Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 1, 2025

<u>pLogo</u>

RRID:SCR_018185 Type: Tool

Proper Citation

pLogo (RRID:SCR_018185)

Resource Information

URL: https://plogo.uconn.edu/

Proper Citation: pLogo (RRID:SCR_018185)

Description: Web tool as probabilistic approach to visualizing protein or nucleic acid sequence motifs. Used for motif visualization in which residue heights are scaled relative to their statistical significance. Supports real time conditional probability calculations and visualizations.

Synonyms: probability logo

Resource Type: software resource, service resource, data access protocol, web service

Defining Citation: PMID:24097270

Keywords: Visualizing protein motif, visualizing nucleic acid motif, sequence motif, conditional probability calculation, probability,

Funding: University of Connecticut Research Foundation ; US Department of Energy

Availability: Restricted

Resource Name: pLogo

Resource ID: SCR_018185

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250501T081438+0000

Ratings and Alerts

No rating or validation information has been found for pLogo.

No alerts have been found for pLogo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lozano-Terol G, et al. (2024) Relative impact of three growth conditions on the Escherichia coli protein acetylome. iScience, 27(2), 109017.

Chancharoen M, et al. (2024) 5-Chloro-2'-deoxycytidine Induces a Distinctive High-Resolution Mutational Spectrum of Transition Mutations In Vivo. Chemical research in toxicology, 37(3), 486.

Marshall S, et al. (2024) In-depth mapping of DNA-PKcs signaling uncovers noncanonical features of its kinase specificity. The Journal of biological chemistry, 300(8), 107513.

She YM, et al. (2024) Region-selective and site-specific glycation of influenza proteins surrounding the viral envelope membrane. Scientific reports, 14(1), 18975.

Lee G, et al. (2023) Distinct phases of cellular signaling revealed by time-resolved protein synthesis. bioRxiv : the preprint server for biology.

Chen L, et al. (2023) A novel two-way rebalancing strategy for identifying carbonylation sites. BMC bioinformatics, 24(1), 429.

Xu S, et al. (2023) Systematic analysis of the impact of phosphorylation and O-GlcNAcylation on protein subcellular localization. Cell reports, 42(7), 112796.

Xu S, et al. (2023) Combining Selective Enrichment and a Boosting Approach to Globally and Site-Specifically Characterize Protein Co-translational O-GlcNAcylation. Analytical chemistry, 95(9), 4371.

Zhang W, et al. (2022) CPLM 4.0: an updated database with rich annotations for protein lysine modifications. Nucleic acids research, 50(D1), D451.

Zecha J, et al. (2022) Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling. Nature communications, 13(1), 165.

Xu S, et al. (2022) Spatial and temporal proteomics reveals the distinct distributions and dynamics of O-GIcNAcylated proteins. Cell reports, 39(11), 110946.

Hariharan A, et al. (2022) Heterogeneous RNA editing and influence of ADAR2 on mesothelioma chemoresistance and the tumor microenvironment. Molecular oncology, 16(22), 3949.

Cullati SN, et al. (2022) Kinase domain autophosphorylation rewires the activity and substrate specificity of CK1 enzymes. Molecular cell, 82(11), 2006.

Gao H, et al. (2022) Protein glycosylation changes during systemic acquired resistance in Arabidopsis thaliana. International journal of biological macromolecules, 212, 381.

Vijayraghavan S, et al. (2022) Acetaldehyde makes a distinct mutation signature in singlestranded DNA. Nucleic acids research, 50(13), 7451.

Zuo Y, et al. (2021) CarSite-II: an integrated classification algorithm for identifying carbonylated sites based on K-means similarity-based undersampling and synthetic minority oversampling techniques. BMC bioinformatics, 22(1), 216.

Kitata RB, et al. (2021) A data-independent acquisition-based global phosphoproteomics system enables deep profiling. Nature communications, 12(1), 2539.

Jiang P, et al. (2021) FSL-Kla: A few-shot learning-based multi-feature hybrid system for lactylation site prediction. Computational and structural biotechnology journal, 19, 4497.

Tan C, et al. (2021) Alterations of Asymmetric Dimethylarginine (ADMA)-Containing Protein Profiles Associated with Chronic Pancreatitis Pathogenesis. Journal of inflammation research, 14, 7381.

Doron S, et al. (2021) SPEAR: A proteomics approach for simultaneous protein expression and redox analysis. Free radical biology & medicine, 176, 366.