BioPharma Finder 3.1 Release Notes

These release notes briefly list new features in the Thermo BioPharma Finder™ 3.1 application (build 3.1.72.22), a mass informatics platform for protein characterization of biotherapeutics. Also included are known issues in the 3.1 release of the application.

Contents

For information on installing the BioPharma Finder software, refer to the DVD insert. For information on configuring and using the BioPharma Finder 3.1 application, refer to the manuals available as PDF files or the Help.

Features

Key features in the BioPharma Finder 3.1 application are workflow-driven experiment creation, method processing, and result review.

Intact Protein Workflow

Features in the intact protein workflow include the following:

- Rapid measurement of the intact molecular weight of biotherapeutics for structural confirmation and characterization
- Confident deconvoluted molecular weight of proteins in both acidic and native conditions
- Target protein sequence matching, which identifies N-linked glycosylations and other common modifications using the intact mass
- Identification of Antibody Drug Conjugates (ADCs) using a sliding window algorithm
- Batch-to-batch comparison
- A novel sliding window algorithm to improve detection on low abundant species

Peptide Mapping Workflow

Features in the peptide mapping workflow include the following:

- Confirmation of amino acid sequences with a novel MS2 prediction algorithm, providing extra confidence in your peptide sequence assignments
- Identification of the site and type of expected and unknown PTMs, providing the relative amount of modification in the sample
- Disulfide bond mapping
- Detection of low-level impurities and sequence variants
- Sequence alterations in stress samples, including the deamidation or oxidation level
- Error tolerant searches for unexpected modifications
- De novo sequence searches for unknown components

Revision A XCALI-98032

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Top Down Workflow

Features in the top down workflow include the following:

- A simple workflow for sequencing intact protein molecules using ProSightBP™ as the core algorithms
- Ability to compare multiple raw files with combined interactive fragmentation coverage maps
- Support for multiple modes of fragmentation: CID, HCD, ETD, EThcD, and UVPD, enabling maximum protein coverage

Intact Protein Analysis

Intact Protein Analysis has these new features and improvements:

- New intact protein deconvolution workflow added to the Chromeleon™ 7.2.9 data system that provides a new compliant solution for molecule weight determination and utilizes the same algorithms as those that are present in BioPharma Finder 3.1
- New intact workbook in BioPharma Finder allowing for simple exchange of information (targeted components and processing method parameters) between BioPharma Finder and Chromeleon
- Better data management for sliding window experiments reducing the size of the stored results on the computer for less disk space usage

Peptide Mapping Analysis and Multi Attribute Method (MAM)

The following are new features and improvements in support of Peptide Mapping Analysis and Multi-Attribute Methods (MAMs):

- New targeted workflow for discovery and monitoring in the same software
- Fast screening of large data sets for targeted Product Quality Attributes (PQAs)
- Identification verification by MS2 spectra, when available, instead of limited verification by accurate mass alone
- Improved relative quantitation in the modification summary with user-defined components for the abundance calculation
- Improved connectivity to Chromeleon using the new peptide workbook for compliant analysis
- New comment column for user-documented results in real time during data review

System Requirements

These are the minimum and recommended hardware and software configurations required for BioPharma Finder 3.1 operation.

System	Minimum requirements	Recommended requirements
Hardware	• Intel™ Core™ i7-4770 CPU@3.40 GHz • 8 GB registered RAM • 100 GB storage hard drive—ST1000DM-003 SCSI disk device • DVD/CD-ROM drives • Resolution display 1280 × 1024 (SXGA)	• Quad-core Intel Xeon™ CPU (E5-1630 v3 3.7 GHz 10 MB 2133 4C) • 32 GB DDR4-2133 (4 × 8 GB) registered RAM • 2 TB storage hard drive (SATA, 7200 rpm)—512 GB solid state boot drive (SATA) • DVD-RW optical drive • Resolution display 1920 × 1080 (WUXGA)
Software	• Microsoft™ Windows™ 7 Professional (English) SP1 (64-bit) • Microsoft .NET Framework 4.6.2 • Microsoft Office 2010 • Adobe™ Acrobat™ Reader™ DC	• Microsoft Windows 10 Professional (English) (64-bit)[a] • Microsoft .NET Framework 4.6.2 • Microsoft Office 2016 • Adobe Acrobat Pro DC

[a] Windows 10 Enterprise LTSB 2016 (English) (64-bit) is also supported.

