

Resource Summary Report

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FoldX

RRID:SCR_008522

Type: Tool

Proper Citation

FoldX (RRID:SCR_008522)

Resource Information

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

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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: service resource, data analysis service, software resource, production service resource, analysis service 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: 20260729T044221+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 794 mentions in open access literature.

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

Hwang J, et al. (2025) Structurally Oriented Classification of FOXA1 Alterations Identifies Prostate Cancers with Opposing Clinical Outcomes and Distinct Molecular and Immunologic Subtypes. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(5), 936.

Bergson S, et al. (2025) HMCN1 variants aggravate epidermolysis bullosa simplex phenotype. *The Journal of experimental medicine*, 222(5).

Ahmadi SF, et al. (2025) Computational and experimental discovery of peptide inhibitors targeting survivin for therapeutic potential in cancer. *Scientific reports*, 15(1), 30599.

Tokatly Latzer I, et al. (2025) Central Dysmyelination in SSADH-Deficient Humans and Mice. *Annals of clinical and translational neurology*, 12(11), 2193.

Akinwumi IA, et al. (2025) Stoichiometric insights into SARS-CoV-2 spike-ACE2 binding across variants. *Computational and structural biotechnology journal*, 27, 3285.

Orlando G, et al. (2025) Charting the structure-sequence landscape of light chain amyloids. *Bioinformatics (Oxford, England)*, 41(5).

Kumar A, et al. (2025) Exploring sequence- and structure-based fitness landscapes to enhance thermal resistance and activity of endoglucanase II with minimal experimental effort. *RSC chemical biology*, 6(6), 975.

Stockinger P, et al. (2025) Computational analysis reveals temperature-induced stabilization of FAST-PETase. *Computational and structural biotechnology journal*, 27, 969.

Ahmed A, et al. (2025) Predicted functional consequences of WNT ligand mutations in colorectal cancer. *Biophysical journal*, 124(9), 1496.

Banerjee A, et al. (2025) Accurate identification and mechanistic evaluation of pathogenic missense variants with Rhapsody-2. *Proceedings of the National Academy of Sciences of the United States of America*, 122(18), e2418100122.

Liu YA, et al. (2025) Heterologous synthesis of a simplified nitrogenase analog in *Escherichia coli*. *Science advances*, 11(18), eadw6785.

Xu P, et al. (2025) The OsbZIP35-COR1-OsTCP19 module modulates cell proliferation to regulate grain length and weight in rice. *Science advances*, 11(37), eadx9815.

Lin JL, et al. (2025) A dirigent protein redirects extracellular terpenoid metabolism for defense against biotic challenges. *Nature communications*, 16(1), 9270.

Woodard J, et al. (2025) A structural machine learning approach for rapid prediction of thermodynamically destabilizing tyrosine phosphorylations. *Cell reports methods*, 5(9), 101169.

Haynes LM, et al. (2025) Thermodynamics and selection of the plasminogen activator inhibitor-1 latency transition. *The Journal of biological chemistry*, 301(12), 110896.

Badonyi M, et al. (2025) Prevalence of loss-of-function, gain-of-function and dominant-negative mechanisms across genetic disease phenotypes. *Nature communications*, 16(1), 8392.

G??mez Borrego J, et al. (2025) Evaluating ligand docking methods for drugging protein-protein interfaces: insights from AlphaFold2 and molecular dynamics refinement. *Journal of cheminformatics*, 17(1), 144.

Zhang H, et al. (2025) The two-component nuclease-active KELShedu system confers broad antiphage activity via abortive infection. *Science advances*, 11(44), eadv4747.

Nair M, et al. (2025) Genetic Diversity of the Malaria Vaccine Candidate PfRIPR in a High Transmission Region of Senegal. *medRxiv : the preprint server for health sciences*.

Hemker SL, et al. (2025) Saturation mapping of MUTYH variant effects using DNA repair reporters. *bioRxiv : the preprint server for biology*.