

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

BeeBase

RRID:SCR_008966

Type: Tool

Proper Citation

BeeBase (RRID:SCR_008966)

Resource Information

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

Proper Citation: BeeBase (RRID:SCR_008966)

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: analysis service resource, data analysis service, data or information resource, data set, database, production service resource, service 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, r3d100010925

Alternate URLs: <https://bio.tools/hgd>, <https://doi.org/10.17616/R3Z629>

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260912T195711+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

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.
- 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.
- 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.
- 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.
- 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.
- 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.
- Prasad N, et al. (2016) A comparative genomic analysis of targets of Hox protein Ultrabithorax amongst distant insect species. *Scientific reports*, 6, 27885.