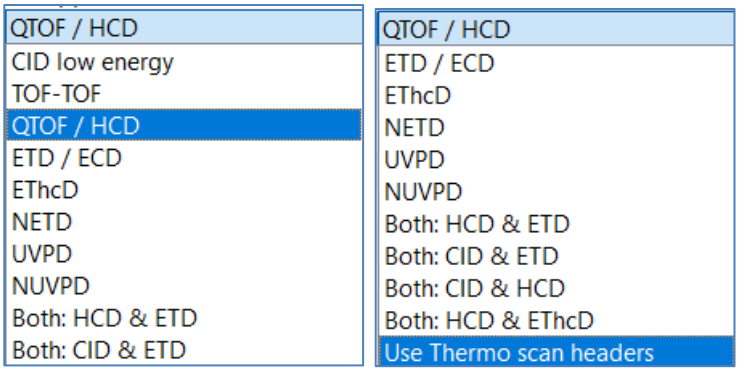


Figure 12: Fragmentation type

Internal models for most fragmentation types are included – CID low energy (ion trap), QTOF / HCD (beam-type CID), and ETD / ECD (electron transfer and electron capture dissociation), as well as a number of combinations of these types. These internal models determine which fragment peak types will be scored and annotated. For example, prominent c- and z-ions and small y-ions are expected for ETD. Prominent oxonium ions are expected from glycopeptides with QTOF / HCD fragmentation, but small or missing oxonium ions from CID low energy.

If a spectrum file contains more than one fragmentation type, for example, alternating HCD and ETD on a Thermo Orbitrap, Byonic will match the labels on the scans to the chosen fragmentation types, so that the MS/MS scans will be scored with the appropriate models. If a scan does not match the selected model, it will be ignored. For example, if the .raw file contains both HCD and ETD scans, the user must select “Both: HCD & ETD” or “Use Thermo scan headers” in order to score both types of scans with the correct model. “Use Thermo scan headers” is a new option that supports all standard combinations of ETD, CID, and HCD, along with choices of mass analyzers. For example, Byonic can now handle “tribrid” data with Orbitrap HCD and EThcD and ion trap CID.

If a spectrum file contains only a single fragmentation type, or as in the case of *.mgf files, does not specify fragmentation type, then the user can choose any single fragmentation model for scoring. For example, HCD can be scored as CID low energy, or EThcD scored as pure ETD. Switching fragmentation models is occasionally advantageous, for example, when EThcD scans use extremely low collision energy.

- **Fragment mass tolerance** is the maximum difference in m/z for matching fragments. Byonic supports both relative (ppm) and absolute (Dalton) tolerances. Relative tolerances are generally recommended for time-of-flight and FTMS mass analyzers, and absolute tolerances for ion trap mass analysis. Fragment tolerances of 0.1 Da or 100 ppm or less apply to high-resolution MS/MS analysis, providing sufficient resolution to distinguish charge states of fragment ions. Fragment tolerances larger than 0.1 Da should be used with low-resolution (ion trap) MS/MS analysis.

Modifications tab

The **Modifications tab** defines specific modification parameter values and Wildcard searches.

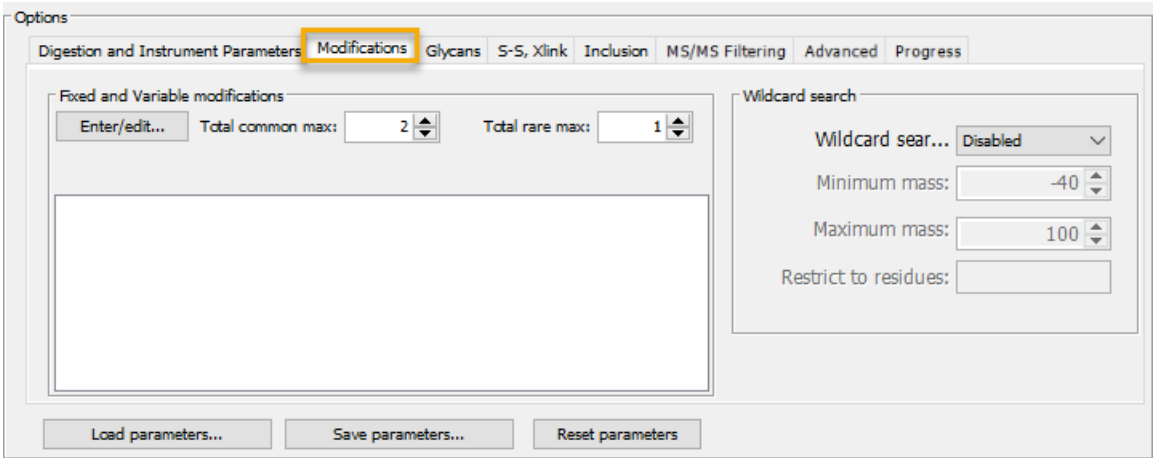


Figure 13: Modifications tab

Like most proteomics search engines, Byonic supports two types of modifications: fixed and variable. A **fixed** modification is assumed to occur on all the residues of that type, but a **variable** modification is optional, so that each site for a variable modification is considered with and without the modification.

Byonic also offers a unique feature not found in other search engines: the user designates each variable modification as either **"common"** or **"rare"**, with the names suggesting their use. Byonic has separate limits on the number of occurrences of each variable modification, so that "common2" means at most two occurrences per peptides. Byonic also has separate limits on the **total number** of common and rare modifications per peptide. A typical search allows a total of at most two common modifications and a total of at most one rare modification per peptide. To search for, say, three phosphoserines per peptide, the user can change Total common modification max to 3 or split phosphorylated serine between two rules: common2 and rare1. Depending upon the other modification rules, the latter approach may give a faster search.

Select Modifications

To add fixed and variable modifications, click **Enter/Edit** to open the **Select Modifications** dialog:

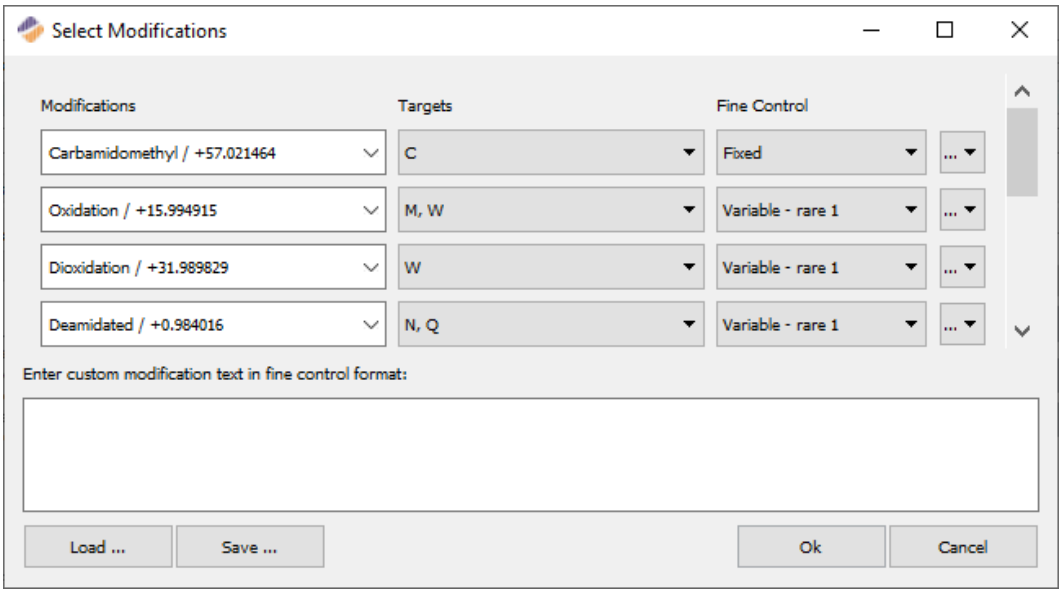


Figure 14: Select Modifications dialog

The modification set can then be edited and extended. Modifications include name and delta mass pairings, modification targets and fine control settings that set modifications as fixed or variable, as well as rare or common. Additional actions can also be performed on the modifications.

- **Modifications** displays a list of common modifications and their corresponding delta masses. The list includes all candidates found in www.unimod.org.

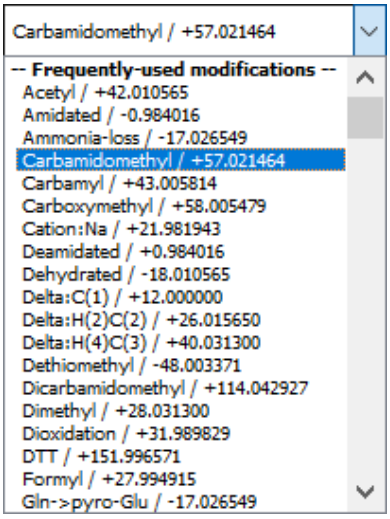


Figure 15: Modification Name / Mass Delta

For convenience, frequently used modifications are listed twice, once at the top and again in the complete list.

- **Targets** displays a list of possible target locations associated with the selected modification name. The Targets field allows the 20 one-letter amino acid abbreviations, as well as four special locations: NTerm, CTerm, Protein NTerm, and Protein CTerm. NTerm, CTerm, Protein NTerm, and Protein CTerm can also be used as modifiers of amino acid residues. Targets form a comma-separated list.

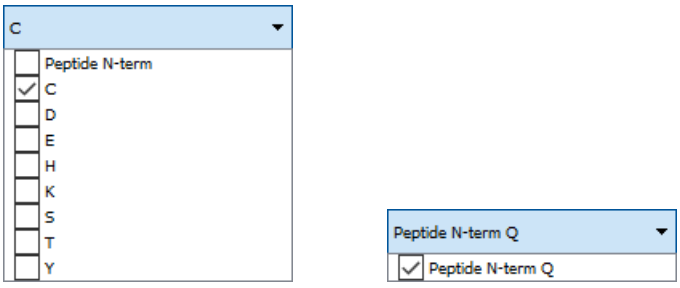


Figure 16: Modification Targets

- **Fine control** marks the modification as “Fixed” or “Variable”, whether the variable modification is considered “Rare” or “Common”, and the maximum count of that modification in the peptide.

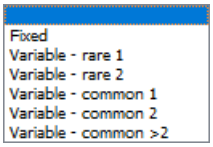


Figure 17: Fine Control

- The ... button in the last column exposes additional actions that can be performed on modifications:

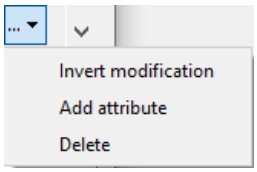


Figure 18: Additional Modification actions

  - **Invert modification** defines a variable modification that is the removal of a fixed modification (for example, under-alkylation. The modification is labeled with the prefix "(De)", as shown in Figure 19:



Figure 19: Invert modification

  - **Add attribute** allow the user to define protein-specific modifications. For example, adding the attribute "ProteinLabel{collagen}" to Oxidation on P allows hydroxyproline only on proteins with "collagen" in their protein names:

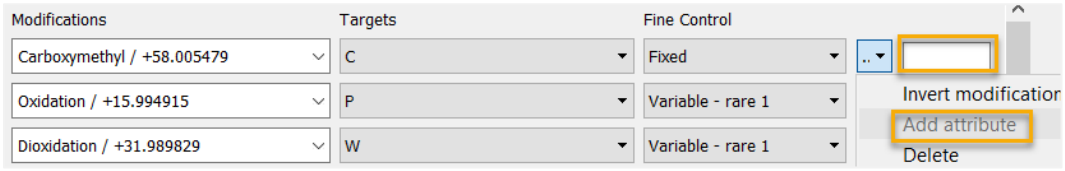


Figure 20: Add modification attribute

  - **Delete** removes that modification record.

To add a new modification, scroll to the bottom of the modification records and add entries for Modifications, Targets and Fine Control:

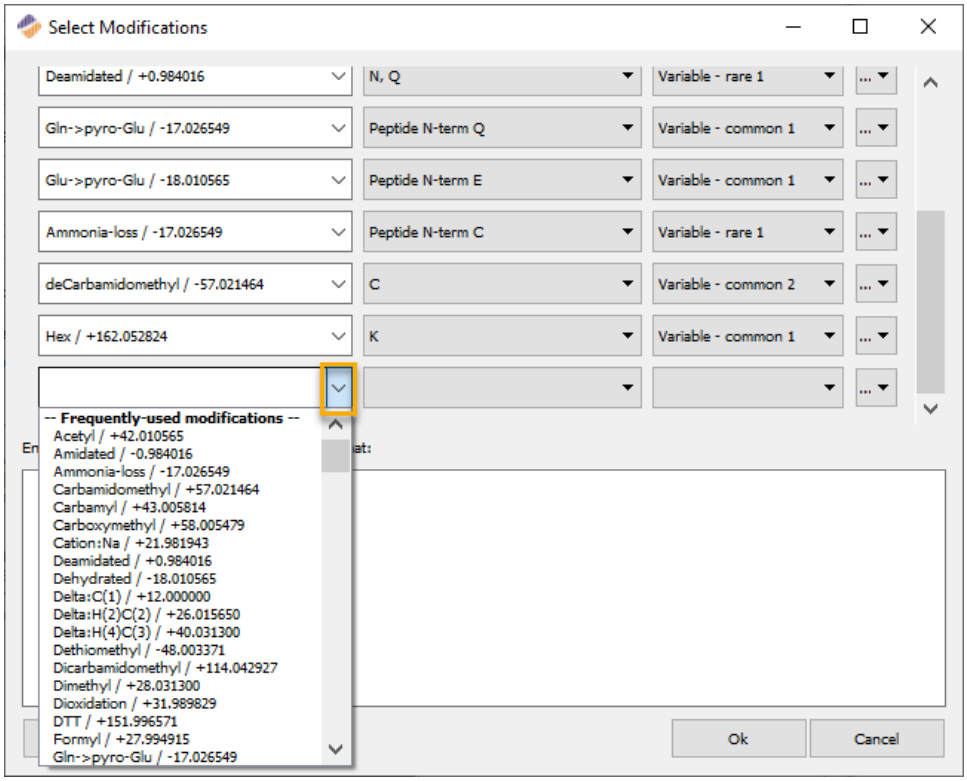


Figure 21: Adding a new modification

An entry for Modification name is optional. The resulting modification record has the format:

Modification_Name / Mass_Delta @ Targets | Fine_Control

Custom modifications can be manually entered in this format in the box labeled **Enter custom modification text in fine control format**. The following is an example of a real modification not (yet) in Unimod:

DehydroFormyl / +9.98435 @ NTerm S, NTerm T | rare1

For **comprehensive sequence variant searches**, or other searches with large numbers of modifications, it is more convenient to paste in a list of modifications in the custom modification box than to add all the modifications via the drop-down menus. Sequence variant lists are available from Protein Metrics by contacting support@proteinmetrics.com.

Click **Save** to export the selected and custom modifications as a text file. This text file can then be loaded into another Byonic session by clicking **Load**. When the list of modifications is complete, click **Ok**. The modification strings are now listed in the Modifications tab.

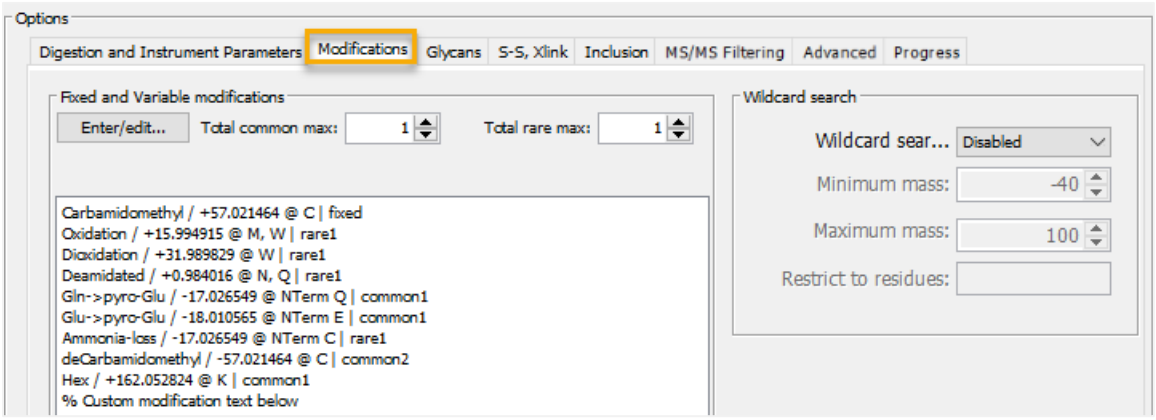


Figure 22: Example set of Fixed and Variable modifications.

To set maximum allowed modifications, set values for **Total common max** and **Total rare max**. To set no maximum, leave the value at zero.

