

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

pLogo

RRID:SCR_018185

Type: Tool

Proper Citation

pLogo (RRID:SCR_018185)

Resource Information

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

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

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: 20260731T043031+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 53 mentions in open access literature.

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

Ning W, et al. (2025) HybridKla: a hybrid deep learning framework for lactylation site prediction. *Briefings in bioinformatics*, 26(4).

Yek KQ, et al. (2025) Legionella effector LpPIP recruits protein phosphatase 1 to the mitochondria to induce dephosphorylation of outer membrane proteins. *PLoS biology*, 23(7), e3003261.

Thongararm P, et al. (2025) Structurally Similar Mycotoxins Aflatoxin B1 and Sterigmatocystin Trigger Different and Distinctive High-Resolution Mutational Spectra in Mammalian Cells. *Toxins*, 17(3).

Lei C, et al. (2025) Chemical Glycoproteomic Profiling in Rice Seedlings Reveals N-glycosylation in the ERAD-L Machinery. *Molecular & cellular proteomics : MCP*, 24(2), 100883.

Sun JK, et al. (2025) Alpha-ketoglutarate mitigates insulin resistance and metabolic inflexibility in a mouse model of Ataxia-Telangiectasia. *Nature communications*, 16(1), 9312.

Adamo M, et al. (2025) AtSnRK2.4 Functions as an ABA-Responsive Protein Kinase in Arabidopsis. *Physiologia plantarum*, 177(5), e70574.

Wright G, et al. (2025) Saskemycin, a potent and selective antimycobacterial agent targeting a unique site on the ribosome. *Research square*.

Ziegler AR, et al. (2025) Employing complementary fractionation-based N-terminomics approaches enhances the identification of legumain cleavage events in naïve and inflamed colon tissue. *Protein science : a publication of the Protein Society*, 34(10), e70186.

Zhang Z, et al. (2025) Unveiling the role of PSD95 phosphorylation after traumatic brain injury: insights from phosphoproteomic analysis. *BMC neurology*, 25(1), 311.

Roffey SE, et al. (2025) Covalent Inhibition of the Peptidyl-Prolyl Isomerase Pin1 by SulfoPin Results in a Broad Impact on the Phosphoproteome of Human Osteosarcoma U2-OS Cells. *Proteomics*, 25(14), e13980.

Wright G, et al. (2025) A Natural Depsipeptide Antibiotic that Targets the E site of the Bacterial Ribosome. Research square.

Doron S, et al. (2025) Two opposing redox signals mediated by 2-cys peroxiredoxin shape the redox proteome during photosynthetic induction. Redox biology, 86, 103810.

Baros-Steyl SS, et al. (2025) A Phosphoproteomic Analysis of Mycobacterial PknG-Mediated Host Immune Evasion. Journal of proteome research, 24(11), 5585.

Zhao MX, et al. (2025) Decoding protein N-phosphorylation functionality and sequence patterns. Briefings in bioinformatics, 26(6).

Kim JY, et al. (2025) Global Profiling of Lysine Lactylation in Prostate Cancer Cells. Cancer genomics & proteomics, 22(6), 929.

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.

Brown GW, et al. (2024) The cytidine deaminase APOBEC3C has unique sequence and genome feature preferences. Genetics, 227(4).