

Sankar Subramanian

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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.

54 papers	4,811 citations	22 h-index	63 g-index
63 ext. papers	5,639 ext. citations	7.3 avg, IF	5.21 L-index

#	Paper	IF	Citations
54	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
53	The comparative RNA web (CRW) site: an online database of comparative sequence and structure information for ribosomal, intron, and other RNAs. <i>BMC Bioinformatics</i> , 2002 , 3, 2	3.6	1094
52	Temporal patterns of fruit fly (<i>Drosophila</i>) evolution revealed by mutation clocks. <i>Molecular Biology and Evolution</i> , 2004 , 21, 36-44	8.3	452
51	Mutation rates in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 803-8	11.5	408
50	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
49	Gene expression intensity shapes evolutionary rates of the proteins encoded by the vertebrate genome. <i>Genetics</i> , 2004 , 168, 373-81	4	183
48	Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau. <i>Nature Communications</i> , 2013 , 4, 2071	17.4	154
47	Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. <i>Virology</i> , 2003 , 316, 90-103	3.6	114
46	Neutral substitutions occur at a faster rate in exons than in noncoding DNA in primate genomes. <i>Genome Research</i> , 2003 , 13, 838-44	9.7	92
45	Patterns of transitional mutation biases within and among mammalian genomes. <i>Molecular Biology and Evolution</i> , 2003 , 20, 988-93	8.3	88
44	High mitogenomic evolutionary rates and time dependency. <i>Trends in Genetics</i> , 2009 , 25, 482-6	8.5	80
43	New developments in ancient genomics. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 386-93	10.9	77
42	Evolutionary anatomies of positions and types of disease-associated and neutral amino acid mutations in the human genome. <i>BMC Genomics</i> , 2006 , 7, 306	4.5	57
41	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014 , 3, 27	7.6	50
40	Signatures of ecological resource availability in the animal and plant proteomes. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1946-51	8.3	48
39	Rapid molecular evolution in a living fossil. <i>Trends in Genetics</i> , 2008 , 24, 106-9	8.5	45
38	The genome of the oyster <i>Saccostrea</i> offers insight into the environmental resilience of bivalves. <i>DNA Research</i> , 2018 , 25, 655-665	4.5	44

37	The effects of sample size on population genomic analyses--implications for the tests of neutrality. <i>BMC Genomics</i> , 2016 , 17, 123	4.5	37
36	Nearly neutrality and the evolution of codon usage bias in eukaryotic genomes. <i>Genetics</i> , 2008 , 178, 2429-32	4.3	35
35	Temporal trails of natural selection in human mitogenomes. <i>Molecular Biology and Evolution</i> , 2009 , 26, 715-7	8.3	23
34	Higher intensity of purifying selection on >90% of the human genes revealed by the intrinsic replacement mutation rates. <i>Molecular Biology and Evolution</i> , 2006 , 23, 2283-7	8.3	23
33	Evidence for a recent origin of penguins. <i>Biology Letters</i> , 2013 , 9, 20130748	3.6	22
32	The abundance of deleterious polymorphisms in humans. <i>Genetics</i> , 2012 , 190, 1579-83	4	20
31	Ancient mtDNA sequences from the First Australians revisited. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 6892-7	11.5	19
30	Time dependency of molecular evolutionary rates? Yes and no. <i>Genome Biology and Evolution</i> , 2011 , 3, 1324-8	3.9	18
29	Quantifying harmful mutations in human populations. <i>European Journal of Human Genetics</i> , 2012 , 20, 1320-2	5.3	17
28	Molecular and morphological evolution in tuatara are decoupled. <i>Trends in Genetics</i> , 2009 , 25, 16-18	8.5	16
27	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018 , 4, eaau5064	14.3	16
26	Ancient population genomics and the study of evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20130381	5.8	14
25	Significance of population size on the fixation of nonsynonymous mutations in genes under varying levels of selection pressure. <i>Genetics</i> , 2013 , 193, 995-1002	4	14
24	Adlie penguins and temperature changes in Antarctica: a long-term view. <i>Integrative Zoology</i> , 2012 , 7, 113-20	1.9	12
23	Next generation sequencing and analysis of a conserved transcriptome of New Zealand's kiwi. <i>BMC Evolutionary Biology</i> , 2010 , 10, 387	3	12
22	Europeans have a higher proportion of high-frequency deleterious variants than Africans. <i>Human Genetics</i> , 2016 , 135, 1-7	6.3	11
21	: a client-side software to construct population phylogeny from genome-wide SNPs. <i>PeerJ</i> , 2019 , 7, e82131	3.1	11
20	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. <i>PLoS ONE</i> , 2019 , 14, e0223964	3.7	10

19	Fixation of deleterious mutations at critical positions in human proteins. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2687-93	8.3	8
18	High proportions of deleterious polymorphisms in constrained human genes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 49-52	8.3	6
17	Selective constraints determine the time dependency of molecular rates for human nuclear genomes. <i>Genome Biology and Evolution</i> , 2012 , 4, 1127-32	3.9	6
16	Greenlip Abalone () Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 3067-3078	3.2	5
15	Distance-dependent patterns of molecular divergences in Tuatara mitogenomes. <i>Scientific Reports</i> , 2015 , 5, 8703	4.9	4
14	BishingIFor Mitochondrial DNA in The Egyptian Sacred Ibis Mummies		4
13	Influence of Effective Population Size on Genes under Varying Levels of Selection Pressure. <i>Genome Biology and Evolution</i> , 2018 , 10, 756-762	3.9	2
12	Using the plurality of codon positions to identify deleterious variants in human exomes. <i>Bioinformatics</i> , 2015 , 31, 301-5	7.2	2
11	Second generation DNA sequencing of the mitogenome of the Chinstrap penguin and comparative genomics of Antarctic penguins. <i>Mitochondrial DNA</i> , 2014 , 25, 271-2		2
10	Complete mitochondrial genomes of Tuatara endemic to different islands of New Zealand. <i>Mitochondrial DNA</i> , 2015 , 26, 25-6		1
9	Abundance of clinical variants in exons included in multiple transcripts. <i>Human Genomics</i> , 2018 , 12, 33	6.8	1
8	Mitogenomic Diversity in Sacred Ibis Mummies sheds light on early Egyptian practices		1
7	Population size influences the type of nucleotide variations in humans. <i>BMC Genetics</i> , 2019 , 20, 93	2.6	1
6	The Long-Term Evolutionary History of Gradual Reduction of CpG Dinucleotides in the SARS-CoV-2 Lineage. <i>Biology</i> , 2021 , 10,	4.9	1
5	Deleterious protein-coding variants in diverse cattle breeds of the world. <i>Genetics Selection Evolution</i> , 2021 , 53, 80	4.9	0
4	Genomic Prediction for Whole Weight, Body Shape, Meat Yield, and Color Traits in the Portuguese Oyster. <i>Frontiers in Genetics</i> , 2021 , 12, 661276	4.5	0
3	NMOSD and MS prevalence in the Indigenous populations of Australia and New Zealand. <i>Journal of Neurology</i> , 2021 , 1	5.5	0
2	Ancient Population Genomics1-10		

- 1 Harmful mutation load in the mitochondrial genomes of cattle breeds. *BMC Research Notes*, **2021**, 14, 241 2.3