

# Simon Whelan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11699064/publications.pdf>

Version: 2024-02-01

33  
papers

15,434  
citations

361296

20  
h-index

434063

31  
g-index

34  
all docs

34  
docs citations

34  
times ranked

22025  
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated Removal of Non-homologous Sequence Stretches with PREQUAL. <i>Methods in Molecular Biology</i> , 2021, 2231, 147-162.	0.4	0
2	Identifying Clusters of High Confidence Homologies in Multiple Sequence Alignments. <i>Molecular Biology and Evolution</i> , 2019, 36, 2340-2351.	3.5	108
3	Physicochemical Amino Acid Properties Better Describe Substitution Rates in Large Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 679-690.	3.5	20
4	PREQUAL: detecting non-homologous characters in sets of unaligned homologous sequences. <i>Bioinformatics</i> , 2018, 34, 3929-3930.	1.8	96
5	Inferring Trees. <i>Methods in Molecular Biology</i> , 2017, 1525, 349-377.	0.4	5
6	Phylogenetic Tree Estimation With and Without Alignment: New Distance Methods and Benchmarking. <i>Systematic Biology</i> , 2016, 66, syw074.	2.7	17
7	ModelOMatic: Fast and Automated Model Selection between RY, Nucleotide, Amino Acid, and Codon Substitution Models. <i>Systematic Biology</i> , 2015, 64, 42-55.	2.7	68
8	GeLL: a generalized likelihood library for phylogenetic models: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2391-2393.	1.8	0
9	Evidence of Statistical Inconsistency of Phylogenetic Methods in the Presence of Multiple Sequence Alignment Uncertainty. <i>Genome Biology and Evolution</i> , 2015, 7, 2102-2116.	1.1	17
10	Covariation Is a Poor Measure of Molecular Coevolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 2456-2468.	3.5	49
11	Assessing the State of Substitution Models Describing Noncoding RNA Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 65-75.	1.1	18
12	Impact of deep coalescence and recombination on the estimation of phylogenetic relationships among species using AFLP markers. <i>Molecular Phylogenetics and Evolution</i> , 2014, 76, 102-109.	1.2	3
13	Class of Multiple Sequence Alignment Algorithm Affects Genomic Analysis. <i>Molecular Biology and Evolution</i> , 2013, 30, 642-653.	3.5	61
14	Characterizing the Phylogenetic Tree-Search Problem. <i>Systematic Biology</i> , 2012, 61, 228.	2.7	23
15	Measuring the distance between multiple sequence alignments. <i>Bioinformatics</i> , 2012, 28, 495-502.	1.8	86
16	Phylogenetic Substitution Models for Detecting Heterotachy during Plastid Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 449-458.	3.5	17
17	Inferring Trees. <i>Methods in Molecular Biology</i> , 2008, 452, 287-309.	0.4	13
18	Determination and validation of principal gene products. <i>Bioinformatics</i> , 2008, 24, 11-17.	1.8	23

#	ARTICLE	IF	CITATIONS
19	The genetic code can cause systematic bias in simple phylogenetic models. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 4003-4011.	1.8	11
20	Spatial and Temporal Heterogeneity in Nucleotide Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2008, 25, 1683-1694.	3.5	36
21	New Approaches to Phylogenetic Tree Search and Their Application to Large Numbers of Protein Alignments. <i>Systematic Biology</i> , 2007, 56, 727-740.	2.7	30
22	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
23	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
24	Statistical Methods in Molecular Evolution. <i>Systematic Biology</i> , 2006, 55, 698-700.	2.7	26
25	Phylogenetics by likelihood: Evolutionary modeling as a tool for understanding the genome. <i>Journal of Biomedical Informatics</i> , 2006, 39, 51-61.	2.5	27
26	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. <i>Nucleic Acids Research</i> , 2006, 34, D327-D331.	6.5	59
27	Estimating the Frequency of Events That Cause Multiple-Nucleotide Changes. <i>Genetics</i> , 2004, 167, 2027-2043.	1.2	81
28	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	2.4	263
29	Pandit: a database of protein and associated nucleotide domains with inferred trees. <i>Bioinformatics</i> , 2003, 19, 1556-1563.	1.8	44
30	A Novel Use of Equilibrium Frequencies in Models of Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2002, 19, 1821-1831.	3.5	46
31	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
32	Molecular phylogenetics: state-of-the-art methods for looking into the past. <i>Trends in Genetics</i> , 2001, 17, 262-272.	2.9	376
33	A General Empirical Model of Protein Evolution Derived from Multiple Protein Families Using a Maximum-Likelihood Approach. <i>Molecular Biology and Evolution</i> , 2001, 18, 691-699.	3.5	2,599