

Filip Bielejec

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11935792/publications.pdf>

Version: 2024-02-01

11
papers

1,940
citations

932766

10
h-index

1281420

11
g-index

13
all docs

13
docs citations

13
times ranked

3683
citing authors

#	ARTICLE	IF	CITATIONS
1	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
2	SpredD3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	3.5	413
3	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016, 2, vew023.	2.2	13
4	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016, 2, e000057.	1.0	4
5	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	2.8	146
6	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015, 1, vev016.	2.2	59
7	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	2.1	330
8	Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography. <i>Systematic Biology</i> , 2014, 63, 493-504.	2.7	75
9	ĪEBUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014, 15, 133.	1.2	22
10	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. <i>Bioinformatics</i> , 2012, 28, 3248-3256.	1.8	75
11	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011, 27, 2910-2912.	1.8	451