License Activation

Use the Thermo Scientific Product Licensing wizard to activate (or deactivate) the BioPharma Finder application. This wizard offers three different licensing options:

- Full features (all workflows—peptide mapping analysis, intact protein analysis, and top down analysis)
- Peptide mapping analysis only
- Intact protein analysis and top down analysis only

Activation of these features is dependent on the product purchased and is controlled by the license activation key. If you would like to add an additional feature to the software, contact your customer service representative.

Before you transfer the license to another computer, you must deactivate the existing BioPharma Finder application and then transfer the license key. If you are upgrading from previous versions of Thermo PepFinder™ or Thermo Protein Deconvolution™, you must obtain a new license key for the BioPharma Finder application.

❖ To activate (or deactivate) the BioPharma Finder application

1. Open the Product Licensing wizard as follows:
   a. Open the BioPharma Finder application.
   b. Choose **File > About BioPharma Finder** to display the License Activation wizard.
   c. Click **Activate** (or **Deactivate**) to start the activation or deactivation process, as applicable.
2. Locate the activation code as follows:
   a. Log in to your account at thermo.flexnetoperations.com.
   b. In the left navigation pane, under Software & Services, click **Order History**.
   c. From the list of ordered products, click the order number.

      The order number is in the Thermo Fisher Scientific "Your Order is Ready" email message. The Order Details table provides the activation code in the last column.
3. Continue through the Product Licensing wizard to activate the license using the activation code.

Installation and Upgrade

Follow these instructions to install the BioPharma Finder 3.1 software. You must be a system administrator on the installation computer to install the software. You may license the application as either an administrator or as a standard user.

During the upgrade of a previous version of BioPharma Finder, two main software folders, C:\ProgramData\ThermoScientific\Databases and C:\ProgramData\ThermoScientific\BioPharma, are automatically backed up.

Copies of the files are placed in the following location using this notation:

C:\ProgramData\ThermoScientific\BioPharma*legacy application version number*_backup_*DateAndTime*

Once the software is successfully installed, you can delete the backup files or move them to another archive location to save space on the processing computer.

❖ To install BioPharma Finder 3.1 software

1. Close all opened Thermo Scientific™ applications.
2. Insert the BioPharma Finder 3.1 DVD into the DVD/CD-ROM drive.

   The Autorun program automatically launches the installer wizard. If the wizard does not start, navigate back to the DVD in Windows Explorer and double-click **BioPharmaFinderSetup.exe**.

   The Welcome to the Thermo BioPharma Finder Suite Installer page opens.
3. Click the links to view the installation instructions, release notes, validation certificate, example data, and documents. Then click **Next**.
4. View the entire license agreement as needed and select the check box to accept the licensing terms.

5. Click **Install**.

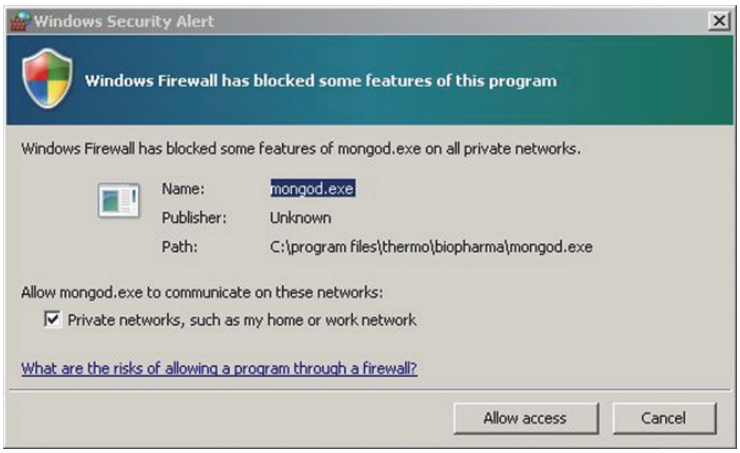
   The wizard automatically checks the minimum system requirements. If there are missing items, a summary report opens with the appropriate links to download and install the required applications.

