Shyam Gopalakrishnan

List of Publications by Year in descending order

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Version: 2024-02-01

		172386	182361
57	3,268	29	51
papers	citations	h-index	g-index
73	73	73	5781

times ranked

citing authors

docs citations

all docs

#	Article	IF	CITATIONS
1	Analysis of independent cohorts of outbred CFW mice reveals novel loci for behavioral and physiological traits and identifies factors determining reproducibility. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	5
2	A multi-omics approach unravels metagenomic and metabolic alterations of a probiotic and synbiotic additive in rainbow trout (Oncorhynchus mykiss). Microbiome, 2022, 10, 21.	4.9	25
3	The rise of genomics in snake venom research: recent advances and future perspectives. GigaScience, 2022, 11, .	3.3	17
4	Probing the genomic limits of de-extinction in the Christmas Island rat. Current Biology, 2022, , .	1.8	8
5	Ancient Maltese genomes and the genetic geography of Neolithic Europe. Current Biology, 2022, 32, 2668-2680.e6.	1.8	9
6	Pervasive Phylogenomic Incongruence Underlies Evolutionary Relationships in Eyebrights (Euphrasia,) Tj ETQq0 (0 1 <u>g</u> BT /C	Overlock 10 Tf
7	Grey wolf genomic history reveals a dual ancestry of dogs. Nature, 2022, 607, 313-320.	13.7	48
8	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. Current Biology, 2021, 31, 198-206.e8.	1.8	26
9	Mitochondrial genomes of Danish vertebrate species generated for the national DNA reference database, DNAmark. Environmental DNA, 2021, 3, 472-480.	3.1	24
10	eDNAâ€based biomonitoring at an experimental German vineyard to characterize how management regimes shape ecosystem diversity. Environmental DNA, 2021, 3, 70-82.	3.1	14
11	Dire wolves were the last of an ancient New World canid lineage. Nature, 2021, 591, 87-91.	13.7	43
12	Extended survival of Pleistocene Siberian wolves into the early 20th century on the island of Honshū. IScience, 2021, 24, 101904.	1.9	9
13	Circumpolar phylogeography and demographic history of beluga whales reflect past climatic fluctuations. Molecular Ecology, 2021, 30, 2543-2559.	2.0	12
14	Biodiversity Soup II: A bulkâ€sample metabarcoding pipeline emphasizing error reduction. Methods in Ecology and Evolution, 2021, 12, 1252-1264.	2.2	21
15	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (<i>Ceratotherium simum</i>). Molecular Ecology, 2021, 30, 6355-6369.	2.0	39
16	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
17	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
18	Evolutionary history of the extinct Sardinian dhole. Current Biology, 2021, 31, 5571-5579.e6.	1.8	7

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19	The genome sequence of the grey wolf, Canis lupus Linnaeus 1758. Wellcome Open Research, 2021, 6, 310.	0.9	9
20	Plasmodium vivax Malaria Viewed through the Lens of an Eradicated European Strain. Molecular Biology and Evolution, 2020, 37, 773-785.	3.5	38
21	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. Current Biology, 2020, 30, 5018-5025.e5.	1.8	34
22	Holo-Omics: Integrated Host-Microbiota Multi-omics for Basic and Applied Biological Research. IScience, 2020, 23, 101414.	1.9	80
23	Multi-omic detection of <i>Mycobacterium leprae</i> in archaeological human dental calculus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190584.	1.8	31
24	The evolutionary history of extinct and living lions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10927-10934.	3.3	70
25	Adapting Genotyping-by-Sequencing and Variant Calling for Heterogeneous Stock Rats. G3: Genes, Genomes, Genetics, 2020, 10, 2195-2205.	0.8	19
26	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. Molecular Biology and Evolution, 2020, 37, 3105-3117.	3.5	20
27	Arctic-adapted dogs emerged at the Pleistocene–Holocene transition. Science, 2020, 368, 1495-1499.	6.0	60
28	Influence of past climate change on phylogeography and demographic history of narwhals, <i>Monodon monoceros</i> . Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192964.	1.2	39
29	Hybridization between two high Arctic cetaceans confirmed by genomic analysis. Scientific Reports, 2019, 9, 7729.	1.6	33
30	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10705-10710.	3.3	119
31	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191929.	1.2	38
32	A 5700 year-old human genome and oral microbiome from chewed birch pitch. Nature Communications, 2019, 10, 5520.	5.8	61
33	MobiSeq: De novo SNP discovery in model and nonâ€model species through sequencing the flanking region of transposable elements. Molecular Ecology Resources, 2019, 19, 512-525.	2.2	4
34	Promises and pitfalls of using highâ€throughput sequencing for diet analysis. Molecular Ecology Resources, 2019, 19, 327-348.	2.2	138
35	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	3.3	64
36	Using <scp>DNA</scp> metabarcoding for simultaneous inference of common vampire bat diet and population structure. Molecular Ecology Resources, 2018, 18, 1050-1063.	2.2	70

