

# WebLogo: A Sequence Logo Generator

Genome Research

14, 1188-1190

DOI: [10.1101/gr.849004](https://doi.org/10.1101/gr.849004)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Amidase domains from bacterial and phage autolysins define a family of $\hat{1}^3$ -d,l-glutamate-specific amidohydrolases. <i>Trends in Biochemical Sciences</i> , 2003, 28, 230-234.	3.7	138
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5	SpliceInfo: an information repository for mRNA alternative splicing in human genome. <i>Nucleic Acids Research</i> , 2004, 33, D80-D85.	6.5	27
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1919	Vipp1: a very important protein in plastids?!. <i>Journal of Experimental Botany</i> , 2012, 63, 1699-1712.	2.4	97
1920	Genome-Wide Analysis of Stowaway-Like MITEs in Wheat Reveals High Sequence Conservation, Gene Association, and Genomic Diversification. <i>Plant Physiology</i> , 2012, 161, 486-496.	2.3	29
1921	Molecular Evolution of Translin Superfamily Proteins Within the Genomes of Eubacteria, Archaea and Eukaryotes. <i>Journal of Molecular Evolution</i> , 2012, 75, 155-167.	0.8	14
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1923	Cuticular Proteins. , 2012, , 134-166.		33
1924	Epi-letters - how to describe epigenetic signatures. <i>BMC Bioinformatics</i> , 2012, 13, .	1.2	1
1925	Genome-wide annotation and analysis of zebra finch microRNA repertoire reveal sex-biased expression. <i>BMC Genomics</i> , 2012, 13, 727.	1.2	39
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1934	Proteomics Strategy to Identify Substrates of LNX, a PDZ Domain-containing E3 Ubiquitin Ligase. <i>Journal of Proteome Research</i> , 2012, 11, 4847-4862.	1.8	29
1935	Mar, a MITE family of hAT transposons in <i>Drosophila</i> . <i>Mobile DNA</i> , 2012, 3, 13.	1.3	27

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1950	CCCH-Type Zinc Finger Family in Maize: Genome-Wide Identification, Classification and Expression Profiling under Abscisic Acid and Drought Treatments. <i>PLoS ONE</i> , 2012, 7, e40120.	1.1	140
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1980	Determination of ribonuclease sequence-specificity using Pentaproboscids and mass spectrometry. <i>Rna</i> , 2012, 18, 1267-1278.	1.6	39
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1991	Regulation and Evolution of Malonate and Propionate Catabolism in Proteobacteria. <i>Journal of Bacteriology</i> , 2012, 194, 3234-3240.	1.0	42
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2055	The Papillomavirus E2 proteins. <i>Virology</i> , 2013, 445, 57-79.	1.1	314
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2059	Structural basis of FliG-FliM interaction in <i>Helicobacter pylori</i> . <i>Molecular Microbiology</i> , 2013, 88, 798-812.	1.2	38
2060	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. <i>Nature</i> , 2013, 500, 350-353.	13.7	466
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5365	Identification of evolutionarily conserved downstream core promoter elements required for the transcriptional regulation of Fushi tarazu target genes. <i>PLoS ONE</i> , 2019, 14, e0215695.	1.1	11
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6200	Prevalence and significance of the commonest phosphorylated motifs in the human proteome: a global analysis. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 5281-5298.	2.4	13
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6211	The round goby genome provides insights into mechanisms that may facilitate biological invasions. <i>BMC Biology</i> , 2020, 18, 11.	1.7	32
6212	Impact of posttranslational modifications on atomistic structure of fibrinogen. <i>PLoS ONE</i> , 2020, 15, e0227543.	1.1	16
6213	Structural Analysis of Rabies Virus Glycoprotein Reveals pH-Dependent Conformational Changes and Interactions with a Neutralizing Antibody. <i>Cell Host and Microbe</i> , 2020, 27, 441-453.e7.	5.1	49
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6230	Genome-wide analysis reveals a regulatory role for G-quadruplexes during Adenovirus multiplication. <i>Virus Research</i> , 2020, 283, 197960.	1.1	21
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