

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, transcriptome, 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

Availability: Free, Freely available

Resource Name: Bgee: dataBase for Gene Expression Evolution

Resource ID: SCR_002028

Alternate IDs: nif-0000-11819, r3d100014596

Alternate URLs: <https://doi.org/10.17616/R31NJNR8>

License: CC0

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260821T193635+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 70 mentions in open access literature.

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

Ivershina A, et al. (2026) Integrated Analysis of Testicular Histology, Sperm Quality, and Gene Expression (TGFB2, DMRT1) in Rooster Semen (*Gallus gallus domesticus*). *Animals* : an open access journal from MDPI, 16(2).

Li S, et al. (2026) Identification of a Diagnostic Gene Signature Associated with Centrosome Amplification in Pressure Injuries: A Cross-Sectional Transcriptome and Machine Learning Study. *Journal of inflammation research*, 19, 580289.

Lamb JW, et al. (2026) Sensory and developmental phenotyping of *C. elegans* parses autism associated genes into behavioural classifications. *bioRxiv* : the preprint server for biology.

Bischof F, et al. (2026) Comparative analysis reveals molecular adaptation of mammalian HCA2 to microbial metabolites. *iScience*, 29(6), 116030.

Oishi K, et al. (2026) The Three Pillars of ATP Production in Mammalian Sperm: Integrating Gluconeogenesis Into the Metabolic Framework. *Reproductive medicine and biology*, 25(1), e70017.

Zhou X, et al. (2025) Role of the human cytochrome b561 family in iron metabolism and tumors (Review). *Oncology letters*, 29(3), 111.

Tackie E, et al. (2025) Whole Exome Sequencing Uncovers Genetic Syndromes Associated with Orofacial Clefts presenting with Limb abnormalities in a Sub-Saharan African cohort. *Research square*.

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.

Kaur H, et al. (2024) A pilot study on the differential urine proteomic profile of subjects with community-acquired acute kidney injury who recover versus those who do not recover completely at 4 months after hospital discharge. *Frontiers in medicine*, 11, 1412561.

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.

Wu Z, et al. (2024) Tumor Heterogeneity of STEAP4 in Malignant Progression of Oral Squamous Cell Carcinoma. *Journal of Cancer*, 15(20), 6754.

Jankovičová 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.

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.

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.

Jankovičová 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.

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

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).