

Desmond G Higgins

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

33
papers

76,839
citations

21
h-index

33
g-index

33
ext. papers

84,292
ext. citations

7.5
avg, IF

7.93
L-index

#	Paper	IF	Citations
33	The Clustal Omega Multiple Alignment Package. <i>Methods in Molecular Biology</i> , 2021 , 2231, 3-16	1.4	31
32	QuanTest2: benchmarking multiple sequence alignments using secondary structure prediction. <i>Bioinformatics</i> , 2020 , 36, 90-95	7.2	5
31	An Integrated Global Analysis of Compartmentalized HRAS Signaling. <i>Cell Reports</i> , 2019 , 26, 3100-3115. e7.6	7.6	22
30	Clustal Omega for making accurate alignments of many protein sequences. <i>Protein Science</i> , 2018 , 27, 135-145	6.3	623
29	TPP riboswitch-dependent regulation of an ancient thiamin transporter in <i>Candida</i> . <i>PLoS Genetics</i> , 2018 , 14, e1007429	6	16
28	Identification of fungi in shotgun metagenomics datasets. <i>PLoS ONE</i> , 2018 , 13, e0192898	3.7	45
27	Protein multiple sequence alignment benchmarking through secondary structure prediction. <i>Bioinformatics</i> , 2017 , 33, 1331-1337	7.2	17
26	MyD88 is an essential component of retinoic acid-induced differentiation in human pluripotent embryonal carcinoma cells. <i>Cell Death and Differentiation</i> , 2017 , 24, 1975-1986	12.7	2
25	ProViz-a web-based visualization tool to investigate the functional and evolutionary features of protein sequences. <i>Nucleic Acids Research</i> , 2016 , 44, W11-5	20.1	44
24	Using de novo protein structure predictions to measure the quality of very large multiple sequence alignments. <i>Bioinformatics</i> , 2016 , 32, 814-20	7.2	15
23	Multiple Origins of the Pathogenic Yeast <i>Candida orthopsilosis</i> by Separate Hybridizations between Two Parental Species. <i>PLoS Genetics</i> , 2016 , 12, e1006404	6	51
22	Identification of Non-Coding RNAs in the <i>Candida parapsilosis</i> Species Group. <i>PLoS ONE</i> , 2016 , 11, e0163375	3.7	8
21	Prolyl hydroxylase-1 regulates hepatocyte apoptosis in an NF- κ B-dependent manner. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 474, 579-586	3.4	21
20	Measuring Transcription Rate Changes via Time-Course 4-Thiouridine Pulse-Labeling Improves Transcriptional Target Identification. <i>Journal of Molecular Biology</i> , 2015 , 427, 3368-74	6.5	11
19	Instability in progressive multiple sequence alignment algorithms. <i>Algorithms for Molecular Biology</i> , 2015 , 10, 26	1.8	13
18	OD-seq: outlier detection in multiple sequence alignments. <i>BMC Bioinformatics</i> , 2015 , 16, 269	3.6	26
17	Reply to Tan et al.: Differences between real and simulated proteins in multiple sequence alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E101	11.5	8

16	Loss of olfactory receptor function in hominin evolution. <i>PLoS ONE</i> , 2014 , 9, e84714	3.7	19
15	Systematic exploration of guide-tree topology effects for small protein alignments. <i>BMC Bioinformatics</i> , 2014 , 15, 338	3.6	10
14	Comparative phenotypic analysis of the major fungal pathogens <i>Candida parapsilosis</i> and <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2014 , 10, e1004365	7.6	80
13	Simple chained guide trees give high-quality protein multiple sequence alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10556-61	11.5	28
12	Clustal omega. <i>Current Protocols in Bioinformatics</i> , 2014 , 48, 3.13.1-16	24.2	267
11	Clustal Omega, accurate alignment of very large numbers of sequences. <i>Methods in Molecular Biology</i> , 2014 , 1079, 105-16	1.4	681
10	Making automated multiple alignments of very large numbers of protein sequences. <i>Bioinformatics</i> , 2013 , 29, 989-95	7.2	40
9	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011 , 7, 539	12.2	8587
8	Sequence embedding for fast construction of guide trees for multiple sequence alignment. <i>Algorithms for Molecular Biology</i> , 2010 , 5, 21	1.8	74
7	Influence of acute phytochemical intake on human urinary metabolomic profiles. <i>American Journal of Clinical Nutrition</i> , 2007 , 86, 1687-1693	7	85
6	Multiple sequence alignment with the Clustal series of programs. <i>Nucleic Acids Research</i> , 2003 , 31, 3497-500	500	3757
5	T-Coffee: A novel method for fast and accurate multiple sequence alignment. <i>Journal of Molecular Biology</i> , 2000 , 302, 205-17	6.5	5330
4	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, 4673-80	20.1	52822
3	CLUSTAL V: multiple alignment of DNA and protein sequences. <i>Methods in Molecular Biology</i> , 1994 , 25, 307-18	1.4	215
2	CLUSTAL V: improved software for multiple sequence alignment. <i>Bioinformatics</i> , 1992 , 8, 189-91	7.2	841
1	CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. <i>Gene</i> , 1988 , 73, 237-44	3.8	3045