   If you are upgrading from legacy software, the installer does the following:

   - Detects legacy software (BioPharma Finder or Protein Deconvolution), uninstalls the legacy software, and upgrades the data. To proceed, click **Yes**.
   - Automatically backs up your legacy results onto the computer and upgrades these results to be compatible with the new software version.

6. To review the IQ report after installation is completed, click the corresponding link. Then click **Finish**.

   If the Windows Security Alert dialog box appears, click **Allow Access**.



You can now start the BioPharma Finder application from the desktop icon or Start menu and activate a license.

The BioPharma Finder installer includes a recently distributed Xcalibur™ security patch. This patch is applied automatically, requiring no user interaction. If Foundation™ is not installed, the patch has no effect. For more information about the patch, consult the website: http://www.thermofisher.com/software-update.

You must reapply the Xcalibur/Foundation update if you install, upgrade, or reinstall Foundation.

❖ To reapply the Xcalibur/Foundation update

1. Locate the cmd.exe file on your PC, and then right-click and choose **Run as administrator**.

   The Windows command prompt opens with Administrator permissions.

2. Navigate to the directory where the update was unzipped.

   For example, if the update was unzipped to c:\Update, type `cd c:\Update`, and then press **Enter**.

3. Type `ThermoXcaliburFoundationSU.exe /uninstall /quiet` and then press **Enter**.
4. Type `ThermoXcaliburFoundationSU.exe /install /passive` and then press **Enter**.

The Xcalibur/Foundation Security Update window opens and then closes when the installation is complete.

Resolved Issues

Table 1 lists defects that were resolved between the BioPharma Finder 1.0, 1.0 SP1, 2.0, and 3.0 applications or are no longer relevant in the 3.1 release. The defects exclude Help issues and cosmetic fixes. In some cases the abstract has been amended or extended from the original to better describe the reported issue. Both an engineering fix and follow-up testing (verified by our product evaluation department) have resolved each of these issues.

Table 1. Resolved issues (Sheet 1 of 4)

Item ID	Software section	Abstract
23543	Intact Analysis	With the 64bit ReSpect dll delivered with BPF1.0, the intensity is very different and missing some low resolution data.
5297	Intact Analysis	Save reference for Xtract sliding shows MS scan numbers as –1–1 in table and Show Details for Sample Reference.

Table 1. Resolved issues (Sheet 2 of 4)

Item ID	Software section	Abstract
4754	Intact Analysis	There should be a reasonable default value for the Sequence Matching Mass Tolerance with Da as the unit.
4158	Intact Analysis	You can export the top-level results only for ReSpect™ sequence matching; the last row shows as an expandable row like Export All.
5145	Intact Analysis	Modification text does not update when switching between the peaks in the zoomed-in state.
5298	Intact Analysis	Attempts to add a sample reference to an Xtract sliding window and then save and run a method do not complete and throw an internal exception.
4999	Intact Analysis	On selecting a result row after zooming and resetting the scale, the chromatogram shows the RT range from a previously loaded raw data file.
5025	Intact Analysis	Run queue becomes corrupted. The experiment type does not match the method type, causing the system to hang in processing.
3532	Intact Analysis	Report -> ReSpect/Xtract Masses table: The order of the matching sequence + modification is not consistent when compared to the deconvolved spectrum and component table in the results view.
4319	Intact Analysis	After the jobs are done, the top jobs (for example, the just finished jobs) should appear.
4234	Intact Analysis	There is a user interface style sheet inconsistency among the different tabs in Protein Deconvolution 4.0.
3087	Intact Analysis	It takes 72 minutes to create 2400 rows using Add Queue. The requirement states 8 minutes.
4449	Intact Analysis	When copying and pasting from the source spectrum, the blue dots are offset from the peaks, which is unexpected.
4637	Intact Analysis	Source spectrum is missing intermittently on a specific file only.
2259	Intact Analysis	On the Parameters > Chromatogram page, if invalid values are entered for the Chromatogram *m/z* range, no tooltip appears with the valid values.
4179	Intact Analysis	There is no averaged spectrum when using an ion trap data "9mix_Lyc_monolith.raw" file.
3388	Intact Analysis	"Reset Method" does not work for the Chromatogram parameters.
4362	Intact Analysis	The XIC for standard Xtract and ReSpect is being represented incorrectly.
40758	Peptide Mapping	MsFileReader is not installed when running the installer in repair mode. Workaround: The BioPharma Finder application now uses RawFileReader instead of MsFileReader.
9206	Peptide Mapping	Memory is not released during the various operations. AlgorithmsLayer has been fixed and there might be some other workflow where memory might not be released. Deferred to the next release, so more improvements can be made.
38277	Peptide Mapping	Refresh issue with loading the protein sequence after reprocessing the data. None of the tabs are selected.
40794	Peptide Mapping	When the MS2/Full window is changed to floating (by dragging the window) and then changed back to dockable, the MS2/Full data is not displayed any more.
15925	Protein Sequence	Feature to add glycan list to the default list of variable modification for the side chain will be redesigned in a future release but a workaround exists. Workaround: Add common glycans as the variable modification, instead of using N-gly as CHO or Human, so the annotation is more specific.