In Figure 22, the user specified Carbamidomethyl / 57.021464 @ C | fixed, meaning carbamidomethylated cysteine (camC). The user also specified Oxidation / +15.994915 @ M | common2, directing the program to consider each methionine residue with and without this modification, up to a limit of 2 such modifications per peptide. In addition, the user specified Ammonia-loss / -17.026549 @ N-term C | rare1, indicating that the program also considers this modification for any N-terminal cysteines as a rare variable modification. Variable modifications are added on top of fixed modifications, so the total mass added to these N-terminal C's will be 57.021+14.016 = 71.037, which represents cysteine propionamide. One way to represent incomplete carbamidomethylation is with these two rules: Carbamidomethyl / +57.021464 @ C | fixed and (De)Carbamidomethyl / -57.021464 @ C | common2.

The rule Carbamidomethyl / +57.021464 @ NTerm | rare1 specifies a common artifact (over-alkylation) on the peptide N-terminus.

The next two rules, +0.984016 @ N | common2 and +0.984016 @ Q | common1, represent deamidation; here the user is allowing up to two deamidated asparagines (the more common deamidation) but only one deamidated glutamine per peptide.

The rule Gln->pyro-Glu / -17.026549 @ NTerm Q | rare1 specifies a modification that occurs only on peptides with N-terminal glutamine.

Conceptually, Byonic has one modification "slot" for each residue, along with slots for the peptide's N- and C-termini. A variable modification such as +0.984016 @ N uses up the residue slot; a nonspecific terminal modification such as +57.021464 @ NTerm uses up the terminal slot; but residue-specific N-terminal modifications, such as -17.026549 @ NTerm Q, use up both the residue and the N-terminal slots.

Byonic can support a limited number of **non-standard amino acid residues** by redefining one-letter amino acid abbreviations using fixed modifications. Starting with version 2.9.77, Byonic accepts B, Z, U, O, J, and X in FASTA protein databases. The non-standard amino acid masses are:

Abbreviation	Mass	Comments
B	114.042927	Same as N
Z	128.058578	Same as Q
U	150.95363	Selenocysteine
O	237.147730	Pyrrolysine
J	100.0	
X	110.05	Close to averagine

For example, by placing a fixed modification of +13.04768 on J, the user can make J in a FASTA database have mass 113.04768, correct for hydroxyproline. Byonic does, however, use amino acid sequence to predict peak intensity, so this fixed modification on J will not give the same scores as a +15.9949 variable modification on P.

For **backwards compatibility**, Byonic still accepts the syntax from earlier versions:

[Residues][Mass_Delta], Fine_Control

Examples of the earlier syntax are [ST][+79.966], common2 for phosphorylation and N-terminal S[+9.984], rare1 for DehydroFormyl.

The **Wildcard search** section of the Modifications tab lets the user turn on wildcard searches, set the range for the wildcard mass, and restrict the wildcard to certain residues if desired.

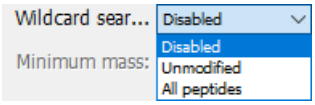


Figure 23: Wildcard search

The **Restrict to residues** box uses the common 20 single-letter residue abbreviations, and (lower case) n denotes peptide N-terminus and (lower case) c denotes peptide C-terminus. A wildcard, even one with a mass range of only 50 or 60 Da, greatly increases the size of the search. It is best used with a focused database (see the Advanced tab section below) and used either alone or with only a few other modifications enabled. Most wildcard mass shifts will be recognizable by an expert; hence, a wildcard can be used to discover which known modifications should be enabled in a subsequent search. For more details about the wildcard search, see the application note "Byonic™: Wildcard Search™" at https://www.proteinmetrics.com/resources/#application-notes.

By specifying most modifications as rare, it is quite feasible to search for 10 – 20 modification types at once with Byonic. Even larger searches are possible with focused protein databases, for example with therapeutic proteins. Such a focused database easily allows efficient mutation searches with 200+ possible substitutions, or oxidative footprinting searches with 50+ types of oxidations. Glycans and wildcards can easily enlarge the search space by 2 to 3 orders of magnitude, so these options should be used with care, and in conjunction with only the most common variable modifications (such as oxidized methionine or pyro-Glu N-terminus). **NOTE**: The single most important factor in search time is Total common max. Roughly speaking, the search time grows as C^T where C is the number of common modifications enabled and T is Total common max.

The **Appendix** of this Manual provides examples of frequently found modifications and appropriate syntax for including those modifications in a Byonic search.

The wildcard search has been expanded to amino acid positions with an already present glycan mass modification. N-linked, O-linked, and other glycan motifs are supported.
The user must use the below parameters:

- **Wildcard search**: All peptides
- **Minimum** and **Maximum mass:** Set values
- **Restrict to residues**: set to "g" to search for wildcard modifications on top of glycan modifications

Glycans tab

The **Glycans tab** allows the user to associate a glycan database with the Byonic search:

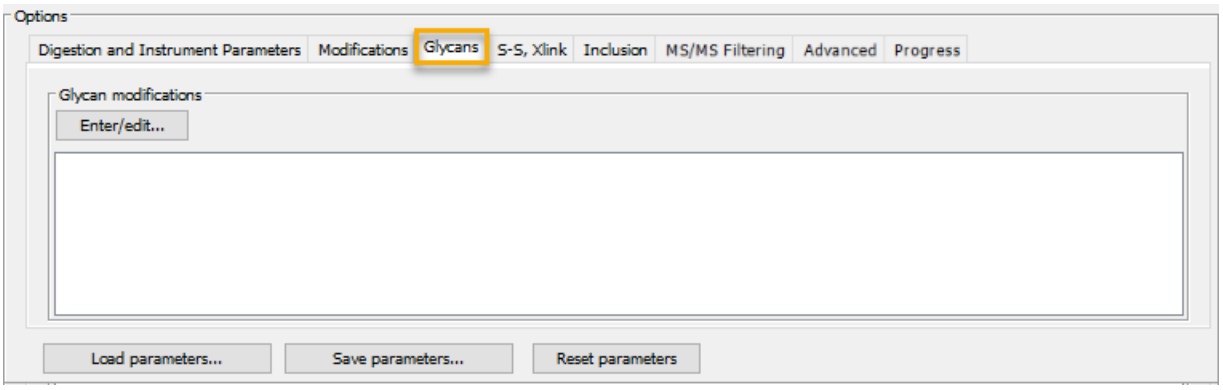


Figure 24: Glycan tab

Byonic offers three ways to define glycan modifications: internal preset tables, external glycan databases, and user-defined glycans. To add glycans, click **Enter/Edit** to open the **Select Glycans** dialog:

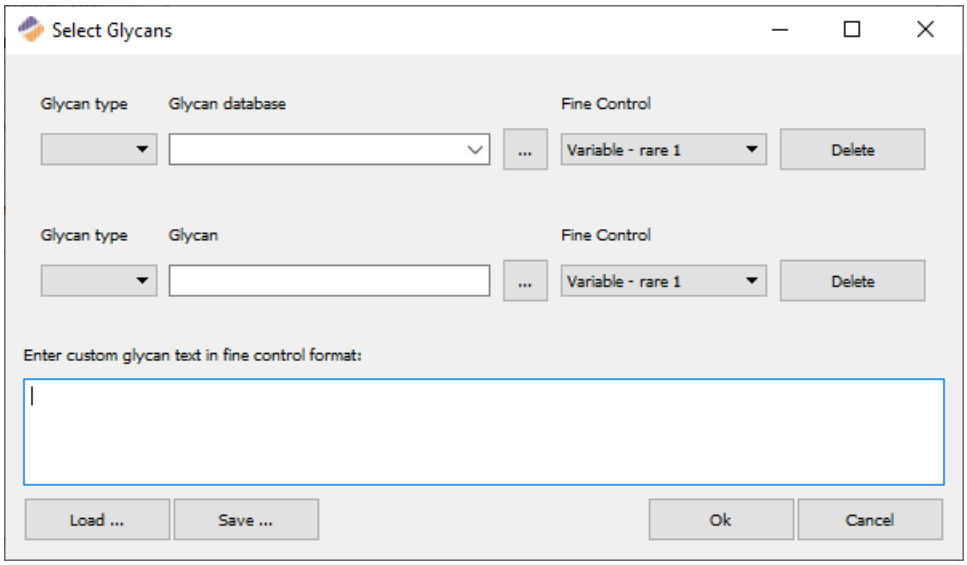


Figure 25: Select Glycans

Similar in look to the Select Modifications dialog, Select Glycans allows the user to set glycan types, choose a glycan database, and define variables as rare or common. The dialog also allows the free entry of glycans in the proper format.

- Glycan type sets it as either an N-glycan or an O-glycan. N-glycans are allowed on Nx{S/T} motif where x is anything except P. O-glycans are allowed on any S/T:

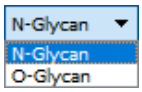


Figure 26: Glycan Type

- Glycan Database allows the user to input a database of glycans:

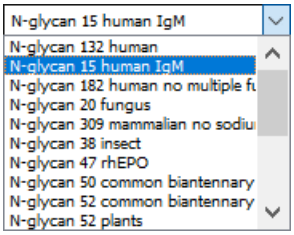


Figure 27: Glycan database options

The database dropdown references a list of glycan database text files found in **C:\Program Files\ProteinMetrics\PMI-Suite\Base\data\GlycanDatabases**. These text files can be edited, and new glycan database text files can be added to the directory, where they become available in the dropdown (after closing and reopening Byonic). This set of glycan databases is continually updated based on customer feedback. Please reach out to support@proteinmetrics.com to request additional content.

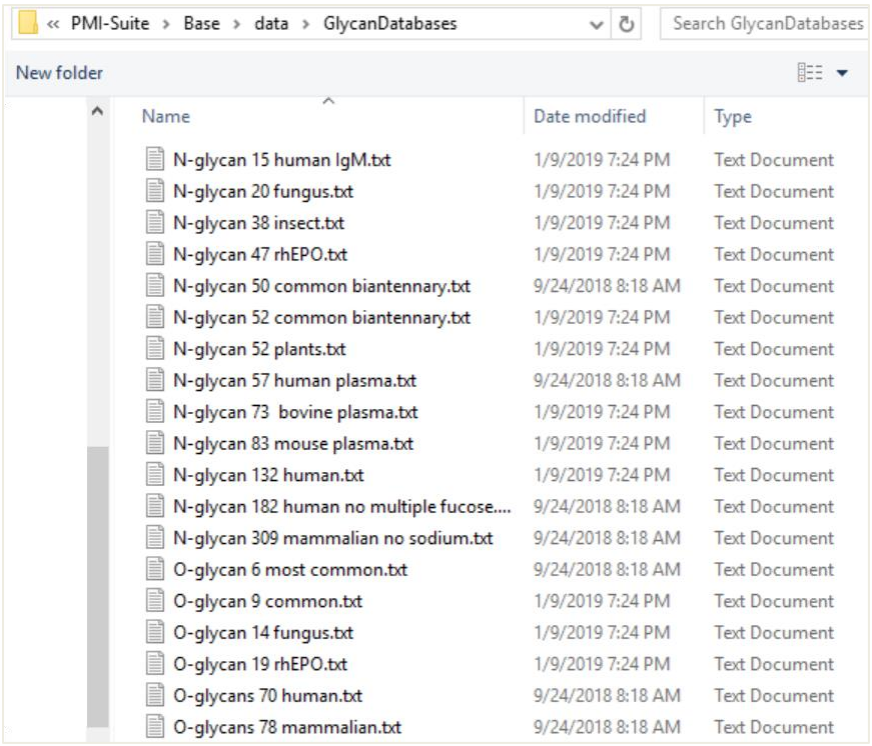


Figure 28: Glycan databases included with installation

Alternatively, a glycan database can be selected from another directory. To open a new glycan database, click the ... button, navigate to the desired directory, select database text file, and click **Open**.

- Fine Control designates the glycan as common or rare, and sets a limit on the count of that glycan per peptide:

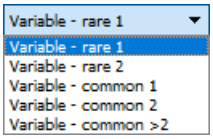


Figure 29: Glycan Fine Control options

- Delete removes the glycan record.

In addition to glycan databases, users can construct a glycan from monosaccharide units in the second section. To assemble a glycan, first select the Glycan type (N-Glycan and O-Glycan) from the dropdown. Next, click the ... button to the right of the Glycan box. This opens the **Edit Glycan** dialog:

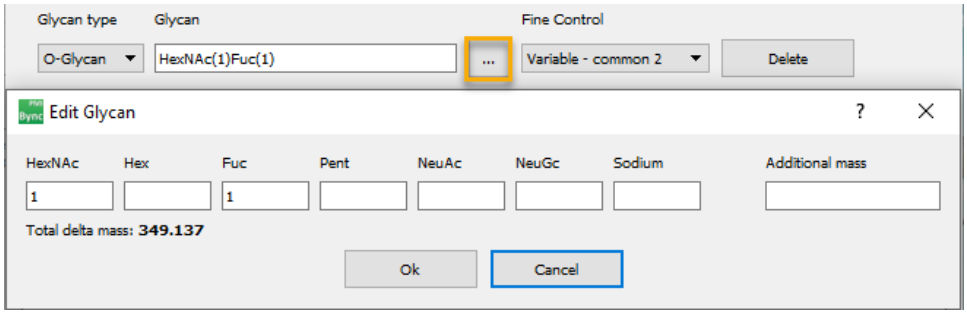


Figure 30: Enter a specific glycan

Enter the count of each used monosaccharide. Six monosaccharide residues are allowed: HexNAc, Hexose, Fucose, Pentose (common in plants), NeuAc, and NeuGc (common in non-humans). There is also a box for Sodium because this is a common adduct on sialic acids. Unused monosaccharides can be left blank or included with zero (0) occurrences. In the resulting text, spaces between monosaccharides units are optional. For example, five common human O-glycans are represented as:

HexNAc(1)
HexNAc(1)Hex(1)
HexNAc(1)Hex(1)NeuAc(1)
HexNAc(1)Hex(1)NeuAc(2)
HexNAc(1)Hex(1)Fuc(1)

Total delta mass displays below for the added monosaccharides. Glycan modifications such as acetylation, phosphorylation, or sulfation or less common monosaccharides such as deaminated neuraminic acid can be added by typing in the correct keywords, “Acetyl”, “Phospho”, “Sulfo”, and “Kdn” respectively. Byonic scoring and annotation will consider peaks for likely placements of these modifications, for example, Acetyl on NeuAc. We are constantly adding to our list of keywords, so it is a good idea to check with info@proteinmetrics.com for unusual glycan components. To support as-yet-undefined glycan components, Byonic also allows arbitrary mass deltas to be input to the Additional mass box. Keywords are preferred over delta masses; a delta mass of 42.010565 does not give the same scoring and spectrum peak annotation as a keyword of “Acetyl”. Click **Ok** to create the glycan:

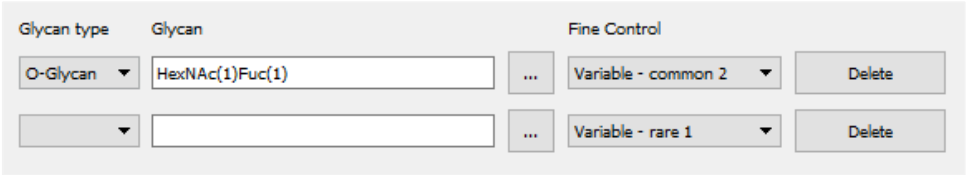


Figure 31: Glycan assembled from monosaccharides

Assign a **Fine Control** value as with the glycan databases.

A third way to enter glycans is to enter or paste glycan text in the **Enter custom glycan text in fine control format** box at the bottom. These glycans are entered using the same format as for individually added glycans: Monosaccharide(count) @ 0 or NGlycan | fine control option

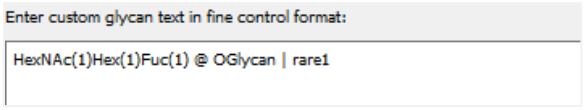


Figure 32: Manually entered or pasted glycan

As with modifications, glycans can be saved and reloaded in other Byonic searches. Click **Ok** to add the various glycans to the Byonic query:

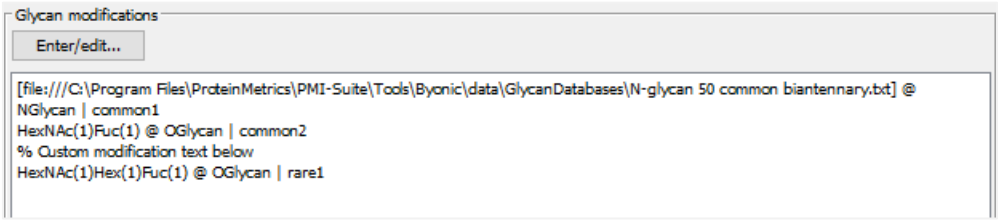


Figure 33: Example of loaded glycan database and individual glycans

Both “OGlycan” and “NGlycan” are modification sites in the sense that modifications other than glycosylation may make use of these keywords. For example, “Heavy deamidation / 2.98826 @ NGlycan | common2” would allow deamidation in O18 water only at N within Nx{S/T}. Conversely, one can place glycans on glycosylation sites besides NGlycan and OGlycan. For example, “HexNAc(1)Hex(1) @ Y | common2” allows (O-linked) glycosylation on Y. For some helpful examples and best practices for conducting N-linked and O-linked glycan searches, see our Application Notes at https://www.proteinmetrics.com/resources/#application-notes.

