

Resource Summary Report

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Babraham Institute Babraham Bioinformatics Core Facility

RRID:SCR_017148

Type: Tool

Proper Citation

Babraham Institute Babraham Bioinformatics Core Facility (RRID:SCR_017148)

Resource Information

URL: <https://www.bioinformatics.babraham.ac.uk>

Proper Citation: Babraham Institute Babraham Bioinformatics Core Facility (RRID:SCR_017148)

Description: Provides bioinformatics services to research groups in Babraham Institute, United Kingdom and external commercial consultancy service. Provides assistance in genomics, proteomics, statistics, microarrays, and custom software development.

Abbreviations: Babraham Bioinformatics

Synonyms: Babraham Bioinformatics, Core Facility, Babraham Institute

Resource Type: service resource, access service resource, core facility

Keywords: genomics, proteomics, statistics, microarrays, software, development, Consulting

Availability: Open

Resource Name: Babraham Institute Babraham Bioinformatics Core Facility

Resource ID: SCR_017148

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260804T043632+0000

Ratings and Alerts

No rating or validation information has been found for Babraham Institute Babraham Bioinformatics Core Facility.

No alerts have been found for Babraham Institute Babraham Bioinformatics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 219 mentions in open access literature.

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

Park H, et al. (2025) Transcriptome Analysis of *Dryadomyces quercus-mongolicae*, a Fungus Associated with Korean Oak Wilt Disease that Causes Oak Mortality in South Korea. *The plant pathology journal*, 41(3), 409.

Biswas J, et al. (2025) E2F1 suppresses Epstein-Barr virus lytic reactivation through cellular and viral transcriptional networks. *PLoS pathogens*, 21(8), e1013410.

Kim SM, et al. (2025) AMPK activation by glycogen expenditure primes the exit of naïve pluripotency. *EMBO reports*, 26(6), 1504.

Yao M, et al. (2025) The whole-genome map of *Astragalus mongholicus* provides ideas for the synthesis of glutathione and flavonoid. *BMC genomics*, 26(1), 1144.

Lüddecke T, et al. (2025) Comparative venomomics suggests an evolutionary adaption of spider venom from predation to defense. *Communications biology*, 8(1), 1496.

Bousquet L, et al. (2025) Life cycle and morphogenetic differentiation in heteromorphic cell types of a cosmopolitan marine microalga. *The New phytologist*, 245(5), 1969.

Li W, et al. (2025) Comprehensive promotion of iPSC-CM maturation by integrating metabolic medium with nanopatterning and electrostimulation. *Nature communications*, 16(1), 2785.

Gao B, et al. (2025) Increased vegetation disturbance intensity reduces soil nutrients while enhancing microbial network interactions. *Frontiers in microbiology*, 16, 1634424.

Stephenson RA, et al. (2025) Triglyceride metabolism controls inflammation and microglial phenotypes associated with APOE4. *Cell reports*, 44(7), 115961.

Bhattacharyya A, et al. (2025) Root exudates protect rhizosphere *Pseudomonas* from water stress. *Applied and environmental microbiology*, 91(9), e0076825.

Kuzmina DO, et al. (2025) Transcriptomic analysis of the symbiotic responsivity trait in pea (*Pisum sativum* L.). *Vavilovskii zhurnal genetiki i selektsii*, 29(2), 248.

Friedson B, et al. (2025) The CDK8 kinase module: A novel player in the transcription of translation initiation and ribosomal genes. *Molecular biology of the cell*, 36(1), ar2.

Park SM, et al. (2025) Integrative transcriptomic analysis identifies emetine as a promising candidate for overcoming acquired resistance to ALK inhibitors in lung cancer. *Molecular oncology*, 19(4), 1155.

Misel-Wuchter KM, et al. (2025) Developmental epigenetic programming by Tet1/3 determines peripheral CD8 T cell fate. *EMBO reports*, 26(10), 2494.

Perçin G, et al. (2025) Embryonic macrophages orchestrate niche cell homeostasis for the establishment of the definitive hematopoietic stem cell pool. *Nature communications*, 16(1), 4428.

Thiel J, et al. (2025) Knock Out of miRNA-30a-5p and Reconstitution of the Actin Network Dynamics Partly Restores the Impaired Terminal Erythroid Differentiation during Blood Pharming. *Stem cell reviews and reports*, 21(8), 2637.

Yilmaz C, et al. (2025) Modulation of microglial phagocytosis via the GAS6-MERTK pathway regulates pathological angiogenesis in the mouse oxygen-induced retinopathy model. *Cell death & disease*, 16(1), 428.

Kavanova K, et al. (2025) Comparative Genome Analysis and Characterization of the Probiotic Properties of Lactic Acid Bacteria Isolated from the Gastrointestinal Tract of Wild Boars in the Czech Republic. *Probiotics and antimicrobial proteins*, 17(4), 1820.

Vemuri K, et al. (2025) Diet-induced obesity mediated through estrogen-related receptor ? is independent of intestinal function. *The Journal of biological chemistry*, 301(2), 108197.

Neyrinck AM, et al. (2025) Fecal transplantation from humans with obesity to mice drives a selective microbial signature without impacting behavioral and metabolic health. *Scientific reports*, 15(1), 15455.