Table 1. Resolved issues (Sheet 3 of 4)

Item ID	Software section	Abstract
20475	Peptide Mapping	Glycosylated peptides will not appear in the results table using the default parameters because their confidence score will be less than 80% if you search for them using variable modifications instead of the N-glycan database. Workaround: Lower the confidence score to 0% to observe this type of variable modification or use the N-glycan database.
9296	Peptide Mapping	Fragment coverage map appears for the components with the ID type as Full MS. This is an error in Mass Analyzer. Improvement has been made but more enhancement needed.
11740	Peptide Mapping	Toggling between the fragmentation types and back to the original shows the predicted spectrum with different scaling and labels. This is an error in Mass Analyzer. Scaling might not be that important, result values need to be correct, and MS/MS values are confirmatory only.
63263	Peptide Mapping	Peptide Mapping -> ID type is incorrect. Workaround: Select the MS2 tab and check to see if the spectrum appears.
38505	Peptide Mapping	In Peptide Mapping, the MS ID Type might be incorrectly labeled. Workaround: Review the results by selecting the component and checking to see if an MS2 spectrum appears in the MS2 pane. If multiple files are present, expand the results table to the raw file level and review each raw file for the MS2 spectra.
35247	Peptide Mapping	Limitation in the components table for displaying peptides with 7 or more modifications.
42105	Peptide Mapping	Feature to double click and load the results is enabled in the queue for Intact Protein Analysis but is not enabled in Peptide Mapping Analysis.
40081	Peptide Mapping	Protein coverage results found in the results table under the shading chromatogram on the Mapping page might not agree with the coverage results on the protein coverage map. This can occur for both the default and user-defined coverages. This issue will be addressed in a future release.
40426	Peptide Mapping	When a peptide mapping experiment is deleted from the Load Results page, the Mapping tab is not removed. Workaround: Exit and restart the application.
17270	Peptide Mapping	All MS/MS Ion runs do not show the Modification Summary report.
17143	Peptide Mapping	Disulfide + Sodium Adduct results in high negative delta mass for the MS2 ID rows.
17030	Peptide Mapping	Gasphase – NH3Loss—seems like the wrong mass for calculation is used. Delta mass is larger than expected.
17015	Peptide Mapping	Isomerization for the same peptide shows up as two different modification masses and shows large delta mass ppm.
14263	Peptide Mapping	When the protein coverage map is copied and pasted into Office 2007, the amino acid is not displayed properly.
62395	Peptide Mapping	Large peptide mapping experiment is only using one file for MS2.
62396	Peptide Mapping	Peptide mapping -> ETD/CID select ETD over higher quality CID.
4169	Intact Analysis	Zooming out to full scale for the MS spectrum does not hide the scrollbar.
3238	Intact Analysis	Reporting -> Source spectrum shows “F:”. We assume this is for Filter; however, we might not have filters for chromatograms.

