

Resource Summary Report

Generated by [NIF](#) on Aug 21, 2026

Genedata Expressionist

RRID:SCR_003298

Type: Tool

Proper Citation

Genedata Expressionist (RRID:SCR_003298)

Resource Information

URL: <http://www.genedata.com/products/expressionist/genomic-profiling.html>

Proper Citation: Genedata Expressionist (RRID:SCR_003298)

Description: Software that provides data processing, analysis, management, and reporting of metabolomics, proteomics and biotherapeutics characterization studies based on mass spectrometry. It can process raw data from various MS instruments, serve MS processing, analysis and reporting needs, and ensure reproducibility and traceability of results.

Synonyms: Genedata Expressionist for Genomic Profiling

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

Keywords: mass spectrometry data processing, mass spectrometry data analysis, mass spectrometry data management, omics software

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Genedata Expressionist

Resource ID: SCR_003298

Alternate IDs: OMICS_00761

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260821T042620+0000

Ratings and Alerts

No rating or validation information has been found for Genedata Expressionist.

No alerts have been found for Genedata Expressionist.

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 [NIF](#) .

Pohl T, et al. (2025) Development, qualification, and application of a highly efficient and robust new peak detection workflow for the LC-MS peptide mapping multi-attribute method. *mAbs*, 17(1), 2572411.

Liang X, et al. (2025) Limited activation interdependence and differing patterns of the in vivo effects of IKK1 and IKK2 downstream of NIK. *Cell reports*, 44(10), 116404.

Goretzki B, et al. (2024) Dual BACH1 regulation by complementary SCF-type E3 ligases. *Cell*, 187(26), 7585.

Seinen J, et al. (2021) Sputum Proteome Signatures of Mechanically Ventilated Intensive Care Unit Patients Distinguish Samples with or without Anti-pneumococcal Activity. *mSystems*, 6(2).

Rangel Pedersen N, et al. (2021) Multicomponent carbohydrase system from *Trichoderma reesei*: A toolbox to address complexity of cell walls of plant substrates in animal feed. *PloS one*, 16(6), e0251556.

Mor N, et al. (2018) Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency. *Cell stem cell*, 23(3), 412.

Yoon S, et al. (2017) MLKL, the Protein that Mediates Necroptosis, Also Regulates Endosomal Trafficking and Extracellular Vesicle Generation. *Immunity*, 47(1), 51.

Shigemura T, et al. (2016) Novel heterozygous C243Y A20/TNFAIP3 gene mutation is responsible for chronic inflammation in autosomal-dominant Behçet's disease. *RMD open*, 2(1), e000223.

Bajaj I, et al. (2014) Functional characterization of a *Penicillium chrysogenum* mutanase gene induced upon co-cultivation with *Bacillus subtilis*. *BMC microbiology*, 14, 114.

Marshall E, et al. (2011) In silico analysis identifies a novel role for androgens in the regulation of human endometrial apoptosis. *The Journal of clinical endocrinology and metabolism*, 96(11), E1746.