UniPROBE

RRID:SCR_005803
Type: Tool

Proper Citation

UniPROBE (RRID:SCR_005803)

Resource Information

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

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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


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

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

### 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 130 mentions in open access literature.

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


Teng M, et al. (2021) Characterizing batch effects and binding site-specific variability in ChIP-seq data. NAR genomics and bioinformatics, 3(4), lqab098.


Broome R, et al. (2021) TET2 is a component of the estrogen receptor complex and controls 5mC to 5hmC conversion at estrogen receptor cis-regulatory regions. Cell reports, 34(8), 108776.