S-S, Xlink tab

The **S-S, Xlink** tab allows the user to search for disulfide-bonded peptide pairs, trisulfide-bonded (also called persulfide-bonded) pairs, and more general cross-linking. This tab provides options to allow a user to search for expected and unexpected disulfide bonds.

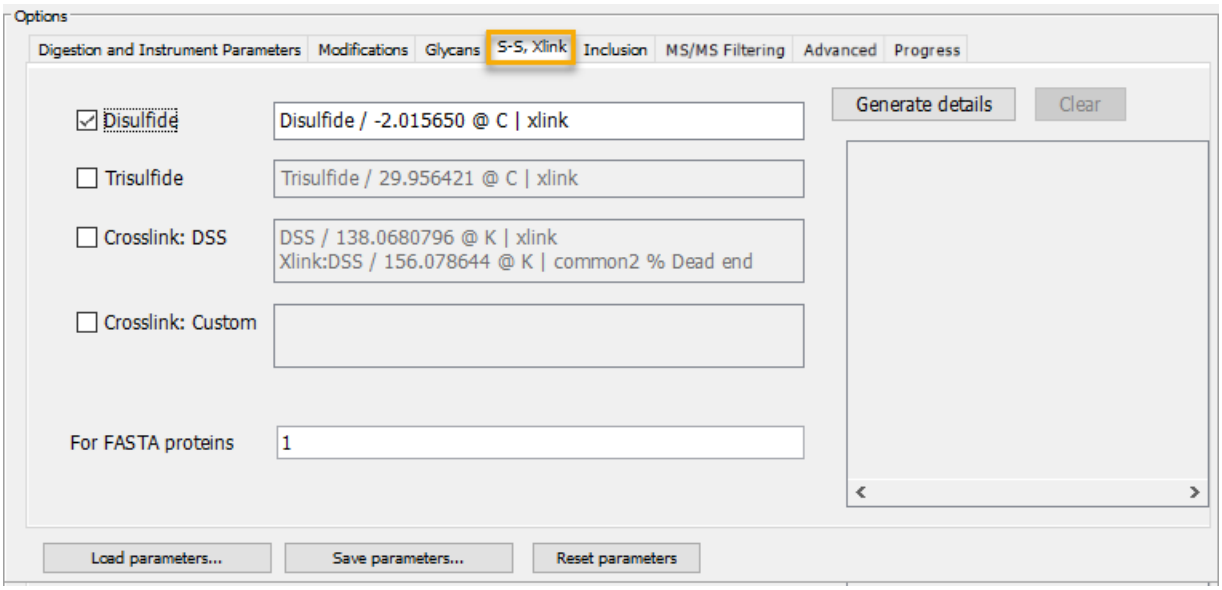


Figure 34: S-S, Xlink tab.

Check the **Disulfide** box on the top left to attempt to pair each peptide that contains a cysteine with each other cysteine-containing peptide in an in-silico digestion. To indicate which protein sequences from the FASTA database to consider for pairings, enter the protein numbers in the **For FASTA proteins** box:

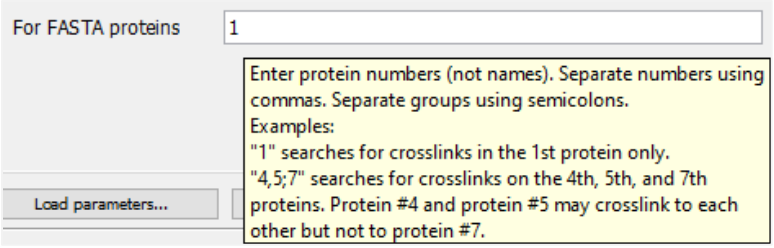


Figure 35: For FASTA proteins entry for designating numerically which protein sequences from the FASTA database to be considered

Commas between protein numbers allow crosslinks between those proteins. Semicolons between protein numbers indicate internal linking for the two proteins but no crosslinking between them.

The **Trisulfide** checkbox includes searches for trisulfides within a single peptide or linking between two peptides.

The **Crosslink: DSS** and **Crosslink: Custom** checkboxes include searches for crosslinks within a single peptide or linking between two peptides.

The **Generate details** button displays all the linked peptides with their mass deltas to be included in the Byonic search, based on the previous settings. To fine-tune the search, this text may be edited.

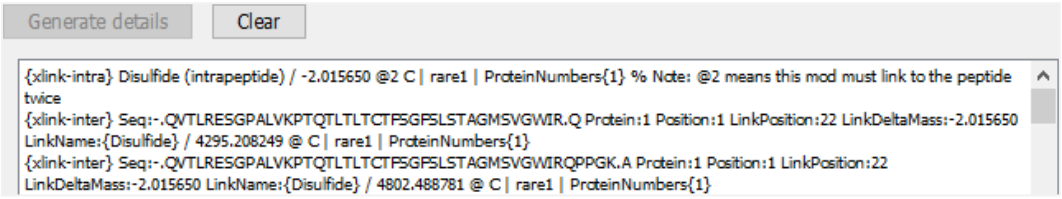


Figure 36: Generate details for S-S, Xlink

Inclusion tab

The **Inclusion** tab allows the user to define a m/z ratio range and/or elution time range segments to include in the search. Enter the begin and end values for one or both range types. A new row is automatically added for additional range definitions.

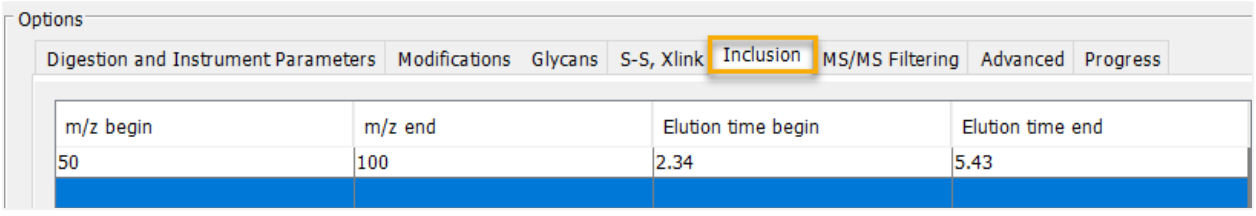


Figure 37: Inclusion tab

MS/MS Filtering tab

The **MS/MS Filtering** tab introduces MS/MS diagnostic peak filtering:

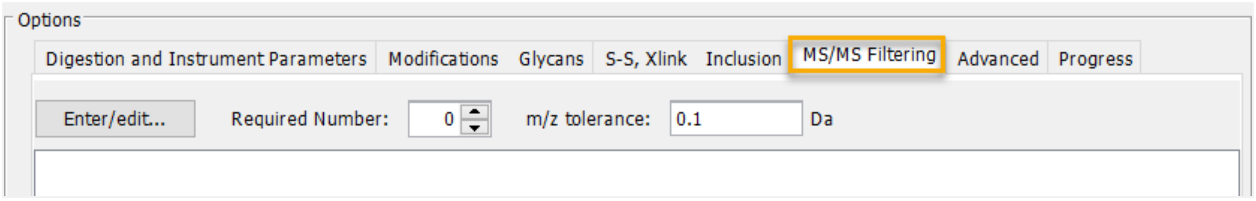


Figure 38: MS/MS Filtering tab

To create an MS/MS diagnostic peak filter, click the **Enter/edit** button. The **Select Peaks** dialog opens:

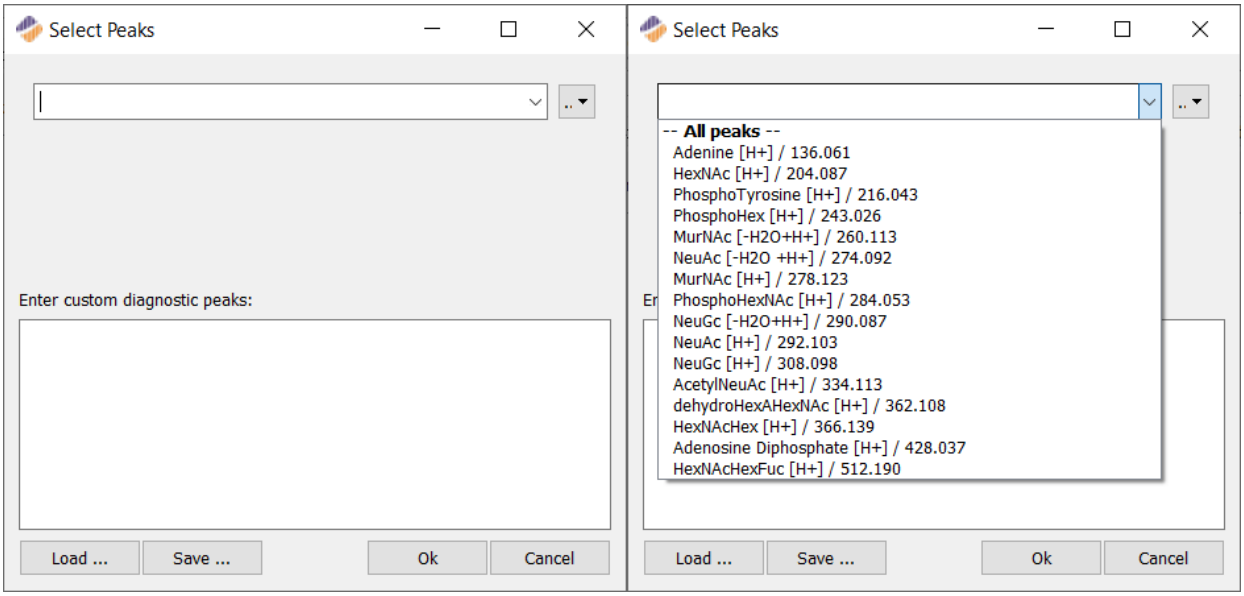


Figure 39: Select Peaks dialog with diagnostic peak drop-down

Click the down arrow to expose the available diagnostic peak. When a peak is selected a new row appears for diagnostic peaks. The  button in the last column exposes additional actions that can be performed on diagnostic peaks:

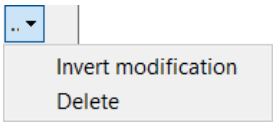


Figure 40: MS/MS peak inversion option

Custom modifications can be manually entered in this format in the box labeled **Enter custom diagnostic peaks**. The following is an example format of a diagnostic peak:

Kdn / 251.076

The selected and custom diagnostic peaks can be exported as a text file by clicking **Save**. This text file can then be loaded into another Byonic session by clicking **Load**. When the list of diagnostic peaks is complete, click **Ok**. The diagnostic peaks strings are now listed in the MS/MS Filtering tab:

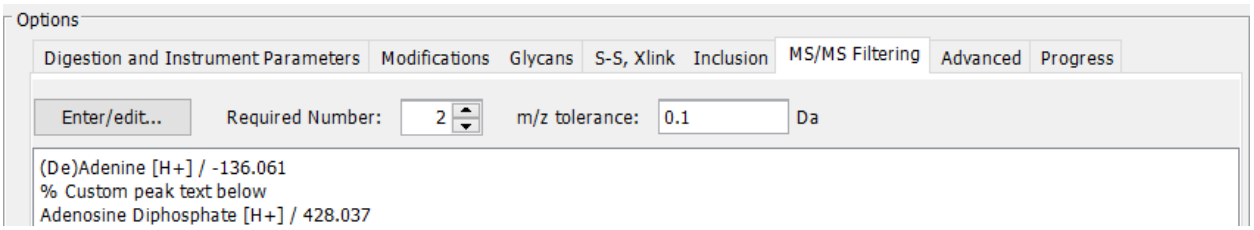


Figure 41: MS/MS Filtering tab with added diagnostic peaks

To set a required count of diagnostic peaks from within the list, enter a value in **Required Number**. To set no minimum requirement, leave the value at zero. A maximum **m/z tolerance** can also be set.

Advanced tab

The **Advanced** tab contains a variety of spectrum, peptide and protein options**.** This tab helps Byonic respond to imperfect inputs. For example, on many MS instruments precursor ion charges are uncertain for some or all spectra

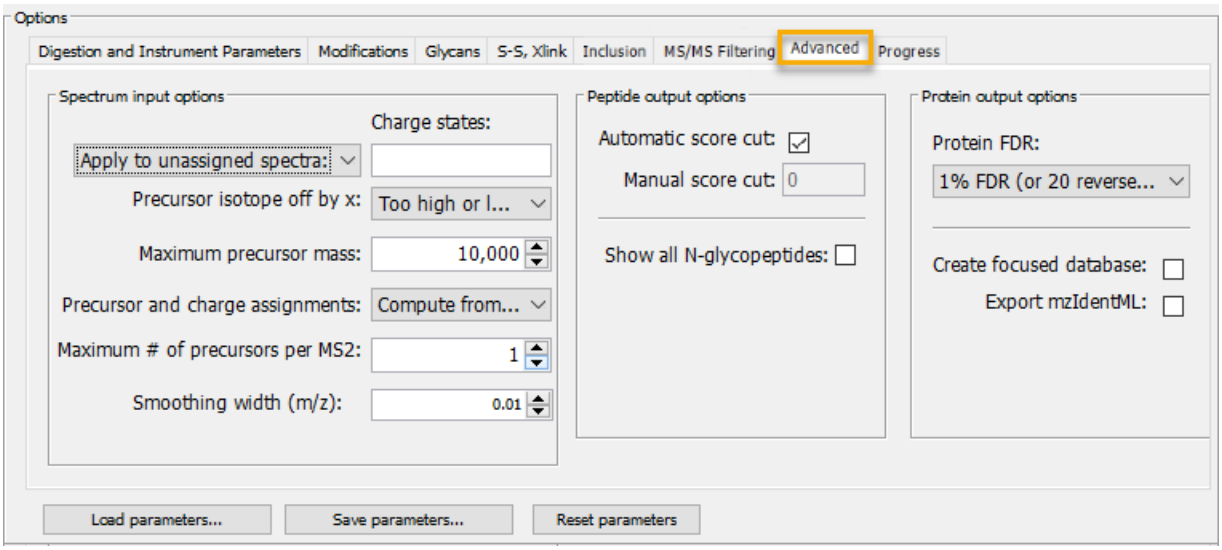


Figure 42: Advanced tab.

Spectrum input options

The **Spectrum input options** section includes precursor and other spectrum settings that are to be applied to the Byonic query.

- **Apply to all spectra/unassigned spectra** allows the user to assign custom charge states to either all spectra or only to unassigned spectra.

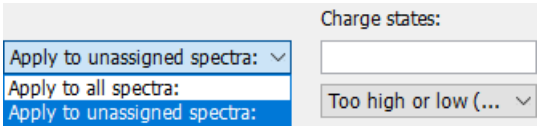


Figure 43: Apply charges to spectra

- **Charge states** sets custom charge states to the applied spectra. By default, the charges +1, +2, +3 are assigned for all CID spectra and the charges +2, +3, +4 are assigned for all ETD spectra. To assign different charges to the spectra, list the charge values, separated by commas.
- **Precursor isotope off by x** allows the user to set an error check for precursor isotope offsets. On many instruments the nominal precursor mass may actually be the mass of a 13C isotope peak rather than of the base (all 12C monoisotopic) peak, so the true precursor mass will within 10 ppm of 2350.120 Da or within 10 ppm of 2351.123 Da.

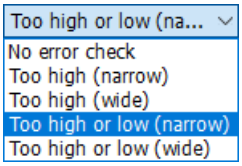


Figure 44 Precursor Isotope off by x

- The tooltip for this setting explains each setting:

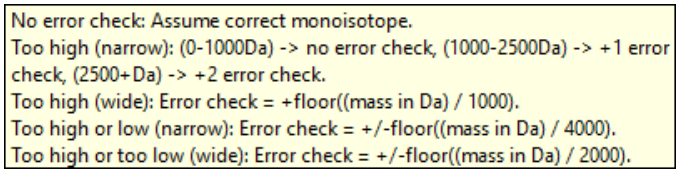


Figure 45: Tooltip for Precursor Isotope off by x

- No error check will use only the assigned precursor; Too high (narrow) allows no errors for precursor up to 1000 Da. For precursors from 1000 to 2500 Da, it allows the assigned precursor to be 1 Da too large in addition to the precursor mass tolerance set on the Digestion and Instrument Parameters tab. For precursors above 2500 Da, the assigned precursor may be 2 Da too large.
- **Maximum precursor mass** allows the user to set a maximum allowed precursor mass
- **Precursor and charge assignments** allows the user to choose between using the pre-assigned precursor and charge assignment values or calculating them from the MS1 data.

