Resource Summary Report

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DP-Bind: a web server for sequence-based prediction of DNA-binding residues in DNA-binding proteins

RRID:SCR_003039
Type: Tool

Proper Citation

DP-Bind: a web server for sequence-based prediction of DNA-binding residues in DNA-binding proteins (RRID:SCR_003039)

Resource Information

URL: http://lcg.rit.albany.edu/dp-bind

Proper Citation: DP-Bind: a web server for sequence-based prediction of DNA-binding residues in DNA-binding proteins (RRID:SCR_003039)

Description: This web-server takes a user-supplied sequence of a DNA-binding protein and predicts residue positions involved in interactions with DNA. Prediction can be performed using a profile of evolutionary conservation of the input sequence automatically generated by the web-server or the input sequence alone. Three prediction methods are run for each input sequence and consensus prediction is generated.

Abbreviations: DP-Bind

Resource Type: analysis service resource, data analysis service, service resource, production service resource

Defining Citation: PMID:17237068, PMID:16568445

Keywords: dna binding

Funding: NLM 1R03LM009034-01

Resource Name: DP-Bind: a web server for sequence-based prediction of DNA-binding residues in DNA-binding proteins

Resource ID: SCR_003039

Alternate IDs: nif-0000-30426

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250409T060232+0000

Ratings and Alerts

No rating or validation information has been found for DP-Bind: a web server for sequence-based prediction of DNA-binding residues in DNA-binding proteins.

No alerts have been found for DP-Bind: a web server for sequence-based prediction of DNA-binding residues in DNA-binding proteins.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Chen J, et al. (2024) Unveiling the repressive mechanism of a PPS-like regulator (PspR) in polyhydroxyalkanoates biosynthesis network. Applied microbiology and biotechnology, 108(1), 265.

Das R, et al. (2023) Functional characterization of a DNA-dependent AAA ATPase in a F-cluster mycobacteriophage. Virus research, 323, 198957.

Filandrová R, et al. (2021) Motif orientation matters: Structural characterization of TEAD1 recognition of genomic DNA. Structure (London, England : 1993), 29(4), 345.

Gomes JR, et al. (2020) Neuronal megalin mediates synaptic plasticity-a novel mechanism underlying intellectual disabilities in megalin gene pathologies. Brain communications, 2(2), fcaa135.

Monteiro JM, et al. (2019) The pentaglycine bridges of Staphylococcus aureus peptidoglycan are essential for cell integrity. Scientific reports, 9(1), 5010.

Lai GH, et al. (2018) Characterization of the DNA binding activity of structural protein VP1 from chicken anaemia virus. BMC veterinary research, 14(1), 155.

Puisac B, et al. (2017) mRNA Quantification of NIPBL Isoforms A and B in Adult and Fetal Human Tissues, and a Potentially Pathological Variant Affecting Only Isoform A in Two

Patients with Cornelia de Lange Syndrome. International journal of molecular sciences, 18(3).

Díaz DJ, et al. (2016) HybridPLAY: A New Technology to Foster Outdoors Physical Activity, Verbal Communication and Teamwork. Sensors (Basel, Switzerland), 16(4).

Lammirato A, et al. (2016) TIS7 induces transcriptional cascade of methylosome components required for muscle differentiation. BMC biology, 14(1), 95.

Zhou HM, et al. (2016) Transgelin increases metastatic potential of colorectal cancer cells in vivo and alters expression of genes involved in cell motility. BMC cancer, 16, 55.

Miao Z, et al. (2015) A Large-Scale Assessment of Nucleic Acids Binding Site Prediction Programs. PLoS computational biology, 11(12), e1004639.

Si J, et al. (2015) An overview of the prediction of protein DNA-binding sites. International journal of molecular sciences, 16(3), 5194.

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Tan BG, et al. (2014) Conformational and thermodynamic hallmarks of DNA operator site specificity in the copper sensitive operon repressor from Streptomyces lividans. Nucleic acids research, 42(2), 1326.

Wu X, et al. (2013) Functional assignment to maize group 1 LEA protein EMB564 within the cell nucleus using computational analysis. Bioinformation, 9(6), 276.

Camerlengo T, et al. (2012) From sequencer to supercomputer: an automatic pipeline for managing and processing next generation sequencing data. AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science, 2012, 1.

Laoong-u-thai Y, et al. (2011) Molecular characterizations of a novel putative DNA-binding protein LvDBP23 in marine shrimp L. vannamei tissues and molting stages. PloS one, 6(5), e19959.

Wu J, et al. (2009) Prediction of DNA-binding residues in proteins from amino acid sequences using a random forest model with a hybrid feature. Bioinformatics (Oxford, England), 25(1), 30.