

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

63 papers	2,777 citations	23 h-index	52 g-index
76 ext. papers	3,860 ext. citations	7.6 avg, IF	5.71 L-index

#	Paper	IF	Citations
63	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020 , 368,	33.3	1366
62	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing		132
61	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021 , 372,	33.3	110
60	Genome-wide footprints of pig domestication and selection revealed through massive parallel sequencing of pooled DNA. <i>PLoS ONE</i> , 2011 , 6, e14782	3.7	103
59	Population genomics from pool sequencing. <i>Molecular Ecology</i> , 2013 , 22, 5561-76	5.7	82
58	Non-Abelian duality from vortex moduli: A dual model of color-confinement. <i>Nuclear Physics B</i> , 2007 , 780, 161-187	2.8	60
57	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021 , 594, 408-412	50.4	57
56	Evolution of recombination in eutherian mammals: insights into mechanisms that affect recombination rates and crossover interference. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013 , 280, 20131945	4.4	54
55	The timing of COVID-19 transmission		48
54	SNP calling by sequencing pooled samples. <i>BMC Bioinformatics</i> , 2012 , 13, 239	3.6	47
53	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013 , 14, 148	4.5	40
52	Massive parallel sequencing in animal genetics: wherefroms and wheretos. <i>Animal Genetics</i> , 2010 , 41, 561-9	2.5	37
51	Epidemiological changes on the Isle of Wight after the launch of the NHS Test and Trace programme: a preliminary analysis. <i>The Lancet Digital Health</i> , 2020 , 2, e658-e666	14.4	34
50	Measuring epistasis in fitness landscapes: The correlation of fitness effects of mutations. <i>Journal of Theoretical Biology</i> , 2016 , 396, 132-43	2.3	34
49	Preferential attachment in growing spatial networks. <i>Physical Review E</i> , 2011 , 84, 016103	2.4	32
48	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021 , 27, 361-362	50.5	32
47	Nucleotide variability at its limit? Insights into the number and evolutionary dynamics of the sex-determining specificities of the honey bee <i>Apis mellifera</i> . <i>Molecular Biology and Evolution</i> , 2014 , 31, 272-87	8.3	28

46	R-symmetry breaking, runaway directions and global symmetries in O’Raifeartaigh models. <i>Journal of High Energy Physics</i> , 2007 , 2007, 064-064	5.4	28
45	OpenABM-Covid19-An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. <i>PLoS Computational Biology</i> , 2021 , 17, e1009146	5	28
44	Neutrality tests for sequences with missing data. <i>Genetics</i> , 2012 , 191, 1397-401	4	25
43	Dosage Compensation in the African Malaria Mosquito <i>Anopheles gambiae</i> . <i>Genome Biology and Evolution</i> , 2016 , 8, 411-25	3.9	25
42	A model of substitution trajectories in sequence space and long-term protein evolution. <i>Molecular Biology and Evolution</i> , 2015 , 32, 542-54	8.3	24
41	Optimal neutrality tests based on the frequency spectrum. <i>Genetics</i> , 2010 , 186, 353-65	4	23
40	OpenABM-Covid19 - an agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing		22
39	Phase diagram of the Bose-Hubbard model on complex networks. <i>Europhysics Letters</i> , 2012 , 99, 18001	1.6	21
38	Flavour from accidental symmetries. <i>Journal of High Energy Physics</i> , 2006 , 2006, 078-078	5.4	20
37	Decomposing the Site Frequency Spectrum: The Impact of Tree Topology on Neutrality Tests. <i>Genetics</i> , 2017 , 207, 229-240	4	19
36	Evolutionary and functional impact of common polymorphic inversions in the human genome. <i>Nature Communications</i> , 2019 , 10, 4222	17.4	18
35	Universality Classes of Interaction Structures for NK Fitness Landscapes. <i>Journal of Statistical Physics</i> , 2018 , 172, 226-278	1.5	16
34	Within-Host Recombination in the Foot-and-Mouth Disease Virus Genome. <i>Viruses</i> , 2018 , 10,	6.2	16
33	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011 , 107, 256-64	3.6	15
32	The Timing of COVID-19 Transmission. <i>SSRN Electronic Journal</i> ,	1	14
31	Beyond fruit-flies: population genomic advances in non-Drosophila arthropods. <i>Briefings in Functional Genomics</i> , 2015 , 14, 424-31	4.9	12
30	Evolutionary constraints in fitness landscapes. <i>Heredity</i> , 2018 , 121, 466-481	3.6	12
29	Persistent Infection of African Buffalo (<i>Syncerus caffer</i>) with Foot-and-Mouth Disease Virus: Limited Viral Evolution and No Evidence of Antibody Neutralization Escape. <i>Journal of Virology</i> , 2019 , 93,	6.6	11