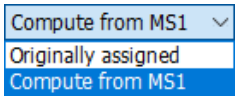


Figure 46: Precursor and Charge Assignments

- **Maximum # of precursors per MS2** sets this limit. It is recommended to set this limit to 2 for complex samples and 5-10 when processing MSe or DIA data.
- Smoothing width (m/z) applies a sigma value in Thomsons for Gaussian smoothing and centroiding of Waters or Sciex data. The default value (0.01 m/z) for half-width at peak half maximum works well in most cases.

Peptide output options

The **Peptide output options** section includes options for filtering the peptide-spectrum matches (PSMs) by score.

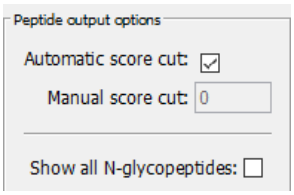


Figure 47: Peptide output options

- **Automatic score cut** uses Byonic to compute this value. By default, PSM filtering is deferred until after protein ranking. It is then filtered to control PSM FDR on the "true" proteins, those ranked above the top-ranking decoy protein. This method gains sensitivity while simultaneously reducing both protein and PSM FDRs. (For more information, see: "Two-dimensional target decoy strategy for shotgun proteomics", *Journal of Proteome Research* 10 (12), 5296-5301, 2011.)
- **Manual score cut** overrides Byonic's algorithm. When Automatic score cut is unchecked, PSMs are filtered before protein ranking, using the minimum score entered into the Manual score cut box. For example, a score threshold of 200 will remove weak matches and a threshold of 400 will remove all but the best matches. Filtering by score may be helpful in special cases, for example to eliminate from consideration all but the best wildcard PSMs.
- **Show all N-glycopeptides** shows the N-glycopeptide matches regardless of score or FDR. This is recommended for simple samples only. This can be especially useful for low energy CID data

Protein output options

The **Protein output options** section includes protein settings applied after the Byonic query is run.

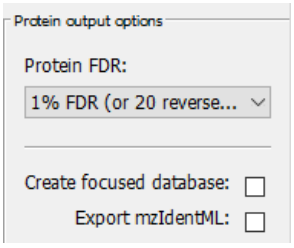


Figure 48: Protein output options

- **Protein FDR** sets the protein list cut-off. By default, the protein list is cut off at 1% protein FDR or 20 decoy proteins, whichever comes last. The user can set the cutoff at 2% protein FDR or 50 decoy proteins, whichever comes last. Finally, the user can select **No Cuts** to produce a completely unfiltered (but still ranked) protein list.

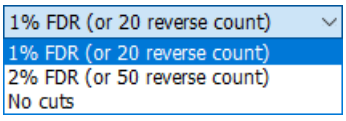


Figure 49: Protein FDR options

- **Create focused database** outputs a new FASTA file containing only the proteins found in the search, along with suitable decoys (>Reverse) for unbiased FDR estimation. The focused database can then be used for subsequent wide searches, including additional modifications and/or a wildcard. Of course, the user can also create focused databases directly by editing existing FASTA files. The FASTA file is named as focused and saved to the designated output folder.

- Export mzIdentML creates mzIdentML and .mgf files that can then be input into third-party tools such as Skyline and Scaffold.

Progress tab

The **Progress** tab sets output options. When the program is launched, this tab will show a progress bar of the current search.

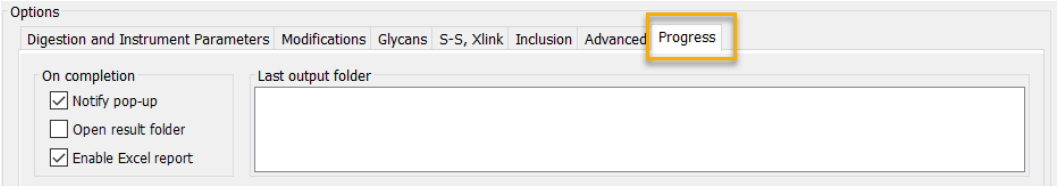


Figure 50: Progress tab

- **Notify pop-up** opens an .html page when the search is done.
- **Open result folder** automatically opens the result folder when the search is done.
- **Enable Excel report** adds an Excel report of the search results that can be shared with collaborators**.**

Additional Settings

Load, Save, and Reset Parameters

Because Byonic has many options and capabilities, writing modification rules and setting parameters can be a nontrivial task. The **Save parameters** button allows the user to save all of the inputs described above. Files are saved with the extension *.byparms. **Load parameters** loads a previously saved set of inputs, which can then be edited as desired. **Reset parameters** clears edited inputs and restores the defaults.

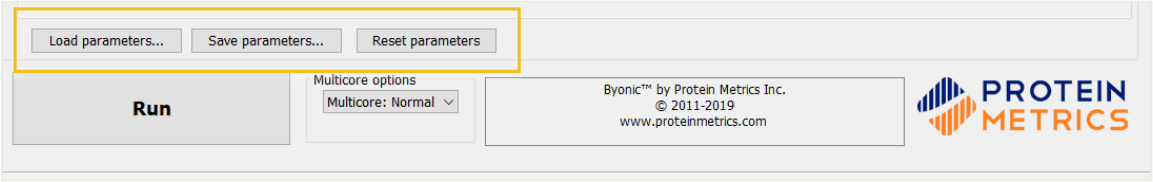


Figure 51: Load, Save, and Reset parameters

Multicore options

The user can control the number of computer cores of the CPU used in the Byonic search. The Light search uses one core, Normal search uses all available cores minus two, and Heavy search uses all available cores. The Light search uses the least CPU resources, while the Heavy search runs the fastest.

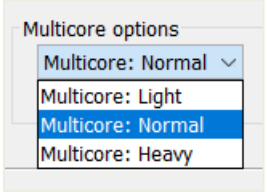


Figure 52: Multicore options

Run

Click the **Run** button to start the analysis.

Byonic Menu Bar

The main menu bar includes three items: **File**, **Edit**, and **Help**.

File Menu

The **File** menu contains three items: **Load params**, **Save params**, and **Exit**.

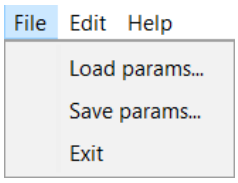


Figure 53: File menu

Save params saves a copy of all the parameters entered in the various tabs of Byonic query to a file with extension *.byparms. **Load params** loads query parameters saved from a previous session. The loaded parameters will replace existing parameters. These functions are the same as the **Load parameters** and **Save parameters** buttons below the tabs. **Exit** closes the application.

Edit Menu

The **Edit** menu formerly contained options that have since been moved to the search tabs. See the **Glycan Tab** section for more information about these Edit options.

Help Menu

The **Help** menu provides information about the software:

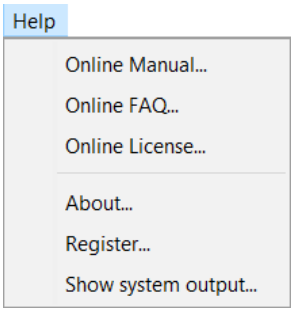


Figure 54: Help menu

The first three menu items open web pages found on www.proteinmetrics.com. **Online Manual** opens a web version of this document, **Online FAQ** opens up summary questions and answers, and **Online License** opens the End User License Agreement for Protein Metrics software.

The **About** menu displays the software version number and system information, which is useful when reporting issues. **Register** is used to activate the software upon first use, along with other license actions.

See the **PMI End-User License Manual** for more information. **Show system output** displays logs for the current Byonic search; these are helpful for troubleshooting problems together with Protein Metrics, Inc. staff via support@proteinmetrics.com.

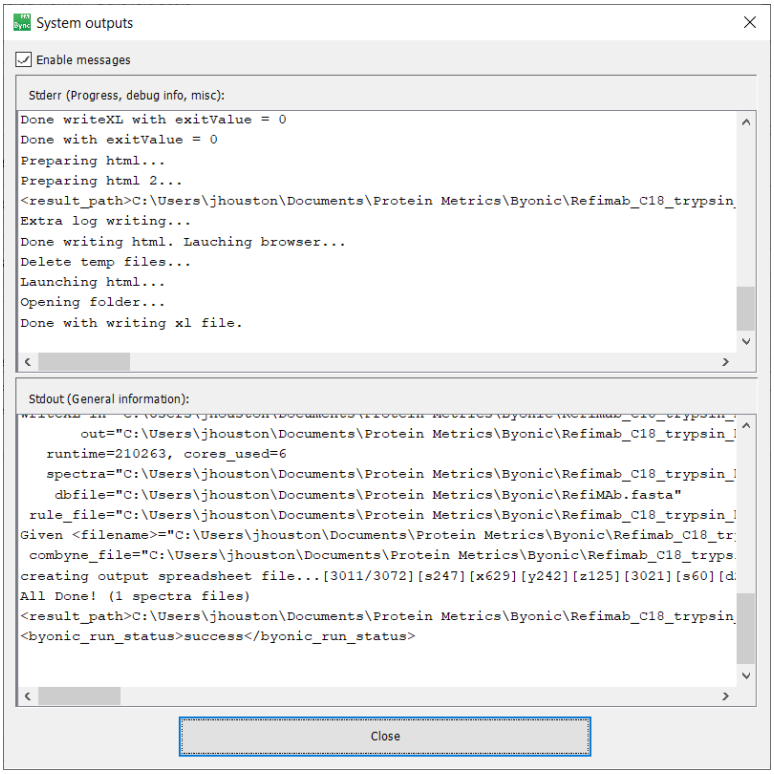


Figure 55: System outputs search logs

Byonic Results

Byonic generates a series of files to the directory defined under **Output folder** in the Search screen. The folder and files are named using the conventions set in the **Results folder name** entry in the Search screen (by default, the MS file name, the date and the term “Byonic”). The Byonic results file (extension *.byrslt) can be viewed and explored interactively using Byonic™ Viewer, a separate program from the Byonic search engine. Byonic also writes the output data to an Excel spreadsheet (.xlsx) for viewing, sorting, importing into other programs, and sharing with collaborators. In both output formats, Byonic organizes its findings into two lists, one for proteins and one for peptide-spectrum matches (PSMs).

Byonic also generates a reformatted spectrum file (extension *.byspec2) that can be loaded into other Protein Metrics applications, such as Peptide Analysis (Byologic®), Intact Analysis (Intact Mass™) or Chromatogram Analysis (Byomap™). Byonic also creates an output of all the parameters used (extension *.byparms) which can be used to reproduce the search later. Finally, the search run creates a subfolder named “objs”, which will contain log files and miscellaneous other output files.

Byos and Byonic Viewer Results

Byonic search result file can be opened in either the Byos® or Byonic™ Viewer applications. Starting with version 3.7.5, a *.byrslt file opens in Byos by default. Therefore, newer versions of Byonic require a co-installation of Byos or Byos Viewer to function correctly. An example *.byrslt file opened in Byos is shown

below in Figure 56:

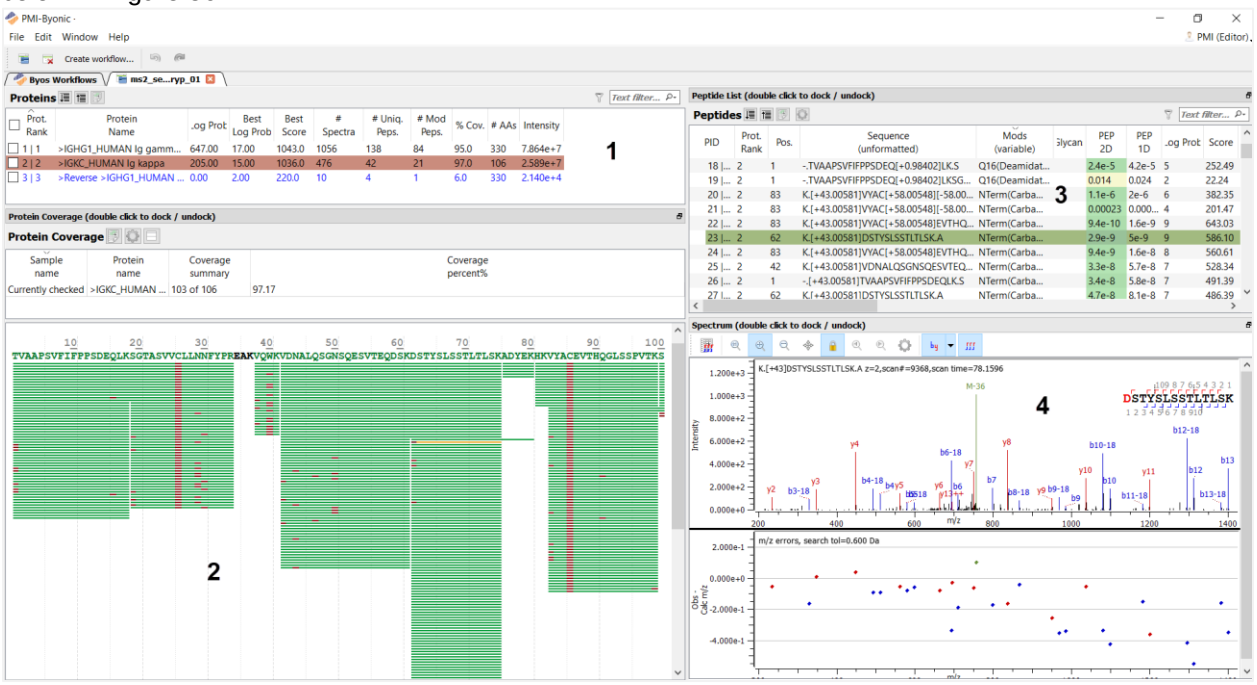


Figure 56: The four Byonic views as displayed in Byos: 1) Proteins table; 2) Protein Coverage map for the selected protein, 3) Peptide table (PSMs) for the selected protein(s), and 4) Annotated Spectrum for the selected PSM.

An example *.byrslt file opened in Byonic Viewer is shown below in Figure 58:

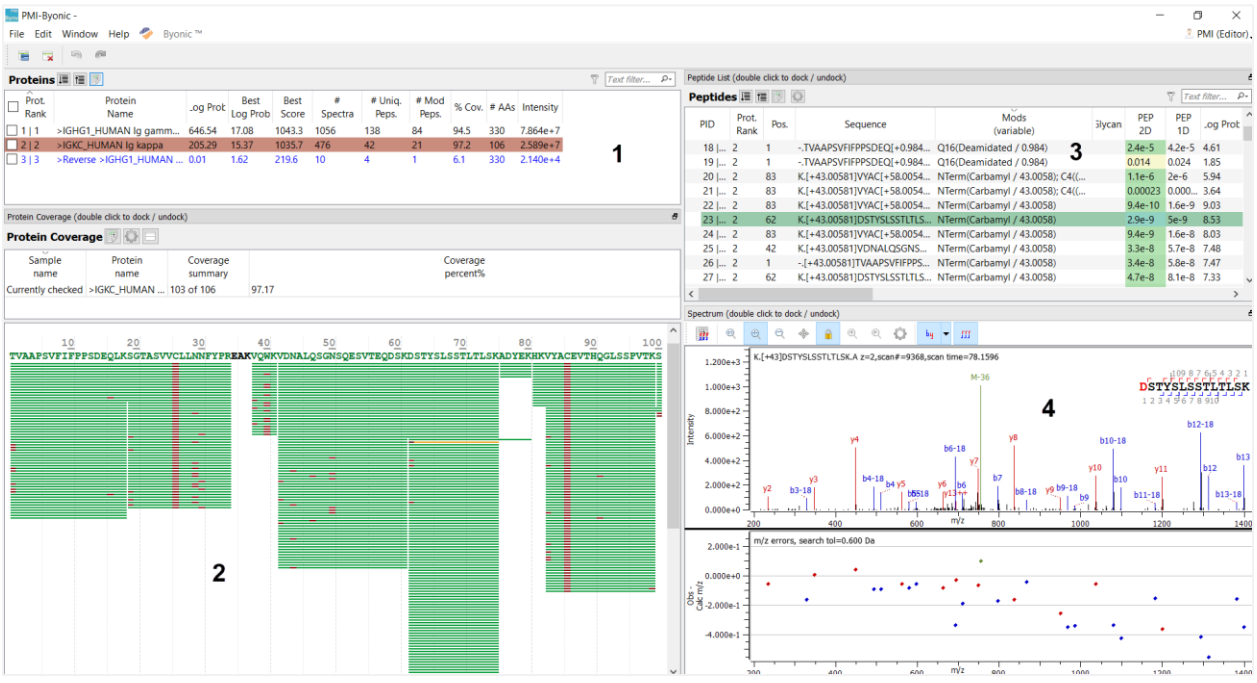


Figure 57: The four Byonic views as displayed in Byonic Viewer: 1) Proteins table; 2) Protein Coverage map for the selected protein, 3) Peptide table (PSMs) for the selected protein(s), and 4) Annotated Spectrum for the selected PSM.

