Resource Summary Report

Generated by dkNET on May 18, 2025

GeneWise

RRID:SCR_015054
Type: Tool

Proper Citation

GeneWise (RRID:SCR_015054)

Resource Information

URL: http://www.ebi.ac.uk/Tools/psa/genewise/

Proper Citation: GeneWise (RRID:SCR_015054)

Description: Gene alignment tool from the EBI which predicts gene structure using similar protein sequences. See also the associated GenomeWise tool.

Resource Type: software resource, web application

Defining Citation: PMID:15123596

Keywords: gene alignment, dna sequence, protein sequence, bio.tools

Funding:

Availability: Freely available, Available for download

Resource Name: GeneWise

Resource ID: SCR_015054

Alternate IDs: biotools:wise

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

Record Creation Time: 20220129T080323+0000

Record Last Update: 20250517T060158+0000

Ratings and Alerts

No rating or validation information has been found for GeneWise.

No alerts have been found for GeneWise.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 914 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Wang MY, et al. (2025) Chromosome-level genome assembly, annotation, and population genomic resource of argali (Ovis ammon). Scientific data, 12(1), 57.

Raynaud M, et al. (2025) PRDM9 drives the location and rapid evolution of recombination hotspots in salmonid fish. PLoS biology, 23(1), e3002950.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries. Molecular horticulture, 5(1), 6.

Zeng J, et al. (2025) Dampened TLR2-mediated Inflammatory Signaling in Bats. Molecular biology and evolution, 42(1).

Chudhary A, et al. (2025) Characterization of chemosensory genes in the subterranean pest Gryllotalpa Orientalis based on genome assembly and transcriptome comparison. BMC genomics, 26(1), 33.

An M, et al. (2025) Chromosome-Level Genome Assembly and Annotation of the Highly Heterozygous Phallus echinovolvatus Provide New Insights into Its Genetics. Journal of fungi (Basel, Switzerland), 11(1).

Yan Y, et al. (2025) Degenerated vision, altered lipid metabolism, and expanded chemoreceptor repertoires enable Lindaspio polybranchiata to thrive in deep-sea cold seeps. BMC biology, 23(1), 13.

Guan DL, et al. (2025) A high-quality chromosome-level genome assembly of the mulberry looper, Phthonandria atrilineata. Scientific data, 12(1), 186.

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of Sesamum species. Plant communications, 5(1), 100729.

Cuello C, et al. (2024) The Madagascar palm genome provides new insights on the evolution of Apocynaceae specialized metabolism. Heliyon, 10(6), e28078.

Gao T, et al. (2024) An improved chromosome-level genome assembly and annotation of Echeneis naucrates. Scientific data, 11(1), 452.

Ruan Z, et al. (2024) Genome sequencing and comparative genomics reveal insights into pathogenicity and evolution of Fusarium zanthoxyli, the causal agent of stem canker in prickly ash. BMC genomics, 25(1), 502.

Yang FS, et al. (2024) Signatures of Adaptation and Purifying Selection in Highland Populations of Dasiphora fruticosa. Molecular biology and evolution, 41(6).

Sun N, et al. (2024) Chromosome-level genome provides insight into the evolution and conservation of the threatened goral (Naemorhedus goral). BMC genomics, 25(1), 92.

Sun R, et al. (2024) Chromosome-level genome assembly and annotation of a potential model organism Gossypium arboreum ZB-1. Scientific data, 11(1), 620.

Hu M, et al. (2024) A chromosome-level genome of the striated frogfish (Antennarius striatus). Scientific data, 11(1), 654.

Liu C, et al. (2024) Comparative analysis of lipid and flavonoid biosynthesis between Pongamia and soybean seeds: genomic, transcriptional, and metabolic perspectives. Biotechnology for biofuels and bioproducts, 17(1), 86.

Li W, et al. (2024) Genome assembly and resequencing shed light on evolution, population selection, and sex identification in Vernicia montana. Horticulture research, 11(7), uhae141.

Rong J, et al. (2024) De novo Whole-Genome Assembly of the 10-Gigabase Fokienia Hodginsii Genome to Reveal Differential Epigenetic Events Between Callus and Xylem. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(40), e2402644.

Zhu H, et al. (2024) The complex hexaploid oil-Camellia genome traces back its phylogenomic history and multi-omics analysis of Camellia oil biosynthesis. Plant biotechnology journal, 22(10), 2890.