

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

Gemma

RRID:SCR_008007

Type: Tool

Proper Citation

Gemma (RRID:SCR_008007)

Resource Information

URL: <http://www.chibi.ubc.ca/Gemma>

Proper Citation: Gemma (RRID:SCR_008007)

Description: Resource for reuse, sharing and meta-analysis of expression profiling data. Database and set of tools for meta analysis, reuse and sharing of genomics data. Targeted at analysis of gene expression profiles. Users can search, access and visualize coexpression and differential expression results.

Abbreviations: Gemma

Resource Type: database, data or information resource

Defining Citation: [PMID:22782548](#)

Keywords: chip, microarray, functional genomics, gene expression, coexpression, differential expression, FASEB list

Funding: NIGMS GM076990;
Canadian Foundation for Innovation ;
Michael Smith Foundation for Health Research ;
Canadian Institutes for Health Research

Availability: Free, Freely available

Resource Name: Gemma

Resource ID: SCR_008007

Alternate IDs: nif-0000-08127, r3d100012747

Alternate URLs: <https://sources.debian.org/src/gemma/>,
<https://doi.org/10.17616/R36R54>, <https://doi.org/10.17616/R36R54>

License: Apache License v2

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260808T190420+0000

Ratings and Alerts

No rating or validation information has been found for Gemma.

No alerts have been found for Gemma.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1145 mentions in open access literature.

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

Rhoads CA, et al. (2026) A Meta-Analysis of the Effects of Acute Sleep Deprivation on the Cortical Transcriptome in Rodent Models. Journal of sleep research, 35(3), e70205.

Liu P, et al. (2026) Integrative Omics Defines Metabolic Biomarkers and Genetic Regulatory Mechanisms of Mortality Risk. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(3), e14464.

Diniz P, et al. (2026) Reasoning-optimised large language models reach near-expert accuracy on board-style orthopaedic exams: A multi-model comparison on 702 multiple-choice questions. Knee surgery, sports traumatology, arthroscopy : official journal of the ESSKA, 34(2), 752.

Brown GS, et al. (2026) Using semantic search to find publicly available gene-expression datasets. Bioinformatics (Oxford, England), 42(3).

Wang P, et al. (2026) Genomic analysis reveals potential involvement of the brain-retina axis in regulating chicken feeding behavior. Poultry science, 105(3), 106438.

Kepesidis G, et al. (2026) Integrative multi-omic and phenotypic analysis of open raceway pond production of *Monoraphidium minutum* 26B-AM reveals distinct stress signatures for scale-up and infection. Biotechnology for biofuels and bioproducts, 19(1), 6.

Wu C, et al. (2026) Genetic dynamics drive maize growth and breeding. Genome biology, 27(1).

Yang Z, et al. (2026) A Pan-TE Map Reveals the Important Role of Transposable Elements in Gene Expression and Phenotypic Diversity in 2,311 Rapeseed Accessions. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(4), e12036.

Zhu P, et al. (2026) Integrated genome-wide domestication and association analyses reveal the complex genetic basis of parthenocarpy during cucumber domestication. *Molecular horticulture*, 6(1), 7.

Gao T, et al. (2026) Revealing the genetic regulation of wood traits and secondary cell wall development in *Ginkgo biloba*: an integrated analysis from the perspectives of GWAS, TWAS, and WGCNA. *Horticulture research*, 13(6), uhag062.

Abitew YA, et al. (2026) Divergent jejunal cis- and trans-eQTLs and their microbiome associations following a diet lacking mineral phosphorus supplements in laying hens. *BMC genomics*, 27(1).

Demir E, et al. (2026) Candidate genes related to growth and milk production in three Anatolian goats revealed by GWAS. *Mammalian genome : official journal of the International Mammalian Genome Society*, 37(1), 30.

Tu Y, et al. (2026) Identification of molecular markers associated with comb traits through genome-wide association study on a specialized strain of yellow feathered broilers. *Poultry science*, 105(1), 106125.

Yang R, et al. (2026) Population structure and genome-wide association study of body conformation traits of two native goat breeds in China. *Animal bioscience*, 39(1), 250334.

Rogic S, et al. (2026) Application of large language models to the annotation of cell lines and mouse strains in genomics data. *bioRxiv : the preprint server for biology*.

Geoghegan EM, et al. (2026) The Converging Effects of Different Categories of Antidepressants on the Brain: A Systematic Meta-Analysis of Public Transcriptional Profiling Data from the Hippocampus and Cortex. *bioRxiv : the preprint server for biology*.

Bardarov S, et al. (2026) A Reproducible Protocol and Framework for Large Language Model (LLM)-Assisted Estrogen and Progesterone Receptor (ER/PR) Scoring. *Cureus*, 18(5), e108708.

Hu L, et al. (2026) High-Resolution Genomic Resources for Trait Mapping and Precision Breeding for Adzuki Bean (*Vigna angularis*). *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(4), e07157.

Zheng J, et al. (2026) Integrative genome-wide association study and transcriptomic analysis to identify candidate genes and pathways for heterophil and lymphocyte traits in white-feathered broilers. *Poultry science*, 105(4), 106407.

Xiong J, et al. (2026) A Meta-Analysis of the Effects of Chronic Stress on the Prefrontal Transcriptome in Animal Models and Convergence With Existing Human Data. *Brain and behavior*, 16(1), e71197.