Resource Summary Report

Generated by RRID on Apr 11, 2025

WEBLOGO

RRID:SCR_010236
Type: Tool

Proper Citation

WEBLOGO (RRID:SCR_010236)

Resource Information

URL: http://weblogo.berkeley.edu

Proper Citation: WEBLOGO (RRID:SCR_010236)

Description: Web application to generate sequence logos, graphical representations of patterns within multiple sequence alignment. Designed to make generation of sequence logos easy. Sequence logo generator.

Synonyms: WebLogo Version 2.8.2, WebLogo3, WebLogo

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

Defining Citation: PMID:15173120

Keywords: Generate sequence logo, pattern graphical representation, multiple sequence alignment, sequence logo generator, amino acid sequence alignment, nucleic acid sequence alignment, sequence alignment representation, bio.tools

Funding: NHGRI K22 HG00056;
Searle Scholars program ;
NIGMS P50 GM62412

Availability: Free, Available for download, Freely available

Resource Name: WEBLOGO

Resource ID: SCR_010236

Alternate IDs: nlx_156853, biotools:weblogo_3

Alternate URLs: http://weblogo.threeplusone.com/, https://bio.tools/weblogo_3

License: MIT Open Source License

Record Creation Time: 20220129T080257+0000

Record Last Update: 20250411T055418+0000

Ratings and Alerts

No rating or validation information has been found for WEBLOGO.

No alerts have been found for WEBLOGO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3355 mentions in open access literature.

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

Seifert-Dávila W, et al. (2025) Structural and kinetic insights into tRNA promoter engagement by yeast general transcription factor TFIIIC. Nucleic acids research, 53(1).

Xiao Q, et al. (2025) Engineered IscB-?RNA system with expanded target range for base editing. Nature chemical biology, 21(1), 100.

Li J, et al. (2025) Genome-Wide Identification and Expression Analysis of bHLH-MYC Family Genes from Mustard That May Be Important in Trichome Formation. Plants (Basel, Switzerland), 14(2).

Liu Q, et al. (2025) RHOBTB2 Variant p.Arg511Gln Causes Developmental and Epileptic Encephalopathy Type 64 in an Infant: A Case Report and Hotspot Variant Analysis. Molecular genetics & genomic medicine, 13(1), e70059.

Knechtel JW, et al. (2025) KMT5C leverages disorder to optimize cooperation with HP1 for heterochromatin retention. EMBO reports, 26(1), 153.

Guillou MC, et al. (2025) Phytocytokine genes newly discovered in Malus domestica and their regulation in response to Erwinia amylovora and acibenzolar-S-methyl. The plant genome, 18(1), e20540.

Renninger KA, et al. (2025) The rise of CLAVATA: evidence for CLAVATA3 and WOX

signaling in the fern gametophyte. The Plant journal : for cell and molecular biology, 121(2), e17207.

Qian C, et al. (2025) Rational design of a triple-type HPV53/56/66 vaccine with one preferable base particle incorporating two identified immunodominant sites. Journal of nanobiotechnology, 23(1), 28.

Huang Y, et al. (2025) A single residue switch mediates the broad neutralization of Rotaviruses. Nature communications, 16(1), 838.

Scribano D, et al. (2025) The periplasmic protein HslJ is the first-line of defense against oxidative stress in Acinetobacter baumannii. Biological research, 58(1), 2.

Knutson BA, et al. (2025) Evolutionary and Structural Insights into the RNA Polymerase I A34 Protein Family: A Focus on Intrinsic Disorder and Phase Separation. Genes, 16(1).

Tong X, et al. (2025) Genome-Wide Characterization of Extrachromosomal Circular DNA in the Midgut of BmCPV-Infected Silkworms and Its Potential Role in Antiviral Responses. International journal of molecular sciences, 26(2).

Ramírez-Montiel FB, et al. (2025) Theoretical Study of Sphingomyelinases from Entamoeba histolytica and Trichomonas vaginalis Sheds Light on the Evolution of Enzymes Needed for Survival and Colonization. Pathogens (Basel, Switzerland), 14(1).

Lyu B, et al. (2025) G-quadruplex structures in 16S rRNA regions correlate with thermal adaptation in prokaryotes. Nucleic acids research, 53(3).

Kamilari E, et al. (2025) Bacillus safensis APC 4099 has broad-spectrum antimicrobial activity against both bacteria and fungi and produces several antimicrobial peptides, including the novel circular bacteriocin safencin E. Applied and environmental microbiology, 91(1), e0194224.

Trasviña-Arenas CH, et al. (2025) Crystal structure of MutYX: A novel clusterless adenine DNA glycosylase with a distinct C-terminal domain and 8-Oxoguanine recognition sphere. bioRxiv : the preprint server for biology.

Németh BZ, et al. (2025) The High-Affinity Chymotrypsin Inhibitor Eglin C Poorly Inhibits Human Chymotrypsin-Like Protease: Gln192 and Lys218 Are Key Determinants. Proteins, 93(2), 543.

Zborowsky S, et al. (2025) Adaptive loss of tRNA gene expression leads to phage resistance in a marine Synechococcus cyanobacterium. Nature microbiology, 10(1), 66.

Gjorgjevikj D, et al. (2025) The Psu protein of phage satellite P4 inhibits transcription termination factor ? by forced hyper-oligomerization. Nature communications, 16(1), 550.

Yang J, et al. (2025) The haemagglutinin gene of bovine-origin H5N1 influenza viruses currently retains receptor-binding and pH-fusion characteristics of avian host phenotype. Emerging microbes & infections, 14(1), 2451052.