

Fabian Sievers

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

16,039
citations

623188

14
h-index

887659

17
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17
all docs

17
docs citations

17
times ranked

32217
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011, 7, 539.	3.2	12,778
2	Clustal Omega for making accurate alignments of many protein sequences. <i>Protein Science</i> , 2018, 27, 135-145.	3.1	1,286
3	Clustal Omega, Accurate Alignment of Very Large Numbers of Sequences. <i>Methods in Molecular Biology</i> , 2014, 1079, 105-116.	0.4	980
4	Clustal Omega. <i>Current Protocols in Bioinformatics</i> , 2014, 48, 3.13.1-16.	25.8	461
5	The Clustal Omega Multiple Alignment Package. <i>Methods in Molecular Biology</i> , 2021, 2231, 3-16.	0.4	144
6	Sequence embedding for fast construction of guide trees for multiple sequence alignment. <i>Algorithms for Molecular Biology</i> , 2010, 5, 21.	0.3	94
7	Making automated multiple alignments of very large numbers of protein sequences. <i>Bioinformatics</i> , 2013, 29, 989-995.	1.8	49
8	OD-seq: outlier detection in multiple sequence alignments. <i>BMC Bioinformatics</i> , 2015, 16, 269.	1.2	42
9	A Complete Analysis of HA and NA Genes of Influenza A Viruses. <i>PLoS ONE</i> , 2010, 5, e14454.	1.1	38
10	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, 10556-10561.	3.3	36
11	Protein multiple sequence alignment benchmarking through secondary structure prediction. <i>Bioinformatics</i> , 2017, 33, 1331-1337.	1.8	35
12	Systematic exploration of guide-tree topology effects for small protein alignments. <i>BMC Bioinformatics</i> , 2014, 15, 338.	1.2	27
13	Instability in progressive multiple sequence alignment algorithms. <i>Algorithms for Molecular Biology</i> , 2015, 10, 26.	0.3	20
14	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
15	QuanTest2: benchmarking multiple sequence alignments using secondary structure prediction. <i>Bioinformatics</i> , 2020, 36, 90-95.	1.8	14
16	Haplotype frequency estimation error analysis in the presence of missing genotype data. <i>BMC Bioinformatics</i> , 2004, 5, 188.	1.2	8
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-E101.	3.3	8