

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Manatee

RRID:SCR_005685

Type: Tool

Proper Citation

Manatee (RRID:SCR_005685)

Resource Information

URL: <http://manatee.sourceforge.net/>

Proper Citation: Manatee (RRID:SCR_005685)

Description: Manatee is a web-based gene evaluation and genome annotation tool; Manatee can store and view annotation for prokaryotic and eukaryotic genomes. The Manatee interface allows biologists to quickly identify genes and make high quality functional assignments, such as GO classifications, using search data, paralogous families, and annotation suggestions generated from automated analysis. Manatee can be downloaded and installed to run under the CGI area of a web server, such as Apache. Platform: Online tool, Linux compatible, Solaris

Abbreviations: Manatee

Resource Type: software resource

Keywords: gene, genome, annotation, ontology or annotation browser, ontology or annotation editor

Availability: Open unspecified license - Free for academic use

Resource Name: Manatee

Resource ID: SCR_005685

Alternate IDs: nlx_149128

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T132540+0000

Ratings and Alerts

No rating or validation information has been found for Manatee.

No alerts have been found for Manatee.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 64 mentions in open access literature.

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

Roggen A, et al. (2025) The MIR157-SPL15 module regulates flowering and inflorescence development in *Arabidopsis thaliana* under short days and in *Arabis alpina*. PLoS genetics, 21(9), e1011799.

Smartt CT, et al. (2025) Changes in the life history traits in *Aedes aegypti* selected for resistance to permethrin and thymol, a spatial repellent. PloS one, 20(8), e0329776.

Zheng H, et al. (2025) Multi-cohort analysis identifies a blood-based immune transcriptomic signature for early lung cancer detection. NPJ precision oncology, 9(1), 246.

Katsis LKD, et al. (2025) A comparison of statistical methods for deriving occupancy estimates from machine learning outputs. Scientific reports, 15(1), 14700.

Sumpio BJ, et al. (2025) Integrated machine learning analysis of proteomic and transcriptomic data identifies healing associated targets in diabetic wound repair. Scientific reports, 15(1), 34355.

Ranches G, et al. (2025) Differentially expressed ncRNAs as key regulators in infection of human bronchial epithelial cells by the SARS-CoV-2 Delta variant. Molecular therapy. Nucleic acids, 36(2), 102559.

Baker L, et al. (2024) Medicaid Managed Care and Pediatric Dental Emergency Department Visits. JAMA health forum, 5(6), e241472.

Yang Y, et al. (2024) The manatee variational autoencoder model for predicting gene expression alterations caused by transcription factor perturbations. Scientific reports, 14(1), 11794.

Rawlings NN, et al. (2024) Cutaneous leishmaniasis in British troops following jungle training in Belize: Cumulative incidence and potential risk practices. Parasite epidemiology and control, 27, e00385.

Burtnick MN, et al. (2024) Identification of *Burkholderia cepacia* strains that express a *Burkholderia pseudomallei*-like capsular polysaccharide. Microbiology spectrum, 12(3), e0332123.

Black KL, et al. (2024) Evidence for gene flow from the Gulf of Mexico to the Atlantic Ocean in bonnethead sharks (*Sphyrna tiburo*). *Ecology and evolution*, 14(9), e70334.

Ayala AJ, et al. (2023) Meteorological associations of *Vibrio vulnificus* clinical infections in tropical settings: Correlations with air pressure, wind speed, and temperature. *PLoS neglected tropical diseases*, 17(7), e0011461.

Kelani AA, et al. (2023) Disruption of the *Aspergillus fumigatus* RNA interference machinery alters the conidial transcriptome. *RNA (New York, N.Y.)*, 29(7), 1033.

Maqueda JJ, et al. (2023) Adapter dimer contamination in sRNA-sequencing datasets predicts sequencing failure and batch effects and hampers extracellular vesicle-sRNA analysis. *Journal of extracellular biology*, 2(6), e91.

Wang Z, et al. (2023) Counting manatee aggregations using deep neural networks and Anisotropic Gaussian Kernel. *Scientific reports*, 13(1), 19793.

Britt K, et al. (2022) Analysis of Citrus Tristeza Virus Incidences within Asian Citrus Psyllid (*Diaphorina citri*) Populations in Florida via High-Throughput Sequencing. *Insects*, 13(3).

Nowell HK, et al. (2022) Impacts of Sugarcane Fires on Air Quality and Public Health in South Florida. *Environmental health perspectives*, 130(8), 87004.

Stumpf RP, et al. (2022) Quantifying *Karenia brevis* bloom severity and respiratory irritation impact along the shoreline of Southwest Florida. *PloS one*, 17(1), e0260755.

Soler-Camargo NC, et al. (2022) The rate and role of pseudogenes of the *Mycobacterium tuberculosis* complex. *Microbial genomics*, 8(10).

Anahtar M, et al. (2022) Host protease activity classifies pneumonia etiology. *Proceedings of the National Academy of Sciences of the United States of America*, 119(25), e2121778119.