

FreeStyle 1.7 Release Notes

These release notes briefly list changes in the Thermo FreeStyle™ 1.7 software, fixes to previously reported issues, and known issues still existing in the FreeStyle 1.7 software release.

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For information on using the FreeStyle 1.7 application, refer to the *FreeStyle 1.7 User Guide*, which is available as a PDF file, or the Help.

Features

This release incorporates a number of new and enhanced features.

New Features

- New Data Analytics View that displays Trailer Extra and Status Log information as a Histogram or Trend plot in a separate window.
- New Mass Defect Filtered (MDF) Chromatogram View for one or more user-defined Mass and Mass Defect Ranges.
- Mass Defect Filtered Spectrum Views linked to MMDF chromatograms.
- Custom periodic table with editable isotope abundance for use in elemental composition calculation and isotope simulations.
- A new customizable File Header view.

Feature Enhancements

- Save and Apply Text and Structure Annotations in the Spectrum View.
- Theoretical Spectral Distance Isotope Pattern now overlaid on Spectrum View and includes Theoretical Mass, Delta Mass and supports Isotope Simulation below.
- Map Ranges available as a right-click option in the Map View and includes Mass Range and Retention Time value fields.
- New peak identification group section in the Peak Detection Info bar page to select Nearest, Highest, or All Peaks detection mode.
- Import component parameters from the processing method to the current or copy of the selected trace.

System Configurations

These are the recommended hardware configuration and required or recommended software configurations for operation of the FreeStyle 1.7 application.

System	Required or <i>recommended</i> configuration
Hardware (Recommended configuration)	<ul style="list-style-type: none">• 3.6 GHz Quad core processor• 16 GB RAM• CD/R-ROM or DVD drive• Video card and monitor capable of 1920 × 1080 resolution• 1 TB hard drive
Software	<ul style="list-style-type: none">• Adobe™ Flash™ Player for animations• Adobe™ Acrobat™ Reader™ 10.1• Microsoft™ Windows™ 7 SP1 (64-bit) or <i>Windows™ 10 (64-bit)</i>, or <i>Windows 10 Enterprise 2016 LTSB</i>• Microsoft Office 2013 or higher• Thermo Xcalibur™4.3 or Thermo Xcalibur™4.4

Important Information

General

The FreeStyle 1.7 application does not require licensing in any form. It is compatible with Windows 7 SP1 (64-bit) and Windows 10 operating systems.

Installation

You must have administrator rights to install and run the FreeStyle 1.7 software on your computer. The FreeStyle 1.7 application is installed as part of the Thermo Xcalibur 4.4 core software suite.

Resolved Issues

Table 1 lists defects that were resolved in the FreeStyle 1.7 release. The table excludes Help issues and any 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 2)

ID	Title	Severity
83315	Application hangs upon performing apply layout operation.	1 - Critical
86000	Elemental composition: Simulated plot from workspace 1 disappears upon closing workspace 2.	2 - High
61471	Application hangs upon opening a corrupted file.	2 - High
109676	Wavelength shown in spectrum list when MS trending is displayed.	2 - High
109687	Noise and Signal/Noise labels are not available from "FT centroid" data.	2 - High
110761	Elemental single mass search does not use exact centroid mass.	2 - High
108758	mmu and amu tolerance modes for elemental composition do not work.	2 - High
116156	"Freestyle Encountered an error" error message occurs when MSMS scan is not present in a spectrum and Elemental composition is performed.	2 - High
50601	MS Paint cannot correctly draw "formula labels" on FreeStyle Spectra when an image is copied to clipboard (but PowerPoint is correct).	3 - Medium
47469	Space is wasted above spectrum plots.	3 - Medium
117669	Unable to open the sequence file, after closing and reopening the workspace containing the sequence file.	3 - Medium
109565	Multispectrum: Mass precision changes when the .raw has both FTMS and ITMS filters.	3 - Medium

Table 1. Resolved issues (Sheet 2 of 2)

