

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 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: data or information resource, database

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: 20260729T044158+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 1112 mentions in open access literature.

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

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.

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.

Liu W, et al. (2025) GRB2 Promotes Malignant Behaviors of Breast Cancer by Modulating the Global Expression and Alternative Splicing Profiles in SK-BR-3 Cells Through Binding mRNA. *Cancer medicine*, 14(10), e70905.

Zhang K, et al. (2025) miR-34a-5p modulation of polycystic ovary syndrome via targeting the NOTCH signaling pathway. *Journal of ovarian research*, 18(1), 55.

Chen D, et al. (2025) Genome-wide association study and subsequent functional analysis reveal regulatory mechanism underlying piglet diarrhea. *Animal bioscience*, 38(4), 612.

Potapova NA, et al. (2025) Genome-Wide Association Study on Imputed Genotypes of 180 Eurasian Soybean Glycine max Varieties for Oil and Protein Contents in Seeds. *Plants (Basel, Switzerland)*, 14(2).

Maciel-Magalhães M, et al. (2025) Amphotericin B Encapsulation in Polymeric Nanoparticles: Toxicity Insights via Cells and Zebrafish Embryo Testing. *Pharmaceutics*, 17(1).

Zhao X, et al. (2025) Genome-wide association study and candidate gene analysis of reproductive traits in Yili geese. *Poultry science*, 104(6), 105127.

Joukhadar R, et al. (2025) Stable pleotropic loci controlling the accumulation of multiple nutritional elements in wheat. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(5), 95.

Lin Y, et al. (2025) Potential common mechanisms between primary Sjögren's syndrome and Hashimoto's thyroiditis: a public databases-based study. Frontiers in genetics, 16, 1520332.

Zhao Y, et al. (2025) GRAMMAR-Lambda Delivers Efficient Understanding of the Genetic Basis for Head Size in Catfish. Biology, 14(1).

Razifard H, et al. (2025) The Evolutionary Dynamics of Genetic Mutational Load Throughout Tomato Domestication History. Molecular ecology, 34(24), e70024.

Zheng P, et al. (2025) Stripe rust fungi hijack a host transcriptional repressor to induce TaSWEET14d for enhanced sugar uptake in wheat. Science advances, 11(28), eadv1760.

Hanchard N, et al. (2025) Aberrant One-Carbon Metabolism and Ancestral Genetics Underlie Edematous Severe Acute Malnutrition. Research square.

Orgil BO, et al. (2025) Unraveling the genetic blueprint of doxorubicin-induced cardiotoxicity through systems genetics approaches. Cardio-oncology (London, England), 11(1), 53.

Luo N, et al. (2025) Identification of regulatory loci and candidate genes related to body weight traits in broilers based on different models. BMC genomics, 26(1), 513.

Santhanam N, et al. (2025) RatXcan: A framework for cross-species integration of genome-wide association and gene expression data. PLoS genetics, 21(3), e1011583.

Sparks CR, et al. (2025) Genomic analyses in Cavalier King Charles spaniels identify loci associated with clinical signs of Chiari-like malformation and Syringomyelia. BMC veterinary research, 21(1), 317.

Xue H, et al. (2025) The Genomic Basis of the Tristylous Floral Polymorphism: Evidence for a Role of Gene Duplications in a Region of Restricted Recombination. Molecular biology and evolution, 42(8).

Zhenyu W, et al. (2025) A meta-analysis of genome-wide association studies revealed significant QTL and candidate genes for loin muscle area in three breeding pigs. Scientific reports, 15(1), 18758.