

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: 20260905T132542+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 [RRID](#) .

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.

Deng L, et al. (2020) Deep neural networks for inferring binding sites of RNA-binding proteins by using distributed representations of RNA primary sequence and secondary structure. *BMC genomics*, 21(Suppl 13), 866.