

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

GENO3D

RRID:SCR_003183

Type: Tool

Proper Citation

GENO3D (RRID:SCR_003183)

Resource Information

URL: <http://geno3d-pbil.ibcp.fr>

Proper Citation: GENO3D (RRID:SCR_003183)

Description: An automatic web server for protein molecular modelling. Starting with a query protein sequence, the server performs the homology modelling in six successive steps: (i) identify homologous proteins with known 3D structures by using PSI-BLAST; (ii) provide the user all potential templates through a very convenient user interface for target selection; (iii) perform the alignment of both query and subject sequences; (iv) extract geometrical restraints (dihedral angles and distances) for corresponding atoms between the query and the template; (v) perform the 3D construction of the protein by using a distance geometry approach and (vi) finally send the results by e-mail to the user. The strategy used in Geno3D is comparative protein structure modelling by spatial restraints (distances and dihedral) satisfaction.

Abbreviations: GENO3D

Resource Type: data analysis service, service resource, analysis service resource, production service resource

Defining Citation: [PMID:11836238](#)

Keywords: protein, molecular modeling, 3d model, homology, comparative protein structure modelling

Funding: Ministere de la recherche ;
Programme Bioinformatique inter-EPST ;
CNRS ;
IMABIO ;
COMI ;
GENOME ;
Region Rhone-Alpes

Availability: Free, Freely available

Resource Name: GENO3D

Resource ID: SCR_003183

Alternate IDs: nif-0000-30608

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260810T040342+0000

Ratings and Alerts

No rating or validation information has been found for GENO3D.

No alerts have been found for GENO3D.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Fu QL, et al. (2025) Novel avian metapneumovirus subtype C variant is a newly emerged pathogen causing hydrosalpinx fluid syndrome in Sheldrake ducks in China. Virulence, 16(1), 2590254.

Koley T, et al. (2022) Structural modeling of Omicron spike protein and its complex with human ACE-2 receptor: Molecular basis for high transmissibility of the virus. Biochemical and biophysical research communications, 592, 51.

Zou Q, et al. (2022) Purification and Mechanism of Microcystinase MlrC for Catalyzing Linearized Cyanobacterial Hepatotoxins Using Sphingopyxis sp. USTB-05. Toxins, 14(9).

Boualem A, et al. (2022) Ethylene plays a dual role in sex determination and fruit shape in cucurbits. Current biology : CB, 32(11), 2390.

Nogara PA, et al. (2020) The Se...S/N interactions as a possible mechanism of ?-aminolevulinic acid dehydratase enzyme inhibition by organoselenium compounds: A computational study. Computational toxicology (Amsterdam, Netherlands), 15, 100127.

Helmová R, et al. (2020) Tick-Borne Encephalitis Virus Adaptation in Different Host Environments and Existence of Quasispecies. Viruses, 12(8).

Dill V, et al. (2018) Influence of cell type and cell culture media on the propagation of foot-and-mouth disease virus with regard to vaccine quality. Virology journal, 15(1), 46.

- Mohanta TK, et al. (2017) Genomics and evolutionary aspect of calcium signaling event in calmodulin and calmodulin-like proteins in plants. *BMC plant biology*, 17(1), 38.
- Gong M, et al. (2016) A newly discovered ubiquitin-conjugating enzyme E2 correlated with the cryogenic autolysis of *Volvariella volvacea*. *Gene*, 583(1), 58.
- Thiyagarajan K, et al. (2016) Genomic Characterization of Phenylalanine Ammonia Lyase Gene in Buckwheat. *PloS one*, 11(3), e0151187.
- Mkaouar H, et al. (2016) Siropins, novel serine protease inhibitors from gut microbiota acting on human proteases involved in inflammatory bowel diseases. *Microbial cell factories*, 15(1), 201.
- Srinivasan M, et al. (2016) Novel Nuclear Factor-KappaB Targeting Peptide Suppresses ?-Amyloid Induced Inflammatory and Apoptotic Responses in Neuronal Cells. *PloS one*, 11(10), e0160314.
- Gaucher JF, et al. (2016) Biophysical Studies of the Induced Dimerization of Human VEGF Receptor 1 Binding Domain by Divalent Metals Competing with VEGF-A. *PloS one*, 11(12), e0167755.
- Boualem A, et al. (2016) The Andromonoecious Sex Determination Gene Predates the Separation of Cucumis and Citrullus Genera. *PloS one*, 11(5), e0155444.
- Devi K, et al. (2015) Novel insights into structure-function mechanism and tissue-specific expression profiling of full-length dxr gene from *Cymbopogon winterianus*. *FEBS open bio*, 5, 325.
- Serrano E, et al. (2015) New Insights into the Phylogeny and Gene Context Analysis of Binder of Sperm Proteins (BSPs). *PloS one*, 10(9), e0137008.
- Begara-Morales JC, et al. (2015) Differential molecular response of monodehydroascorbate reductase and glutathione reductase by nitration and S-nitrosylation. *Journal of experimental botany*, 66(19), 5983.
- Mamgain S, et al. (2015) Computer aided screening of natural compounds targeting the E6 protein of HPV using molecular docking. *Bioinformation*, 11(5), 236.
- Pandey V, et al. (2015) Comparative interactions of withanolides and sterols with two members of sterol glycosyltransferases from *Withania somnifera*. *BMC bioinformatics*, 16(1), 120.
- Gallo LI, et al. (2014) TBC1D9B functions as a GTPase-activating protein for Rab11a in polarized MDCK cells. *Molecular biology of the cell*, 25(23), 3779.