

Sudhir Kumar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2238075/publications.pdf>

Version: 2024-02-01

85
papers

37,734
citations

318942

23
h-index

84171

75
g-index

90
all docs

90
docs citations

90
times ranked

47842
citing authors

#	ARTICLE	IF	CITATIONS
1	Crp/fnr family protein binds to promoters of atxA and sodm genes that regulate the expression of exotoxins in Bacillus anthracis. Protein Expression and Purification, 2022, 193, 106059.	0.6	1
2	Embracing Green Computing in Molecular Phylogenetics. Molecular Biology and Evolution, 2022, 39, .	3.5	10
3	MOCA for Integrated Analysis of Gene Expression and Genetic Variation in Single Cells. Frontiers in Genetics, 2022, 13, 831040.	1.1	1
4	Dynamic coupling of residues within proteins as a mechanistic foundation of many enigmatic pathogenic missense variants. PLoS Computational Biology, 2022, 18, e1010006.	1.5	16
5	Epistasis Creates Invariant Sites and Modulates the Rate of Molecular Evolution. Molecular Biology and Evolution, 2022, 39, .	3.5	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.	3.3	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, , .	3.6	0
8	TreeMap: a structured approach to fine mapping of eQTL variants. Bioinformatics, 2021, 37, 1125-1134.	1.8	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.	2.2	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.	1.2	1
12	Common Treatment, Common Variant: Evolutionary Prediction of Functional Pharmacogenomic Variants. Journal of Personalized Medicine, 2021, 11, 131.	1.1	8
13	MEGA11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution, 2021, 38, 3022-3027.	3.5	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.	3.3	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.	3.5	54
16	Molecular and morphological clocks for estimating evolutionary divergence times. BMC Ecology and Evolution, 2021, 21, 83.	0.7	7
17	Data-driven speciation tree prior for better species divergence times in calibration-poor molecular phylogenies. Bioinformatics, 2021, 37, i102-i110.	1.8	8
18	Evolutionary Sparse Learning for Phylogenomics. Molecular Biology and Evolution, 2021, 38, 4674-4682.	3.5	4

#	ARTICLE	IF	CITATIONS
19	Migrations of cancer cells through the lens of phylogenetic biogeography. <i>Scientific Reports</i> , 2021, 11, 17184.	1.6	7
20	The somatic molecular evolution of cancer: Mutation, selection, and epistasis. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 165, 56-65.	1.4	11
21	Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. <i>Nature Computational Science</i> , 2021, 1, 573-577.	3.8	10
22	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. <i>Lancet Microbe</i> , The, 2021, 2, e666-e675.	3.4	147
23	Assessing Rapid Relaxed-Clock Methods for Phylogenomic Dating. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
24	A Report by the Editor-in-Chief for <i>Molecular Biology and Evolution</i> (MBE), Volume 37. <i>Molecular Biology and Evolution</i> , 2021, 38, 5830-5830.	3.5	0
25	Tumors Are Evolutionary Island-Like Ecosystems. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
26	Deep Model Based Transfer and Multi-Task Learning for Biological Image Analysis. <i>IEEE Transactions on Big Data</i> , 2020, 6, 322-333.	4.4	101
27	Somatic selection distinguishes oncogenes and tumor suppressor genes. <i>Bioinformatics</i> , 2020, 36, 1712-1717.	1.8	27
28	Molecular Biology and Evolution of Cancer: From Discovery to Action. <i>Molecular Biology and Evolution</i> , 2020, 37, 320-326.	3.5	43
29	Molecular Evolutionary Genetics Analysis (MEGA) for macOS. <i>Molecular Biology and Evolution</i> , 2020, 37, 1237-1239.	3.5	1,067
30	Reliable Confidence Intervals for RelTime Estimates of Evolutionary Divergence Times. <i>Molecular Biology and Evolution</i> , 2020, 37, 280-290.	3.5	36
31	Functional, Morphological, and Evolutionary Characterization of Hearing in Subterranean, Eusocial African Mole-Rats. <i>Current Biology</i> , 2020, 30, 4329-4341.e4.	1.8	19
32	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020, 32, 107949.	2.9	26
33	A Report by the Editor-in-Chief for <i>Molecular Biology and Evolution</i> (MBE), Volume 36. <i>Molecular Biology and Evolution</i> , 2020, 37, 3699-3700.	3.5	0
34	Interactive effect of TLR SNPs and exposure to sexually transmitted infections on prostate cancer risk in Jamaican men. <i>Prostate</i> , 2020, 80, 1365-1372.	1.2	2
35	Where Did SARS-CoV-2 Come From?. <i>Molecular Biology and Evolution</i> , 2020, 37, 2463-2464.	3.5	22
36	Power and pitfalls of computational methods for inferring clone phylogenies and mutation orders from bulk sequencing data. <i>Scientific Reports</i> , 2020, 10, 3498.	1.6	21

