

Resource Summary Report

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FreeStyle 1.8 SP1

RRID:SCR_022877

Type: Tool

Proper Citation

FreeStyle 1.8 SP1 (RRID:SCR_022877)

Resource Information

URL: <https://www.thermofisher.com/de/de/home/technical-resources/technical-reference-library/mass-spectrometry-support-center/liquid-chromatography-mass-spectrometry-software-support/freestyle-software-support/freestyle-software-support-getting-started.html>

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Description: Software to visualize and qualitatively analyze mass spectrometry data. Used to display chromatograms and spectra, detect and integrate chromatographic peaks, search mass spectral libraries, simulate mass spectra, subtract background spectra, apply scan filters, annotate plots with text and graphics, create and save layouts, view the status of various instrument parameters during data acquisition, and create a 2D or 3D representation of an analysis displaying the acquired mass/wavelength scans. Part of liquid chromatography mass spectrometry system.

Resource Type: data analysis software, data processing software, software resource, software application

Keywords: Fisher Scientific, liquid chromatography, mass spectrometry, visualize and qualitatively analyze mass spectrometry data

Availability: Restricted

Resource Name: FreeStyle 1.8 SP1

Resource ID: SCR_022877

Record Creation Time: 20221013T050144+0000

Record Last Update: 20260812T044427+0000

Ratings and Alerts

No rating or validation information has been found for FreeStyle 1.8 SP1.

No alerts have been found for FreeStyle 1.8 SP1.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Schmidt L, et al. (2025) Protocol for generating protein profiles and distance-based network analysis of murine tissue slices. STAR protocols, 6(1), 103578.

Bestehorn A, et al. (2025) Cytoplasmic mRNA decay controlling inflammatory gene expression is determined by pre-mRNA fate decision. Molecular cell, 85(4), 742.

Schmidt L, et al. (2024) Spatial proteomics of skeletal muscle using thin cryosections reveals metabolic adaptation at the muscle-tendon transition zone. Cell reports, 43(7), 114374.

Trendafilova A, et al. (2023) Phytochemical Profile, Antioxidant Potential, Antimicrobial Activity, and Cytotoxicity of Dry Extract from Rosa damascena Mill. Molecules (Basel, Switzerland), 28(22).

Tareq FS, et al. (2023) An Untargeted Metabolomics Approach to Study the Variation between Wild and Cultivated Soybeans. Molecules (Basel, Switzerland), 28(14).

Shajahan A, et al. (2023) Site specific N- and O-glycosylation mapping of the spike proteins of SARS-CoV-2 variants of concern. Scientific reports, 13(1), 10053.

Ramaprasad A, et al. (2022) A choline-releasing glycerophosphodiesterase essential for phosphatidylcholine biosynthesis and blood stage development in the malaria parasite. eLife, 11.

Lofaro FD, et al. (2021) Age-Related Changes in the Matrisome of the Mouse Skeletal Muscle. International journal of molecular sciences, 22(19).

Liu L, et al. (2021) Secondary metabolites of Hülle cells mediate protection of fungal reproductive and overwintering structures against fungivorous animals. eLife, 10.

Villageliú DN, et al. (2018) Production of the Neurotoxin Salsolinol by a Gut-Associated Bacterium and Its Modulation by Alcohol. Frontiers in microbiology, 9, 3092.