

Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 2026

ProNIT

RRID:SCR_003431

Type: Tool

Proper Citation

ProNIT (RRID:SCR_003431)

Resource Information

URL: <http://www.abren.net/pronit/>

Proper Citation: ProNIT (RRID:SCR_003431)

Description: Database that provides experimentally determined thermodynamic interaction data between proteins and nucleic acids. It contains the properties of the interacting protein and nucleic acid, bibliographic information and several thermodynamic parameters such as the binding constants, changes in free energy, enthalpy and heat capacity.

Abbreviations: ProNIT

Resource Type: data or information resource, database

Defining Citation: [PMID:16381846](#), [PMID:11987161](#), [PMID:11724731](#)

Keywords: interaction, protein, nucleic acid, protein-nucleic acid interaction, thermodynamic, binding constant, free energy, enthalpy, heat capacity

Funding: Japan Society for the Promotion of Science ;
Advanced Technology Institute Inc.

Availability: Free, Freely available

Resource Name: ProNIT

Resource ID: SCR_003431

Alternate IDs: nif-0000-03347, OMICS_00541

Old URLs: <http://gibk26.bse.kyutech.ac.jp/jouhou/pronit/pronit.html>,
<http://www.rtc.riken.go.jp/jouhou/pronit/pronit.html>

Record Creation Time: 20220129T080219+0000

Ratings and Alerts

No rating or validation information has been found for ProNIT.

No alerts have been found for ProNIT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Yu X, et al. (2026) iDLDDG: predicting protein stability changes from missense mutations in DNA-binding proteins using integrated deep learning features. Briefings in bioinformatics, 27(1).

Rimal P, et al. (2025) Further Development of SAMPDI-3D: A Machine Learning Method for Predicting Binding Free Energy Changes Caused by Mutations in Either Protein or DNA. Genes, 16(1).

Mei LC, et al. (2021) HISNAPI: a bioinformatic tool for dynamic hot spot analysis in nucleic acid-protein interface with a case study. Briefings in bioinformatics, 22(5).

Jiang Y, et al. (2021) Systematic comparison and prediction of the effects of missense mutations on protein-DNA and protein-RNA interactions. PLoS computational biology, 17(4), e1008951.

Nguyen TB, et al. (2021) mmCSM-NA: accurately predicting effects of single and multiple mutations on protein-nucleic acid binding affinity. NAR genomics and bioinformatics, 3(4), lqab109.

Liu J, et al. (2021) Nabe: an energetic database of amino acid mutations in protein-nucleic acid binding interfaces. Database : the journal of biological databases and curation, 2021.

Zhu X, et al. (2020) iPNHOT: a knowledge-based approach for identifying protein-nucleic acid interaction hot spots. BMC bioinformatics, 21(1), 289.

Pan Y, et al. (2020) Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. BMC bioinformatics, 21(Suppl 13), 384.

Zhang N, et al. (2020) PremPRI: Predicting the Effects of Missense Mutations on Protein-RNA Interactions. International journal of molecular sciences, 21(15).

Zhao F, et al. (2018) Computational Approaches to Prioritize Cancer Driver Missense Mutations. *International journal of molecular sciences*, 19(7).

Zhang N, et al. (2018) PremPDI estimates and interprets the effects of missense mutations on protein-DNA interactions. *PLoS computational biology*, 14(12), e1006615.

Pires DEV, et al. (2017) mCSM-NA: predicting the effects of mutations on protein-nucleic acids interactions. *Nucleic acids research*, 45(W1), W241.