

Sudhir Kumar

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

37,734
citations

279798
23
h-index

74163
75
g-index

90
all docs

90
docs citations

90
times ranked

44246
citing authors

#	ARTICLE	IF	CITATIONS
1	Crp/fnr family protein binds to promoters of atxA and sodmn genes that regulate the expression of exotoxins in Bacillus anthracis. Protein Expression and Purification, 2022, 193, 106059.	1.3	1
2	Embracing Green Computing in Molecular Phylogenetics. Molecular Biology and Evolution, 2022, 39, .	8.9	10
3	MOCA for Integrated Analysis of Gene Expression and Genetic Variation in Single Cells. Frontiers in Genetics, 2022, 13, 831040.	2.3	1
4	Dynamic coupling of residues within proteins as a mechanistic foundation of many enigmatic pathogenic missense variants. PLoS Computational Biology, 2022, 18, e1010006.	3.2	16
5	Epistasis Creates Invariant Sites and Modulates the Rate of Molecular Evolution. Molecular Biology and Evolution, 2022, 39, .	8.9	2
6	Co-metabolism of 4-bromophenol by Pseudomonas sp. EN-4 and toxicity evaluation of biotransformed samples. Journal of Environmental Chemical Engineering, 2022, 10, 108223.	6.7	4
7	Structural and functional studies of serine acetyltransferase isoform from Entamoeba histolytica reveals novel role of the C-terminal tail in loss of regulation from feedback inhibition. International Journal of Biological Macromolecules, 2022, , .	7.5	0
8	TreeMap: a structured approach to fine mapping of eQTL variants. Bioinformatics, 2021, 37, 1125-1134.	4.1	6
9	Molecular dating for phylogenies containing a mix of populations and species by using Bayesian and RelTime approaches. Molecular Ecology Resources, 2021, 21, 122-136.	4.8	18
10	Proteins Involved in Colorectal Cancer: Identification Strategies and Possible Roles. , 2021, , 179-194.		0
11	Co-morbid conditions in COVID-19 patients in Uttarakhand state of India. Journal of Global Health, 2021, 11, 03029.	2.7	1
12	Common Treatment, Common Variant: Evolutionary Prediction of Functional Pharmacogenomic Variants. Journal of Personalized Medicine, 2021, 11, 131.	2.5	8
13	MEGA11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution, 2021, 38, 3022-3027.	8.9	6,189
14	Epistasis produces an excess of invariant sites in neutral molecular evolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2018767118.	7.1	2
15	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.	8.9	54
16	Molecular and morphological clocks for estimating evolutionary divergence times. BMC Ecology and Evolution, 2021, 21, 83.	1.6	7
17	Data-driven speciation tree prior for better species divergence times in calibration-poor molecular phylogenies. Bioinformatics, 2021, 37, i102-i110.	4.1	8
18	Evolutionary Sparse Learning for Phylogenomics. Molecular Biology and Evolution, 2021, 38, 4674-4682.	8.9	4

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19	Migrations of cancer cells through the lens of phylogenetic biogeography. Scientific Reports, 2021, 11, 17184.	3.3	7
20	The somatic molecular evolution of cancer: Mutation, selection, and epistasis. Progress in Biophysics and Molecular Biology, 2021, 165, 56-65.	2.9	11
21	Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. Nature Computational Science, 2021, 1, 573-577.	8.0	10
22	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. Lancet Microbe, The, 2021, 2, e666-e675.	7.3	147
23	Assessing Rapid Relaxed-Clock Methods for Phylogenomic Dating. Genome Biology and Evolution, 2021, 13, .	2.5	7
24	A Report by the Editor-in-Chief for <i>Molecular Biology and Evolution</i> (MBE), Volume 37. Molecular Biology and Evolution, 2021, 38, 5830-5830.	8.9	0
25	Tumors Are Evolutionary Island-Like Ecosystems. Genome Biology and Evolution, 2021, 13, .	2.5	2
26	Deep Model Based Transfer and Multi-Task Learning for Biological Image Analysis. IEEE Transactions on Big Data, 2020, 6, 322-333.	6.1	101
27	Somatic selection distinguishes oncogenes and tumor suppressor genes. Bioinformatics, 2020, 36, 1712-1717.	4.1	27
28	Molecular Biology and Evolution of Cancer: From Discovery to Action. Molecular Biology and Evolution, 2020, 37, 320-326.	8.9	43
29	Molecular Evolutionary Genetics Analysis (MEGA) for macOS. Molecular Biology and Evolution, 2020, 37, 1237-1239.	8.9	1,067
30	Reliable Confidence Intervals for RelTime Estimates of Evolutionary Divergence Times. Molecular Biology and Evolution, 2020, 37, 280-290.	8.9	36
31	Functional, Morphological, and Evolutionary Characterization of Hearing in Subterranean, Eusocial African Mole-Rats. Current Biology, 2020, 30, 4329-4341.e4.	3.9	19
32	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. Cell Reports, 2020, 32, 107949.	6.4	26
33	A Report by the Editor-in-Chief for Molecular Biology and Evolution (MBE), Volume 36. Molecular Biology and Evolution, 2020, 37, 3699-3700.	8.9	0
34	Interactive effect of TLR SNPs and exposure to sexually transmitted infections on prostate cancer risk in Jamaican men. Prostate, 2020, 80, 1365-1372.	2.3	2
35	Where Did SARS-CoV-2 Come From?. Molecular Biology and Evolution, 2020, 37, 2463-2464.	8.9	22
36	Power and pitfalls of computational methods for inferring clone phylogenies and mutation orders from bulk sequencing data. Scientific Reports, 2020, 10, 3498.	3.3	21

