Resource Summary Report

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Bgee: dataBase for Gene Expression Evolution

RRID:SCR_002028
Type: Tool

Proper Citation

Bgee: dataBase for Gene Expression Evolution (RRID:SCR_002028)

Resource Information

URL: https://www.bgee.org/

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Description: Database to retrieve and compare gene expression patterns between animal species. Bgee first maps heterogeneous expression data (currently bulk RNA-Seq, scRNA-Seq, Affymetrix, in situ hybridization, and EST data) to anatomy and development of different species. Bgee is based exclusively on curated healthy wild-type expression data (e.g., no gene knock-out, no treatment, no disease), to provide a comparable reference of gene expression.

Abbreviations: Bgee

Synonyms: Bgee: dataBase Gene Expression Evolution, dataBase Gene Expression Evolution

Resource Type: data or information resource, database

Keywords: gene expression, scrna-seq, rna-seq, affymetrix, in situ hybridization, expressed sequence tag, cross specie, comparison, homology, anatomy, developmental stage, gene expression pattern, development, genome, function, chordate, fish, transcriptiome, embryo, adult, mirna, protein coding, prenatal, immature, post-embryonic development, alimentary system, cardiovascular system, nervous system, renal system, reproductive system, respiratory system, skeletal system, ortholog, ontology, FASEB list

Funding:

Availability: Free, Freely available

Resource Name: Bgee: dataBase for Gene Expression Evolution

Resource ID: SCR_002028

Alternate IDs: nif-0000-11819

License: CC0

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250507T060031+0000

Ratings and Alerts

No rating or validation information has been found for Bgee: dataBase for Gene Expression Evolution.

No alerts have been found for Bgee: dataBase for Gene Expression Evolution.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Bastian FB, et al. (2025) Bgee in 2024: focus on curated single-cell RNA-seq datasets, and query tools. Nucleic acids research, 53(D1), D878.

Sartorius AM, et al. (2024) An evolutionary timeline of the oxytocin signaling pathway. Communications biology, 7(1), 471.

Nakamura M, et al. (2024) Unraveling the DNA methylation landscape in dog blood across breeds. BMC genomics, 25(1), 1089.

Jankovi?ová J, et al. (2024) The extracellular vesicle tetraspanin CD63 journey from the testis through the epididymis to mature bull sperm. Scientific reports, 14(1), 29449.

Majewska AM, et al. (2024) Secreted novel AID/APOBEC-like deaminase 1 (SNAD1) - a new important player in fish immunology. Frontiers in immunology, 15, 1340273.

Mehta K, et al. (2024) Predictions of Bedaquiline Central Nervous System Exposure in Patients with Tuberculosis Meningitis Using Physiologically based Pharmacokinetic

Modeling. Clinical pharmacokinetics, 63(5), 657.

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. PloS one, 18(2), e0279597.

Jankovi?ová J, et al. (2023) Distribution of tetraspanins in bovine ovarian tissue and fresh/vitrified oocytes. Histochemistry and cell biology, 159(2), 163.

Goo BS, et al. (2023) Schizophrenia-associated Mitotic Arrest Deficient-1 (MAD1) regulates the polarity of migrating neurons in the developing neocortex. Molecular psychiatry, 28(2), 856.

Liang XZ, et al. (2023) IRF8 and its related molecules as potential diagnostic biomarkers or therapeutic candidates and immune cell infiltration characteristics in steroid-induced osteonecrosis of the femoral head. Journal of orthopaedic surgery and research, 18(1), 27.

Pedroni L, et al. (2023) A Computational Inter-Species Study on Safrole Phase I Metabolism-Dependent Bioactivation: A Mechanistic Insight into the Study of Possible Differences among Species. Toxins, 15(2).

Ni P, et al. (2023) Influence of N6-methyladenosine (m6A) modification on cell phenotype in Alzheimer's disease. PloS one, 18(8), e0289068.

Baindara P, et al. (2023) Preventing Respiratory Viral Diseases with Antimicrobial Peptide Master Regulators in the Lung Airway Habitat. Clinics and practice, 13(1), 125.

Cordes H, et al. (2023) Gene expression databases for physiologically based pharmacokinetic modeling of humans and animal species. CPT: pharmacometrics & systems pharmacology, 12(3), 311.

Alonso AM, et al. (2023) Dicodon-based measures for modeling gene expression. Bioinformatics (Oxford, England), 39(6).

Li Z, et al. (2023) Identification of a potential bioinformatics-based biomarker in keloids and its correlation with immune infiltration. European journal of medical research, 28(1), 476.

Antalíková J, et al. (2022) Expression of ?V integrin and its potential partners in bull reproductive tissues, germ cells and spermatozoa. International journal of biological macromolecules, 209(Pt A), 542.

Mendes de Farias T, et al. (2022) Lessons learned to boost a bioinformatics knowledge base reusability, the Bgee experience. GigaScience, 12.

Jovanovic VM, et al. (2021) Positive Selection in Gene Regulatory Factors Suggests Adaptive Pleiotropic Changes During Human Evolution. Frontiers in genetics, 12, 662239.

Giachelle F, et al. (2021) Search, access, and explore life science nanopublications on the Web. PeerJ. Computer science, 7, e335.