Steven Weaver

List of Publications by Year
in descending order

22 papers	5,940 citations	471371 17 h-index	713332 21 g-index
29 all docs	29 docs citations	29 times ranked	9380 citing authors

#	Article	IF	Citations
1	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	5.8	101
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	13.7	1,210
3	TopHap: rapid inference of key phylogenetic structures from common haplotypes in large genome collections with limited diversity. Bioinformatics, 2022, 38, 2719-2726.	1.8	7
4	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular Biology and Evolution, 2022, 39, .	3.5	84
5	Contrast-FEL—A Test for Differences in Selective Pressures at Individual Sites among Clades and Sets of Branches. Molecular Biology and Evolution, 2021, 38, 1184-1198.	3.5	33
6	Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes. PLoS ONE, 2021, 16, e0248337.	1.1	13
7	Detection of a SARS-CoV-2 variant of concern in South Africa. Nature, 2021, 592, 438-443.	13.7	1,381
8	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. PLoS Biology, 2021, 19, e3001115.	2.6	172
9	An Evolutionary Portrait of the Progenitor SARS-CoV-2 and Its Dominant Offshoots in COVID-19 Pandemic. Molecular Biology and Evolution, 2021, 38, 3046-3059.	3.5	54
10	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	13.5	186
11	Characteristics and growth of the genetic HIV transmission network of Mexico City during 2020. Journal of the International AIDS Society, 2021, 24, e25836.	1.2	7
12	HyPhy 2.5—A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. Molecular Biology and Evolution, 2020, 37, 295-299.	3.5	342
13	No more business as usual: Agile and effective responses to emerging pathogen threats require open data and open analytics. PLoS Pathogens, 2020, 16, e1008643.	2.1	22
14	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2019, 1910, 427-468.	0.4	48
15	HIV-TRACE (TRAnsmission Cluster Engine): a Tool for Large Scale Molecular Epidemiology of HIV-1 and Other Rapidly Evolving Pathogens. Molecular Biology and Evolution, 2018, 35, 1812-1819.	3.5	206
16	Datamonkey 2.0: A Modern Web Application for Characterizing Selective and Other Evolutionary Processes. Molecular Biology and Evolution, 2018, 35, 773-777.	3.5	643
17	Full-Length Envelope Analyzer (FLEA): A tool for longitudinal analysis of viral amplicons. PLoS Computational Biology, 2018, 14, e1006498.	1.5	5
18	phylotree.js - a JavaScript library for application development and interactive data visualization in phylogenetics. BMC Bioinformatics, 2018, 19, 276.	1.2	40

#	Article	IF	Citations
19	Less Is More: An Adaptive Branch-Site Random Effects Model for Efficient Detection of Episodic Diversifying Selection. Molecular Biology and Evolution, 2015, 32, 1342-1353.	3.5	631
20	Gene-Wide Identification of Episodic Selection. Molecular Biology and Evolution, 2015, 32, 1365-1371.	3.5	493
21	IDEPI: Rapid Prediction of HIV-1 Antibody Epitopes and Other Phenotypic Features from Sequence Data Using a Flexible Machine Learning Platform. PLoS Computational Biology, 2014, 10, e1003842.	1.5	24
22	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 0, , .	13.7	61