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37	Relative Efficiencies of Simple and Complex Substitution Models in Estimating Divergence Times in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2020, 37, 1819-1831.	8.9	16
38	The Role of Conformational Dynamics and Allostery in Modulating Protein Evolution. <i>Annual Review of Biophysics</i> , 2020, 49, 267-288.	10.0	101
39	A Report by the Editor-in-Chief for <i>Molecular Biology and Evolution</i> (MBE), Volume 35. <i>Molecular Biology and Evolution</i> , 2020, 37, 300-300.	8.9	0
40	A new method for inferring timetrees from temporally sampled molecular sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007046.	3.2	19
41	Wastewater ferti-irrigation: an eco-technology for sustainable agriculture. <i>Sustainable Water Resources Management</i> , 2020, 6, 1.	2.1	19
42	MBE Transitions to the Open Access Publication Model in 2021. <i>Molecular Biology and Evolution</i> , 2020, 37, 3397-3398.	8.9	0
43	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. <i>BMC Genetics</i> , 2019, 20, 52.	2.7	10
44	On estimating evolutionary probabilities of population variants. <i>BMC Evolutionary Biology</i> , 2019, 19, 133.	3.2	5
45	<i>MBE</i> Citation Classics (2019 Edition). <i>Molecular Biology and Evolution</i> , 2019, 36, 1-3.	8.9	3
46	A Machine Learning Method for Detecting Autocorrelation of Evolutionary Rates in Large Phylogenies. <i>Molecular Biology and Evolution</i> , 2019, 36, 811-824.	8.9	45
47	Biological relevance of computationally predicted pathogenicity of noncoding variants. <i>Nature Communications</i> , 2019, 10, 330.	12.8	44
48	N-terminal residues are crucial for quaternary structure and active site conformation for the phosphoserine aminotransferase from enteric human parasite <i>E. histolytica</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 132, 1012-1023.	7.5	8
49	Adventures in Evolution: The Narrative of Tardigrada, Trundlers in Time. <i>American Biology Teacher</i> , 2019, 81, 543-552.	0.2	0
50	Delineation of Tumor Migration Paths by Using a Bayesian Biogeographic Approach. <i>Cancers</i> , 2019, 11, 1880.	3.7	7
51	A Report by the Editor-in-Chief for <i>Molecular Biology and Evolution</i> (MBE), Volume 34. <i>Molecular Biology and Evolution</i> , 2019, 36, 202-202.	8.9	0
52	Annotation of a hypothetical protein (WP_002969292.1) from <i>Brucella abortus</i> . <i>Bioinformatics</i> , 2019, 15, 315-320.	0.5	1
53	Neutral Theory, Disease Mutations, and Personal Exomes. <i>Molecular Biology and Evolution</i> , 2018, 35, 1297-1303.	8.9	6
54	MBE Citation Classics (2018 Edition). <i>Molecular Biology and Evolution</i> , 2018, 35, 1-2.	8.9	17

