# **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

# **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: database, data or information resource

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:** Creative Commons Attribution-NonCommercial-ShareAlike License, v3 Unported, Commercial use with permission

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

Record Last Update: 20250430T055221+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: <u>SciCrunch Registry</u>

#### **Usage and Citation Metrics**

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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).

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.

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.

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).

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

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

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