The four views are interconnected: when a protein is selected in the Proteins table (view 1), the Protein Coverage map (view 2) and the Peptides table PSMs (view 3) are displayed for that protein. When a PSM is selected in the Peptides table, the annotated Spectrum (view 4) is displayed for that peptide. To view all the proteins at once, check the box at the top left of the Proteins table. All of the PSMs will display in the Peptides table. The four views can be undocked and rearranged for a customized screen layout; this is especially useful for double-headed displays. To undock (detach) a pane from the others, click the icon at the top right of the pane:

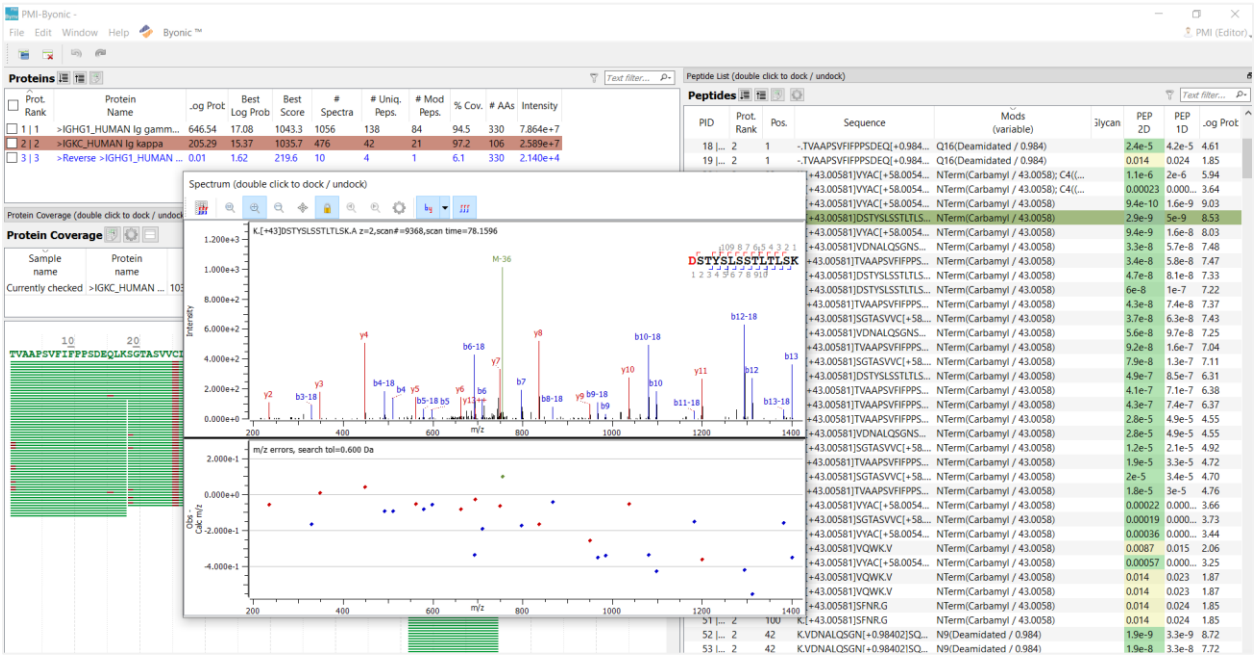


Figure 58: Byonic Viewer with the Spectrum view (MS2 plot and fragment errors) undocked

To return the panes to their original locations, choose **Windows > Restore Default Layout**.

Byonic Viewer Menu Bar

The main menu bar includes three items: **File**, **Edit, Window**, and **Help**.

File Menu

The **File** menu manages Byonic project files:

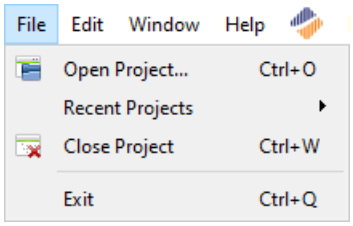


Figure 59: File menu

The File menus includes items to open previously created projects from saved files, close a project (yet leave the application open), and exit Byonic. Mouse over the **Recent Projects** menu to open a side window with a list of recently visited projects that can be reopened. The button and button below the File and Edit menus can also be used to open and close projects, respectively.

Edit Menu

The **Edit** menu contains the **Undo** and **Redo** features. The button and button below the Window and Help menus also perform undo and redo, respectively.

Window Menu

The **Window** menu manages layouts:

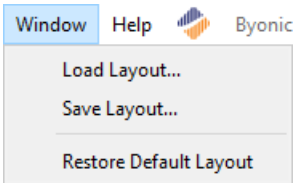


Figure 60: Window Menu

Load Layout opens a saved layout for how the different views are arranged and customized. These are stored to files with extension *.ini. **Save Layout** saves the current layout to an .ini file for use in other sessions. **Restore Default Layout** applies the layout used when the application is first opened.

The current layout is customized by hovering over the vertical or horizontal edges between table and plot views so that the cursor changes to arrows: or . Left click and drag the edges up or down or right or left to change the sizes of the views. Columns in the table views can be made larger or smaller in same manner. To reorder columns in a table, left click the name of the column and drag it to the new location. To do a simple sort, left click the header once to sort ascending and twice to sort descending. Mouse over a column header to see a description of that field.

To hide or display columns, right-click any column header. The **Column Header Editor** opens:

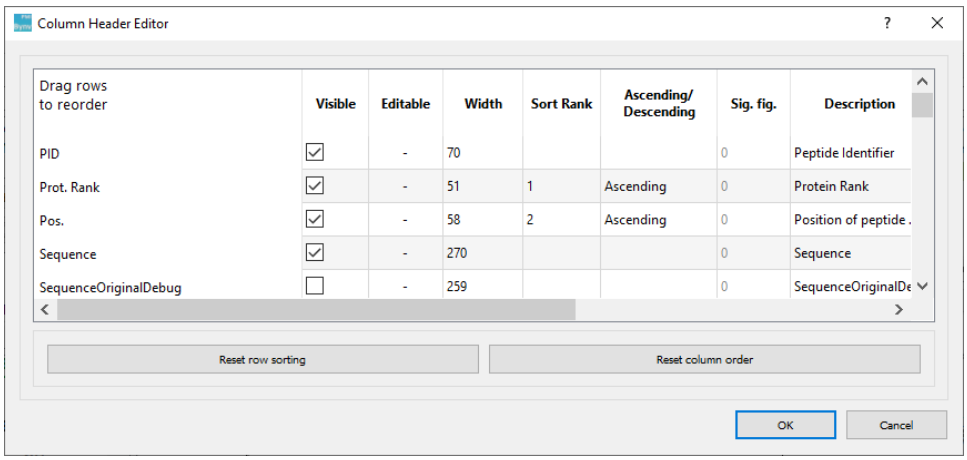


Figure 61: Column Header Editor

Check the column fields to display and uncheck the fields to hide. The dialog contains brief descriptions of each field. Alternatively, hover over the column names to display the descriptions as tooltips. Note that the Byonic Viewer layout persists on exit.

Help Menu

The **Help** menu provides information about the software:

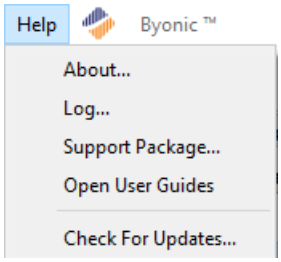


Figure 62: Help Menu

The **About** menu shows the software version number, which is needed when reporting issues. The **Log** menu opens a log containing recent activity; this is helpful for troubleshooting problems together with Protein Metrics staff via support@proteinmetrics.com. **Support Package** collects all relevant information helpful for troubleshooting problems together with Protein Metrics staff via support@proteinmetrics.com. **Open User Guides** opens the Document directory where this and other useful guides can be found, including PMI Reporting Manual.pdf. **Check For Updates** checks whether software updates are available on www.proteinmetrics.com. Note that the **Register** function is available in the Help menu from the Byonic search application.

Table Menus

The menu bars at the top of the three table views, Project, Peaks, and Candidates, share icons that manage hierarchical lists and filter on data.

- The  icon expands rows to show “sub-rows”.
- The  icon collapses rows to hide sub-rows. The use of sub-row depends on the table. For example, in the Peptides table, a row is a peptide record and a sub-row is the data resulting from an individual sample that contained the peptide.
- The  icon exports the table to a .csv file for opening with Excel.
- The  icon opens a dialog to create custom filters specific to columns in that data table:

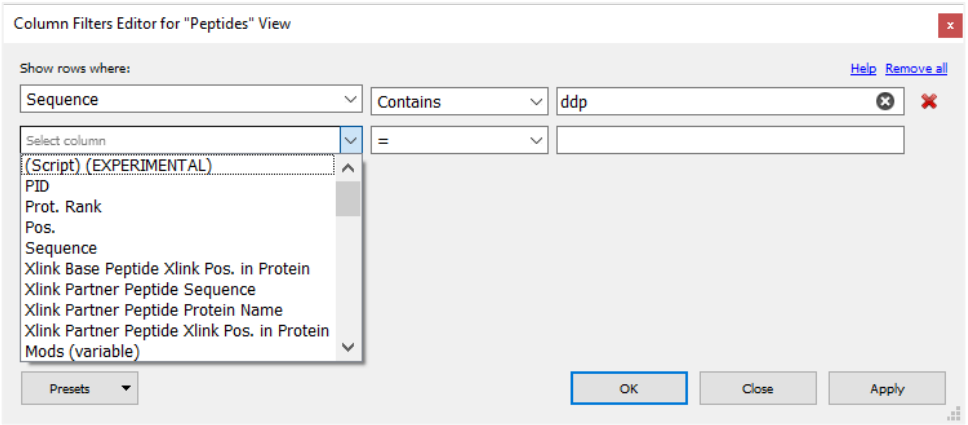


Figure 63: Column Filters Editor

Select a column in the first cell, select an operator in the second cell, and enter text in the third cell. A second filter row becomes available for further entry. Click the red X after a filter row to delete it. Custom filters allow masses to be filtered by mass range, annotation, intensity, and so

forth. Custom filters can be stored with the project document or exported and imported using the **Presets** dropdown.

- The 

cell filters the entered text across the content of all columns in the protein and peptide tables. The records are filtered automatically as text is entered. Click the icon to search the string as a whole word or as case sensitive.
- To sort the contents of a column by ascending value, click the column header. Click the column header again to sort by descending value.

Table Right-Click Menus

The Project and Peptides tables have context menu items revealed by a right-click on the rows within the tables. (Recall that a right-click on the header of these tables opens the Column Header Editor dialog.)

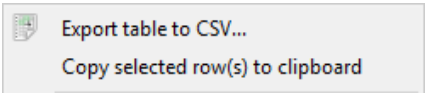


Figure 64: Table right-click menus

- **Export table to CSV** saves the table content and headers to a .csv file using parameters chosen in the **Export data** dialog.
- **Copy selected row(s) to clipboard** copies selected table rows, with their headers to be available for pasting into another application. (This menu is not available in the Protein Coverage table.)
- Table context menus contain a set of query options for searching the clicked text value using any of the available search operators. This is an easy way to filter a table based on a specific field value:

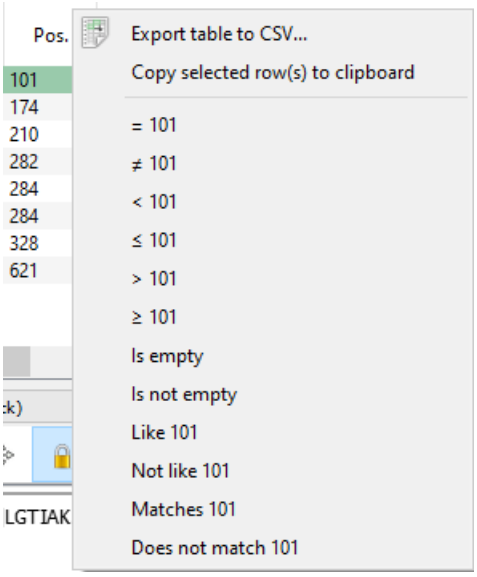


Figure 65: Search table values through a right-click menu

The context menu shows all the possible queries for that data in that column, in this case, for value 101 in the Pos. column of the Peptides table.

Proteins Table

The **Proteins** table contains information about the identified proteins, including name, rank and scores:

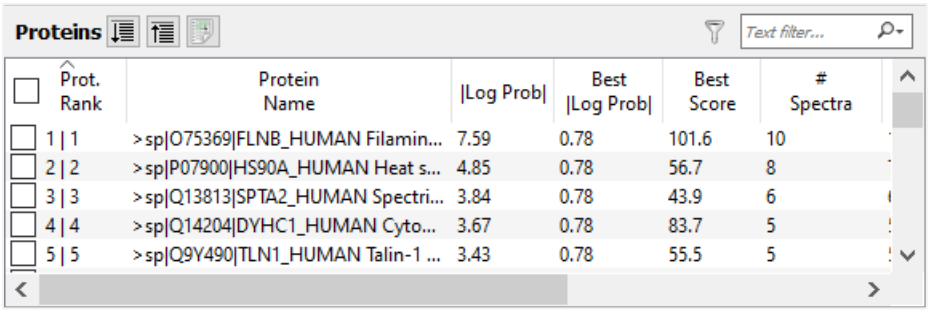


Figure 66: Proteins table

To display or remove the associated views of a protein in the Protein Coverage and Peptides tables, check or uncheck the box at left of the protein. To view all of the proteins together, check the box at the top left.

Protein Coverage Table and Menu

The **Protein Coverage** table displays peptide sequences and corresponding protein coverage. The accompanying display maps the protein sequences of detected peptides to colored lines below each sequence:

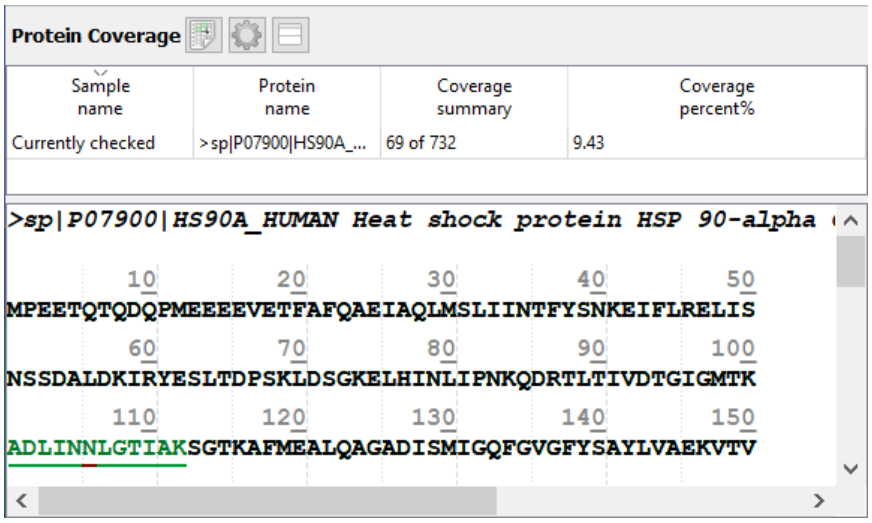


Figure 67: Protein Coverage table

The Protein Coverage table also includes the following specialized menu icon button:

- The  icon opens the Protein coverage rendering options dialog:

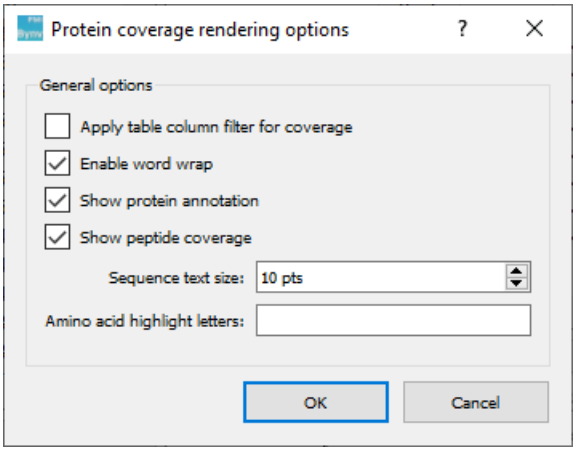


Figure 68: Protein coverage rendering options

- The  icon turns on and off the display of the tabular protein coverage data.

