

Resource Summary Report

Generated by [ASWG](#) on Sep 18, 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, service resource, software resource, 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: 20260912T195858+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 67 mentions in open access literature.

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

Tang L, et al. (2026) Pyramiding elite alleles of the genetically linked OsNRAMP5 and OsHMA3 confers low Cd accumulation in rice grains without compromising stress tolerance. *Plant communications*, 7(4), 101690.

Liu XY, et al. (2026) Hepatic glutathione depletion ameliorates MASLD through selective protein oxidation and inhibition of lipogenesis. *The Journal of clinical investigation*, 136(8).

Jonak K, et al. (2026) Integrated analysis of the redoxome and zinc proteome links ribosomal protein oxidation to zinc homeostasis. *Redox biology*, 93, 104152.

Cao G, et al. (2026) Global discovery of RNA modifications and functional analysis of m5C methylome in cyanobacteria. *The Journal of biological chemistry*, 302(2), 111133.

Laposchan S, et al. (2026) Development of motif-specific monoclonal antibodies for global protein citrullination detection with minimal cross-reactivity to homocitrullination. *Cell reports methods*, 6(4), 101345.

Franciosa G, et al. (2026) The proteomics and phosphoproteomics landscape of melanoma under T cell attack. *Cell reports. Medicine*, 7(6), 102829.

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).

Cheng X, et al. (2025) Proteomics and Phosphoproteomics Revealed Dysregulated Kinases and Potential Therapy for Liver Fibrosis. *Molecular & cellular proteomics : MCP*, 24(6), 100991.

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.

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.

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

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.

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

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.

Lee M, et al. (2025) Profiling tyrosine kinase substrate recognition using bacterial peptide display and deep sequencing. *bioRxiv : the preprint server for biology*.

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*.

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

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