FreeStyle 1.8 SP1 Release Notes

These release notes briefly list the changes in the Thermo FreeStyle™ 1.8 SP1 software, new features and enhancements, fixes to the previously reported issues, and known issues that exist in the FreeStyle 1.8 SP1 software release. Additionally, system requirements for the software installation are included in these release notes.

Contents

For information on using the FreeStyle 1.8 SP1 application, refer to the user guide available as PDF file or the embedded Help.

New Features

This release incorporates the following fixed issues, new and enhanced features.

- Display peak labels produced by the Advanced Peak Determination (APD) algorithm that runs on the embedded instrument computer during data acquisition
  - Thermo Scientific™ Orbitrap Exploris™ MS Series: ICSW 4.0 or later
  - Thermo Scientific Orbitrap Tribrid™ MS Series: Tune 3.5 or later

- Elemental composition calculation based on mass only

- Thermo Scientific FAIMS Pro interface CV optimization data processing and export for TSQ™ ICSW version 3.4 or later

- Apply Xtract All deconvolution to chromatograms

- Peak area label with full numerical display

- MSn browser mass tolerance and precursor masses support 4 decimals

- Improved usability by reorganizing the ribbon menu and right-click menu options

- Backward compatibility with Thermo Scientific Foundation™ software 3.1 SP6 or later

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System Requirements

These are the minimum required and recommended hardware and software configurations for operation of the FreeStyle 1.8 SP1 application.

System	Required or *recommended* configuration
Hardware	• 3.6 GHz Quad core processor with a minimum of 8 GB RAM (16 GB recommended) • CD/R-ROM or DVD drive • 1 TB hard drive • Video card and monitor capable of 1920×1080 resolution
Software	• Adobe Acrobat™ Reader™ 10.1 or later • Microsoft™ .NET Framework 4.7.2 • Microsoft Office 2013 (for exported data) • Microsoft Windows™ 7 SP1 (64-bit) or Windows 10 (64-bit) • Thermo Foundation™ Platform 3.1 SP6 or later

Important Information

General

The FreeStyle 1.8 SP1 application does not require licensing in any form. The software may be installed on Windows 7 SP1 64-bit or Windows 10 64-bit operating systems.

Installation

You must have administrator rights to install the FreeStyle 1.8 SP1 software on your computer.

Compatibility

The FreeStyle 1.8 SP1 application requires Foundation 3.1 SP6 or later.

Install the FreeStyle 1.8 SP1 Application

Before upgrading to FreeStyle 1.8 SP1, verify the Foundation version installed on your system by going to Version Info.

Follow these instructions:

• To upgrade to the FreeStyle 1.8 SP1 application for a system with the Foundation Platform 3.1 SP6 or later

• To upgrade to the FreeStyle 1.8 SP1 application for a system with the Foundation Platform 3.1 SP5 or earlier

❖ **To upgrade to the FreeStyle 1.8 SP1 application for a system with the Foundation Platform 3.1 SP6 or later**

1. Download the FreeStyle 1.8 SP1 software from Flexera (https://thermo.flexnetoperations.com/control/thmo/login) to your local processing computer.
2. Open the Windows Control Panel and click **Programs and Features**.
3. Uninstall the previous version of the FreeStyle application.
4. Install the FreeStyle 1.8 SP1 application.

❖ **To upgrade to the FreeStyle 1.8 SP1 application for a system with the Foundation Platform 3.1 SP5 or earlier**

1. Download the FreeStyle 1.8 SP1 software from Flexera (https://thermo.flexnetoperations.com/control/thmo/login) to your local processing computer.
2. Open the Windows Control Panel and click **Programs and Features**.
3. Uninstall the FreeStyle application.
4. Uninstall any installed version of the Xcalibur application.
5. Uninstall any installed version of the Foundation Platform.
6. (Optional) Install the Xcalibur 4.2 SP1 application (or later.)
7. Install the FreeStyle 1.8 SP1 application.

Windows 10 Tip

In Windows 10, follow these steps to specify the FreeStyle application as the default application used to open all .RAW files.

1. In a File Explorer window, right-click a .RAW file and choose **Properties**.
2. On the General page of the Properties dialog box, click **Change**.
3. Select FreeStyle 1.8(C:\Program Files\Thermo\FreeStyle) and click **OK**.
4. In the Properties dialog box, click **OK**.

Supported Local Language for the Data System Computer

The FreeStyle 1.8 SP1 application was tested and supported for US-English Only locale settings.

To change the format on your computer, go to Control Panel > Region and specify the language format.

