

Desmond G Higgins

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

91,592
citations

257450

24
h-index

414414

32
g-index

33
all docs

33
docs citations

33
times ranked

90190
citing authors

#	ARTICLE	IF	CITATIONS
1	CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. <i>Nucleic Acids Research</i> , 1994, 22, 4673-4680.	14.5	59,168
2	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011, 7, 539.	7.2	12,778
3	T-coffee: a novel method for fast and accurate multiple sequence alignment 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2000, 302, 205-217.	4.2	6,404
4	Multiple sequence alignment with the Clustal series of programs. <i>Nucleic Acids Research</i> , 2003, 31, 3497-3500.	14.5	4,221
5	CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. <i>Gene</i> , 1988, 73, 237-244.	2.2	3,454
6	CLUSTAL V: improved software for multiple sequence alignment. <i>Bioinformatics</i> , 1992, 8, 189-191.	4.1	1,479
7	Clustal Omega for making accurate alignments of many protein sequences. <i>Protein Science</i> , 2018, 27, 135-145.	7.6	1,286
8	Clustal Omega, Accurate Alignment of Very Large Numbers of Sequences. <i>Methods in Molecular Biology</i> , 2014, 1079, 105-116.	0.9	980
9	Clustal Omega. <i>Current Protocols in Bioinformatics</i> , 2014, 48, 3.13.1-16.	25.8	461
10	Clustal V: Multiple Alignment of DNA and Protein Sequences. , 1994, 25, 307-318.		255
11	The Clustal Omega Multiple Alignment Package. <i>Methods in Molecular Biology</i> , 2021, 2231, 3-16.	0.9	144
12	Multiple Origins of the Pathogenic Yeast <i>Candida orthopsilosis</i> by Separate Hybridizations between Two Parental Species. <i>PLoS Genetics</i> , 2016, 12, e1006404.	3.5	125
13	Comparative Phenotypic Analysis of the Major Fungal Pathogens <i>Candida parapsilosis</i> and <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004365.	4.7	108
14	Sequence embedding for fast construction of guide trees for multiple sequence alignment. <i>Algorithms for Molecular Biology</i> , 2010, 5, 21.	1.2	94
15	Influence of acute phytochemical intake on human urinary metabolomic profiles. <i>American Journal of Clinical Nutrition</i> , 2007, 86, 1687-1693.	4.7	88
16	Identification of fungi in shotgun metagenomics datasets. <i>PLoS ONE</i> , 2018, 13, e0192898.	2.5	83
17	ProVizâ€”a web-based visualization tool to investigate the functional and evolutionary features of protein sequences. <i>Nucleic Acids Research</i> , 2016, 44, W11-W15.	14.5	68
18	Making automated multiple alignments of very large numbers of protein sequences. <i>Bioinformatics</i> , 2013, 29, 989-995.	4.1	49

#	ARTICLE	IF	CITATIONS
19	OD-seq: outlier detection in multiple sequence alignments. BMC Bioinformatics, 2015, 16, 269.	2.6	42
20	Simple chained guide trees give high-quality protein multiple sequence alignments. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10556-10561.	7.1	36
21	An Integrated Global Analysis of Compartmentalized HRAS Signaling. Cell Reports, 2019, 26, 3100-3115.e7.	6.4	36
22	Protein multiple sequence alignment benchmarking through secondary structure prediction. Bioinformatics, 2017, 33, 1331-1337.	4.1	35
23	TPP riboswitch-dependent regulation of an ancient thiamin transporter in Candida. PLoS Genetics, 2018, 14, e1007429.	3.5	29
24	Systematic exploration of guide-tree topology effects for small protein alignments. BMC Bioinformatics, 2014, 15, 338.	2.6	27
25	Loss of Olfactory Receptor Function in Hominin Evolution. PLoS ONE, 2014, 9, e84714.	2.5	26
26	Prolyl hydroxylase-1 regulates hepatocyte apoptosis in an NF- κ B-dependent manner. Biochemical and Biophysical Research Communications, 2016, 474, 579-586.	2.1	26
27	Instability in progressive multiple sequence alignment algorithms. Algorithms for Molecular Biology, 2015, 10, 26.	1.2	20
28	Using <i>de novo</i> protein structure predictions to measure the quality of very large multiple sequence alignments. Bioinformatics, 2016, 32, 814-820.	4.1	19
29	QuanTest2: benchmarking multiple sequence alignments using secondary structure prediction. Bioinformatics, 2020, 36, 90-95.	4.1	14
30	Measuring Transcription Rate Changes via Time-Course 4-Thiouridine Pulse-Labeling Improves Transcriptional Target Identification. Journal of Molecular Biology, 2015, 427, 3368-3374.	4.2	13
31	Identification of Non-Coding RNAs in the Candida parapsilosis Species Group. PLoS ONE, 2016, 11, e0163235.	2.5	11
32	Reply to Tan et al.: Differences between real and simulated proteins in multiple sequence alignments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E101-E101.	7.1	8
33	MyD88 is an essential component of retinoic acid-induced differentiation in human pluripotent embryonal carcinoma cells. Cell Death and Differentiation, 2017, 24, 1975-1986.	11.2	5