Resource Summary Report

Generated by NIF on Apr 25, 2025

iceLogo

RRID:SCR_012137
Type: Tool

Proper Citation

iceLogo (RRID:SCR_012137)

Resource Information

URL: https://code.google.com/p/icelogo/

Proper Citation: iceLogo (RRID:SCR_012137)

Description: Software that builds on probability theory to visualize significant conserved sequence patterns in multiple peptide sequence alignments against background (reference) sequence sets that can be tailored to the studied system and the used protocol.

Resource Type: software resource

Defining Citation: PMID:19876014

Keywords: standalone software, web app, bio.tools

Funding:

Availability: Apache License

Resource Name: iceLogo

Resource ID: SCR_012137

Alternate IDs: biotools:icelogo, OMICS_05885

Alternate URLs: https://bio.tools/icelogo

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014607+0000

Ratings and Alerts

No rating or validation information has been found for iceLogo.

No alerts have been found for iceLogo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 164 mentions in open access literature.

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

Tyl MD, et al. (2025) Infection-induced lysine lactylation enables herpesvirus immune evasion. Science advances, 11(2), eads6215.

Wang L, et al. (2025) Serpina3k lactylation protects from cardiac ischemia reperfusion injury. Nature communications, 16(1), 1012.

Wang S, et al. (2024) Amino acid insertion in Bat MHC-I enhances complex stability and augments peptide presentation. Communications biology, 7(1), 586.

Song F, et al. (2024) Cleavage site-directed antibodies reveal the prion protein in humans is shed by ADAM10 at Y226 and associates with misfolded protein deposits in neurodegenerative diseases. Acta neuropathologica, 148(1), 2.

Koch LB, et al. (2024) Rewiring of the phosphoproteome executes two meiotic divisions in budding yeast. The EMBO journal, 43(7), 1351.

Du R, et al. (2024) Sirtuin 1/sirtuin 3 are robust lysine delactylases and sirtuin 1-mediated delactylation regulates glycolysis. iScience, 27(10), 110911.

Gou Y, et al. (2024) GPS-SUMO 2.0: an updated online service for the prediction of SUMOylation sites and SUMO-interacting motifs. Nucleic acids research, 52(W1), W238.

Dong H, et al. (2024) Targeting PRMT9-mediated arginine methylation suppresses cancer stem cell maintenance and elicits cGAS-mediated anticancer immunity. Nature cancer, 5(4), 601.

Madzharova E, et al. (2024) Substrate O-glycosylation actively regulates extracellular proteolysis. Protein science : a publication of the Protein Society, 33(8), e5128.

Walcher S, et al. (2024) Deciphering fucosylated protein-linked O-glycans in oral Tannerella serpentiformis: Insights from NMR spectroscopy and glycoproteomics. Glycobiology, 34(12).

Cai J, et al. (2024) Peptidomic analysis of endogenous and bacterial protease activity in human plasma and wound fluids. iScience, 27(2), 109005.

Celebic D, et al. (2024) Qualitative rather than quantitative phosphoregulation shapes the end of meiosis I in budding yeast. The EMBO journal, 43(7), 1325.

Desai M, et al. (2024) A quest for cytosolic sequons and their functions. Scientific reports, 14(1), 7736.

Wang S, et al. (2024) PTMoreR-enabled cross-species PTM mapping and comparative phosphoproteomics across mammals. Cell reports methods, 4(9), 100859.

Ye T, et al. (2024) Characterization of acidic lysine acylations in mycobacteria. Frontiers in microbiology, 15, 1503184.

Cesar Ramos de Jesus H, et al. (2024) Optimization of quenched fluorescent peptide substrates of SARS-CoV-2 3CLpro main protease (Mpro) from proteomic identification of P6-P6' active site specificity. Journal of virology, 98(6), e0004924.

Liu F, et al. (2024) Acetylome analyses provide novel insights into the effects of chronic intermittent hypoxia on hippocampus-dependent cognitive impairment. Frontiers in molecular neuroscience, 17, 1324458.

Kunová N, et al. (2024) Polyphosphate and tyrosine phosphorylation in the N-terminal domain of the human mitochondrial Lon protease disrupts its functions. Scientific reports, 14(1), 9923.

Qu JH, et al. (2024) Reprogramming of cardiac phosphoproteome, proteome, and transcriptome confers resilience to chronic adenylyl cyclase-driven stress. eLife, 12.

Jiang Z, et al. (2024) Development of subunit selective proteasome substrates for Schistosoma species. bioRxiv : the preprint server for biology.