ID	Title	Severity
109567	Empirical Formula not updated when the Peak detection algorithm for a trace is changed in chromatogram view.	3 - Medium
114381	Composition column does not appear on the Spectrum List when elemental composition button is enabled.	3 - Medium
114695	Correct Base peak mass does not get updated, when elemental composition is performed for single mass mode for first time on an Averaged spectrum.	3 - Medium
115082	Spectrum List - Theo.Mass and Delta mass display zero.	3 - Medium
115152	Undeleted peak missing in the Peak List.	3 - Medium
109807	Scan header can display the actual instrument name instead of the generic name "Instrument data".	3 - Medium
110145	Selection retained in "To CSV File" when user opt for "Selection As" and then moved to "Workspace As".	3 - Medium
62409	ETD Ions are not updated on the results table .	3 - Medium
50834	Toolbox is removed when Selecting "text and graphics annotation".	3 - Medium
50835	Units are missing from "Label Threshold".	3 - Medium
86276	Peak List view becomes blank upon switching between two chromatogram views.	3 - Medium
84427	Layout - Incorrect trending data is displayed in chromatogram.	3 - Medium
29962	CV Plot cannot be re-enabled if closed while floating.	3 - Medium
29963	CV Plot does not update after re-ordering in Active Traces window.	3 - Medium
29969	Peak Detection is not applied from the Default Layout.	3 - Medium
29978	Many spectra are added automatically upon applying layout.	3 - Medium
29983	File name alignment is incorrect when many windows are open.	3 - Medium
29987	Layouts - Spectrum pane is displayed on opening a raw file applied with layout having MultiSpectrum pane floated and no Spectrum pane.	3 - Medium
30483	RT marker doesn't move while navigating thru keyboard.	3 - Medium
30571	Enhancement request: Isotope Simulation Window is too Wide for Very Long Peptide Sequences.	3 - Medium
30573	The copied and pasted data doesn't match if the user hide the data using "Field Chooser".	3 - Medium
44242	Enhancement request: Request that FS enables the "bold" and "italic" check boxes for text labels.	3 - Medium
47203	Custom Axis Name is not copied when we open new workspace.	3 - Medium
47210	Map ranges: Red border shown for valid filter.	4 - Low
89414	"Detect in All plot" button does not get toggled/enabled as expected.	4 - Low

Known Issues

Suggested Recovery Actions

- For some issues, restarting the application is the appropriate recovery action.
- In some cases (particularly issues that arise during data acquisition), restarting applications, such as the Home Page, might not ensure complete recovery. Typically, restarting the data system computer resolves issues, but some devices with error conditions might require power cycling.
- As a fix, Thermo Fisher Scientific generally does not recommend reinstalling the software or the operating system, which more commonly occurs after you install a new hard drive.

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.

Known Defects

Table 2 contains known defects in the software, categorized by severity with a brief abstract. 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. Software defects (Sheet 1 of 4)

ID	Title	Severity
29974	Export workspace as EMF with dimensions does not work correctly on Windows 10.	3 - Medium
29975	Minimum trace height feature does not work correctly on 4K screens.	3 - Medium
29976	MultiSpectrum: Unable to change the color from 9th plot onwards.	3 - Medium
29977	Peak detection is randomly applied when trace is deleted.	3 - Medium
29979	Toolbox will not relocate to my cursor position: moves about twice as fast as mouse.	3 - Medium
29980	Manufacturing layouts: Position of chromatogram and spectrum are changed.	3 - Medium
29981	PPD S/N threshold sometimes not applied to filtered chromatograms for some raw files.	3 - Medium
29988	Product displays blank screen during remote access.	3 - Medium
44777	Unchecking and rechecking the trace from chromatogram ranges makes to the annotated text to disappear.	3 - Medium
44875	Instrument method view does not correctly show which method is being displayed.	3 - Medium
44883	Text annotation: Add/Edit text is not working for a long statement.	3 - Medium
47273	SN display format is not ideal (decimals and scientific notation).	3 - Medium
37166	Display Options- Subtabs corresponding to both chromatogram and spectrum are shown.	3 - Medium

Table 2. Software defects (Sheet 2 of 4)