  The Protein Coverage view has context menu items revealed by a right-click on the graphical portion of the display:

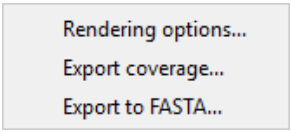
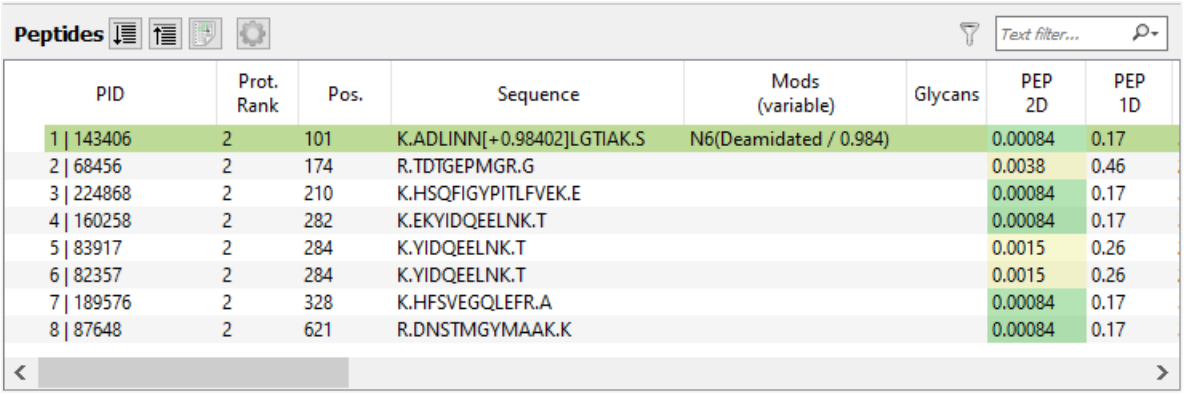


Figure 69: Protein Coverage right-click menu

- **Rendering options** also opens the Protein coverage rendering options dialog show above.
- **Export coverage** creates a *.png file of the graphical protein coverage display.
- **Export to FASTA** creates a *.fasta file of the proteins found in the Protein Coverage view. The *.fasta file is then available for import into new projects.

Peptides Table and Menu

The **Peptides** table contains detailed information about all identified peptides for the protein(s) checked or selected in the Proteins table:



PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Glycans	PEP 2D	PEP 1D
1 | 143406	2	101	K.ADLINN[+0.98402]LGTIAK.S	N6(Deamidated / 0.984)		0.00084	0.17
2 | 68456	2	174	R.TDTGEPMGR.G			0.0038	0.46
3 | 224868	2	210	K.HSQFIGYPITLFVEK.E			0.00084	0.17
4 | 160258	2	282	K.EKYIDQEELNK.T			0.00084	0.17
5 | 83917	2	284	K.YIDQEELNK.T			0.0015	0.26
6 | 82357	2	284	K.YIDQEELNK.T			0.0015	0.26
7 | 189576	2	328	K.HFSVEGQLEFR.A			0.00084	0.17
8 | 87648	2	621	R.DNSTMGYMAAK.K			0.00084	0.17

Figure 70: Peptides (PSM) table

The **Peptide** table includes a large number of possible column fields. The most important ones are the peptide sequence, Byonic score and log probability, and scan number (often also found in the Comment field). In the case of an identification that includes a glycan from the predefined glycan tables, the Glycan column displays the glycan's monosaccharide composition as a sequence of 6 numbers: the counts of HexNAc, Hex, Fuc, NeuAc, NeuGc, and sodium. The order of monosaccharides is displayed in the tooltip for the Glycan column header.

In addition to the usual table menu buttons, the Peptides table contains the icon button which opens the Peptide view options dialog. This allows the table to be grouped by unique peptides:

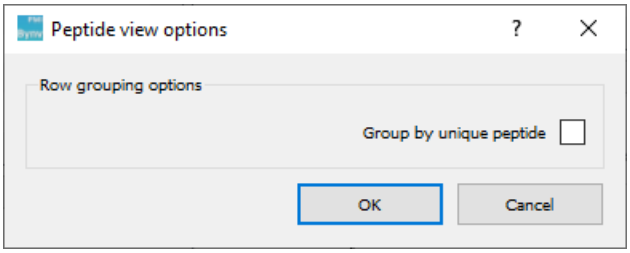


Figure 71: Peptide view options

Spectrum View and Menu

The annotated **Spectrum** view allows the user to inspect identified peaks and associated fragment errors to manually validate peak identifications and modification placements.

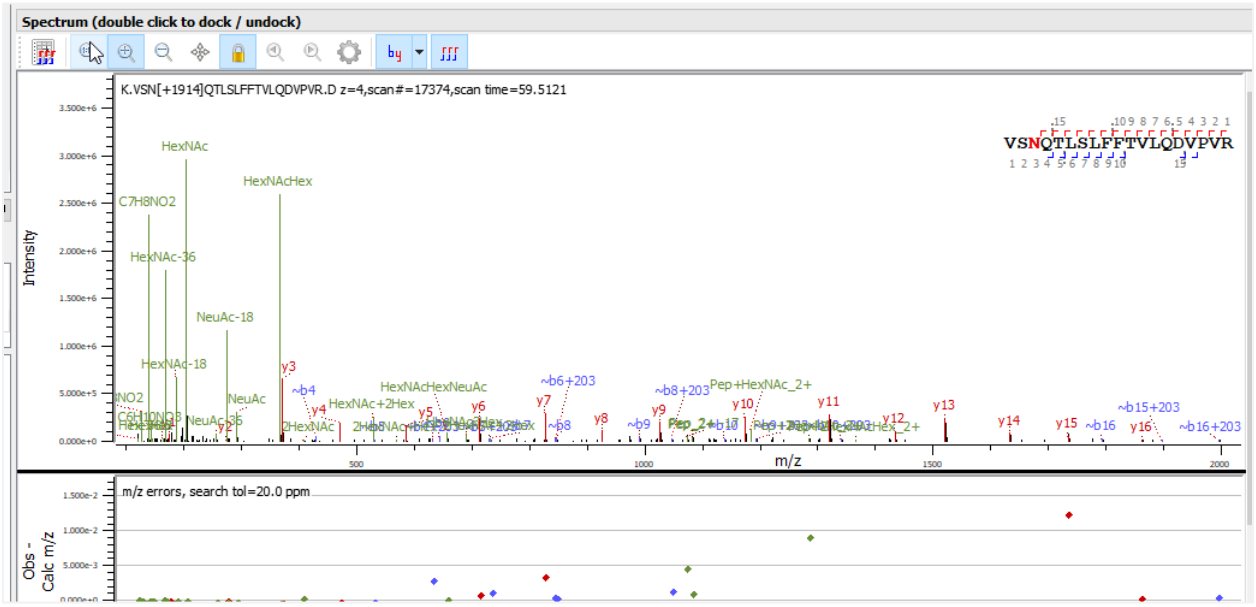


Figure 72: Annotated Spectrum view

Byonic annotates key elements of the spectrum. It annotates the most commonly observed ion series (a, b, y, c, z, b++, y++, etc.) for the type of fragmentation. It annotates common neutral losses from the precursor (e.g., M–98 for loss of phosphoric acid). It annotates immonium ions for certain amino acids and oxonium ions for glycans. Finally, Byonic annotates key diagnostic peaks such as imm_pY at 216 Da for phosphotyrosine, 243 for phopho-Hex, and 284 for phospho-HexNAc. For Byonic, M alone refers to a precursor in its original charge state, so M+e in an ETD spectrum represents a charge-reduced precursor, and M_2+ – HexNAcHex in a spectrum of a plus-three precursor represents the loss of HexNAc, Hexose, and a proton. In a glycopeptide spectrum, Pep refers to the neutral (possibly modified) peptide without

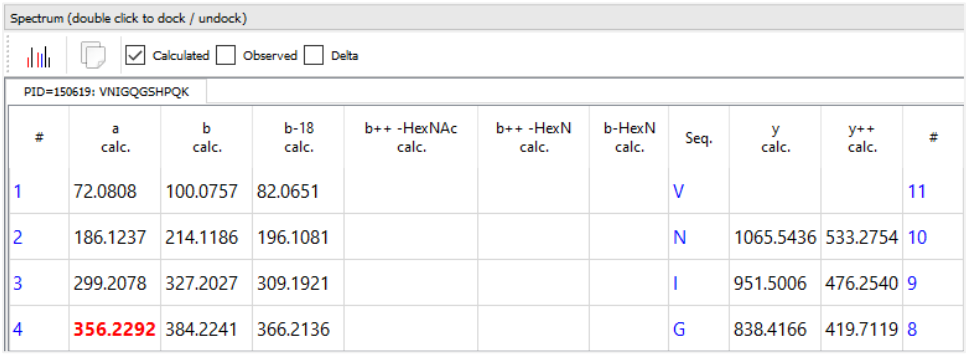
glycans. For example, Pep+HexNAc_2+ represents the peptide with HexNAc and two protons, that is, the Y1++ ion.

Most of Byonic's annotations of product ions are standard, but a few of the conventions may require additional explanation. If Byonic does not indicate charge, the charge is plus one. If Byonic does not indicate isotopes, the peak is the monoisotopic peak. For high-mass fragments, Byonic will append annotations to identify higher-isotope peaks, for example, _iso1, _iso2. Common neutral losses are shown by removed nominal masses, for example, –17 = ammonia, –18 = water, –36 = two water molecules, –54 = three water molecules (a common loss from glycated lysine), –80 = loss of SO_3 from sulfation, and –98 = loss of H_3PO_4 from phosphorylation. An apostrophe before a z-ion, for example, 'z6 shows loss of (alkylated) side-chain on an N-terminal cysteine. A tilde shows loss of labile modifications, for example, ~y7 means y7 with loss of all labile modifications. Labile modifications are defined to be O- and N-linked glycosylation, sulfation, histidine phosphorylation, and gamma-carboxylation. (In order to accommodate all the various types and modifications of O-linked glycans, Byonic treats any sufficiently heavy modification on S/T as labile.) For GalNAc- or GlcNAc-initiated glycosylation, Byonic will annotate peaks with a single base HexNAc, for example, ~y7+203. Byonic annotates oxonium ions from glycans, either with names like "NeuAc–18" or atomic formulas when names are not definitive.

Spectrum Menus

The menu bar at the top includes icons for operations on plots. These icons appear in almost all Protein Metrics, Inc. software products.

- The  icon switches between the default plot view and the mass table view:



#	a calc.	b calc.	b-18 calc.	b++ -HexNAc calc.	b++ -HexN calc.	b-HexN calc.	Seq.	y calc.	y++ calc.	#
1	72.0808	100.0757	82.0651				V			11
2	186.1237	214.1186	196.1081				N	1065.5436	533.2754	10
3	299.2078	327.2027	309.1921				I	951.5006	476.2540	9
4	**356.2292**	384.2241	366.2136				G	838.4166	419.7119	8

Figure 73: Mass table view of the Spectrum view

When the **Mass table** view is shown, the observed values are shown in RED by default. The user can optionally expand to show observed and Delta masses in separate columns. The  button that allows an analyst to copy the table to the clipboard. The  button returns to the spectrum view.

- The  icon resets the plot to default zoom level. Shortcut = double left-click.
- The  icon enables zooming in. The cursor changes to this icon. Drag across the range of the plot to display to zoom to that x-range. By default, the plot's y-range scales according to the maximum y-value within the x-range, but the software also supports freeform zooming as enabled under the  icon.
- The  icon enables zooming out. Click anywhere in the plot to zoom out.
- The  icon enables moving (panning) across the plot. The cursor changes to this icon. Click the plot and drag up or down, right or left to view a part of the plot that is off-screen.

- The icon locks the x-axis for stacked plots in a plot view to use the same ranges. Unselecting this allows stacked plots to apply independent x-axis ranges.
- The icon performs an undo of the last zoom step. Shortcut = Shift-left arrow key.
- The icon performs a redo of the last zoom step. Shortcut = Shift-right arrow key.
- The icon manages how plots are displayed (render options), as well as zoom modes. The Render and zoom options include:

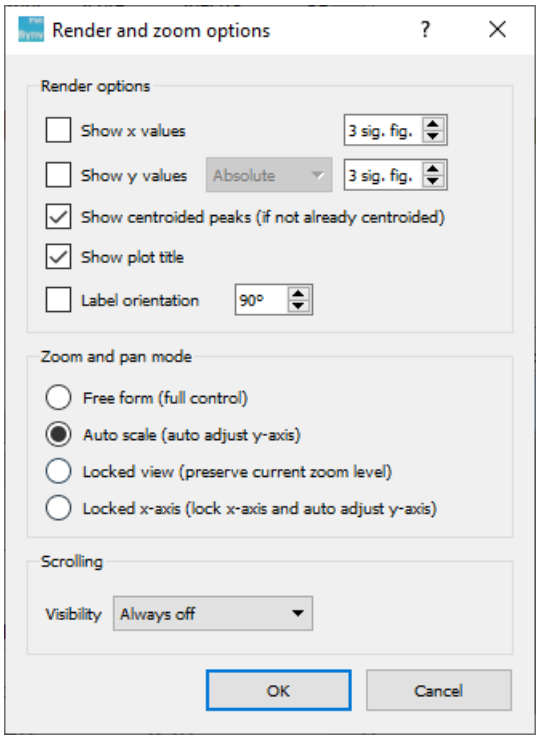


Figure 74: Render and zoom options

  - **Show x values** and **Show y values** display the x- or y-coordinates beside plot peaks to the chosen number of significant figures. When x-coordinates are displayed, hovering the cursor over an x-coordinate label, will display x-coordinate (that is, m/z differences). This feature is invaluable for identifying unlabeled peak. For example, a mass delta of 18.011 indicates water loss (or gain).
  - **Show centroided peaks** darkens the peak positions that are determined to be centroided.
  - **Show plot title** displays the title of the plot, as generated from field values.
  - **Label orientation**, when checked, orients labels to some angle other than horizontal.

  The **Zoom and pan mode** options include:

  - **Free form** mode to manually select the desired y range as well as x range
  - **Auto scale** mode to select only the x range (the y range is then adjusted to the value of the highest peak)
  - **Locked view** mode to keep the current x range (for either *m/z* and/or m) when moving between elution peaks. In Isotope plots

- **Locked x-axis** mode turns off autoscaling for the x-axis (but not the y-axis) and applies the current x-axis scale across all Peptide table selections

Under **Scrolling**, the **Visibility** setting controls display of the scroll bars:

- **Always on** displays scroll bars even when the full plot is shown
- **Always off** turns off display of the scroll bars even when a partial plot is shown
- **Show as needed** displays scroll bars only when a partial plot is shown

- The by icon switches between showing and hiding the b and y ion labels. The icon is accompanied by a drop-down arrow that reveals three sub-menus:
  - **Open annotation options** opens a dialog that allows the user to set options for determining the assignment of the MS2 annotations:

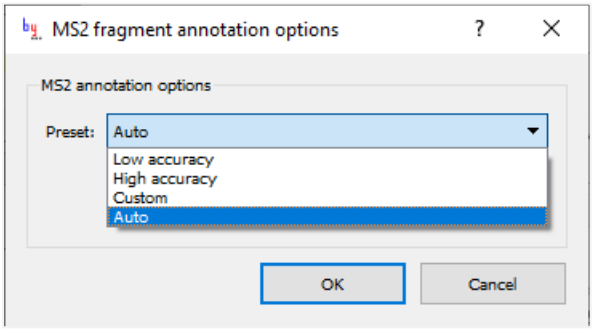


Figure 75: MS2 fragment annotation options

The MS2 mass-accuracy tolerance options can use presets for Low accuracy, High accuracy, or Custom, in which the user sets these values. The dialog defaults to the Auto preset, in which the software determines the MS2 fragment annotation settings.

  - **Remove fragment coverage cache** clears the existing cache of detected fragments used for the protein fragment coverage rendering.
  - **Export fragment to CSV**, exports the fragment sequence to a *.csv file.
- The icon turns on or off the fragment sequences displayed in the top right of the plot. The cleavage diagram for the amino acid sequence is a standard summarization of the evidence for the identification

Spectrum Right-Click Menus

The Spectrum plot has a variety of context menus for plot styling and exporting revealed by a right-click on the plot:

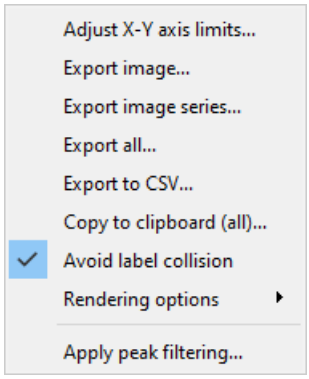


Figure 76: Spectrum context menus

Figures exported can be useful for reports, publications, regulatory filings, or internal communications. There are many options for rendering and exporting so that the user has much freedom to prepare a plot or figure style as needed.

