

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Gene3D

Synonyms: Gene3D - Structures assigned to Genomes

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

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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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260905T132614+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 272 mentions in open access literature.

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

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.

Li R, et al. (2025) Phosphoproteomic insights into the regulation of root length in rice (*Oryza sativa* L. cv. KDML 105): uncovering key events and pathways involving phosphorylated proteins. *PeerJ*, 13, e19361.

Shen R, et al. (2025) Chromosome-level genome of the shining chafer *Kibakoganea tamdaoensis* (Coleoptera: Scarabaeidae: Rutelinae). *Scientific data*, 12(1), 1345.

- Gil-Gomez A, et al. (2025) Proteome remodeling in the zoospore-to-vegetative cell transition of the stramenopile *Aurantiochytrium limacinum* reveals candidate ectoplasmic network proteins. *PLoS one*, 20(7), e0326651.
- Huang R, et al. (2025) High-quality genome assembly and annotation of the crested gecko (*Correlophus ciliatus*). *G3 (Bethesda, Md.)*, 15(2).
- Cheng L, et al. (2025) Genome assembly of *Stewartia sinensis* reveals origin and evolution of orphan genes in Theaceae. *Communications biology*, 8(1), 354.
- Paulo DF, et al. (2025) Functional genomics implicates ebony in the black pupae phenotype of tephritid fruit flies. *Communications biology*, 8(1), 60.
- Vysakh VG, et al. (2025) The transcriptomic footprint of *Mytella strigata*: de novo transcriptome assembly of a major invasive species. *Scientific data*, 12(1), 201.
- Otte A, et al. (2025) High-resolution multiomics links nutrients and mixotrophy to toxicity in a harmful bloom of the haptophyte *Chrysochromulina leadbeateri*. *Science advances*, 11(26), eadv3390.
- Ding Y, et al. (2025) High-quality assembly of the chromosomal genome for *Flemingia macrophylla* reveals genomic structural characteristics. *BMC genomics*, 26(1), 535.
- Gu??rin N, et al. (2025) Transcriptomic response of the picoalga *Pelagomonas calceolata* to nitrogen availability: new insights into cyanate lyase function. *Microbiology spectrum*, 13(5), e0265424.
- Asghar R, et al. (2025) Computational studies reveal structural characterization and novel families of *Puccinia striiformis* f. sp. *tritici* effectors. *PLoS computational biology*, 21(3), e1012503.
- Li R, et al. (2025) Chromosome-Level Genome Assembly of the Heptageniid Mayfly *Parafronurus youi* (Ephemeroptera), and Its Annotation. *Genome biology and evolution*, 17(3).
- Rao DM, et al. (2025) Systematic identification and characterization of eukaryotic and viral 2A peptide-bond-skipping sequences. *Cell reports*, 44(7), 115822.
- Parlar SC, et al. (2025) LRRK2 rare-variant per-domain genetic burden in Parkinson's Disease: association confined to the kinase domain. *NPJ Parkinson's disease*, 11(1), 102.
- Talo M, et al. (2025) ProtFun: A Protein Function Prediction Model Using Graph Attention Networks with a Protein Large Language Model. *bioRxiv : the preprint server for biology*.
- Liu K, et al. (2025) Chromosome-level genome of a multivoltine biotype *Ostrinia furnacalis* strain. *Scientific data*, 12(1), 881.
- Wei Z, et al. (2025) Chromosome-level genome assembly of *Sambus kanssuensis* (Coleoptera: Buprestidae). *Scientific data*, 12(1), 895.
- Oraon PK, et al. (2025) A chromosome-scale reference assembly of *Vigna radiata* enables delineation of centromeres and telomeres. *Scientific data*, 12(1), 305.

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