

# Resource Summary Report

Generated by [RRID](#) on Apr 10, 2025

## [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](#)

**Funding:**

**Resource Name:** openBIS

**Resource ID:** SCR\_011815

**Alternate IDs:** OMICS\_01009

**Record Creation Time:** 20220129T080306+0000

**Record Last Update:** 20250410T070207+0000

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## Ratings and Alerts

No rating or validation information has been found for openBIS.

No alerts have been found for openBIS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 12 mentions in open access literature.

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

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.

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

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

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.

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.

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 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.