

# Amol C Shetty

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Translatome changes in acute myeloid leukemia cells post-exposure to pegcrisantaspace and venetoclax. <i>Experimental Hematology</i> , 2022, , .	0.4	2
2	Multiple genetic paths including massive gene amplification allow <i>Mycobacterium tuberculosis</i> to overcome loss of ESX-3 secretion system substrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	9
3	Therapeutic implications of <i>C. albicans</i> - <i>S. aureus</i> mixed biofilm in a murine subcutaneous catheter model of polymicrobial infection. <i>Virulence</i> , 2021, 12, 835-851.	4.4	37
4	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. <i>MSystems</i> , 2021, 6, .	3.8	8
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
6	Determining <i>Aspergillus fumigatus</i> transcription factor expression and function during invasion of the mammalian lung. <i>PLoS Pathogens</i> , 2021, 17, e1009235.	4.7	28
7	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	8.8	51
8	Tissue Damage in Radiation-Induced Oral Mucositis Is Mitigated by IL-17 Receptor Signaling. <i>Frontiers in Immunology</i> , 2021, 12, 687627.	4.8	11
9	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.	5.9	8
10	Venetoclax and pegcrisantaspace for complex karyotype acute myeloid leukemia. <i>Leukemia</i> , 2020, 35, 1907-1924.	7.2	19
11	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.	3.3	16
12	Tobacco Hornworm ( <i>Manduca sexta</i> ) caterpillars as a novel host model for the study of fungal virulence and drug efficacy. <i>Virulence</i> , 2020, 11, 1075-1089.	4.4	12
13	Integrated analysis of miRNAs and DNA methylation identifies miR-32 as a tumor suppressor in lung adenocarcinoma. <i>Thoracic Cancer</i> , 2020, 11, 2112-2124.	1.9	6
14	Oral epithelial IL-22/STAT3 signaling licenses IL-17-mediated immunity to oral mucosal candidiasis. <i>Science Immunology</i> , 2020, 5, .	11.9	66
15	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. <i>Nature Communications</i> , 2020, 11, 1499.	12.8	125
16	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.	2.5	2
17	Evolutionary history of modern Samoans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9458-9465.	7.1	14
18	Monocyte Subsets With High Osteoclastogenic Potential and Their Epigenetic Regulation Orchestrated by IRF8. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 199-214.	2.8	13

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19	Cost effective, experimentally robust differential-expression analysis for human/mammalian, pathogen and dual-species transcriptomics. <i>Microbial Genomics</i> , 2020, 6, .	2.0	0
20	Dual RNA-Seq of Chlamydia and Host Cells. <i>Methods in Molecular Biology</i> , 2019, 2042, 123-135.	0.9	7
21	<i>Candida albicans</i> quorum-sensing molecule farnesol modulates staphyloxanthin production and activates the thiol-based oxidative-stress response in <i>Staphylococcus aureus</i> . <i>Virulence</i> , 2019, 10, 625-642.	4.4	35
22	Genomic structure and diversity of <i>Plasmodium falciparum</i> in Southeast Asia reveal recent parasite migration patterns. <i>Nature Communications</i> , 2019, 10, 2665.	12.8	46
23	Whole blood transcriptomic profiles can differentiate vulnerability to chronic low back pain. <i>PLoS ONE</i> , 2019, 14, e0216539.	2.5	39
24	Cross-species transcriptional analysis reveals conserved and host-specific neoplastic processes in mammalian glioma. <i>Scientific Reports</i> , 2018, 8, 1180.	3.3	22
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.	3.7	13
26	A comparative analysis of library prep approaches for sequencing low input transcriptome samples. <i>BMC Genomics</i> , 2018, 19, 696.	2.8	66
27	A Genome-Wide Association Study of Idiopathic Dilated Cardiomyopathy in African Americans. <i>Journal of Personalized Medicine</i> , 2018, 8, 11.	2.5	38
28	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018, 8, 13377.	3.3	17
29	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.	7.1	115
30	Inhibition of EGFR Signaling Protects from Mucormycosis. <i>MBio</i> , 2018, 9, .	4.1	45
31	Iron restriction inside macrophages regulates pulmonary host defense against <i>Rhizopus</i> species. <i>Nature Communications</i> , 2018, 9, 3333.	12.8	85
32	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.	4.0	102
33	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.	3.3	45
34	Transcriptional Variation of Diverse Enteropathogenic <i>Escherichia coli</i> Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017, 2, .	3.8	12
35	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017, 3, e000122.	2.0	13
36	<i>Streptococcus pneumoniae</i> in the heart subvert the host response through biofilm-mediated resident macrophage killing. <i>PLoS Pathogens</i> , 2017, 13, e1006582.	4.7	62

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37	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. Nature Communications, 2016, 7, 12218.	12.8	103
38	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	12.8	68
39	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
40	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
41	New signaling pathways govern the host response to <i>C. albicans</i> infection in various niches. Genome Research, 2015, 25, 679-689.	5.5	82
42	Brain feminization requires active repression of masculinization via DNA methylation. Nature Neuroscience, 2015, 18, 690-697.	14.8	339
43	Drosophila anti-nematode and antibacterial immune regulators revealed by RNA-Seq. BMC Genomics, 2015, 16, 519.	2.8	55
44	Transcriptomic Analysis of Vulvovaginal Candidiasis Identifies a Role for the NLRP3 Inflammasome. MBio, 2015, 6, .	4.1	114
45	Molecular epidemiology and genomics of group A Streptococcus. Infection, Genetics and Evolution, 2015, 33, 393-418.	2.3	65
46	MNKs act as a regulatory switch for eIF4E1 and eIF4E3 driven mRNA translation in DLBCL. Nature Communications, 2014, 5, 5413.	12.8	73
47	Characterization of microRNA transcriptome in lung cancer by next-generation deep sequencing. Molecular Oncology, 2014, 8, 1208-1219.	4.6	73
48	Simultaneous Transcriptional Profiling of Bacteria and Their Host Cells. PLoS ONE, 2013, 8, e80597.	2.5	125