Resource Summary Report

Generated by NIF on Apr 21, 2025

DPInteract

RRID:SCR_007627
Type: Tool

Proper Citation

DPInteract (RRID:SCR_007627)

Resource Information

URL: http://arep.med.harvard.edu/dpinteract/

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Description: DPInteract is a database of DNA-binding site matrices. This dataset is being collected with several purposes in mind: 1. Cataloging demonstrated sites and non-sites for E.coli DNA-binding proteins; 2. Aiding the annotation of such sites in other E.coli databases and sequence entries; 3. Interpreting the results of whole-genome in vivo methylation protection experiments; 4. Developing better computational tools for recognizing DNA binding proteins in sequence data.

Synonyms: DPInteract

Resource Type: database, data or information resource

Keywords: e. coli dna-binding proteins, e. coli gene matrice, e. coli protein, dna-binding, dna-binding site

Funding:

Resource Name: DPInteract

Resource ID: SCR_007627

Alternate IDs: nif-0000-02763

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250420T015556+0000

Ratings and Alerts

No rating or validation information has been found for DPInteract.

No alerts have been found for DPInteract.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Feng H, et al. (2023) Deep-learning-assisted Sort-Seq enables high-throughput profiling of gene expression characteristics with high precision. Science advances, 9(45), eadg5296.

Tretina K, et al. (2016) Cis regulatory motifs and antisense transcriptional control in the apicomplexan Theileria parva. BMC genomics, 17, 128.

GuhaThakurta D, et al. (2006) Computational identification of transcriptional regulatory elements in DNA sequence. Nucleic acids research, 34(12), 3585.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Kechris KJ, et al. (2004) Detecting DNA regulatory motifs by incorporating positional trends in information content. Genome biology, 5(7), R50.