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55	MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. <i>Molecular Biology and Evolution</i> , 2018, 35, 1547-1549.	8.9	25,630
56	Theoretical Foundation of the RelTime Method for Estimating Divergence Times from Variable Evolutionary Rates. <i>Molecular Biology and Evolution</i> , 2018, 35, 1770-1782.	8.9	164
57	Computational enhancement of single-cell sequences for inferring tumor evolution. <i>Bioinformatics</i> , 2018, 34, i917-i926.	4.1	32
58	Adaptive Landscape of Protein Variation in Human Exomes. <i>Molecular Biology and Evolution</i> , 2018, 35, 2015-2025.	8.9	10
59	RelTime Relaxes the Strict Molecular Clock throughout the Phylogeny. <i>Genome Biology and Evolution</i> , 2018, 10, 1631-1636.	2.5	25
60	The Reliability and Stability of an Inferred Phylogenetic Tree from Empirical Data. <i>Molecular Biology and Evolution</i> , 2017, 34, msw272.	8.9	4
61	TimeTree: A Resource for Timelines, Timetrees, and Divergence Times. <i>Molecular Biology and Evolution</i> , 2017, 34, 1812-1819.	8.9	2,017
62	MBE Citation Classics (2017 Edition). <i>Molecular Biology and Evolution</i> , 2017, 34, 1-3.	8.9	14
63	Fast and Accurate Estimates of Divergence Times from Big Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 45-50.	8.9	52
64	Advances in Time Estimation Methods for Molecular Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 863-869.	8.9	96
65	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. <i>3 Biotech</i> , 2016, 6, 16.	2.2	13
66	MBE Citation Classics (2016 Edition). <i>Molecular Biology and Evolution</i> , 2016, 33, 1-3.	8.9	25
67	A Molecular Evolutionary Reference for the Human Variome. <i>Molecular Biology and Evolution</i> , 2016, 33, 245-254.	8.9	20
68	Using Disease-Associated Coding Sequence Variation to Investigate Functional Compensation by Human Paralogous Proteins. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S30594.	1.2	0
69	MBE Citation Classics (2015 Edition). <i>Molecular Biology and Evolution</i> , 2015, 32, 1-3.	8.9	11
70	Integration of structural dynamics and molecular evolution via protein interaction networks: a new era in genomic medicine. <i>Current Opinion in Structural Biology</i> , 2015, 35, 135-142.	5.7	29
71	Tree of Life Reveals Clock-Like Speciation and Diversification. <i>Molecular Biology and Evolution</i> , 2015, 32, 835-845.	8.9	862
72	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. <i>American Journal of Botany</i> , 2015, 102, 1115-1127.	1.7	137

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73	Structural basis of <i>Bacillus anthracis</i> MoxXT disruption and the modulation of MoxT ribonuclease activity by rationally designed peptides. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 606-624.	3.5	12
74	Reply to: "Proper reporting of predictor performance". <i>Nature Methods</i> , 2014, 11, 781-782.	19.0	2
75	Society for Molecular Biology and Evolution A Report by Editor-in-Chief MBE Volume 30. <i>Molecular Biology and Evolution</i> , 2014, 31, 3373-3374.	8.9	1
76	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014, 46, 1303-1310.	21.4	174
77	Biophysical aspects of lysozyme adduct with monocrotophos. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 5477-5485.	3.7	5
78	Crystal structure of serine acetyl transferase from <i>Brucella abortus</i> and its complex with coenzyme A. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1741-1748.	2.3	13
79	No Positive Selection for G Allele in a p53 Response Element in Europeans. <i>Cell</i> , 2014, 157, 1497-1499.	28.9	2
80	Prospects for Building Large Timetrees Using Molecular Data with Incomplete Gene Coverage among Species. <i>Molecular Biology and Evolution</i> , 2014, 31, 2542-2550.	8.9	57
81	Single Residue Mutation in Active Site of Serine Acetyltransferase Isoform 3 from <i>Entamoeba histolytica</i> Assists in Partial Regaining of Feedback Inhibition by Cysteine. <i>PLoS ONE</i> , 2013, 8, e55932.	2.5	10
82	The narrow active-site cleft of <i>O</i> -acetylserine sulfhydrylase from <i>Leishmania donovani</i> allows complex formation with serine acetyltransferases with a range of C-terminal sequences. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 909-919.	2.5	35
83	Impact of Fly Ash on Soil Properties. <i>The National Academy of Sciences, India</i> , 2012, 35, 13-16.	1.3	21
84	Structural and Biochemical Studies of Serine Acetyltransferase Reveal Why the Parasite <i>Entamoeba histolytica</i> Cannot Form a Cysteine Synthase Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 12533-12541.	3.4	50
85	CODON-BASED DETECTION OF POSITIVE SELECTION CAN BE BIASED BY HETEROGENEOUS DISTRIBUTION OF POLAR AMINO ACIDS ALONG PROTEIN SEQUENCES. , 2006, , .		13