Resource Summary Report

Generated by NIF on May 15, 2025

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

Alternate URLs: https://sources.debian.org/src/gemma/

License: Apache License v2

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250507T060540+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 936 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Guzman A, et al. (2025) Arbuscular mycorrhizal interactions and nutrient supply mediate floral trait variation and pollinator visitation. The New phytologist, 245(1), 406.

Luo Y, et al. (2025) Experimental validation of genome-environment associations in Arabidopsis. bioRxiv : the preprint server for biology.

Huang Y, et al. (2025) Genetic factors shaping the plasma lipidome and the relations to cardiometabolic risk in children and adolescents. EBioMedicine, 112, 105537.

Zemmoto C, et al. (2025) Genome-wide study suggests inheritance of personality traits in Toy Poodles and Miniature Dachshunds. Animal genetics, 56(1), e13508.

Raffle J, et al. (2025) Identification of novel genetic variants associated with feline cardiomyopathy using targeted next-generation sequencing. Scientific reports, 15(1), 3871.

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

Laghouaouta H, et al. (2025) Sequence variants associated with resilient responses in growing pigs. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 142(1), 79.

Akinbiyi T, et al. (2025) ADELLE: A global testing method for trans-eQTL mapping. PLoS genetics, 21(1), e1011563.

Tao Y, et al. (2025) O-sialoglycoprotein Endopeptidase (OSGEP) Suppresses Hepatic Ischemia-Reperfusion Injury-Induced Ferroptosis Through Modulating the MEK/ERK Signaling Pathway. Molecular biotechnology, 67(2), 689.

Ko WH, et al. (2025) Genome-wide statistical evidence elucidates candidate factors of life expectancy in dogs. Molecules and cells, 48(1), 100162.

Eynard SE, et al. (2025) Sequence-Based Multi Ancestry Association Study Reveals the Polygenic Architecture of Varroa destructor Resistance in the Honeybee Apis mellifera. Molecular ecology, 34(3), e17637.

Li M, et al. (2025) QTL mapping and candidate gene analysis of element accumulation in rice grains via genome-wide association study and population genetic analysis. BMC plant biology, 25(1), 93.

Purnama PR, et al. (2025) Uncovering genetic determinants of antioxidant properties in Thai landrace rice through genome-wide association analysis. Scientific reports, 15(1), 1443.

Yang X, et al. (2025) Novel candidate genes and genetic basis analysis of kernel starch content in tropical maize. BMC plant biology, 25(1), 105.

Guo H, et al. (2025) Natural variation of CTB5 confers cold adaptation in plateau japonica rice. Nature communications, 16(1), 1032.

Bilgili A, et al. (2025) The effectiveness of arbuscular mycorrhizal fungal species (Funneliformis mosseae, Rhizophagus intraradices, and Claroideoglomus etunicatum) in the biocontrol of root and crown rot pathogens, Fusarium solani and Fusarium mixture in pepper. PeerJ, 13, e18438.

Hu T, et al. (2025) Generative language models exhibit social identity biases. Nature computational science, 5(1), 65.

Debaenst S, et al. (2025) Crispant analysis in zebrafish as a tool for rapid functional screening of disease-causing genes for bone fragility. eLife, 13.