Table 1. Resolved issues (Sheet 4 of 4)

Item ID	Software section	Abstract
62577	Peptide Mapping	After placing a peptide mapping experiment on the run queue, the Home page still shows the method as checked.
62580	Protein Sequence	Loading an incorrect MSQC file causes an exception dialog. Workaround: To load MAM results, browse and select only *.msqc files.

Known Issues

Suggested recovery actions

- For some issues, restarting the application is the appropriate recovery action.
- As a fix we generally do not recommend reinstalling the software or the operating system, which more commonly occurs after you install a new hard drive.
- If you observe a problem with the Chromeleon instrument service not starting after installing the BioPharma Finder software, try downloading and installing the Visual C++™ 2013 redistributable package (x86) to reestablish communication.

Feature requests and other removed items

- We do not include issues where there is insufficient information logged to successfully reproduce the reported problem.
- We do not list feature requests as software issues, regardless of the reported significance or severity of the request. Product managers evaluate logged feature requests for future releases.
- We report only discrepancies in the documented software as known issues.

Terminology

Severity	Interpretation
Critical	A problem that renders the system unusable because either an entire function is unusable and no workaround exists, or use of the current system compromises data integrity or results in data loss. Catastrophic problems also include significant and non-obvious quantitative errors, and all human and instrument safety issues.
High	A serious issue that does not affect data integrity (meaning data loss, corruption of data, or the wrong answer), but affects the customer's ability to use the product as designed. It can be a failure, design issue, or documentation error or omission. A workaround might or might not exist.
Medium	A minor error or poor behavior of a product feature. There is probably a workaround.
Low	An issue that has a limited effect on customer usage of the product; for defects with visibility so low that a customer might never see it; or for ease of use issues or other items not causing any performance degradation.

Risk	Interpretation
High	Occurrence is likely to happen and can compromise operation.
Medium	Occurrence is uncommon, but if it occurs, can compromise operation.
Low	Issue is minor; however, the software might operate differently from a user's expectations. A workaround is often available.
No Risk	This issue causes no problems but is commonly an inconsistency or a cosmetic issue.

Known defects

Table 2 contains known defects in the software, with a brief abstract and information related to each defect's severity and risk. The Item ID is the internal number assigned to each issue. Product management assesses risk, which can differ significantly from the reported severity.

Table 2. Known defects (Sheet 1 of 6)

Severity	Abstract	Risk	Item ID
High	Duplicate copies of a chromatogram, deconvolution, and source spectra (from the same raw file) are created for a multiconsensus experiment when the raw file contains more than one component that passes the multiconsensus merge parameters. This might appear as a bug; however, if you view the raw file information, the individual component information is displayed for review.	High	32986
High	The protein sequence information might not be displayed correctly in the load results table and the identification parameters when upgrading a legacy Protein Deconvolution 4.0 result. Workaround: Reprocess the results in BioPharma Finder 3.1 using the same protein sequence (added manually) and then save the results.	High	37244
High	Missing retention time: The design was changed in Protein Deconvolution 4.0, and this error surfaced as a side error. To fix it requires redesigning the algorithm.	High	10137
High	When three chains are added to a FASTA file, the components are missing the "matched sequences." This issue is as designed; when three chains are added to the same sequence, the target mass of the protein is higher than the component. As a result, none of the sequence is matching. This issue has been documented in Protein Deconvolution 4.0. Workaround: Import each chain as a separate FASTA file and add these sequences to the method. A sequence match gives the expected result. In a future release, the algorithm will be updated so that you can add all chains in the same sequence.	High	14421
High	Copied images from BioPharma Finder to Microsoft Word or PowerPoint™ that are then saved as PDF images might be corrupted. The Save as PDF command in Word and PowerPoint requires the installation of Adobe Acrobat Pro, which would then display the images correctly in a PDF file.	High	9716
High	Performance of "finalizing results" is slow.	High	2235
High	The Auto ReSpect feature cannot find the expected components.	High	3281
High	Top Down: Intact deconvolution spectrum might not update correctly when changing between peaks in the Results table. Workaround: Load another result, and then load this result again. For intact deconvolution, select the empty peak first.	High	63112
High	During the upgrade from BioPharma Finder 3.0 to 3.1, if there is not enough disk space and you select the Ignore option, the application still tries to create a backup database and installation fails. Workaround: Run the BPF 3.1 installer. Since no previous version exists anymore, this is considered a fresh installation. Install version 3.1 successfully and the installer will automatically run the Database Upgrade Utility which upgrades all of the 3.0 experiments once space on the drive is available.	High	81326
Medium	Drug load values are only assigned to components with identifications.	Medium	30767

