Resource Summary Report

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Gene3D

RRID:SCR_007672
Type: Tool

Proper Citation

Gene3D (RRID:SCR_007672)

Resource Information

URL: http://gene3d.biochem.ucl.ac.uk/Gene3D/

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Description: A large database of CATH protein domain assignments for ENSEMBL genomes and Uniprot sequences. Gene3D is a resource of form studying proteins and the component domains. Gene3D takes CATH domains from Protein Databank (PDB) structures and assigns them to the millions of protein sequences with no PDB structures using Hidden Markov models. Assigning a CATH superfamily to a region of a protein sequence gives information on the gross 3D structure of that region of the protein. CATH superfamilies have a limited set of functions and so the domain assignment provides some functional insights. Furthermore most proteins have several different domains in a specific order, so looking for proteins with a similar domain organization provides further functional insights. Strict confidence cut-offs are used to ensure the reliability of the domain assignments. Gene3D imports functional information from sources such as UNIPROT, and KEGG. They also import experimental datasets on request to help researchers integrate there data with the corpus of the literature. The website allows users to view descriptions for both single proteins and genes and large protein sets, such as superfamilies or genomes. Subsets can then be selected for detailed investigation or associated functions and interactions can be used to expand explorations to new proteins. The Gene3D web services provide programmatic access to the CATH-Gene3D annotation resources and in-house software tools. These services include Gene3DScan for identifying structural domains within protein sequences, access to pre-calculated annotations for the major sequence databases, and linked functional annotation from UniProt, GO and KEGG.

Abbreviations: Gene3D

Synonyms: Gene3D - Structures assigned to Genomes

Resource Type: database, data access protocol, web service, data or information resource, service resource, software resource, storage service resource, data repository

Defining Citation: PMID:19906693, PMID:18032434

Keywords: protein domain, protein, protein superfamily, hidden markov model, structural domain, genome, sequence, domain assignments, protein structure, bio.tools, FASEB list

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Resource Name: Gene3D

Resource ID: SCR_007672

Alternate IDs: nif-0000-02877, biotools:gene3d

Alternate URLs: https://bio.tools/gene3d

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250411T055154+0000

Ratings and Alerts

No rating or validation information has been found for Gene3D.

No alerts have been found for Gene3D.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 255 mentions in open access literature.

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

Vysakh VG, et al. (2025) De novo transcriptome assembly of the Perna viridis: A novel invertebrate model for ecotoxicological studies. Scientific data, 12(1), 147.

Paulo DF, et al. (2025) Functional genomics implicates ebony in the black pupae phenotype of tephritid fruit flies. Communications biology, 8(1), 60.

Schikora-Tamarit MÀ, et al. (2024) Recent gene selection and drug resistance underscore clinical adaptation across Candida species. Nature microbiology, 9(1), 284.

Neale DB, et al. (2024) A genome sequence for the threatened whitebark pine. G3 (Bethesda, Md.), 14(5).

Senkevich K, et al. (2024) Are rare heterozygous SYNJ1 variants associated with Parkinson's disease? medRxiv : the preprint server for health sciences.

Ma X, et al. (2024) Seagrass genomes reveal ancient polyploidy and adaptations to the marine environment. Nature plants, 10(2), 240.

Javed MA, et al. (2024) Telomere-to-telomere Genome Assembly of the Clubroot Pathogen Plasmodiophora Brassicae. Genome biology and evolution, 16(6).

Ang'ang'o LM, et al. (2024) Bioinformatics analysis of the Microsporidia sp. MB genome: a malaria transmission-blocking symbiont of the Anopheles arabiensis mosquito. BMC genomics, 25(1), 1132.

Borujeni PM, et al. (2024) Revisiting the functional annotation of TriTryp using sequence similarity tools. Heliyon, 10(20), e39243.

Puginier C, et al. (2024) Phylogenomics reveals the evolutionary origins of lichenization in chlorophyte algae. Nature communications, 15(1), 4452.

Kaur H, et al. (2024) Genome-wide identification and characterization of flowering genes in Citrus sinensis (L.) Osbeck: a comparison among C. Medica L., C. Reticulata Blanco, C. Grandis (L.) Osbeck and C. Clementina. BMC genomic data, 25(1), 20.

Frey B, et al. (2024) Searching for new plastic-degrading enzymes from the plastisphere of alpine soils using a metagenomic mining approach. PloS one, 19(4), e0300503.

Senkevich K, et al. (2024) Are rare heterozygous SYNJ1 variants associated with Parkinson's disease? NPJ Parkinson's disease, 10(1), 201.

Hallee L, et al. (2024) Annotation Vocabulary (Might Be) All You Need. bioRxiv : the preprint server for biology.

Li R, et al. (2024) Chromosome-level genome assembly of the pygmy grasshopper Eucriotettix oculatus (Orthoptera: Tetrigoidea). Scientific data, 11(1), 431.

Zhong D, et al. (2024) A haplotype-like, chromosome-level assembled and annotated genome of Biomphalaria glabrata, an important intermediate host of schistosomiasis and the best studied model of schistosomiasis vector snails. PLoS neglected tropical diseases, 18(2), e0011983.

Liu F, et al. (2024) Niche-dependent sponge hologenome expression profiles and the host-microbes interplay: a case of the hawaiian demosponge Mycale Grandis. Environmental microbiome, 19(1), 22.

Lin S, et al. (2024) A genetic toolkit underlying the queen phenotype in termites with totipotent workers. Scientific reports, 14(1), 2214.

Roy AS, et al. (2024) A computational approach for structural and functional analyses of disease-associated mutations in the human CYLD gene. Genomics & informatics, 22(1), 4.

Peters DL, et al. (2024) Functional domains of Acinetobacter bacteriophage tail fibers. Frontiers in microbiology, 15, 1230997.