

# Resource Summary Report

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## UniPROBE

RRID:SCR\_005803

Type: Tool

### Proper Citation

UniPROBE (RRID:SCR\_005803)

### Resource Information

**URL:** [http://the\\_brain.bwh.harvard.edu/uniprobe/](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:** data or information resource, database

**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

**Availability:** Acknowledgement requested, Academic research use license

**Resource Name:** UniPROBE

**Resource ID:** SCR\_005803

**Alternate IDs:** nif-0000-03611, OMICS\_00546, r3d100010557

**Alternate URLs:** [http://thebrain.bwh.harvard.edu/pbms/webworks\\_pub/](http://thebrain.bwh.harvard.edu/pbms/webworks_pub/),  
<https://doi.org/10.17616/R35C9J>

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260905T133132+0000

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## Ratings and Alerts

No rating or validation information has been found for UniPROBE.

No alerts have been found for UniPROBE.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 151 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. Science advances, 12(1), eady2539.

Hermant C, et al. (2026) TBP regulates transposable element expression in early mouse embryos. The EMBO journal, 45(9), 3073.

Hu Y, et al. (2026) TF2TG: an online resource mining the potential gene targets of transcription factors in Drosophila. Genetics, 232(1).

Ball KF, et al. (2025) The 3' region of the ZPA regulatory sequence (ZRS) is required for activity and contains a critical E-box. Frontiers in cell and developmental biology, 13, 1569573.

Shen T, et al. (2025) A Modified Method Incorporating Multiplex PCR Reveals Fusobacterium Prevalence in Southern Chinese Population and Its Correlations in Cancers. Microbial biotechnology, 18(12), e70292.

Zhao K, et al. (2025) Endogenous fine-mapping and prioritization of functional regulatory elements in complex genetic loci. Cell genomics, 100982.

Yuan Q, et al. (2025) Inferring gene regulatory networks from single-cell multiome data using atlas-scale external data. Nature biotechnology, 43(2), 247.

Hermant C, et al. (2025) The transcription factor SRF regulates MERV1 retrotransposons and gene expression during zygotic genome activation. *Genes & development*, 39(7-8), 490.

Feng Z, et al. (2025) Modeling combinatorial regulation from single-cell multi-omics provides regulatory units underpinning cell type landscape using cRegulon. *Genome biology*, 26(1), 220.

Durval MC, et al. (2025) Transcription factors and candidate functional SNPs associated with variation in fatty acid composition from skeletal muscle of pigs. *Animal genetics*, 56(5), e70051.

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

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

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

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) ExplainNN: 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*.