

Resource Summary Report

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Pyteomics

RRID:SCR_024988

Type: Tool

Proper Citation

Pyteomics (RRID:SCR_024988)

Resource Information

URL: <https://pypi.org/project/pyteomics/>

Proper Citation: Pyteomics (RRID:SCR_024988)

Description: Software library providing Python interfaces to proteomic data. Provides set of modules to facilitate the most common tasks in proteomics data analysis.

Synonyms: Pyteomics 4.0

Resource Type: source code, software library, software resource, software toolkit

Defining Citation: [PMID:30576148](#)

Keywords: Python interfaces, proteomics data analysis, proteomic data,

Funding: Russian Foundation for Basic Research

Availability: Free, Available for download, Freely available

Resource Name: Pyteomics

Resource ID: SCR_024988

Alternate URLs: <https://github.com/levitsky/pyteomics>

License: Apache v2.0

Record Creation Time: 20240202T050227+0000

Record Last Update: 20250429T060355+0000

Ratings and Alerts

No rating or validation information has been found for Pyteomics.

No alerts have been found for Pyteomics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Deng Y, et al. (2024) An end-to-end deep learning method for mass spectrometry data analysis to reveal disease-specific metabolic profiles. Nature communications, 15(1), 7136.

Abdollahnia A, et al. (2024) Mass spectrometric analysis of Odonthobuthus Doriae scorpion venom and its non-neutralized fractions after interaction with commercial antivenom. Scientific reports, 14(1), 10389.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Korolkova Y, et al. (2021) New Insectotoxin from Tibellus Oblongus Spider Venom Presents Novel Adaptation of ICK Fold. Toxins, 13(1).

Sorensen M, et al. (2020) Rapid microbial identification and colistin resistance detection via MALDI-TOF MS using a novel on-target extraction of membrane lipids. Scientific reports, 10(1), 21536.

Lam MP, et al. (2016) Cardiovascular proteomics in the era of big data: experimental and computational advances. Clinical proteomics, 13, 23.