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37	Agriculture shapes the trophic niche of a bat preying on multiple pest arthropods across Europe: Evidence from <scp>DNA</scp> metabarcoding. Molecular Ecology, 2018, 27, 815-825.	2.0	110
38	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. Molecular Biology and Evolution, 2018, 35, 287-298.	3.5	41
39	Singleâ€ŧube library preparation for degraded <scp>DNA</scp> . Methods in Ecology and Evolution, 2018, 9, 410-419.	2.2	261
40	Population genomics of grey wolves and wolf-like canids in North America. PLoS Genetics, 2018, 14, e1007745.	1.5	54
41	Interspecific Gene Flow Shaped the Evolution of the Genus Canis. Current Biology, 2018, 28, 3441-3449.e5.	1.8	110
42	Ancient genomes from Iceland reveal the making of a human population. Science, 2018, 360, 1028-1032.	6.0	62
43	The evolutionary history of dogs in the Americas. Science, 2018, 361, 81-85.	6.0	140
44	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	1.2	73
45	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.	3.3	137
46	Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice. Nature Genetics, 2016, 48, 919-926.	9.4	119
47	An Anthropocene map of genetic diversity. Science, 2016, 353, 1532-1535.	6.0	251
48	Genome Sequence of a 5,310-Year-Old Maize Cob Provides Insights into the Early Stages of Maize Domestication. Current Biology, 2016, 26, 3195-3201.	1.8	130
49	Mapping of Craniofacial Traits in Outbred Mice Identifies Major Developmental Genes Involved in Shape Determination. PLoS Genetics, 2015, 11, e1005607.	1.5	67
50	Variation in the Form of Pavlovian Conditioned Approach Behavior among Outbred Male Sprague-Dawley Rats from Different Vendors and Colonies: Sign-Tracking vs. Goal-Tracking. PLoS ONE, 2013, 8, e75042.	1.1	116
51	Assessing the Impact of Non-Differential Genotyping Errors on Rare Variant Tests of Association. Human Heredity, 2011, 72, 153-160.	0.4	18
52	Extending Rare-Variant Testing Strategies: Analysis of Noncoding Sequence and Imputed Genotypes. American Journal of Human Genetics, 2010, 87, 604-617.	2.6	121
53	Familyâ€based SNP association study on 8q24 in bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 612-618.	1.1	22
54	An efficient comprehensive search algorithm for tagSNP selection using linkage disequilibrium criteria. Bioinformatics, 2006, 22, 220-225.	1.8	74

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55	TagSNP selection based on pairwise LD criteria and power analysis in association studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 511-22.	0.7	1
56	TAGSNP SELECTION BASED ON PAIRWISE LD CRITERIA AND POWER ANALYSIS IN ASSOCIATION STUDIES. , 2005, , .		4
57	Conservation genomics of the endangered Seychelles Magpieâ€Robin (Copsychus sechellarum): A unique insight into the history of a precious endemic bird. Ibis, 0, , .	1.0	4