

Resource Summary Report

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GraphProt

RRID:SCR_005842

Type: Tool

Proper Citation

GraphProt (RRID:SCR_005842)

Resource Information

URL: <http://www.bioinf.uni-freiburg.de/Software/GraphProt/>

Proper Citation: GraphProt (RRID:SCR_005842)

Description: Software for modeling binding preferences of RNA-binding proteins from high-throughput experiments such as CLIP-seq and RNAcompete.

Abbreviations: GraphProt

Resource Type: software resource

Defining Citation: [PMID:24451197](#)

Keywords: sequence-binding preference, structure-binding preference, rna-binding protein, high-throughput sequencing, clip-seq, rnacompete, rna, bio.tools

Availability: Free, Public

Resource Name: GraphProt

Resource ID: SCR_005842

Alternate IDs: OMICS_02252, biotools:graphprot

Alternate URLs: <https://bio.tools/graphprot>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260919T195100+0000

Ratings and Alerts

No rating or validation information has been found for GraphProt.

No alerts have been found for GraphProt.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

He J, et al. (2026) Augmented prediction of multi-species protein-RNA interactions using evolutionary conservation of RNA-binding proteins. Nature communications, 17(1).

Schmerer N, et al. (2025) A searchable atlas of pathogen-sensitive lncRNA networks in human macrophages. Nature communications, 16(1), 4733.

Zhang J, et al. (2025) RMDNet: RNA-aware dung beetle optimization-based multi-branch integration network for RNA-protein binding sites prediction. BMC bioinformatics, 26(1), 176.

Qiao Y, et al. (2024) DeepFusion: A deep bimodal information fusion network for unraveling protein-RNA interactions using in vivo RNA structures. Computational and structural biotechnology journal, 23, 617.

Niu M, et al. (2024) CircRNA identification and feature interpretability analysis. BMC biology, 22(1), 44.

Vaculík O, et al. (2023) Transfer Learning Allows Accurate RBP Target Site Prediction with Limited Sample Sizes. Biology, 12(10).

Horlacher M, et al. (2023) A systematic benchmark of machine learning methods for protein-RNA interaction prediction. Briefings in bioinformatics, 24(5).

Xu Y, et al. (2023) PrismNet: predicting protein-RNA interaction using in vivo RNA structural information. Nucleic acids research, 51(W1), W468.

Akbari Rokn Abadi S, et al. (2023) KDeep: a new memory-efficient data extraction method for accurately predicting DNA/RNA transcription factor binding sites. Journal of translational medicine, 21(1), 727.

Chalupová E, et al. (2022) ENNGene: an Easy Neural Network model building tool for Genomics. BMC genomics, 23(1), 248.

Laverty KU, et al. (2022) PRIESSTEES: interpretable, high-performing models of the sequence and structure preferences of RNA-binding proteins. Nucleic acids research, 50(19), e111.

Uhl M, et al. (2021) RNAProt: an efficient and feature-rich RNA binding protein binding site predictor. GigaScience, 10(8).

Sohrabi-Jahromi S, et al. (2021) Thermodynamic modeling reveals widespread multivalent binding by RNA-binding proteins. *Bioinformatics (Oxford, England)*, 37(Suppl_1), i308.

Sharma NK, et al. (2021) RBPSpot: Learning on appropriate contextual information for RBP binding sites discovery. *iScience*, 24(12), 103381.

Sun L, et al. (2021) Predicting dynamic cellular protein-RNA interactions by deep learning using in vivo RNA structures. *Cell research*, 31(5), 495.

Xiong F, et al. (2021) RNA m6A modification orchestrates a LINE-1-host interaction that facilitates retrotransposition and contributes to long gene vulnerability. *Cell research*, 31(8), 861.

Grønning AGB, et al. (2020) DeepCLIP: predicting the effect of mutations on protein-RNA binding with deep learning. *Nucleic acids research*, 48(13), 7099.

Zhang G, et al. (2020) Identifying Circular RNA and Predicting Its Regulatory Interactions by Machine Learning. *Frontiers in genetics*, 11, 655.

Uhl M, et al. (2020) Improving CLIP-seq data analysis by incorporating transcript information. *BMC genomics*, 21(1), 894.

Ilik IA, et al. (2020) FLASH: ultra-fast protocol to identify RNA-protein interactions in cells. *Nucleic acids research*, 48(3), e15.