

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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: 20260905T133002+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 [RRID](#) .

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.