

Amol C Shetty

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1816399/amol-c-shetty-publications-by-citations.pdf>

Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

1,736
citations

22
h-index

41
g-index

54
ext. papers

2,744
ext. citations

9.2
avg, IF

4.31
L-index

#	Paper	IF	Citations
46	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268
45	Brain feminization requires active repression of masculinization via DNA methylation. <i>Nature Neuroscience</i> , 2015 , 18, 690-7	25.5	264
44	Simultaneous transcriptional profiling of bacteria and their host cells. <i>PLoS ONE</i> , 2013 , 8, e80597	3.7	85
43	Transcriptomic analysis of vulvovaginal candidiasis identifies a role for the NLRP3 inflammasome. <i>MBio</i> , 2015 , 6,	7.8	83
42	Association of a Novel Mutation in the Plasmodium falciparum Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. <i>Journal of Infectious Diseases</i> , 2017 , 216, 468-476	7	75
41	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016 , 7, 12218	17.4	69
40	Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E6526-E6535	11.5	68
39	Characterization of microRNA transcriptome in lung cancer by next-generation deep sequencing. <i>Molecular Oncology</i> , 2014 , 8, 1208-19	7.9	59
38	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. <i>Nature Communications</i> , 2020 , 11, 1499	17.4	58
37	New signaling pathways govern the host response to C. albicans infection in various niches. <i>Genome Research</i> , 2015 , 25, 679-89	9.7	57
36	MNKs act as a regulatory switch for eIF4E1 and eIF4E3 driven mRNA translation in DLBCL. <i>Nature Communications</i> , 2014 , 5, 5413	17.4	55
35	Iron restriction inside macrophages regulates pulmonary host defense against Rhizopus species. <i>Nature Communications</i> , 2018 , 9, 3333	17.4	48
34	Molecular epidemiology and genomics of group A Streptococcus. <i>Infection, Genetics and Evolution</i> , 2015 , 33, 393-418	4.5	47
33	Genome-wide diversity and gene expression profiling of Babesia microti isolates identify polymorphic genes that mediate host-pathogen interactions. <i>Scientific Reports</i> , 2016 , 6, 35284	4.9	47
32	Drosophila anti-nematode and antibacterial immune regulators revealed by RNA-Seq. <i>BMC Genomics</i> , 2015 , 16, 519	4.5	45
31	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. <i>Nature Communications</i> , 2016 , 7, 12521	17.4	45
30	Streptococcus pneumoniae in the heart subvert the host response through biofilm-mediated resident macrophage killing. <i>PLoS Pathogens</i> , 2017 , 13, e1006582	7.6	38

29	A comparative analysis of library prep approaches for sequencing low input translome samples. <i>BMC Genomics</i> , 2018 , 19, 696	4.5	30
28	Oral epithelial IL-22/STAT3 signaling licenses IL-17-mediated immunity to oral mucosal candidiasis. <i>Science Immunology</i> , 2020 , 5,	2.8	29
27	Inhibition of EGFR Signaling Protects from Mucormycosis. <i>MBio</i> , 2018 , 9,	7.8	28
26	Comparative genomics and transcriptomics of Escherichia coli isolates carrying virulence factors of both enteropathogenic and enterotoxigenic E. coli. <i>Scientific Reports</i> , 2017 , 7, 3513	4.9	27
25	quorum-sensing molecule farnesol modulates staphyloxanthin production and activates the thiol-based oxidative-stress response in. <i>Virulence</i> , 2019 , 10, 625-642	4.7	24
24	Genomic structure and diversity of Plasmodium falciparum in Southeast Asia reveal recent parasite migration patterns. <i>Nature Communications</i> , 2019 , 10, 2665	17.4	20
23	A Genome-Wide Association Study of Idiopathic Dilated Cardiomyopathy in African Americans. <i>Journal of Personalized Medicine</i> , 2018 , 8,	3.6	20
22	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic Escherichia coli prototype isolates. <i>Frontiers in Microbiology</i> , 2015 , 6, 569	5.7	19
21	Whole blood transcriptomic profiles can differentiate vulnerability to chronic low back pain. <i>PLoS ONE</i> , 2019 , 14, e0216539	3.7	17
20	Cross-species transcriptional analysis reveals conserved and host-specific neoplastic processes in mammalian glioma. <i>Scientific Reports</i> , 2018 , 8, 1180	4.9	15
19	Therapeutic implications of mixed biofilm in a murine subcutaneous catheter model of polymicrobial infection. <i>Virulence</i> , 2021 , 12, 835-851	4.7	13
18	Identification of a gene expression signature associated with the metastasis suppressor function of NME1: prognostic value in human melanoma. <i>Laboratory Investigation</i> , 2018 , 98, 327-338	5.9	9
17	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018 , 8, 13377	4.9	9
16	Transcriptional Variation of Diverse Enteropathogenic Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017 , 2,	7.6	8
15	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017 , 3, e000122	4.4	8
14	Venetoclax and pegcrisantaspase for complex karyotype acute myeloid leukemia. <i>Leukemia</i> , 2021 , 35, 1907-1924	10.7	6
13	Tobacco Hornworm () caterpillars as a novel host model for the study of fungal virulence and drug efficacy. <i>Virulence</i> , 2020 , 11, 1075-1089	4.7	6
12	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021 , 22, 121	18.3	6

11	Determining <i>Aspergillus fumigatus</i> transcription factor expression and function during invasion of the mammalian lung. <i>PLoS Pathogens</i> , 2021 , 17, e1009235	7.6	5
10	Repeated sampling facilitates within- and between-subject modeling of the human sperm transcriptome to identify dynamic and stress-responsive sncRNAs. <i>Scientific Reports</i> , 2020 , 10, 17498	4.9	4
9	Integrated analysis of miRNAs and DNA methylation identifies miR-132-3p as a tumor suppressor in lung adenocarcinoma. <i>Thoracic Cancer</i> , 2020 , 11, 2112-2124	3.2	3
8	Evolutionary history of modern Samoans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 9458-9465	11.5	3
7	Detecting geospatial patterns of <i>Plasmodium falciparum</i> parasite migration in Cambodia using optimized estimated effective migration surfaces. <i>International Journal of Health Geographics</i> , 2020 , 19, 13	3.5	2
6	Altered Huntingtin-Chromatin Interactions Predict Transcriptional and Epigenetic Changes in Huntington's Disease		2
5	Tissue Damage in Radiation-Induced Oral Mucositis Is Mitigated by IL-17 Receptor Signaling. <i>Frontiers in Immunology</i> , 2021 , 12, 687627	8.4	2
4	Monocyte Subsets With High Osteoclastogenic Potential and Their Epigenetic Regulation Orchestrated by IRF8. <i>Journal of Bone and Mineral Research</i> , 2021 , 36, 199-214	6.3	2
3	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. <i>MSystems</i> , 2021 , 6,	7.6	2
2	Dual RNA-Seq of Chlamydia and Host Cells. <i>Methods in Molecular Biology</i> , 2019 , 2042, 123-135	1.4	1
1	Comprehensive molecular profiling of UV-induced metastatic melanoma in Nme1/Nme2-deficient mice reveals novel markers of survival in human patients. <i>Oncogene</i> , 2021 , 40, 6329-6342	9.2	1