#	ARTICLE	IF	CITATIONS
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.	3.5	16
38	The Role of Conformational Dynamics and Allostery in Modulating Protein Evolution. <i>Annual Review of Biophysics</i> , 2020, 49, 267-288.	4.5	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.	3.5	0
40	A new method for inferring timetrees from temporally sampled molecular sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007046.	1.5	19
41	Wastewater ferti-irrigation: an eco-technology for sustainable agriculture. <i>Sustainable Water Resources Management</i> , 2020, 6, 1.	1.0	19
42	MBE Transitions to the Open Access Publication Model in 2021. <i>Molecular Biology and Evolution</i> , 2020, 37, 3397-3398.	3.5	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.	3.5	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.	3.5	45
47	Biological relevance of computationally predicted pathogenicity of noncoding variants. <i>Nature Communications</i> , 2019, 10, 330.	5.8	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.	3.6	8
49	Adventures in Evolution: The Narrative of Tardigrada, Trundlers in Time. <i>American Biology Teacher</i> , 2019, 81, 543-552.	0.1	0
50	Delineation of Tumor Migration Paths by Using a Bayesian Biogeographic Approach. <i>Cancers</i> , 2019, 11, 1880.	1.7	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.	3.5	0
52	Annotation of a hypothetical protein (WP_002969292.1) from <i>Brucella abortus</i> . <i>Bioinformatics</i> , 2019, 15, 315-320.	0.2	1
53	Neutral Theory, Disease Mutations, and Personal Exomes. <i>Molecular Biology and Evolution</i> , 2018, 35, 1297-1303.	3.5	6
54	MBE Citation Classics (2018 Edition). <i>Molecular Biology and Evolution</i> , 2018, 35, 1-2.	3.5	17

#	ARTICLE	IF	CITATIONS
55	MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. <i>Molecular Biology and Evolution</i> , 2018, 35, 1547-1549.	3.5	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.	3.5	164
57	Computational enhancement of single-cell sequences for inferring tumor evolution. <i>Bioinformatics</i> , 2018, 34, i917-i926.	1.8	32
58	Adaptive Landscape of Protein Variation in Human Exomes. <i>Molecular Biology and Evolution</i> , 2018, 35, 2015-2025.	3.5	10
59	RelTime Relaxes the Strict Molecular Clock throughout the Phylogeny. <i>Genome Biology and Evolution</i> , 2018, 10, 1631-1636.	1.1	25
60	The Reliability and Stability of an Inferred Phylogenetic Tree from Empirical Data. <i>Molecular Biology and Evolution</i> , 2017, 34, msw272.	3.5	4
61	TimeTree: A Resource for Timelines, Timetrees, and Divergence Times. <i>Molecular Biology and Evolution</i> , 2017, 34, 1812-1819.	3.5	2,017
62	MBE Citation Classics (2017 Edition). <i>Molecular Biology and Evolution</i> , 2017, 34, 1-3.	3.5	14
63	Fast and Accurate Estimates of Divergence Times from Big Data. <i>Molecular Biology and Evolution</i> , 2017, 34, 45-50.	3.5	52
64	Advances in Time Estimation Methods for Molecular Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 863-869.	3.5	96
65	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. <i>3 Biotech</i> , 2016, 6, 16.	1.1	13
66	MBE Citation Classics (2016 Edition). <i>Molecular Biology and Evolution</i> , 2016, 33, 1-3.	3.5	25
67	A Molecular Evolutionary Reference for the Human Variome. <i>Molecular Biology and Evolution</i> , 2016, 33, 245-254.	3.5	20
68	Using Disease-Associated Coding Sequence Variation to Investigate Functional Compensation by Human Paralogous Proteins. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S30594.	0.6	0
69	MBE Citation Classics (2015 Edition). <i>Molecular Biology and Evolution</i> , 2015, 32, 1-3.	3.5	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.	2.6	29
71	Tree of Life Reveals Clock-Like Speciation and Diversification. <i>Molecular Biology and Evolution</i> , 2015, 32, 835-845.	3.5	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.	0.8	137

#	ARTICLE	IF	CITATIONS
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.	2.0	12
74	Reply to: "Proper reporting of predictor performance". <i>Nature Methods</i> , 2014, 11, 781-782.	9.0	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.	3.5	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.	9.4	174
77	Biophysical aspects of lysozyme adduct with monocrotophos. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 5477-5485.	1.9	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.	1.1	13
79	No Positive Selection for G Allele in a p53 Response Element in Europeans. <i>Cell</i> , 2014, 157, 1497-1499.	13.5	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.	3.5	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.	1.1	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.	0.8	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.	1.6	50
85	CODON-BASED DETECTION OF POSITIVE SELECTION CAN BE BIASED BY HETEROGENEOUS DISTRIBUTION OF POLAR AMINO ACIDS ALONG PROTEIN SEQUENCES. , 2006, , .		13