

Amol C Shetty

List of Publications by Year in Descending Order

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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	Venetoclax and pegcrisantaspace for complex karyotype acute myeloid leukemia. <i>Leukemia</i> , 2021 , 35, 1907-1924	10.7	6
45	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
44	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021 , 22, 121	18.3	6
43	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
42	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
41	Therapeutic implications of mixed biofilm in a murine subcutaneous catheter model of polymicrobial infection. <i>Virulence</i> , 2021 , 12, 835-851	4.7	13
40	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. <i>MSystems</i> , 2021 , 6,	7.6	2
39	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268
38	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
37	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
36	Oral epithelial IL-22/STAT3 signaling licenses IL-17-mediated immunity to oral mucosal candidiasis. <i>Science Immunology</i> , 2020 , 5,	28	29
35	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. <i>Nature Communications</i> , 2020 , 11, 1499	17.4	58
34	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
33	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
32	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
31	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
30	Genomic structure and diversity of <i>Plasmodium falciparum</i> in Southeast Asia reveal recent parasite migration patterns. <i>Nature Communications</i> , 2019 , 10, 2665	17.4	20

29	Whole blood transcriptomic profiles can differentiate vulnerability to chronic low back pain. <i>PLoS ONE</i> , 2019 , 14, e0216539	3.7	17
28	Dual RNA-Seq of Chlamydia and Host Cells. <i>Methods in Molecular Biology</i> , 2019 , 2042, 123-135	1.4	1
27	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
26	Cross-species transcriptional analysis reveals conserved and host-specific neoplastic processes in mammalian glioma. <i>Scientific Reports</i> , 2018 , 8, 1180	4.9	15
25	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
24	Inhibition of EGFR Signaling Protects from Mucormycosis. <i>MBio</i> , 2018 , 9,	7.8	28
23	Iron restriction inside macrophages regulates pulmonary host defense against <i>Rhizopus</i> species. <i>Nature Communications</i> , 2018 , 9, 3333	17.4	48
22	A comparative analysis of library prep approaches for sequencing low input transcriptome samples. <i>BMC Genomics</i> , 2018 , 19, 696	4.5	30
21	A Genome-Wide Association Study of Idiopathic Dilated Cardiomyopathy in African Americans. <i>Journal of Personalized Medicine</i> , 2018 , 8,	3.6	20
20	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018 , 8, 13377	4.9	9
19	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
18	Association of a Novel Mutation in the <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. <i>Journal of Infectious Diseases</i> , 2017 , 216, 468-476	7	75
17	Comparative genomics and transcriptomics of <i>Escherichia coli</i> isolates carrying virulence factors of both enteropathogenic and enterotoxigenic <i>E. coli</i> . <i>Scientific Reports</i> , 2017 , 7, 3513	4.9	27
16	Transcriptional Variation of Diverse Enteropathogenic Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017 , 2,	7.6	8
15	<i>Streptococcus pneumoniae</i> in the heart subvert the host response through biofilm-mediated resident macrophage killing. <i>PLoS Pathogens</i> , 2017 , 13, e1006582	7.6	38
14	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017 , 3, e000122	4.4	8
13	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016 , 7, 12218	17.4	69
12	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

11	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
10	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
9	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
8	Brain feminization requires active repression of masculinization via DNA methylation. <i>Nature Neuroscience</i> , 2015 , 18, 690-7	25.5	264
7	Drosophila anti-nematode and antibacterial immune regulators revealed by RNA-Seq. <i>BMC Genomics</i> , 2015 , 16, 519	4.5	45
6	Transcriptomic analysis of vulvovaginal candidiasis identifies a role for the NLRP3 inflammasome. <i>MBio</i> , 2015 , 6,	7.8	83
5	Molecular epidemiology and genomics of group A Streptococcus. <i>Infection, Genetics and Evolution</i> , 2015 , 33, 393-418	4.5	47
4	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
3	Characterization of microRNA transcriptome in lung cancer by next-generation deep sequencing. <i>Molecular Oncology</i> , 2014 , 8, 1208-19	7.9	59
2	Simultaneous transcriptional profiling of bacteria and their host cells. <i>PLoS ONE</i> , 2013 , 8, e80597	3.7	85
1	Altered Huntingtin-Chromatin Interactions Predict Transcriptional and Epigenetic Changes in Huntington's Disease		2