Amol C Shetty

List of Publications by Year
in descending order

48 papers	3,476 citations	201674 27 h-index	206112 48 g-index
54 all docs	54 docs citations	54 times ranked	7915 citing authors

#	Article	IF	Citations
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	Brain feminization requires active repression of masculinization via DNA methylation. Nature Neuroscience, 2015, 18, 690-697.	14.8	339
3	Simultaneous Transcriptional Profiling of Bacteria and Their Host Cells. PLoS ONE, 2013, 8, e80597.	2.5	125
4	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. Nature Communications, 2020, 11, 1499.	12.8	125
5	Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6526-E6535.	7.1	115
6	Transcriptomic Analysis of Vulvovaginal Candidiasis Identifies a Role for the NLRP3 Inflammasome. MBio, 2015, 6, .	4.1	114
7	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. Nature Communications, 2016, 7, 12218.	12.8	103
8	Association of a Novel Mutation in the Plasmodium falciparum Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. Journal of Infectious Diseases, 2017, 216, 468-476.	4.0	102
9	Iron restriction inside macrophages regulates pulmonary host defense against Rhizopus species. Nature Communications, 2018, 9, 3333.	12.8	85
10	New signaling pathways govern the host response to *C. albicans* infection in various niches. Genome Research, 2015, 25, 679-689.	5.5	82
11	Genome-wide diversity and gene expression profiling of Babesia microti isolates identify polymorphic genes that mediate host-pathogen interactions. Scientific Reports, 2016, 6, 35284.	3.3	74
12	MNKs act as a regulatory switch for eIF4E1 and eIF4E3 driven mRNA translation in DLBCL. Nature Communications, 2014, 5, 5413.	12.8	73
13	Characterization of microRNA transcriptome in lung cancer by next†generation deep sequencing. Molecular Oncology, 2014, 8, 1208-1219.	4.6	73
14	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	12.8	68
15	A comparative analysis of library prep approaches for sequencing low input translatome samples. BMC Genomics, 2018, 19, 696.	2.8	66
16	Oral epithelial IL-22/STAT3 signaling licenses IL-17†"mediated immunity to oral mucosal candidiasis. Science Immunology, 2020, 5, .	11.9	66
17	Molecular epidemiology and genomics of group A Streptococcus. Infection, Genetics and Evolution, 2015, 33, 393-418.	2.3	65
18	Streptococcus pneumoniae in the heart subvert the host response through biofilm-mediated resident macrophage killing. PLoS Pathogens, 2017, 13, e1006582.	4.7	62

#	Article	IF	Citations
19	Drosophila anti-nematode and antibacterial immune regulators revealed by RNA-Seq. BMC Genomics, 2015, 16, 519.	2.8	55
20	Best practices on the differential expression analysis of multi-species RNA-seq. Genome Biology, 2021, 22, 121.	8.8	51
21	Genomic structure and diversity of Plasmodium falciparum in Southeast Asia reveal recent parasite migration patterns. Nature Communications, 2019, 10, 2665.	12.8	46
22	Comparative genomics and transcriptomics of Escherichia coli isolates carrying virulence factors of both enteropathogenic and enterotoxigenic E. coli. Scientific Reports, 2017, 7, 3513.	3.3	45
23	Inhibition of EGFR Signaling Protects from Mucormycosis. MBio, 2018, 9, .	4.1	45
24	Whole blood transcriptomic profiles can differentiate vulnerability to chronic low back pain. PLoS ONE, 2019, 14, e0216539.	2.5	39
25	A Genome-Wide Association Study of Idiopathic Dilated Cardiomyopathy in African Americans. Journal of Personalized Medicine, 2018, 8, 11.	2.5	38
26	Therapeutic implications of <i>C. albicans-S. aureus</i> mixed biofilm in a murine subcutaneous catheter model of polymicrobial infection. Virulence, 2021, 12, 835-851.	4.4	37
27	<i>Candida albicans</i> quorum-sensing molecule farnesol modulates staphyloxanthin production and activates the thiol-based oxidative-stress response in <i>Staphylococcus aureus</i>. Virulence, 2019, 10, 625-642.	4.4	35
28	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic Escherichia coli prototype isolates. Frontiers in Microbiology, 2015, 6, 569.	3.5	32
29	Determining Aspergillus fumigatus transcription factor expression and function during invasion of the mammalian lung. PLoS Pathogens, 2021, 17, e1009235.	4.7	28
30	Cross-species transcriptional analysis reveals conserved and host-specific neoplastic processes in mammalian glioma. Scientific Reports, 2018, 8, 1180.	3.3	22
31	Venetoclax and pegcrisantaspase for complex karyotype acute myeloid leukemia. Leukemia, 2020, 35, 1907-1924.	7.2	19
32	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. Scientific Reports, 2018, 8, 13377.	3.3	17
33	Repeated sampling facilitates within- and between-subject modeling of the human sperm transcriptome to identify dynamic and stress-responsive sncRNAs. Scientific Reports, 2020, 10, 17498.	3.3	16
34	Evolutionary history of modern Samoans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9458-9465.	7.1	14
35	Identification of a gene expression signature associated with the metastasis suppressor function of NME1: prognostic value in human melanoma. Laboratory Investigation, 2018, 98, 327-338.	3.7	13
36	Monocyte Subsets With High Osteoclastogenic Potential and Their Epigenetic Regulation Orchestrated by IRF8. Journal of Bone and Mineral Research, 2020, 36, 199-214.	2.8	13

#	Article	IF	Citations
37	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. Microbial Genomics, 2017, 3, e000122.	2.0	13
38	Transcriptional Variation of Diverse Enteropathogenic Escherichia coli Isolates under Virulence-Inducing Conditions. MSystems, 2017, 2, .	3.8	12
39	Tobacco Hornworm (*Manduca sexta*) caterpillars as a novel host model for the study of fungal virulence and drug efficacy. Virulence, 2020, 11, 1075-1089.	4.4	12
40	Tissue Damage in Radiation-Induced Oral Mucositis Is Mitigated by IL-17 Receptor Signaling. Frontiers in Immunology, 2021, 12, 687627.	4.8	11
41	Multiple genetic paths including massive gene amplification allow *Mycobacterium tuberculosis* to overcome loss of ESX-3 secretion system substrates. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
42	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. MSystems, 2021, 6, .	3.8	8
43	Comprehensive molecular profiling of UV-induced metastatic melanoma in Nme1/Nme2-deficient mice reveals novel markers of survival in human patients. Oncogene, 2021, 40, 6329-6342.	5.9	8
44	Dual RNA-Seq of Chlamydia and Host Cells. Methods in Molecular Biology, 2019, 2042, 123-135.	0.9	7
45	Integrated analysis of miRNAs and DNA methylation identifies miRâ€132â€3p as a tumor suppressor in lung adenocarcinoma. Thoracic Cancer, 2020, 11, 2112-2124.	1.9	6
46	Detecting geospatial patterns of Plasmodium falciparum parasite migration in Cambodia using optimized estimated effective migration surfaces. International Journal of Health Geographics, 2020, 19, 13.	2.5	2
47	Translatome changes in acute myeloid leukemia cells post-exposure to pegcrisantaspase and venetoclax. Experimental Hematology, 2022, , .	0.4	2
48	Cost effective, experimentally robust differential-expression analysis for human/mammalian, pathogen and dual-species transcriptomics. Microbial Genomics, 2020, 6, .	2.0	0