- **Adjust X-Y axis limits** opens a dialog for the user to manually edit the plots x and y maxima and minima. This is a less convenient but more precise (and reproducible) alternative to the  and  icons.
- **Export image** allows the user to save the plot as a *.pdf or *.png file. It opens the **Plot Exporting Settings** dialog, which controls image size, file name and folder, and x and y minima and maxima:

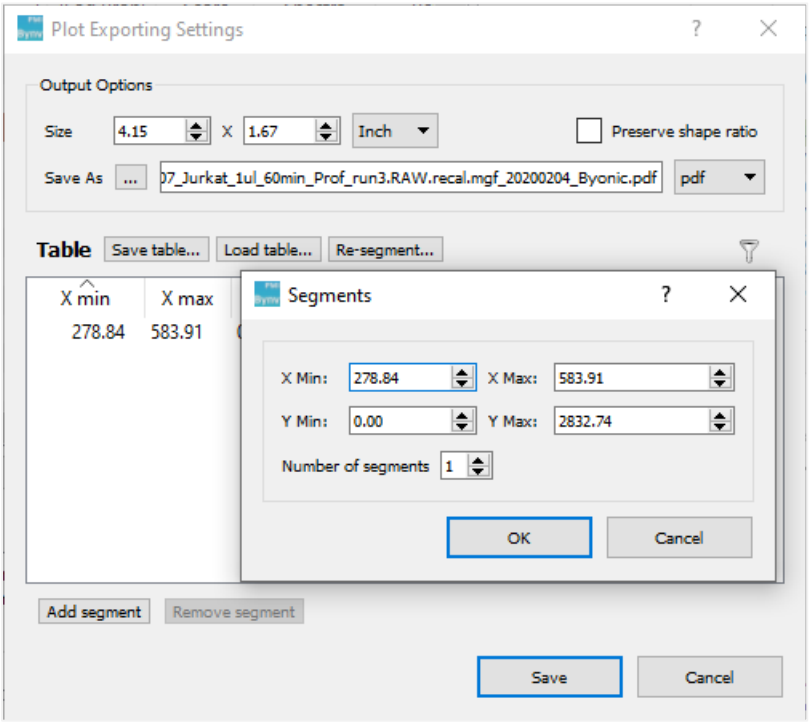


Figure 77: Plot export settings

Sometimes a user wishes to display a wide range across the x-axis and yet retain significant detail. This can be done by breaking up the plot into a series of panels. The **Add segment** button

creates segments with user-defined x and y values. A series of these segments eliminates unneeded portions of the plot and increases the effective detail in the image. This is also a useful function for automated reporting. The **Re-segment** button allows edits to the reported x and y minima and maxima for existing segments

- **Export image series** also opens the Plot Exporting Settings dialog, except that the segments are prepopulated with six equal sized segments. This simplifies the edits of the segments. The **Add segment** and **Remove segment** buttons control the number of segments that divide up the plot.
- **Export all** also opens the Plot Exporting Settings dialog, except that the wildtype peptide plots are exported along with the peptide plots. Segment editing functions are disabled for this option.
- **Export to CSV** exports the plot trace x-y points to a *.csv file.
- **Copy to clipboard (all)** enables pasting the plot image into another application.
- **Avoid label collision** staggers the label text to reduce overlap.
- **Rendering options** controls how a plot is displayed in the application. It includes several sub-menus:

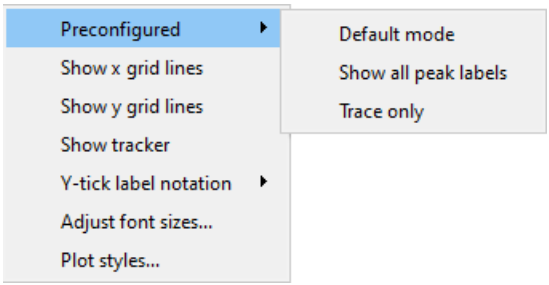


Figure 78: Rendering options sub-menu

  - **Preconfigured** sub-menus control what is displayed in the plots. **Default mode** displays the trace, peak labels and plot title. **Show all peak labels** does exactly that. **Trace only** turns off the peak labels and plot title.
  - **Show x grid lines** turns on and off the x grid lines.
  - **Show y grid lines** turns on and off the y grid lines.
  - **Show tracker** displays a vertical dotted line that follows the cursor when moved in the plot. This allows the user to line up annotated peaks with their associated m/z errors.
  - **Y-tick label notation** toggles between y-axis notation options of absolute amounts or as percentages of the highest peak.
  - **Adjust font sizes** controls the font size for each type of text on the plot.
  - **Plot styles** allows changes to the graphic styling of the plot, including trace width, axis width, and total *m/z* dot colors to be used.
- **Apply peak filtering** sets the signal-to-noise ratio (set to zero by default).

When the cursor is positioned exactly over a spectrum peak, the reported m/z and intensity of that peak is shown inside curly brackets { }. When the cursor is not directly over a peak, these numbers give the m/z and intensity (x, y coordinates) of the cursor position.

Excel Report

A Byonic search generates an Excel report summarizing much of tabular data found in the *.byrslt file:

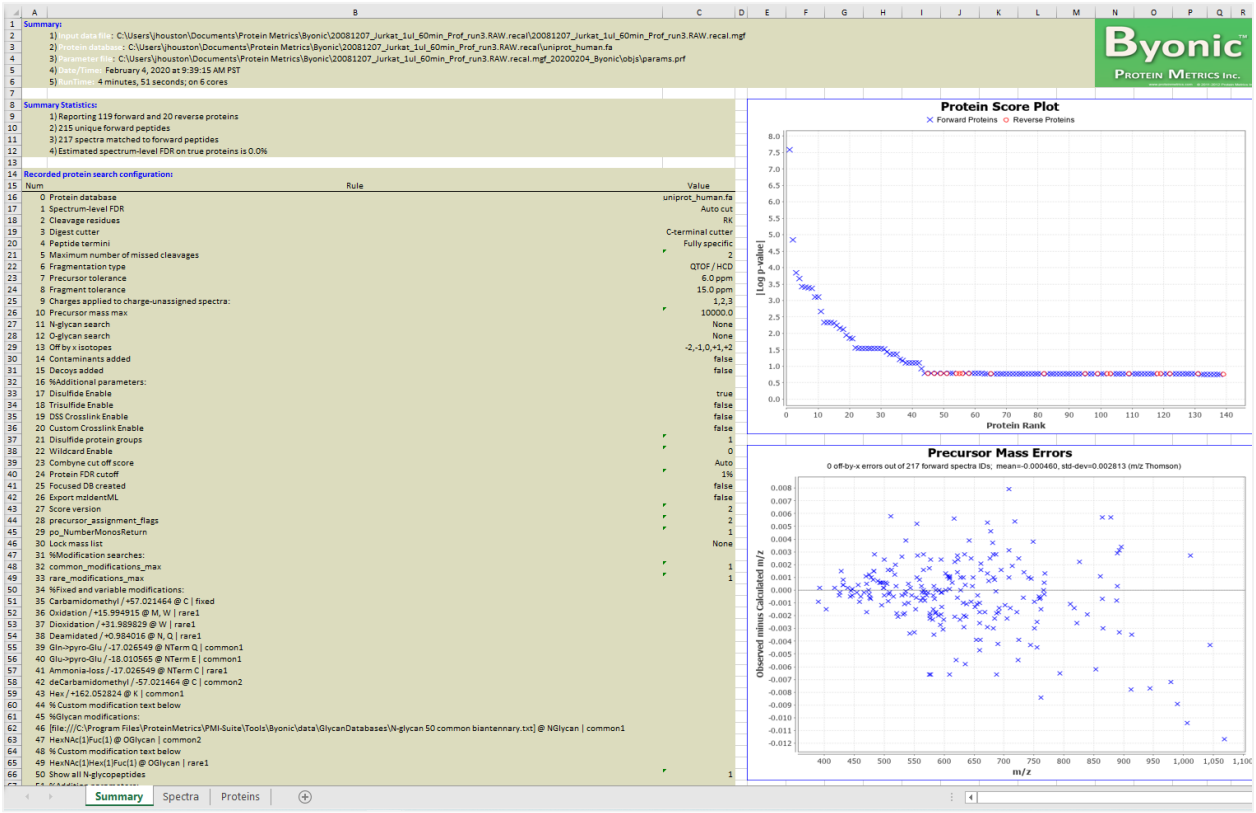
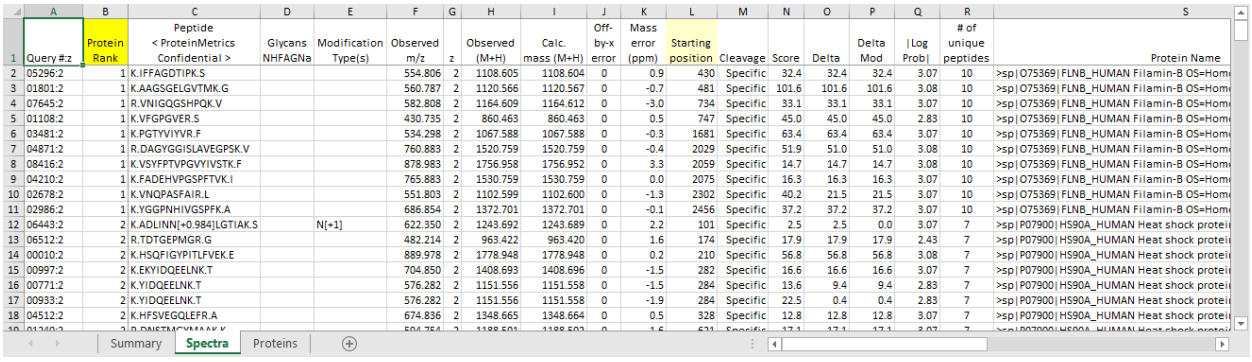


Figure 79: Byonic results (Summary sheet) as viewed in Excel

The *.xlsx file is saved to the same download directory as the *.byrslt file. Note that the Byonic logo graphic may need to be enlarged from a single cell to be viewed. The shaded areas of the Summary sheet display the initial search parameters. The top Protein Score plot charts protein rank vs. log p-value. The bottom Precursor Mass Errors plot charts m/z vs. observed minus calculated m/z.

The **Spectra** sheet displays the Peptides (PSM) table data:

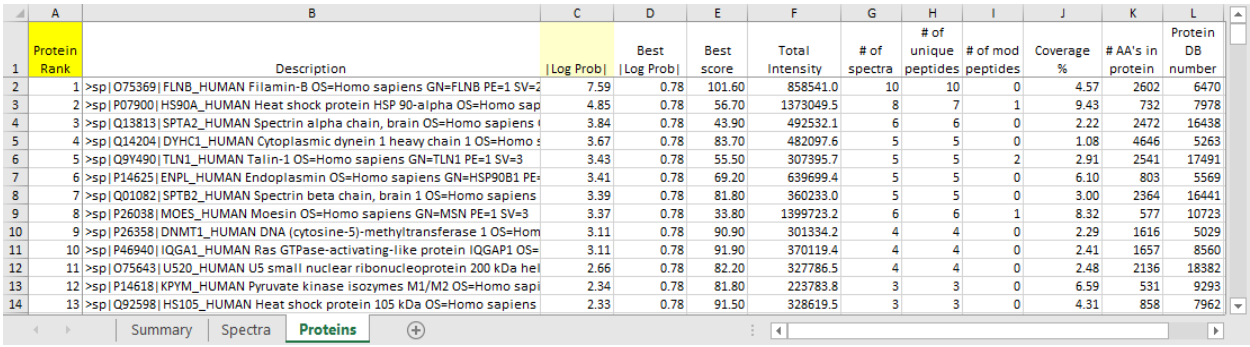


Query #:z	Protein Rank	Peptide < ProteinMetrics Confidential >	Glycans NHFAGNa	Modification Type(s)	Observed m/z	z	Observed (M+H)	Calc. mass (M+H)	Off-by-x error	Mass error (ppm)	Starting position	Cleavage	Score	Delta	Delta Mod	|Log Prob|	# of unique peptides	Protein Name
05296:2	1	K.IFFAGDTIPK.S			554.806	2	1108.605	1108.604	0	0.9	430	Specific	32.4	32.4	32.4	3.07	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
01801:2	1	K.AAGSGELGVTMK.G			560.787	2	1120.566	1120.567	0	-0.7	481	Specific	101.6	101.6	101.6	3.08	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
07645:2	1	R.VNIGQQSHPQK.V			582.808	2	1164.609	1164.612	0	-3.0	734	Specific	33.1	33.1	33.1	3.07	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
01108:2	1	K.VFGPGVER.S			430.735	2	860.463	860.463	0	0.5	747	Specific	45.0	45.0	45.0	2.83	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
03481:2	1	K.PGTYVIYVR.F			534.298	2	1067.588	1067.588	0	-0.3	1681	Specific	63.4	63.4	63.4	3.07	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
04871:2	1	R.DAGYGGISLAVEGPSK.V			760.883	2	1520.759	1520.759	0	-0.4	2029	Specific	51.9	51.0	51.0	3.08	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
08416:2	1	K.VSYFPTVPGVYIVSTK.F			878.983	2	1756.958	1756.952	0	3.3	2059	Specific	14.7	14.7	14.7	3.08	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
04210:2	1	K.FADEHVPGSPFTVK.I			765.883	2	1530.759	1530.759	0	0.0	2075	Specific	16.3	16.3	16.3	3.07	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
02678:2	1	K.VNQPASFAIR.L			551.803	2	1102.599	1102.600	0	-1.3	2302	Specific	40.2	21.5	21.5	3.07	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
02986:2	1	K.YGGPNHIVGSPFK.A			686.854	2	1372.701	1372.701	0	-0.1	2456	Specific	37.2	37.2	37.2	3.07	10	>sp|O75369|FLNB_HUMAN Filamin-B OS=Hom
06443:2	2	K.ADLINN[+0.984]LGTIAK.S		N[+1]	622.350	2	1243.692	1243.689	0	2.2	101	Specific	2.5	2.5	0.0	3.07	7	>sp|P07900|HS90A_HUMAN Heat shock protei
06512:2	2	R.TDTGEPMGR.G			482.214	2	963.422	963.420	0	1.6	174	Specific	17.9	17.9	17.9	2.43	7	>sp|P07900|HS90A_HUMAN Heat shock protei
00010:2	2	K.HSQFIGYPITLFVEK.E			889.978	2	1778.948	1778.948	0	0.2	210	Specific	56.8	56.8	56.8	3.08	7	>sp|P07900|HS90A_HUMAN Heat shock protei
00997:2	2	K.EKYIDQEELNK.T			704.850	2	1408.693	1408.696	0	-1.5	282	Specific	16.6	16.6	16.6	3.07	7	>sp|P07900|HS90A_HUMAN Heat shock protei
00771:2	2	K.YIDQEELNK.T			576.282	2	1151.556	1151.558	0	-1.5	284	Specific	13.6	9.4	9.4	2.83	7	>sp|P07900|HS90A_HUMAN Heat shock protei
00933:2	2	K.YIDQEELNK.T			576.282	2	1151.556	1151.558	0	-1.9	284	Specific	22.5	0.4	0.4	2.83	7	>sp|P07900|HS90A_HUMAN Heat shock protei
04512:2	2	K.HFSVEGQLEFR.A			674.836	2	1348.665	1348.664	0	0.5	328	Specific	12.8	12.8	12.8	3.07	7	>sp|P07900|HS90A_HUMAN Heat shock protei

Summary Spectra Proteins

Figure 80: Excel Spectra sheet displaying Peptides table data

The **Proteins** sheet displays the Proteins table data:



	A	B	C	D	E	F	G	H	I	J	K	L
1	Protein Rank	Description	|Log Prob|	Best |Log Prob|	Best score	Total Intensity	# of spectra	# of unique peptides	# of mod peptides	Coverage %	# AA's in protein	Protein DB number
2	1	>sp|O75369|FLNB_HUMAN Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	7.59	0.78	101.60	858541.0	10	10	0	4.57	2602	6470
3	2	>sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sap	4.85	0.78	56.70	1373049.5	8	7	1	9.43	732	7978
4	3	>sp|Q13813|SPTA2_HUMAN Spectrin alpha chain, brain OS=Homo sapiens (	3.84	0.78	43.90	492532.1	6	6	0	2.22	2472	16438
5	4	>sp|Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo s	3.67	0.78	83.70	482097.6	5	5	0	1.08	4646	5263
6	5	>sp|Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	3.43	0.78	55.50	307395.7	5	5	2	2.91	2541	17491
7	6	>sp|P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=	3.41	0.78	69.20	639699.4	5	5	0	6.10	803	5569
8	7	>sp|Q01082|SPTB2_HUMAN Spectrin beta chain, brain 1 OS=Homo sapiens	3.39	0.78	81.80	360233.0	5	5	0	3.00	2364	16441
9	8	>sp|P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	3.37	0.78	33.80	1399723.2	6	6	1	8.32	577	10723
10	9	>sp|P26358|DNMT1_HUMAN DNA (cytosine-5)-methyltransferase 1 OS=Hom	3.11	0.78	90.90	301334.2	4	4	0	2.29	1616	5029
11	10	>sp|P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=	3.11	0.78	91.90	370119.4	4	4	0	2.41	1657	8560
12	11	>sp|O75643|U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa hel	2.66	0.78	82.20	327786.5	4	4	0	2.48	2136	18382
13	12	>sp|P14618|KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapi	2.34	0.78	81.80	223783.8	3	3	0	6.59	531	9293
14	13	>sp|Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens	2.33	0.78	91.50	328619.5	3	3	0	4.31	858	7962

Summary | Spectra | Proteins

Figure 81: Excel Proteins sheet displaying Proteins table data

Byonic Field Descriptions

The Byonic Viewer, as well as the Excel report, contain many fields in the Proteins table and sheet and the Peptides table and Spectra sheet. The following tables contain descriptions of these Proteins and Peptides fields.