ID	Title	Severity
47478	m/z bandwidth text box should not wait for the click of ENTER button.	3 - Medium
48108	Installer shows up a warning though latest version of MS office is installed.	3 - Medium
50023	Separate axis should be automatically enabled when a new chromatogram trace is added to the chromatogram view.	3 - Medium
50639	NIST Search: Mass labels are missing in exclusion plot.	3 - Medium
50769	Enabling "Show within the Workspace" for isotope simulation and checking profile resolution triggers simulated isotope plot.	3 - Medium
51144	Labels from simulated plot (Elemental Composition, NIST) disappear after applying "Show within the Workspace" for isotope simulation.	3 - Medium
30251	Blank spectrum is displayed when background subtraction 2 range is performed in the new chromatogram view.	3 - Medium
29982	Mass tolerance - different for mzVault verses mzCloud - Example FTMS and ITMS.	3 - Medium
29985	Mass tolerance is not updated when chemical formula/Peptide sequence is present.	3 - Medium
30469	Layouts: MultiSpectrum position changes and new spectra is added upon performing apply default.	3 - Medium
30470	Splash screen which appears before FS main window on starting application is very small on a 4K screen.	3 - Medium
30473	Window placement arrows are disabled.	3 - Medium
30480	Layout - Peak List - Empirical formula is not displayed upon apply default although settings is 'Saved as Default'.	3 - Medium
30493	Averaging on spectrum with multi segment data is merged to single segment scan in MultiSpectrum.	3 - Medium
30494	Chromatogram pot title and hover box do not reflect user-selected decimal places.	3 - Medium
29966	The chromatogram RT marker stops tracking, after releasing a spectrum.	3 - Medium
29967	Legends > Scan header options do not work for composite & average spectra.	3 - Medium
29971	Averaging and background subtraction icons in the toolbox disappear when chromatogram is zoomed.	3 - Medium
29972	Sequence file name is not synced with current chromatogram view.	3 - Medium
29973	Mass labels appear for every profile point from ITMS profile file.	3 - Medium
29391	Missing labels in chromatogram plots during print.	3 - Medium
29959	Manual peak detection for UV data files.	3 - Medium
29960	PPD Chromatogram peak label missing for 1 peak but those adjacent OK.	3 - Medium
29964	Little variation noticed in exported averaged/background subtracted spectrum.	3 - Medium
29965	PPD Chromatogram peak tip occasionally cut off.	3 - Medium
30574	Sum button does not stay active.	3 - Medium
30652	Usability Issue - Cursor or RT marker does not move when delay time is given in chromatogram ranges and move to end RT using keyboard arrow keys.	3 - Medium

Table 2. Software defects (Sheet 3 of 4)

ID	Title	Severity
30658	Deleting unselected, unreferenced chromatogram plot affects selected, reference plot.	3 - Medium
30660	Average with multiple chromatogram - RT value within limits but looks like limit is for second chromatogram.	3 - Medium
30467	Application does not accept decimal values as expected in mass range entry.	3 - Medium
30468	Mismatch in elemental composition result for PPD peak top vs user-selected peak top.	3 - Medium
30662	Layouts are not applied if we open the same raw file or different raw file again.	3 - Medium
30670	Isotope simulation: The plot title does not match with the plot selected.	3 - Medium
30699	FS layout default overrides smoothing, delay time, reference, applies invalid settings to raw files.	3 - Medium
30709	Incorrect file name is displayed in the spectrum view title bar.	3 - Medium
30695	Chromatogram display options - RT labels are missing in 'Stick' view.	3 - Medium
30661	.Raw file name is replaced by selected file name from sequence when both .raw and .sld files are opened together.	3 - Medium
29953	Adjusting the Chromatogram Range window to a certain size shows the chemical formula window - partially hidden the chemical formula floating window.	3 - Medium
29954	Performing mzVault/NIST search on MultiSpectrum - Opens new spectrum window each time search is performed.	3 - Medium
29955	Elemental Composition MS/MS scan number accepts SRM scan filters.	3 - Medium
29956	PPD chromatogram copy to clipboard does not reflect PPD peak.	3 - Medium
29957	Template can cause m/z range to be set to 0-1 if raw file is outside template m/z range.	3 - Medium
29958	Scrolling up Vertically for chromatogram and MultiSpectrum hides the horizontal scrollbar.	3 - Medium
62330	Chemical Formula or Peptide Sequence EIC Info not retained in Layout.	3 - Medium
63283	HRAM Data not Exported if Quick, Normal Search Types Selected.	3 - Medium
63563	Undo Zoom does not function when chromatogram has been averaged followed by zoomed.	3 - Medium
82778	Chromatogram becomes blank for a particular trace type.	3 - Medium
86938	Reports - Configured width and height is not used in "To Clipboard in EMF"	3 - Medium
107758	NIST similarity search type Neutral Loss results mismatch in FreeStyle and NIST browser.	3 - Medium
113322	Cannot export tab delimited data to clipboard.	3 - Medium
113915	Elemental results table does not track selected spectrum.	3 - Medium
115117	Layout : Blank Map view window is displayed on applying layout for an invalid filter but Map ranges displays no filter as shown in default scenario.	3 - Medium
115443	"Show Peptide Results Table" is disabled for spectrum 1 when spectrum 2 is closed.	3 - Medium

Trademarks

Table 2. Software defects (Sheet 4 of 4)

ID	Title	Severity
115599	Columns in Elemental Composition Results table cannot be resized.	3 - Medium
56308	Write to .raw does not include reference / exception peak information.	3 - Medium
61791	Layout: Incorrect averaging done upon applying layout.	3 - Medium

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