28	Condensation and topological phase transitions in a dynamical network model with rewiring of the links. <i>Physical Review E</i> , 2014 , 89, 042810	2.4	11
27	Non-neutral theory of biodiversity. <i>Europhysics Letters</i> , 2009 , 87, 28001	1.6	11
26	Dynamics of condensation in growing complex networks. <i>Physical Review E</i> , 2008 , 78, 056102	2.4	11
25	Features and heterogeneities in growing network models. <i>Physical Review E</i> , 2012 , 85, 066110	2.4	10
24	The effect of single recombination events on coalescent tree height and shape. <i>PLoS ONE</i> , 2013 , 8, e60137	3.7	9
23	Femaleless Controls Sex Determination and Dosage Compensation Pathways in Females of Anopheles Mosquitoes. <i>Current Biology</i> , 2021 , 31, 1084-1091.e4	6.3	8
22	The neutral frequency spectrum of linked sites. <i>Theoretical Population Biology</i> , 2018 , 123, 70-79	1.2	7
21	SiNPLE: Fast and Sensitive Variant Calling for Deep Sequencing Data. <i>Genes</i> , 2019 , 10,	4.2	7
20	Duality between preferential attachment and static networks on hyperbolic spaces. <i>Europhysics Letters</i> , 2014 , 105, 38001	1.6	6
19	PRDM9 Diversity at Fine Geographical Scale Reveals Contrasting Evolutionary Patterns and Functional Constraints in Natural Populations of House Mice. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1686-1700	8.3	5
18	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
17	Pervasive within-host recombination and epistasis as major determinants of the molecular evolution of the foot-and-mouth disease virus capsid. <i>PLoS Pathogens</i> , 2020 , 16, e1008235	7.6	5
16	The third moments of the site frequency spectrum. <i>Theoretical Population Biology</i> , 2018 , 120, 16-28	1.2	4
15	The neutral frequency spectrum of linked sites		4
14	Lessons for preparedness and reasons for concern from the early COVID-19 epidemic in Iran. <i>Epidemics</i> , 2021 , 36, 100472	5.1	4
13	COVID-19 incidence and R decreased on the Isle of Wight after the launch of the Test, Trace, Isolate programme		5
12	Ongoing outbreak of COVID-19 in Iran: challenges and signs of concern with under-reporting of prevalence and deaths		3
11	Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages. <i>Molecular Biology and Evolution</i> , 2021 , 38, 4346-4361	8.3	3

10	Pervasive within-host recombination and epistasis as major determinants of the molecular evolution of the Foot-and-Mouth Disease Virus capsid		2
9	The Site Frequency/Dosage Spectrum of Autopolyploid Populations. <i>Frontiers in Genetics</i> , 2018 , 9, 480	4.5	2
8	A generalized Watterson estimator for next-generation sequencing: From trios to autopolyploids. <i>Theoretical Population Biology</i> , 2015 , 100C, 79-87	1.2	1
7	Patterns of RNA Editing in Newcastle Disease Virus Infections. <i>Viruses</i> , 2020 , 12,	6.2	1
6	Decomposing the site frequency spectrum: the impact of tree topology on neutrality tests		1
5	Genomic Diversity and Evolution of Quasispecies in Newcastle Disease Virus Infections. <i>Viruses</i> , 2020 , 12,	6.2	1
4	A framework for reconstructing SARS-CoV-2 transmission dynamics using excess mortality data. <i>Nature Communications</i> , 2022 , 13,	17.4	1
3	Establishment and a comparative transcriptomic analysis of a male-specific cell line from the African malaria mosquito <i>Anopheles gambiae</i> .. <i>Scientific Reports</i> , 2022 , 12, 6885	4.9	0
2	Detecting correlations among functional-sequence motifs. <i>Physical Review E</i> , 2012 , 85, 066124	2.4	
1	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , 2022 , 8, veac022	3.7	