Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

FoldX

RRID:SCR_008522
Type: Tool

Proper Citation

FoldX (RRID:SCR_008522)

Resource Information

URL: http://foldx.crg.es/

Proper Citation: FoldX (RRID:SCR_008522)

Description: A computer algorithm that provides a fast and quantitative estimation of the importance of the interactions contributing to the stability of proteins and protein complexes. The predictive power of FOLDEF has been tested on a very large set of point mutants (1088 mutants) spanning most of the structural environments found in proteins . FoldX uses a full atomic description of the structure of the proteins. The different energy terms taken into account in FoldX have been weighted using empirical data obtained from protein engineering experiments.

Abbreviations: FoldX

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

Defining Citation: PMID:15980494, PMID:16006526

Keywords: interaction, stability, protein, protein complex

Availability: Acknowledgement requested

Resource Name: FoldX

Resource ID: SCR_008522

Alternate IDs: OMICS_00129, nif-0000-30580

Alternate URLs: http://fold-x.embl.de, http://fold-x.embl-heidelberg.de

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260912T200013+0000

Ratings and Alerts

No rating or validation information has been found for FoldX.

No alerts have been found for FoldX.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 855 mentions in open access literature.

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

Ahmed S, et al. (2026) Identification of the ACTB p.Ser348Leu de novo variant in individuals with syndromic neonatal diabetes. EBioMedicine, 128, 106286.

Cisneros AF, et al. (2026) Paralog interference contributes to the preservation of genetic redundancy. Current biology : CB, 36(6), 1373.

Kálmán ZE, et al. (2026) Structural Modeling and Dynamics of the Full-Length Homer1 Multimer. Proteins, 94(4), 947.

da Rosa LM, et al. (2026) Chronic Granulomatous Disease: Clinical and Molecular Characterization of Brazilian Patients. The journal of gene medicine, 28(2), e70086.

Zhu X, et al. (2026) Biosynthesis of pyomelanin from methanol with engineered Komagataella phaffii and its characterizations. Nature communications, 17(1).

Guzmán-Vega FJ, et al. (2026) VarLand: A pipeline to map the structural landscape of missense variants at the proteome scale. The Journal of biological chemistry, 302(2), 111071.

Mbaye M, et al. (2026) Integrative Computational Analysis of TP53 Exon 5-6 Mutations in Oral Cavity, Prostate, and Breast Cancers in a Senegalese Population. Genes, 17(2).

Wagenknecht JB, et al. (2026) Multi-State Structural Genomics Enables Large-Scale, Mechanistic, and Context-Specific Classification of ABCC6 Genetic Variants Implicated in Calcification Diseases. International journal of molecular sciences, 27(4).

Wong RS, et al. (2026) Quantifying electrostatic control of docking and binding energetics in functional Cx36 gap junctions. Communications biology, 9(1).

Wang L, et al. (2026) In Silico Saturation-Mutagenesis-Based Genomic Mutation Risk Assessment for Enterovirus B. Viruses, 18(6).

Yang Y, et al. (2026) Combined computational, rational, and empirical design of boiling-resistant keratinase. Applied and environmental microbiology, 92(1), e0186025.

Baid S, et al. (2026) Mapping the Mutational Landscape for Streptokinase Binding to Plasminogen. bioRxiv : the preprint server for biology.

Kumar A, et al. (2026) Variants in MTNAP1 underlie a neurodegenerative disorder by impairing mitochondrial stability. NPJ genomic medicine, 11(1).

Akiyama M, et al. (2026) Cross-species gene redesign leveraging ortholog information and generative modeling. Nature communications, 17(1).

Hou P, et al. (2026) Structural basis of transcription-coupled RNA damage by incorporation of oxidized ribonucleotides. Proceedings of the National Academy of Sciences of the United States of America, 123(16), e2602266123.

Stammnitz MR, et al. (2026) The genetic architecture of an allosteric hormone receptor. Nature communications, 17(1).

Yu D, et al. (2026) Susceptibility of naturally human papillomavirus type 16 major capsid protein L1 variants to vaccines and predictions of future evolutionary trends. Tumour virus research, 21, 200341.

Ding K, et al. (2026) Deconvolving mutation effects on protein stability and function with disentangled protein language models. bioRxiv : the preprint server for biology.

Nair M, et al. (2026) Genetic diversity of the malaria vaccine candidate PfRIPR in a high transmission region of Senegal. iScience, 29(3), 114883.

Ortega Del Campo S, et al. (2026) Synergistic antiviral effects of structure-guided peptides and a mutagenic base analog on SARS-CoV-2 replication. Antimicrobial agents and chemotherapy, 70(6), e0188525.