Table 2. Known defects (Sheet 2 of 6)

Severity	Abstract	Risk	Item ID
Medium	For multiconsensus Average DAR experiments, if a raw file does not contain the component being used for the Average DAR calculation, the table will display empty spaces instead of the raw file name.	Medium	35097
Medium	If a processing method has an error, the application allows you to save the method. Workaround: Do not save methods with errors.	Medium	30357
Medium	If multiple resolutions are used during the data acquisition, the application requires two different processing methods that use the appropriate resolution values to obtain the best results.	Medium	24386
Medium	If the raw file folder path and the raw file name are greater than 256 characters, the number of components detected in the queue is listed as 0. However the experiment still processes correctly. Workaround: The number of components detected value appears correctly in the Load Results table.	Medium	38426
Medium	In the summary table found in the Parameters > Save Method page, the report parameters are listed and enabled for multiconsensus experiments. Note that reporting is not a feature for multiconsensus or DAR-enabled experiments and reports will only be produced for single file experiments.	Medium	36231
Medium	In this release, the deconvolution is processed every time you reprocess the experiment, even if no deconvolution parameters are changed. This feature will be redesigned in a future release to improve performance.	Medium	34061
Medium	Multiconsensus merging parameters are not deactivated for single file experiments.	Medium	34626
Medium	N-term and C-term modifications are not included in the DAR list of modifications. Therefore, they cannot be used for assigning drug load values in this release.	Medium	31909
Medium	When the component you want to override is an unchecked row and other rows are checked, overriding the drug load does not work. Workaround: Uncheck all of the components in the main results table. Select the component you would like to change the drug load value and select the override check box.	Medium	34990
Medium	Canceling peptide mapping can crash the application. This defect seems to be related to clicking the button to cancel. Workaround: If the application crashes when canceling, reopen it to continue processing.	Medium	35934
Medium	The peptide sequence coverage map does not paste correctly into MS Word. Workaround: Use the Windows Snipping tool to capture the image or do a screen copy.	Medium	20965
Medium	Sometime a peptide might not be highlighted in the protein sequence pane.	Medium	24538
Medium	The chain mass is not updated when linking disulfide bonds in the Protein Sequence Editor. Workaround: When a search is performed, only the target protein mass is used for searching. Therefore, this issue will not cause problems in your results because the application does not use the individual chain mass information.	Medium	14419

Table 2. Known defects (Sheet 3 of 6)

Severity	Abstract	Risk	Item ID
Medium	When exporting a multiconsensus experiment and there is a component with a raw file containing multiple peaks, only the first component is exported. Workaround: Export all components at all levels.	Medium	39426
Medium	Application error/crash occurs when launching a second instance of the application for a different user on the same machine.	Medium	41418
Medium	Disulfide bond is not properly highlighted in the Protein sequence pane. If the peptide sequence is overlapping, the first part of the sequence is not highlighted.	Medium	16720
Medium	Save the results after you recalculate the average DAR using the selected check boxes. The open results and drug load are zero for the non-checked rows. Workaround: Uncheck all rows and then click Recalculate. The drug load values appear for all rows with a drug load.	Medium	41362
Medium	Mass Std Dev and PPM Std Dev are present in the report but are not present in the results table or the exported file for ReSpect sliding window.	Medium	42104
Medium	Single-scan raw data files exported from Qual Browser can cause the source spectrum to be blank when switching from sliding window to average over RT deconvolution. Workaround: Create a method with a sliding window deconvolution that is within the RT range of the file.	Medium	40422
Medium	Using a restricted time that is greater than the actual chromatogram time causes the chromatogram and source spectrum to be empty. Work around: Adjust the restricted time to fit into the actual chromatogram window.	Medium	40735
Medium	When upgrading BioPharma Finder 1.0 SP1 to version 3.1, for custom methods, the RT range is set to 0 instead of the value set in the time limit parameter. The RT range parameter had a different meaning in past releases. Workaround: Change the RT range manually.	Medium	39721
Medium	When changing the MS2 window to floating (by dragging the window) and back to dockable, the MS2 data is no longer displayed. Workaround: When you encounter this error, select another experiment and then load this experiment again. Data will be displayed.	Medium	40794
Medium	With a remote desktop to a Windows 10 machine, when you load/open the results, a blank screen appears instead of the results on the Process and Review page. Workaround: Close and restart the application, and then load/open the results to see them displayed on the Process and Review page.	Medium	42050
Medium	The Mapping tab for results is missing for duplicate disulfide chain—shows on the Process and Review page.	Medium	14079
Medium	The resolution displayed on the experimental HCD spectra might be incorrect.	Medium	11778
Medium	The later loaded raw data file should not overwrite the previously loaded data.	Medium	5910
Medium	An apex RT should be within its RT range.	Medium	11958

