Resource Summary Report

Generated by RRID on May 18, 2025

UniPROBE

RRID:SCR_005803

Type: Tool

Proper Citation

UniPROBE (RRID:SCR_005803)

Resource Information

URL: http://the_brain.bwh.harvard.edu/uniprobe/

Proper Citation: UniPROBE (RRID:SCR_005803)

Description: Database that hosts experimental data from universal protein binding microarray (PBM) experiments (Berger et al., 2006) and their accompanying statistical analyses from prokaryotic and eukaryotic organisms, malarial parasites, yeast, worms, mouse, and human. It provides a centralized resource for accessing comprehensive data on the preferences of proteins for all possible sequence variants ("words") of length k ("k-mers"), as well as position weight matrix (PWM) and graphical sequence logo representations of the k-mer data. The database's web tools include a text-based search, a function for assessing motif similarity between user-entered data and database PWMs, and a function for locating putative binding sites along user-entered nucleotide sequences.

Abbreviations: UniPROBE

Synonyms: UniPROBE Database, Universal Protein Binding Microarray Resource for Oligonucleotide Binding Evaluation, Universal PBM Resource for Oligonucleotide Binding Evaluation

Resource Type: database, data or information resource

Defining Citation: PMID:21037262, PMID:18842628

Keywords: protein, in vitro, dna binding, protein binding, genetics, dna, nucleotide sequence, sequence variant, k-mer, position weight matrix, graphical sequence logo, motif, motif similarity, binding site, microarray, protein-dna interaction, protein binding microarray probe sequence, probe, FASEB list

Funding:

Availability: Acknowledgement requested, Academic research use license

Resource Name: UniPROBE

Resource ID: SCR_005803

Alternate IDs: nif-0000-03611, OMICS_00546

Alternate URLs: http://thebrain.bwh.harvard.edu/pbms/webworks_pub/

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250517T055722+0000

Ratings and Alerts

No rating or validation information has been found for UniPROBE.

No alerts have been found for UniPROBE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 141 mentions in open access literature.

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

Song C, et al. (2024) eRNAbase: a comprehensive database for decoding the regulatory eRNAs in human and mouse. Nucleic acids research, 52(D1), D81.

Lim F, et al. (2024) Affinity-optimizing enhancer variants disrupt development. Nature, 626(7997), 151.

Ren YY, et al. (2024) Characterization of Single-Cell Cis-regulatory Elements Informs Implications for Cell Differentiation. Genome biology and evolution, 16(11).

Zhang B, et al. (2024) Sustained mucosal colonization and fecal metabolic dysfunction by Bacteroides associates with fecal microbial transplant failure in ulcerative colitis patients. Scientific reports, 14(1), 18558.

Hill C, et al. (2023) ChromDL: A Next-Generation Regulatory DNA Classifier. bioRxiv: the

preprint server for biology.

Song BP, et al. (2023) Diverse logics and grammar encode notochord enhancers. Cell reports, 42(2), 112052.

Novakovsky G, et al. (2023) ExplaiNN: interpretable and transparent neural networks for genomics. Genome biology, 24(1), 154.

Nappi A, et al. (2023) Loss of p53 activates thyroid hormone via type 2 deiodinase and enhances DNA damage. Nature communications, 14(1), 1244.

Luan Y, et al. (2023) Intra-Domain Residue Coevolution in Transcription Factors Contributes to DNA Binding Specificity. Microbiology spectrum, 11(2), e0365122.

Cornwell A, et al. (2023) The C. elegans Myc-family of transcription factors coordinate a dynamic adaptive response to dietary restriction. bioRxiv: the preprint server for biology.

Hwang J, et al. (2023) Mapping Chromatin Occupancy of Ppp1r1b-lncRNA Genome-Wide Using Chromatin Isolation by RNA Purification (ChIRP)-seq. Cells, 12(24).

Hwang J, et al. (2023) Mapping Chromatin Occupancy of Ppp1r1b-lncRNA Genome-Wide Using Chromatin Isolation by RNA Purification (ChIRP)-seq. bioRxiv: the preprint server for biology.

Wang Z, et al. (2023) An autoimmune pleiotropic SNP modulates IRF5 alternative promoter usage through ZBTB3-mediated chromatin looping. Nature communications, 14(1), 1208.

Recio PS, et al. (2023) Zinc cluster transcription factors frequently activate target genes using a non-canonical half-site binding mode. Nucleic acids research, 51(10), 5006.

Yuan Q, et al. (2023) Continuous lifelong learning for modeling of gene regulation from single cell multiome data by leveraging atlas-scale external data. bioRxiv: the preprint server for biology.

Zhang Y, et al. (2022) TcoFBase: a comprehensive database for decoding the regulatory transcription co-factors in human and mouse. Nucleic acids research, 50(D1), D391.

Heller IS, et al. (2022) Characterization of mouse Bmp5 regulatory injury element in zebrafish wound models. Bone, 155, 116263.

Aneas I, et al. (2021) Asthma-associated genetic variants induce IL33 differential expression through an enhancer-blocking regulatory region. Nature communications, 12(1), 6115.

Greulich F, et al. (2021) The glucocorticoid receptor recruits the COMPASS complex to regulate inflammatory transcription at macrophage enhancers. Cell reports, 34(6), 108742.

Mehta TK, et al. (2021) Evolution of regulatory networks associated with traits under selection in cichlids. Genome biology, 22(1), 25.