

Resource Summary Report

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WEBLOGO

RRID:SCR_010236

Type: Tool

Proper Citation

WEBLOGO (RRID:SCR_010236)

Resource Information

URL: <http://weblogo.berkeley.edu>

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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: data access protocol, service resource, software resource, 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;
NIGMS P50 GM62412;
Searle Scholars program

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: 20260905T132637+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 3980 mentions in open access literature.

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

Stanojcic S, et al. (2026) Stranded short nascent strand sequencing reveals the topology of DNA replication origins in *Trypanosoma brucei*. *eLife*, 14.

Zhang JW, et al. (2026) Phylogenetic Comparison and Splice Site Conservation of the Animal SMNDC1 Gene Family. *Genesis (New York, N.Y. : 2000)*, 64(3), e70054.

Esposito-Verza A, et al. (2026) Molecular requirements for PLK1 activation by T-loop phosphorylation. *The EMBO journal*, 45(5), 1496.

Chorozian K, et al. (2026) Characterization of an AA9 LPMO from *Fusarium oxysporum* and its role in cellulose hydrolysis and functionalization. *Biotechnology for biofuels and bioproducts*, 19(1).

Domanski P, et al. (2026) Origin of class B J-domain proteins involved in amyloid transactions. *Proceedings of the National Academy of Sciences of the United States of America*, 123(2), e2522403123.

Tang ZM, et al. (2026) The crucial but insufficient role of E2s domain's residues 490 and 492 in determining the host tropism of hepatitis E virus. *Nature communications*, 17(1).

Cheng SS, et al. (2026) Small molecule splicing modulators that disrupt O-GlcNAc homeostasis. *Nature communications*, 17(1), 1548.

Xiong C, et al. (2026) Genome-wide identification of AP2/ERF transcription factors in *Populus trichocarpa*: structural analysis, expression patterns, and response to *Melampsora larici-populina*. *BMC plant biology*, 26(1).

Arad D, et al. (2026) Landscape and dynamics of TadA-dependent RNA editing in *Escherichia coli* reveal a role in nutrient-rich growth. *mBio*, 17(5), e0055126.

Liu J, et al. (2026) Epidemiological Survey of Porcine Circovirus Types 2 and 3 in Liaoning Region of China and Preparation of Monoclonal Antibodies Against PCV3 Cap Protein. *Veterinary sciences*, 13(3).

Zhong L, et al. (2026) Mechanistic insights into substrate-targeting modification effects on interfacial kinetics of raw starch-degrading amylases. *Applied and environmental microbiology*, 92(5), e0190825.

Wu SY, et al. (2026) A host-derived volatile primes context-dependent foraging behavior in parasitic nematodes via a lysosome-associated neural pathway. *Proceedings of the National Academy of Sciences of the United States of America*, 123(8), e2520778123.

Shi LD, et al. (2026) Reduced methane emissions in transgenic rice genotypes are associated with altered rhizosphere microbial hydrogen cycling. *Nature communications*, 17(1).

Unlu I, et al. (2026) High-throughput analyses of a reconstituted diversity-generating retroelement identify intrinsic and extrinsic determinants of diversification. *PLoS genetics*, 22(2), e1012038.

Zhao T, et al. (2026) A tandem recruitment site in the pseudokinase scaffold PEAK3 is subject to phosphorylation-dependent regulation and cancer-associated mutations. *The Journal of biological chemistry*, 302(5), 111365.

Zhao F, et al. (2026) Identification of a novel N-terminal linear B-cell epitope on the FIPV nucleocapsid protein by a monoclonal antibody. *BMC veterinary research*, 22(1).

Singh J, et al. (2026) Structure of a Stand-Alone Homodimeric NRPS Condensation Domain Reveals Occlusion of the Canonical Carrier-Protein Interface. *bioRxiv : the preprint server for biology*.

Gao A, et al. (2026) Structural basis of QueC-family protein function in qatABCD anti-phage defense. *Nature communications*, 17(1).

Yeh YH, et al. (2026) A standardized toolkit for programmable protein secretion and surface display in *Bacteroides thetaiotaomicron*. *bioRxiv : the preprint server for biology*.

Lim S, et al. (2026) Compensatory evolution facilitates loss of prfB autoregulation in *Pseudomonas fluorescens* SBW25. *Molecular biology and evolution*, 43(6).