

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

[openBIS](#)

RRID:SCR_011815

Type: Tool

Proper Citation

openBIS (RRID:SCR_011815)

Resource Information

URL: <http://www.cisd.ethz.ch/software/openBIS>

Proper Citation: openBIS (RRID:SCR_011815)

Description: Software for an open, distributed system for managing biological information that supports biological research data workflows from the source (i.e. the measurement instruments) to facilitate the process of answering biological questions by means of cross-domain queries against raw data, processed data, knowledge resources and its corresponding metadata. The openBIS software framework can be easily extended and has been customized for the following technologies: * High Content Screening * Proteomics * Deep Sequencing * Metabolomics

Abbreviations: openBIS

Synonyms: open Biology Information System

Resource Type: software resource

Defining Citation: [PMID:22151573](#)

Resource Name: openBIS

Resource ID: SCR_011815

Alternate IDs: OMICS_01009

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260725T190722+0000

Ratings and Alerts

No rating or validation information has been found for openBIS.

No alerts have been found for openBIS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Broman A, et al. (2025) Proteomic Profiling of Acoustically Isolated Extracellular Vesicles from Blood Plasma during Murine Bacterial Sepsis. *Journal of proteome research*, 24(8), 4126.

Palm F, et al. (2023) Phenotypic Characterization of Acoustically Enriched Extracellular Vesicles from Pathogen-Activated Platelets. *Journal of innate immunity*, 15(1), 599.

Kuhn Cuellar L, et al. (2022) A data management infrastructure for the integration of imaging and omics data in life sciences. *BMC bioinformatics*, 23(1), 61.

Broman A, et al. (2021) Multinodal Acoustic Trapping Enables High Capacity and High Throughput Enrichment of Extracellular Vesicles and Microparticles in miRNA and MS Proteomics Studies. *Analytical chemistry*, 93(8), 3929.

Olsson TSG, et al. (2019) Lightweight data management with dtool. *PeerJ*, 7, e6562.

Carbonell P, et al. (2018) An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. *Communications biology*, 1, 66.

Prasser F, et al. (2018) Data Integration for Future Medicine (DIFUTURE). *Methods of information in medicine*, 57(S 01), e57.

Åhrman E, et al. (2018) Quantitative proteomic characterization of the lung extracellular matrix in chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. *Journal of proteomics*, 189, 23.

Okada H, et al. (2016) Proteome-wide association studies identify biochemical modules associated with a wing-size phenotype in *Drosophila melanogaster*. *Nature communications*, 7, 12649.

Malmström E, et al. (2016) Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. *Nature communications*, 7, 10261.

Malmström L, et al. (2015) Quantitative proteogenomics of human pathogens using DIA-MS. *Journal of proteomics*, 129, 98.

Antony PM, et al. (2013) Light microscopy applications in systems biology: opportunities and challenges. *Cell communication and signaling : CCS*, 11(1), 24.

Bauch A, et al. (2011) openBIS: a flexible framework for managing and analyzing complex data in biology research. BMC bioinformatics, 12, 468.