

# 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

933447

10  
h-index

1281871

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.	27.8	346
2	SpredD3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	8.9	413
3	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016, 2, vew023.	4.9	13
4	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016, 2, e000057.	2.0	4
5	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	6.0	146
6	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015, 1, vev016.	4.9	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.	4.7	330
8	Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography. <i>Systematic Biology</i> , 2014, 63, 493-504.	5.6	75
9	€BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014, 15, 133.	2.6	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.	4.1	75
11	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011, 27, 2910-2912.	4.1	451