Resolved Issues

Table 1 lists the defects that were resolved between the FreeStyle 1.7 SP2 and the FreeStyle 1.8 SP1 release. The table excludes Help issues and any cosmetic fixes. In some cases, the Title has been amended or extended from the original to better describe the reported issue. The ID is the internal number assigned to each 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) in FreeStyle 1.8 SP1

ID	Title	Severity
187459	Chromatogram ranges freeze up with a 5 GB data file.	1 - Critical
184964	FreeStyle crashed after applying peak detection on certain layout.	1 - Critical
184982	Layout: Application crashes upon clicking on Auto Filter after unchecking all traces from chromatogram ranges.	1 - Critical
187460	Increase charge state upper limit to 99 in isotope simulation.	2 - High
175187	Dimensions are not correct for Export the plots to EMF.	2 - High
171819	MSn Browser - Allow to enter mass tolerance in 4 decimal places.	2 - High
172925	Application crash when entering invalid species in isotope simulation info bar.	2 - High
150666	Application crashes when map view is saved as layout and applied to corrupt raw file.	2 - High
185538	AcquireX raw file with a long exclusion list takes more than 20 seconds to open the Instrument method.	3 - Medium
150836	Elemental composition is not performed on an averaged spectrum when Multispecrum is present.	3 - Medium
150866	Both spectra display refresh wheel on navigating the scan using keyboard when background subtraction followed by Averaging is performed for a chromatogram linked to those spectra.	3 - Medium
151098	Chromatogram header is copied multiple times, on applying peak detection to a EIC chromatogram of mass obtained from chemical formula applied.	3 - Medium
44875	Instrument method view does not correctly show which method is being displayed.	3 - Medium
56308	Write to .raw does not include reference / exception peak information.	3 - Medium
140790	Export to csv: Spectrum list is incomplete upon exporting after performing elemental composition.	3 - Medium
140791	Entered grayed out charge state should not be used for EC.	3 - Medium
149596	Averaging gets performed for complete RT Range for a raw file, on performing Averaging for a RT range followed by Save as default and Apply default.	3 - Medium
174280	Averaging not applied correctly when two chromatogram views with only one spectrum view is present.	3 - Medium
175844	Incorrect cursor symbol scenarios and incorrect blue ball position scenario.	3 - Medium

Table 1. Resolved issues (Sheet 2 of 2) in FreeStyle 1.8 SP1

ID	Title	Severity
176687	Header error when making negative ion isotope simulations.	3 - Medium
177019	Incorrect EIC is plotted for a Peptide sequence when an invalid species is present.	3 - Medium
151419	Averaging range gets updated to a different value when save to default layout is performed on an Averaged and background subtracted spectra for a MS filtered trace and raw file is opened in new workspace.	3 - Medium
152946	Flags toggle button not working for Spectrum List in Display Options.	3 - Medium
163199	Chemical formula does not appear in right side title in a chromatogram view.	3 - Medium
163877	Spectrum data with background subtraction is not correctly copied from an existing spectrum when a new spectrum is created second time.	3 - Medium
163882	Refresh issue in spectrum scan header and title update linking to a trace having the same raw file.	3 - Medium
165408	Layout: Ranges in chromatogram ranges does not display all the mass ranges used for EIC creation upon applying layout.	3 - Medium
29391	Missing labels in chromatogram plots during print.	3 - Medium
29975	Minimum trace height feature does not work correctly on 4K screens.	3 - Medium
30694	Landing page- "Don't show again" check box does not hide links/page.	4 - Low
151334	Trace selection is not saved correctly in when multiple traces are present in a chromatogram and Save as default layout is performed.	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 these 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

Risk	Interpretation
1 - 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.
2 - 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.

Risk	Interpretation
3 - Medium	A minor error or poor behavior of a product feature. There is probably a workaround.
4 - 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 table 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. Known defects

ID	Title	Severity
29988	Product displays blank screen during remote access.	3 - Medium
30251	Blank spectrum is displayed when background subtraction 2 range is performed in the new chromatogram view.	3 - Medium
30467	Application does not accept decimal values as expected in mass range entry.	3 - Medium
44777	Unchecking and rechecking the trace from chromatogram ranges makes to the annotated text to disappear.	3 - Medium
63283	HRAM Data not Exported if Quick, Normal Search Types Selected.	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
113915	Elemental results table does not track selected spectrum.	3 - Medium
163242	Undo zoom does not perform as expected upon toggling and un-toggling EIC mass and EIC range.	3 - Medium
172824	Xtract - Incorrect monoisotopic mass for large protein.	3 - Medium
178143	Unexpected message After Changing Something in Default Options When NIST Info Tab is Open.	3 - Medium
178155	Communicator Bar "No Results" Message Is Not Cleared When There Is Results.	3 - Medium
179721	Refresh issue in info bar Xtract *m/z* range fields.	3 - Medium
180146	Structure annotations are getting lost upon performing Undo Zoom.	3 - Medium
181647	Xtract - Monoisotopic Mass Mode is Off by 1amu for CAH Protein.	3 - Medium
187534	FreeStyle crashes when the layout is saved after moving Chromatogram as tabbed view with Spectrum View.	3 - Medium

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