Resource Summary Report

Generated by <u>dkNET</u> on May 19, 2025

BeeBase

RRID:SCR_008966 Type: Tool

Proper Citation

BeeBase (RRID:SCR_008966)

Resource Information

URL: http://hymenopteragenome.org/beebase/

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Description: Gene sequences and genomes of Bombus terrestris, Bombus impatiens, Apis mellifera and three of its pathogens, that are discoverable and analyzed via genome browsers, blast search, and apollo annotation tool. The genomes of two additional species, Apis dorsata and A. florea are currently under analysis and will soon be incorporated.BeeBase is an archive and will not be updated. The most up-to-date bee genome data is now available through the navigation bar on the HGD Home page.

Abbreviations: BeeBase

Synonyms: Hymenoptera Genome Database

Resource Type: service resource, production service resource, data analysis service, database, data set, analysis service resource, data or information resource

Defining Citation: PMID:21071397

Keywords: genome, gene set, sequence, bee, genomics, entomology, blast, annotation, pest, pathogen, honey, beehive, insect, bee pollen, bee product, bee culture, pollination, pollinator, bio.tools, FASEB list

Funding: Texas Agricultural Experiment Station ; Golden Heritage Foods and Sioux Honey Association ; NHGRI 5-P41-HG000739-13; USDA 2008-35302-18804 Availability: Open unspecified license, Acknowledgement requested, Data Usage Policy

Resource Name: BeeBase

Resource ID: SCR_008966

Alternate IDs: nlx_152034, biotools:hgd

Alternate URLs: https://bio.tools/hgd

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250517T055918+0000

Ratings and Alerts

No rating or validation information has been found for BeeBase.

No alerts have been found for BeeBase.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 56 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Liu J, et al. (2024) An orthology-based methodology as a complementary approach to retrieve evolutionarily conserved A-to-I RNA editing sites. RNA biology, 21(1), 29.

Dickey M, et al. (2023) Transcriptomic analysis of the honey bee (Apis mellifera) queen brain reveals that gene expression is affected by pesticide exposure during development. PloS one, 18(4), e0284929.

Yin Z, et al. (2023) A postmeiotically bifurcated roadmap of honeybee spermatogenesis marked by phylogenetically restricted genes. PLoS genetics, 19(12), e1011081.

Rangel J, et al. (2021) Transcriptomic analysis of the honey bee (Apis mellifera) queen spermathecae reveals genes that may be involved in sperm storage after mating. PloS one, 16(1), e0244648.

Xing L, et al. (2021) The landscape of lncRNAs in Cydia pomonella provides insights into their signatures and potential roles in transcriptional regulation. BMC genomics, 22(1), 4.

Rowland BW, et al. (2021) Identifying the climatic drivers of honey bee disease in England and Wales. Scientific reports, 11(1), 21953.

Henriques D, et al. (2021) A SNP assay for assessing diversity in immune genes in the honey bee (Apis mellifera L.). Scientific reports, 11(1), 15317.

Budge GE, et al. (2020) Chronic bee paralysis as a serious emerging threat to honey bees. Nature communications, 11(1), 2164.

Xie J, et al. (2020) Functional analysis of a novel orthologous small heat shock protein (shsp) hsp21.8a and seven species-specific shsps in Tribolium castaneum. Genomics, 112(6), 4474.

Porath HT, et al. (2019) RNA editing is abundant and correlates with task performance in a social bumblebee. Nature communications, 10(1), 1605.

Ding X, et al. (2019) Genome-Wide Identification and Expression Profiling of Wnt Family Genes in the Silkworm, Bombyx mori. International journal of molecular sciences, 20(5).

Liberti J, et al. (2019) Seminal fluid compromises visual perception in honeybee queens reducing their survival during additional mating flights. eLife, 8.

Xie J, et al. (2019) Characterization and functional analysis of hsp18.3 gene in the red flour beetle, Tribolium castaneum. Insect science, 26(2), 263.

Salcedo-Porras N, et al. (2019) Rhodnius prolixus: Identification of missing components of the IMD immune signaling pathway and functional characterization of its role in eliminating bacteria. PloS one, 14(4), e0214794.

Eimanifar A, et al. (2018) Population genomics and morphometric assignment of western honey bees (Apis mellifera L.) in the Republic of South Africa. BMC genomics, 19(1), 615.

Nie H, et al. (2018) Genome-Wide Identification and Characterization of Fox Genes in the Honeybee, Apis cerana, and Comparative Analysis with Other Bee Fox Genes. International journal of genomics, 2018, 5702061.

Schatton A, et al. (2018) FoxP in bees: A comparative study on the developmental and adult expression pattern in three bee species considering isoforms and circuitry. The Journal of comparative neurology, 526(9), 1589.

Avalos A, et al. (2017) A soft selective sweep during rapid evolution of gentle behaviour in an Africanized honeybee. Nature communications, 8(1), 1550.

Badaoui B, et al. (2017) RNA-sequence analysis of gene expression from honeybees (Apis mellifera) infected with Nosema ceranae. PloS one, 12(3), e0173438.

Jiang H, et al. (2016) Ligand selectivity in tachykinin and natalisin neuropeptidergic systems of the honey bee parasitic mite Varroa destructor. Scientific reports, 6, 19547.