Table 2. Known defects (Sheet 4 of 6)

Severity	Abstract	Risk	Item ID
Medium	When you upgrade from an earlier version of Protein Deconvolution to BioPharma Finder with a permanent license key, the experiment type and loaded results are deactivated until you restart the application.	Medium	13612
Medium	(UXLib 14705) When you have a remote desktop to a machine with a trial license for BioPharma Finder, intact protein is not enabled.	Medium	14462
Medium	Unexpected exception, RunQueueViewModel.StatusHandler, encountered for a large run queue with the PepFinder (tryptic digest) file nativeLYSCETDCID2.raw.	Medium	5291
Medium	The resolution for mixed data of FTMS Full MS and ITMS full MS is not correct.	Medium	1918
Medium	You can set different time limits for processing a sliding window and chromatogram. During processing, the chromatogram window is shown.	Medium	4565
Medium	The RT Range for sliding window can be zero for start and finish, and in automatic mode, you do not get the suboptimal warning in the run queue message.	Medium	4258
Medium	For top down analysis, when you delete the sequence that you added from the Home page, the proteoform is not present after processing. Workaround: If the sequence is used in an experiment being processed or in a submitted state, do not delete this sequence from the Global Sequence Reference table.	Medium	63260
Medium	Peptide Mapping: The best fragmentation MS2 is now selected, but the predicted MS2 spectrum is not the correct fragmentation type. Workaround: Manually select the correct fragmentation type in the Predicted Peptide MS/MS dialog box.	Medium	62682
Medium	Top down Xtract parameters for intact deconvolution: *m/z* range does not correspond with the range on the source spectrum's scan filter header when Intact Deconvolution is unchecked after selecting an RT range. Workaround: Manually change the *m/z* range in the Parameters > Intact Deconvolution tab and save the method.	Medium	63022
Medium	Intact: When the queue is paused and BioPharma Finder is upgraded to version 3.1, the application crashes after prompting you to start the queue. Workaround: Process all data experiment in the queue before upgrading to the later version.	Medium	61937
Medium	Top down: The ProSightBP table is not sorted by relative abundance on initially clicking a proteoform. Workaround: Sort manually on relative abundance.	Medium	62214
Medium	For MSQC, when copying peptide sequences into the sequence box with "> name", this information does not show in the table.	Medium	60347
Medium	Intact -> Process and Review: XIC disappears in an auto peak detection experiment when reviewing data. Workaround: Reload the results to view the XIC.	Medium	60726
Medium	Licensing: In offline deactivation, the response file for "Deactivation.req" is called "Activation.xml". Workaround: Edit the default name and name it "Deactivation.req".	Medium	61014

Table 2. Known defects (Sheet 5 of 6)

