

# Desmond G Higgins

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

91,592  
citations

293460

24  
h-index

466096

32  
g-index

33  
all docs

33  
docs citations

33  
times ranked

99720  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Clustal Omega Multiple Alignment Package. <i>Methods in Molecular Biology</i> , 2021, 2231, 3-16.	0.4	144
2	QuanTest2: benchmarking multiple sequence alignments using secondary structure prediction. <i>Bioinformatics</i> , 2020, 36, 90-95.	1.8	14
3	An Integrated Global Analysis of Compartmentalized HRAS Signaling. <i>Cell Reports</i> , 2019, 26, 3100-3115.e7.	2.9	36
4	Clustal Omega for making accurate alignments of many protein sequences. <i>Protein Science</i> , 2018, 27, 135-145.	3.1	1,286
5	TPP riboswitch-dependent regulation of an ancient thiamin transporter in <i>Candida</i> . <i>PLoS Genetics</i> , 2018, 14, e1007429.	1.5	29
6	Identification of fungi in shotgun metagenomics datasets. <i>PLoS ONE</i> , 2018, 13, e0192898.	1.1	83
7	Protein multiple sequence alignment benchmarking through secondary structure prediction. <i>Bioinformatics</i> , 2017, 33, 1331-1337.	1.8	35
8	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.	5.0	5
9	Multiple Origins of the Pathogenic Yeast <i>Candida orthopsilosis</i> by Separate Hybridizations between Two Parental Species. <i>PLoS Genetics</i> , 2016, 12, e1006404.	1.5	125
10	Identification of Non-Coding RNAs in the <i>Candida parapsilosis</i> Species Group. <i>PLoS ONE</i> , 2016, 11, e0163235.	1.1	11
11	Prolyl hydroxylase-1 regulates hepatocyte apoptosis in an NF- $\kappa$ B-dependent manner. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 579-586.	1.0	26
12	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.	6.5	68
13	Using <i>de novo</i> protein structure predictions to measure the quality of very large multiple sequence alignments. <i>Bioinformatics</i> , 2016, 32, 814-820.	1.8	19
14	OD-seq: outlier detection in multiple sequence alignments. <i>BMC Bioinformatics</i> , 2015, 16, 269.	1.2	42
15	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-E101.	3.3	8
16	Measuring Transcription Rate Changes via Time-Course 4-Thiouridine Pulse-Labeling Improves Transcriptional Target Identification. <i>Journal of Molecular Biology</i> , 2015, 427, 3368-3374.	2.0	13
17	Instability in progressive multiple sequence alignment algorithms. <i>Algorithms for Molecular Biology</i> , 2015, 10, 26.	0.3	20
18	Loss of Olfactory Receptor Function in Hominin Evolution. <i>PLoS ONE</i> , 2014, 9, e84714.	1.1	26

#	ARTICLE	IF	CITATIONS
19	Systematic exploration of guide-tree topology effects for small protein alignments. BMC Bioinformatics, 2014, 15, 338.	1.2	27
20	Comparative Phenotypic Analysis of the Major Fungal Pathogens <i>Candida parapsilosis</i> and <i>Candida albicans</i> . PLoS Pathogens, 2014, 10, e1004365.	2.1	108
21	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.	3.3	36
22	Clustal Omega. Current Protocols in Bioinformatics, 2014, 48, 3.13.1-16.	25.8	461
23	Clustal Omega, Accurate Alignment of Very Large Numbers of Sequences. Methods in Molecular Biology, 2014, 1079, 105-116.	0.4	980
24	Making automated multiple alignments of very large numbers of protein sequences. Bioinformatics, 2013, 29, 989-995.	1.8	49
25	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Molecular Systems Biology, 2011, 7, 539.	3.2	12,778
26	Sequence embedding for fast construction of guide trees for multiple sequence alignment. Algorithms for Molecular Biology, 2010, 5, 21.	0.3	94
27	Influence of acute phytochemical intake on human urinary metabolomic profiles. American Journal of Clinical Nutrition, 2007, 86, 1687-1693.	2.2	88
28	Multiple sequence alignment with the Clustal series of programs. Nucleic Acids Research, 2003, 31, 3497-3500.	6.5	4,221
29	T-coffee: a novel method for fast and accurate multiple sequence alignment 1 Edited by J. Thornton. Journal of Molecular Biology, 2000, 302, 205-217.	2.0	6,404
30	CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research, 1994, 22, 4673-4680.	6.5	59,168
31	Clustal V: Multiple Alignment of DNA and Protein Sequences. , 1994, 25, 307-318.		255
32	CLUSTAL V: improved software for multiple sequence alignment. Bioinformatics, 1992, 8, 189-191.	1.8	1,479
33	CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. Gene, 1988, 73, 237-244.	1.0	3,454