Proteins Field	Description
Prot. Rank	The rank of the protein by p-value. The p-value is the likelihood of the protein arising by random chance. For example, for a protein p-value of 0.001, a search against a database containing 10,000 independent proteins, should find only about ten p-values better than 0.001 arising at random. Byonic's p-values are only as accurate as the probabilistic model, so the user should also check the ranking of the proteins relative to the decoy (>Reverse) proteins. Byonic actually outputs the absolute value of the logarithm base 10 of the p-value. Logarithms are useful to prevent numerical underflow, and the absolute value offers compatibility with follow-on tools that expect a larger-is-better score. Byonic's protein table includes a number of columns that reflect the quality of the PSMs for each protein:
Protein Name	The name of the protein
|Log Prob|	Absolute value of the log base 10 of the protein p-value
Best |Log Prob|	Largest |Log Prob| of an individual PSM assigned to the protein
Best Score	Largest Byonic score of a PSM assigned to the protein. For "one-peptide-per-protein" samples, for example top-down proteomics or N-glycopeptide samples, sorting by Best Score may give a better protein list (lower-ranking decoys) than protein |Log Prob|
# Spectra	Total number of PSMs, including duplicate PSMs
# Uniq. Peps.	Total number of PSMs, discounting duplicates (the same modification in a different place is treated as a distinct PSM)
# Mod Preps	Total number of modified peptides
% Cov.	Percent of the protein sequence covered by PSMs. Byonic groups together if their spectra match exactly. An ambiguous PSM, one matching a peptide that is found in two or more proteins, is always assigned to the higher-ranking of those proteins. For example, if PSM P1 has separate evidence but P2 does not, P2 will not be shown. If P1 has more separate evidence than P2, then P1 will be ranked according to all its evidence, but P2 will be ranked according to only its separate evidence. For this reason, as well as others, none of Byonic's outputs (# of spectra, intensity, etc.) is an accurate measure of protein abundance.

# AAs	Number of amino acids
Intensity	Total intensity of MS/MS peaks
ProteinsId	Internal Byonic ID used to identify the protein records

Peptides/Spectra Field	**Description**
PID	Byonic ID used to identify the peptide records
Prot. Rank	Protein Rank (see Proteins Field description, above)
Pos.	Position within the protein sequence of the N-terminal residue of the peptide
Sequence	The peptide sequence
Xlink Base Peptide Xlink Pos. in Protein	The amino acid position of the link in the base protein
Xlink Partner Peptide Sequence	Crosslinked pairs include "base" (under Sequence column) and "partner" (this column)
Xlink Partner Peptide Protein Name	The crosslink bridge's “partner” protein
Xlink Partner Peptide Xlink Pos. in Protein	The amino acid position of the link in the partner protein
Mods (variable)	Modification list (common and rare)
Glycans	Glycan composition. If in numeric form (e.g. 0 1 2 0 0 0): HexNAc Hex Fuc NeuAc NeuGc Sodium
PEP 2D	Protein-aware posterior error probability
PEP 1D	Protein-oblivious posterior error probability
|Log Prob|	The absolute value of the log10 of the posterior error probability (PEP). The PEP takes into account the Byonic score, delta, precursor mass error, digestion specificity, and so forth (10 features in all). For PSMs with non-negligible error probabilities, say error probabilities > 0.0001, and hence |Log Prob| < 4.0, PEPs are in good agreement with “local FDR” measured by the decoy sequences. |Log Prob| incorporates more evidence than Byonic scores, so that sorting by |Log Prob| will almost always give a better ROC curve than sorting by score.
Score	Byonic score, the “raw” indicator of PSM correctness. Byonic scores reflect the absolute quality of the peptide-spectrum match, not the relative quality compared to other candidate peptides. Byonic scores range from 0 to about 1000, with 300 a good score, 400 a very good score, and PSMs with scores over 500 almost sure to be correct.
Xlink Score	The score of the lower-scoring peptide in a crosslinked pair of peptides
Delta Score	The drop in Byonic score from the top-scoring peptide to the next *distinct* peptide. In this computation, the same peptide with different modifications is not considered distinct.
Delta Mod. Score	The drop in Byonic score from the top-scoring peptide to the next peptide different in any way, including placement of modifications. DeltaMod gives an indication of whether modifications are confidently localized; DeltaMod over 10.0 means that there is a high likelihood that all modification placements are correct.
z	Charge

Obs. m/z	Observed m/z
Calc. m/z	Calculated m/z
ppm err.	ppm mass error (observed - calculated), or more specifically, 10^6 x ($M_{Observed}$ – $M_{Computed}$) / ($M_{Computed}$). The ppm mass error is computed after correcting for off-by-x errors
Off -By-X	[$M_{Observed}$ – $M_{Computed}$], where $M_{Observed}$ is the observed M+H (singly charged) precursor mass and $M_{Computed}$ is the computed M+H precursor mass, and [ ] means closest integer
Obs. MH	Observed M+H (singly protonated mass)
Calc. MH	Calculated M+H (singly protonated mass)
Cleavage	Digestion specificity, where Specific means fully specific, Nragged refers to nonspecific at the N-terminus, Cragged refers to nonspecific at the C-terminus, and Non refers to nonspecific at both termini.
Glycans Pos.	Glycan position within the peptide
Z-Score	Z-Score
Protein Name	Protein Name
Prot. Id	Protein record identifier
Scan Time	Scan time, usually reported in seconds (depending on the input data file format). This is usually also the retention time (R.T.) in LC-MS experiments.
Scan #	Scan number(s) for the MS/MS spectrum
QID	Query Identifier (QueriesId)
Mods (fixed)	Modification list (fixed)
Comment	Comment is derived from TITLE= [line] of the source data file. This sometimes contains the scan number from the raw file.
Fragment Type	Fragmentation type (MS2)
Obs.M	Observed neutral mass
Calc.M	Calculated neutral mass
FDR 2D	(# Decoy PSMs) / (# Target PSMs) in full PSM list ranked by PEP 2D
FDR 1D	(# Decoy PSMs) / (# Target PSMs) in full PSM list ranked by PEP 1D
FDR uniq. 2D	(# Decoy Peptides) / (# Target Peptides) in full peptides list ranked by PEP 2D
FDR uniq. 1D	(# Decoy Peptides) / (# Target Peptides) in full peptides list ranked by PEP 2D
q-value 2D	Estimated FDR for the full list of PSMs thresholded at this PSM by PEP 2D
q-value 1D	Estimated FDR for the full list of PSMs thresholded at this PSM by PEP 1D

Modifications

The following contains additional details about Byonic's modification rules.

Bundled Modifications. A modification rule can specify more than one target residue at a time. For example, the one rule

Phospho / +79.966331 @ S, T | common2

is identical to the two rules

Phospho / +79.966331 @ S | common2
Phospho / +79.966331 @ T | common2

Protein Terminal Modifications. The following rule specifies acetylation on the protein, but not peptide, N-terminus:

Acetyl / +42.010565 @ Protein NTerm | rare1

Protein-Specific Modifications. The following rule specifies hydroxyproline only on proteins that include the string “collagen” in their FASTA file names.

Oxidation / +15.994915 @ P | common3 | ProteinLabel[icase]{collagen}

The last field is an example of a modification attribute; to add an attribute pull down the menu highlighted in an orange box in Figure 14: Select Modifications dialog

.

The keyword [icase] specifies case-insensitive match, so that collagen will also match “Collagen”, “procollagen”, “collegenase”, etc. The keyword [case] specifies case-sensitive match. To match a single protein, use a unique identifier such as the accession number. Protein-specific modifications offer even finer control of the size and focus of a Byonic search and can be extremely useful when search space would otherwise be unnecessarily large, as mentioned below.

Glycopeptide searches. The fully automatic, pre-set, glycopeptide searches (the checkboxes under Glycan preset tables) allow only one glycan per peptide. The limitation of one glycan per peptide is not a severe restriction for N-linked glycosylation, because few peptides contain two N-glycosylation motifs, that is, two occurrences of NX{S/T}. However, this limitation is a serious restriction for O-linked glycosylation, especially mucin glycosylation, and for O-GlcNAc-ylation on S/T, because sites for these modifications often cluster together. The following rule gives a reasonable O-GlcNAc search:

HexNAc / +203.079373 @ S, T | common3, or alternatively,
HexNAc @ OGlycan | common3.
HexNAc @ S, T | common3

The third expression lets the software compute the mass applicable to the specific cases of glycan compositions only.

For a faster but narrower search, use:

HexNAc @ S, T | common2

For an intermediate search, designate the modification as both common2 and rare1.

An example of a slightly expanded search rule is:

HexNAc / +203.079373 @ NGlycan, S, T | common3

NGlycan as a modification target means the asparagine in the N-glycosylation motif NX{S/T}, where X is any residue except proline. The expanded rule searches for truncated N-glycans; with the earlier rule a peptide with a truncated N-glycan is likely to be mistaken for an O-GlcNAc peptide.

The NGlycan keyword enables the user to search for more than one N-glycan per peptide. The keyword also enables the user to customize the N-glycosylation search to specific glycan masses, rather than rely on Byonic’s predefined tables. For example, a researcher may have already acquired detailed knowledge of the glycan masses through detached glycan analysis. For human blood serum samples, one of the most common N-glycans is usually HexNAc(4)Hex(5)NeuAc(2) at 2204.77 Da.

Mucin-type O-glycosylation sites tend to cluster, so that a single tryptic peptide may have 5 or more glycosylation sites. Searches allowing 4 or more common modifications are computationally intensive, so these searches are best run with small protein databases and limited lists of glycan masses. With Total common modification max set to 5, a search involving 10 proteins (typically the protein of interest, along with trypsin and contaminants) and 10 likely O-glycans (for example, HexNAc(1), HexNAc(1)Hex(1),

HexNAc(1)Hex(1)NeuAc(1), HexNAc(1)Hex(1)NeuAc(2), HexNAc(2)Hex(1), etc.) may already be an undesirably large search. Specifying fully specific digestion, no more than one missed cleavage, and making the glycosylation protein-specific using the ProteinLabel attribute are ways to help control the combinatorial explosion by limiting the large glycosylation part of the search to just the relevant protein(s).

Byonic allows the user to combine handcrafted modification rules with one or both of the predefined glycopeptide searches. One strategy is to use the predefined searches for exploration, and then iteratively move the modification masses found in confident identifications into handcrafted rules in order to focus the range of modification masses while simultaneously increasing the number of allowed instances of each modification.

Wildcard mass defect. If the precursor mass tolerance is low (less than 100 ppm) Byonic obtains the exact mass of the wildcard from the difference between the observed precursor mass and the calculated mass of the candidate peptide. If the precursor mass tolerance is high (within 100 ppm), Byonic uses a mass defect (fractional part of the mass) characteristic of an organic molecule. In either case, Byonic will show the wildcard mass it used in the output. With precursor masses good to 5 ppm, a modest-size wildcard, say in the range –40 Da to 40 Da, may pinpoint the elemental composition.

False Discovery Rate

Byonic uses a two-dimensional false discovery rate (2D-FDR) estimation method. For more details on this method, see the journal article: “Two-dimensional target decoy strategy for shotgun proteomics,” by M. Bern and Y. Kil in J. Proteome Res., 2011, vol 10(12), 5296-5301. PMID 22010998

Internally, Byonic retains all PSMs and all proteins. For presentation to the user, however, Byonic by default cuts the protein list after the 20th decoy protein or at the point in the list at which the protein FDR first reaches 1%, whichever cut gives more proteins. On most data sets, almost all the true proteins will be on this truncated list. Researchers with special knowledge of their samples, along with the time to examine protein identifications manually, may choose to make a lower protein cut using the options on the Advanced tab of the Byonic input window. (For making a focused database for subsequent searches, a 2% FDR is generally recommended to make the resulting FASTA file liberal in inclusion of protein sequences.)

After making the protein cut, Byonic makes a PSM cut in order to keep the spectrum-level FDR to a reasonable level, that is, in order to discard false matches to the reported proteins. By default, Byonic makes this cut by discarding the n PSMs with the lowest Byonic scores, where n is the expected number of random PSMs matching the reported proteins. Byonic then estimates the spectrum-level FDR of the remaining PSMs to the reported proteins; this FDR will typically be in the range 0 – 5%. Alternatively, using the Advanced tab, the user can ask Byonic to make a manual score cut in order to obtain a desired spectrum-level FDR. Warning: A significant number of true PSMs may be lost by imposing an arbitrary low FDR limit rather than accepting Byonic’s automatic cutoff.

And a final word of caution: The target-decoy strategy gives an accurate estimate of the rate of completely false identifications at both the protein and PSM levels, but it does not give any estimate of “partially correct” identifications, for example, wrong homologues or splice variants in the case of proteins, or misplaced or incorrect modifications in the case of peptides. Peptide identifications that may be only partially correct can usually be recognized by low DeltaMod (often zero), and manual inspection of the annotated spectrum may in some cases resolve the ambiguity. Even with all of Byonic’s advances over the previous state of the art, human judgment remains the ultimate arbiter of subtle identification clues.

Appendix – Common Modifications

Below are examples of modifications that are often encountered and the appropriate syntax for including those modifications in a Byonic search.

Table 1. Cysteine Treatments + Artifacts of Treatment

The modifications **in blue** apply to samples with the cysteine treatment **in black** above them. The syntax for the rules from the pull-down menu are also accepted in the custom modification entry box as well as the “old syntax” pre-dating the new pull-down menu interface.

Rule from Pull-Down Menu	Explanation
Carbamidomethyl / +57.021464 @ C | fixed	Iodoacetamide treatment
(De)Carbamidomethyl / -57.021464 @ C | common1	Under-alkylation
Ammonia-loss / -17.026549 @ NTerm C | rare1	Pyro-glu from camC
Methyl / +14.01565 @ C | rare1	Propionamide (from gel)
DTT / +151.996571 @ C | rare1	Total mass delta ≈ 209 Da
Carbamidomethyl / +57.021464 @ NTerm, H, K | common2	Over-alkylation
Carboxymethyl / +58.005479 @ C | fixed	Iodoacetic acid treatment
DTT / +151.996571 @ C | rare1	Total mass delta ≈ 210 Da
Methylthio / +45.987721 @ C | fixed	MMTS treatment
Propionamide / +71.037114 @ C | common2	Common in gel samples

Table 2. Other Chemical Treatments

Mixtures of isotopically labeled and unlabeled peptides (e.g., SILAC) are best run as two searches with fixed modifications, rather than as variable modifications, because peptides should be either completely labeled or completely unlabeled.

Rule from Pull-Down Menu	Explanation
Propionyl / +56.026215 @ NTerm, K | fixed	Propionylation
TMT / +224.152478 @ NTerm, K | fixed	TMT0 labeling
TMT2plex / +225.155833 @ NTerm, K | fixed	TMT2 labeling
iTRAQ4plex / +144.102063 @ NTerm, K | fixed	iTRAQ labeling
Label:13C(6)15N(2) / +8.014199 @ K | fixed	Heavy Lysine for SILAC
Label:13C(8)15N(2) / +10.020909 @ R | fixed	Heavy Arginine for SILAC

Table 3. Common In Vitro Modifications

Rule from Pull-Down Menu
Deamidated / +0.984016 @ N, Q | common2
Carbamyl / +43.005814 @ NTerm | common1
Gln->pyro-Glu / -17.026549 @ NTerm Q | common1
Glu->pyro-Glu / -18.010565 @ NTerm E | common1
Delta:H(2)C(2) / +26.01565 @ NTerm | common1
Oxidation / +15.994915 @ M | common2
Dioxidation / +31.989829 @ M, W | rare1
Trioxidation / +47.984744 @ C | rare1
Dethiomethyl / -48.003371 @ M | common2
Cation:Na / +21.981943 @ D, E | common1
Methyl / +14.01565 @ E | common1
Dehydrated / -18.010565 @ S, T | rare1

Table 4. Common In Vivo (Biological) Modifications

Rule from Pull-Down Menu
Oxidation / +15.994915 @ P | common3 | ProteinLabel[icase]{collagen}
Phospho / +79.966331 @ S, T | common3
Phospho / +79.966331 @ Y | common2
Methyl / +14.01565 @ K, R | common2
Dimethyl / +28.0313 @ K | common2
Acetyl / +42.010565 @ K | common2
Trimethyl / +42.04695 @ K | common2
Acetyl / +42.010565 @ Protein NTerm | common1
Amidated / -0.984016 @ Protein CTerm | rare1
Sulfo / +79.956815 @ C, S, T, Y | common2
HexNAc / +203.079373 @ S, T | common2
HexNAc(1)Hex(1) @ OGlycan | common2
HexNAc(4)Hex(5)NeuAc(2) @ NGlycan | rare1
HexNAc(4)Hex(5)NeuAc(2)Sodium(1) @ NGlycan | rare1
Hex / +162.052824 @ K | common2