Severity	Abstract	Risk	Item ID
Medium	Peptide Mapping: In a single file experiment, for some components, the ID Type appears as Full, even though the MS2 spectra and fragment coverage map are present when mixed modes of MS2 are present in the raw data file.	Medium	76529
Medium	In a non-targeted/targeted experiment with multiple (and single) raw data file(s), the predicted MS2 is not working when some peptides with MS2 spectrum are searched.	Medium	77170
Medium	Targeted Peptide Mapping: On the Modification Summary page, the % Abundance values for modifications that use unique peptides in the calculation might be incorrect.	Medium	79541
Medium	On a few Windows 7 machines, when running the BioPharma Finder installer, it might get stuck at the "Initializing" step.	Medium	81000
Medium	Installer: During installation, the mongodb access dialog box should be visible (not hidden). Workaround to partially fix this issue: 1. While the installer is still running (while it is showing the 1920 error), go to the C:\Program Files\Thermo\BioPharma Finder folder. 2. Select the ThermoFisher.BioPharma.DBUpgradeUtility.exe file and then run it as an administrator. In the displayed mongodb access dialog box, click **Allow Access**. 3. In the BioPharma Finder installer, in the 1920 error dialog box, click **Retry**. The Biopharma Finder installation successfully completes.	Medium	81387
Medium	Peptide Mapping for targeted experiment: On the Modification Summary page, the relative abundance calculations does not use the defined peptides when more than one modification is on the same peptide. This modification is excluded from the numerator.	Medium	80050
Medium	Peptide Mapping: The Theoretical Monoisotopic Mass is slightly different for targeted vs. non-targeted experiments.	Medium	80599
Medium	Peptide Mapping: There are multiple labels for glycan fragments for the same peptide in some MS2 spectra.	Medium	81002
Medium	When comparing BioPharma Finder 3.0 vs. 3.1, you see a large delta ppm for Mannosylation + GasPhase – B40.	Medium	81132
Medium	Peptide Mapping: NIST 2:V84-R99 NH3 loss results are significantly different in the BioPharma Finder application compared to the Mass Analyzer application.	Medium	68410
Medium	Peptide Mapping: When comparing BioPharma Finder 3.0 vs. 3.1, the confidence score is less than 3.0 for a few IDs and hence it is getting missed.	Medium	70896
Medium	Peptide Mapping: The missing Column "Level" causes data overlapping in the results table after exporting to Save As Displayed.	Medium	78060
Medium	Peptide Mapping: A crash occurs when zooming in on the chromatogram plot for a targeted experiment.	Medium	79771
Medium	When comparing non-targeted and targeted experiments for the same settings in created workbooks, Deamidation seems off by 1 amu.	Medium	79790
Medium	Peptide Mapping: The plot axis is not readable.	Medium	79794

Table 2. Known defects (Sheet 6 of 6)

Severity	Abstract	Risk	Item ID
Low	Xtract should block the use of a raw data file such as 20130511_RP-4H_100umlDx100cm_PAO1_GF9_135m in 1uL01.raw including ITMS Full MS and FTMS MS/MS.	Low	5275
Low	MSDimer Predicted Spectrum does not show up correctly in the sequence dialog box (assume MS/MS predicted spectrum is incorrect as well).	Low	12896
Low	Top Down Analysis: Selecting a method or typing an experiment name triggers the Clear Settings dialog box when clicking the Home tab.	Low	61013
Low	Top Down: UI items are not properly aligned on the Identification tab; PPM label is truncated. Workaround: This issue is specific to a certain VGA card only.	Low	51752
Low	The communicator bar does not display an error for the peak selection and deconvolution parameters when the window is dragged and floating.	Low	52498
Low	Peptide Mapping: The communicator bar messages are out of sync when changing the focus.	Low	71690
Low	File order is reversed in the Results table.	Low	53190
Low	Peptide Mapping: Low S/N can cause problems with keeping IDs with confidence = 0.0, even though the confidence threshold is greater than 80%.	Low	55881
Low	Peptide Mapping: Clearing the filter for a column does not set back to the original filter type.	Low	80017
Low	Peptide Mapping: The Trend MS Area plot is missing the raw file labels on the x-axis for a 100-file experiment.	Low	73403
Low	Peptide Mapping workbook: For the RT (Min) parameter, the red error message in the communicator bar does not disappear even after fixing the parameter value. You have to click on another row.	Low	75306
Low	Peptide Mapping: The test cases take a longer time on a XE2 machine vs. a Dell 9020 optiplex machine.	Low	77108

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