

# Sujai Kumar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/432021/publications.pdf>

Version: 2024-02-01

28  
papers

3,519  
citations

331670

21  
h-index

501196

28  
g-index

37  
all docs

37  
docs citations

37  
times ranked

6454  
citing authors

#	ARTICLE	IF	CITATIONS
1	MolluscDB: a genome and transcriptome database for molluscs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200157.	4.0	17
2	Extracellular vesicles from <i>Heligmosomoides bakeri</i> and <i>Trichuris muris</i> contain distinct microRNA families and small RNAs that could underpin different functions in the host. <i>International Journal for Parasitology</i> , 2020, 50, 719-729.	3.1	16
3	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	12.6	365
4	Secretion of an Argonaute protein by a parasitic nematode and the evolution of its siRNA guides. <i>Nucleic Acids Research</i> , 2019, 47, 3594-3606.	14.5	75
5	Comparative analysis of small RNAs released by the filarial nematode <i>Litomosoides sigmodontis</i> in vitro and in vivo. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007811.	3.0	19
6	Sexually dimorphic gene expression and transcriptome evolution provide mixed evidence for a fast effect in <i>Heliconius</i> . <i>Journal of Evolutionary Biology</i> , 2019, 32, 194-204.	1.7	31
7	A high-coverage draft genome of the mycalesine butterfly <i>Bicyclus anynana</i> . <i>GigaScience</i> , 2017, 6, 1-7.	6.4	55
8	GenomeHubs: simple containerized setup of a custom Ensembl database and web server for any species. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	13
9	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	5.6	170
10	No evidence for extensive horizontal gene transfer in the genome of the tardigrade <i>Hypsibius dujardini</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5053-5058.	7.1	214
11	Exosomes secreted by nematode parasites transfer small RNAs to mammalian cells and modulate innate immunity. <i>Nature Communications</i> , 2014, 5, 5488.	12.8	640
12	Comparative Analysis of the Secretome from a Model Filarial Nematode ( <i>Litomosoides sigmodontis</i> ) Reveals Maximal Diversity in Gravid Female Parasites. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2527-2544.	3.8	32
13	The complex hybrid origins of the root knot nematodes revealed through comparative genomics. <i>PeerJ</i> , 2014, 2, e356.	2.0	99
14	Sulfur Amino Acids Regulate Translational Capacity and Metabolic Homeostasis through Modulation of tRNA Thiolation. <i>Cell</i> , 2013, 154, 416-429.	28.9	189
15	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. <i>BMC Genomics</i> , 2013, 14, 923.	2.8	43
16	Phylogenomics and Analysis of Shared Genes Suggest a Single Transition to Mutualism in <i>Wolbachia</i> of Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1668-1674.	2.5	49
17	Blobology: exploring raw genome data for contaminants, symbionts and parasites using taxon-annotated GC-coverage plots. <i>Frontiers in Genetics</i> , 2013, 4, 237.	2.3	258
18	Toward 959 nematode genomes. <i>Worm</i> , 2012, 1, 42-50.	1.0	51

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19	The genome of the heartworm, <i>Dirofilaria immitis</i> , reveals drug and vaccine targets. FASEB Journal, 2012, 26, 4650-4661.	0.5	124
20	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. Developmental Cell, 2012, 23, 1072-1080.	7.0	101
21	959 Nematode Genomes: a semantic wiki for coordinating sequencing projects. Nucleic Acids Research, 2012, 40, D1295-D1300.	14.5	44
22	Genomics and transcriptomics across the diversity of the Nematoda. Parasite Immunology, 2012, 34, 108-120.	1.5	22
23	Simultaneous genome sequencing of symbionts and their hosts. Symbiosis, 2011, 55, 119-126.	2.3	37
24	Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. BMC Genomics, 2010, 11, 499.	2.8	74
25	Comparing de novo assemblers for 454 transcriptome data. BMC Genomics, 2010, 11, 571.	2.8	217
26	Characterization of a hotspot for mimicry: assembly of a butterfly wing transcriptome to genomic sequence at the <i>HmYb/Sb</i> locus. Molecular Ecology, 2010, 19, 240-254.	3.9	70
27	Analysis of the genome sequences of three <i>Drosophila melanogaster</i> spontaneous mutation accumulation lines. Genome Research, 2009, 19, 1195-1201.	5.5	343
28	Let SMIL be your umbrella: Software tools for transcribing, coding, and presenting digital video in behavioral research. Behavior Research Methods, 2005, 37, 359-367.	4.0	10