

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Bisque

RRID:SCR_005564

Type: Tool

Proper Citation

Bisque (RRID:SCR_005564)

Resource Information

URL: <http://biodev.ece.ucsb.edu/projects/bisquik/wiki>

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Description: A scalable web-based system for biological image analysis, management and exploration. The Bisque system incorporates many features useful to imaging researchers from image capture to extensible image analysis and querying. At the core, bisque maintains a flexible database of images and experimental metadata. Image analyses can be incorporated into the system and deployed on clusters and desktops. Search and comparison of datasets by image data and content is supported. Novel semantic analyses are integrated into the system allowing high level semantic queries and comparison of image content. New features and testing of Bisque version: 0.5.1, among many others are: # Parallel execution of datasets # Rich interfaces for autogenerated module UI # Abstracted storage system for local, irods, etc.. They are using Mercurial for their source control system. This should be installed before proceeding. Browse source on-line, <http://biodev.ece.ucsb.edu/projects/bisquik/browser> Bisque Installation, <http://biodev.ece.ucsb.edu/projects/bisquik/wiki/InstallationInstructions05> Bisque DOWNLOAD, <http://biodev.ece.ucsb.edu/projects/bisquik/wiki/download>, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Bisque

Synonyms: Bio-Image Semantic Query User Environment, Bisque - Bio-Image Semantic Query User Environment

Resource Type: software resource, source code

Defining Citation: [PMID:20031971](#)

Keywords: image, biology, annotate, metadata, analysis, magnetic resonance

Funding: NSF ITR-0331697;
NSF IIS-0808772

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Bisque

Resource ID: SCR_005564

Alternate IDs: nlx_144653

Alternate URLs: <http://www.nitrc.org/projects/bisque>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T133326+0000

Ratings and Alerts

No rating or validation information has been found for Bisque.

No alerts have been found for Bisque.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Kim J, et al. (2025) Functional maturation of preterm intestinal epithelium through CFTR activation. Communications biology, 8(1), 540.

Zhao J, et al. (2025) Brain 5-hydroxymethylcytosine alterations are associated with Alzheimer's disease neuropathology. Nature communications, 16(1), 2842.

Wang Z, et al. (2025) Pathway-based cancer transcriptome deciphers a high-resolution intrinsic heterogeneity within bladder cancer classification. Journal of translational medicine, 23(1), 666.

Zhao W, et al. (2025) A prognostic signature for lung adenocarcinoma in people who have never smoked. bioRxiv : the preprint server for biology.

Willis C, et al. (2025) Gene expression differences associated with alcohol use disorder in human brain. Molecular psychiatry, 30(4), 1617.

Lee SHT, et al. (2024) Single nucleus RNA-sequencing integrated into risk variant colocalization discovers 17 cell-type-specific abdominal obesity genes for metabolic dysfunction-associated steatotic liver disease. EBioMedicine, 106, 105232.

Li M, et al. (2024) ReCIDE: robust estimation of cell type proportions by integrating single-reference-based deconvolutions. *Briefings in bioinformatics*, 25(5).

Dai R, et al. (2024) Evaluating performance and applications of sample-wise cell deconvolution methods on human brain transcriptomic data. *Science advances*, 10(21), eadh2588.

Guo X, et al. (2024) Highly Accurate Estimation of Cell Type Abundance in Bulk Tissues Based on Single-Cell Reference and Domain Adaptive Matching. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(7), e2306329.

Larsen JH, et al. (2024) Benchmarking transcriptome deconvolution methods for estimating tissue- and cell-type-specific extracellular vesicle abundances. *Journal of extracellular vesicles*, 13(9), e12511.

Xu X, et al. (2024) Cell-type deconvolution for bulk RNA-seq data using single-cell reference: a comparative analysis and recommendation guideline. *Briefings in bioinformatics*, 26(1).

Carter JK, et al. (2024) Identifying novel gene dysregulation associated with opioid overdose death: A meta-analysis of differential gene expression in human prefrontal cortex. *medRxiv : the preprint server for health sciences*.

Wang W, et al. (2024) Identification of hypoxic macrophages in glioblastoma with therapeutic potential for vasculature normalization. *Cancer cell*, 42(5), 815.

Dai R, et al. (2023) Evaluating performance and applications of sample-wise cell deconvolution methods on human brain transcriptomic data. *bioRxiv : the preprint server for biology*.

Safrastyan A, et al. (2023) Decoding cell-type contributions to the cfRNA transcriptomic landscape of liver cancer. *Human genomics*, 17(1), 90.

Schulmann A, et al. (2023) Antipsychotic drug use complicates assessment of gene expression changes associated with schizophrenia. *Translational psychiatry*, 13(1), 93.

Nambala P, et al. (2023) Differences in gene expression profiles in early and late stage rhodesiense HAT individuals in Malawi. *PLoS neglected tropical diseases*, 17(12), e0011803.

Namulondo J, et al. (2023) Transcriptome analysis of peripheral blood of *Schistosoma mansoni* infected children from the Albert Nile region in Uganda reveals genes implicated in fibrosis pathology. *PLoS neglected tropical diseases*, 17(11), e0011455.

Gambardella G, et al. (2022) A single-cell analysis of breast cancer cell lines to study tumour heterogeneity and drug response. *Nature communications*, 13(1), 1714.

Hong SR, et al. (2021) Bisulfite-Converted DNA Quantity Evaluation: A Multiplex Quantitative Real-Time PCR System for Evaluation of Bisulfite Conversion. *Frontiers in genetics*, 12, 618955.