

Apurva Narechania

List of Publications by Year in Descending Order

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Version: 2024-04-27

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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.

49
papers

19,947
citations

27
h-index

52
g-index

52
ext. papers

22,894
ext. citations

11.6
avg, IF

4.87
L-index

#	Paper	IF	Citations
49	Multidrug-Resistant Methicillin-Resistant Staphylococcus aureus Associated with Bacteremia and Monocyte Evasion, Rio de Janeiro, Brazil. <i>Emerging Infectious Diseases</i> , 2021 , 27, 2825-2835	10.2	1
48	Adaptation by Ancient Horizontal Acquisition of Butyrate Metabolism Genes in <i>Aggregatibacter actinomycetemcomitans</i> . <i>MBio</i> , 2021 , 12,	7.8	1
47	Genetic variation of staphylococcal LukAB toxin determines receptor tropism. <i>Nature Microbiology</i> , 2021 , 6, 731-745	26.6	3
46	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. <i>Systematic Biology</i> , 2021 , 70, 360-375	8.4	6
45	Genomic Epidemiology of Vancomycin-Resistant Enterococcus faecium (VREfm) in Latin America: Revisiting The Global VRE Population Structure. <i>Scientific Reports</i> , 2020 , 10, 5636	4.9	23
44	Genomic variant-identification methods may alter transmission inferences. <i>Microbial Genomics</i> , 2020 , 6,	4.4	10
43	Local Diversification of Methicillin- Resistant ST239 in South America After Its Rapid Worldwide Dissemination. <i>Frontiers in Microbiology</i> , 2019 , 10, 82	5.7	13
42	Strains of Staphylococcus aureus that Colonize and Infect Skin Harbor Mutations in Metabolic Genes. <i>IScience</i> , 2019 , 19, 281-290	6.1	12
41	CFTR-PTEN-dependent mitochondrial metabolic dysfunction promotes airway infection. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	32
40	Pre-detection history of extensively drug-resistant tuberculosis in KwaZulu-Natal, South Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23284-23291	11.5	12
39	Antimicrobial sensing coupled with cell membrane remodeling mediates antibiotic resistance and virulence in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 ,	11.5	27
38	1232. Phylogenomics of Enterococcus faecium From South America: Revisiting Worldwide VRE Population Structure. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S374-S374	1	78
37	Mobile-Genetic-Element-Encoded Hypertolerance to Copper Protects Staphylococcus aureus from Killing by Host Phagocytes. <i>MBio</i> , 2018 , 9,	7.8	23
36	Transmission of Extensively Drug-Resistant Tuberculosis in South Africa. <i>New England Journal of Medicine</i> , 2017 , 376, 243-253	59.2	167
35	A Prospective Cohort Multicenter Study of Molecular Epidemiology and Phylogenomics of Staphylococcus aureus Bacteremia in Nine Latin American Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	45
34	Architecture of a Species: Phylogenomics of Staphylococcus aureus. <i>Trends in Microbiology</i> , 2017 , 25, 153-166	12.4	37
33	The mitogenome of the bed bug (Hemiptera: Cimicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 425-427	0.5	5

32	Genomic epidemiology of Lineage 4 Mycobacterium tuberculosis subpopulations in New York City and New Jersey, 1999-2009. <i>BMC Genomics</i> , 2016 , 17, 947	4.5	7
31	Clusterflock: a flocking algorithm for isolating congruent phylogenomic datasets. <i>GigaScience</i> , 2016 , 5, 44	7.6	6
30	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016 , 7, 10164	17.4	46
29	Spermatogenesis Drives Rapid Gene Creation and Masculinization of the X Chromosome in Stalk-Eyed Flies (Diopsidae). <i>Genome Biology and Evolution</i> , 2016 , 8, 896-914	3.9	4
28	Co-existence of BRAF and NRAS driver mutations in the same melanoma cells results in heterogeneity of targeted therapy resistance. <i>Oncotarget</i> , 2016 , 7, 77163-77174	3.3	39
27	Rickettsial endosymbiont in the "early-diverging" streptophyte green alga <i>Mesostigma viride</i> . <i>Journal of Phycology</i> , 2016 , 52, 219-29	3	11
26	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016 , 48, 593-9	36.3	204
25	Comparative Genomics of a Bacterivorous Green Alga Reveals Evolutionary Causalities and Consequences of Phago-Mixotrophic Mode of Nutrition. <i>Genome Biology and Evolution</i> , 2015 , 7, 3047-61 ^{3.9}	3.9	24
24	Methicillin-Susceptible, Vancomycin-Resistant <i>Staphylococcus aureus</i> , Brazil. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1844-8	10.2	28
23	Parallel Epidemics of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Infection in North and South America. <i>Journal of Infectious Diseases</i> , 2015 , 212, 1874-82	7	75
22	Transferable vancomycin resistance in a community-associated MRSA lineage. <i>New England Journal of Medicine</i> , 2014 , 370, 1524-31	59.2	110
21	Evolution of hypervirulence by a MRSA clone through acquisition of a transposable element. <i>Molecular Microbiology</i> , 2014 , 93, 664-81	4.1	61
20	Complete Genome Sequence of <i>Streptococcus agalactiae</i> CNCTC 10/84, a Hypervirulent Sequence Type 26 Strain. <i>Genome Announcements</i> , 2014 , 2,		14
19	Induction of type I interferon signaling determines the relative pathogenicity of <i>Staphylococcus aureus</i> strains. <i>PLoS Pathogens</i> , 2014 , 10, e1003951	7.6	69
18	Genome Sequence of Bacterial Interference Strain <i>Staphylococcus aureus</i> 502A. <i>Genome Announcements</i> , 2014 , 2,		20
17	Emergence of the epidemic methicillin-resistant <i>Staphylococcus aureus</i> strain USA300 coincides with horizontal transfer of the arginine catabolic mobile element and <i>speG</i> -mediated adaptations for survival on skin. <i>MBio</i> , 2013 , 4, e00889-13	7.8	82
16	Insect phylogenomics: exploring the source of incongruence using new transcriptomic data. <i>Genome Biology and Evolution</i> , 2012 , 4, 1295-309	3.9	47
15	Gene duplication, tissue-specific gene expression and sexual conflict in stalk-eyed flies (Diopsidae). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012 , 367, 2357-75	5.8	20

14	Random Addition Concatenation Analysis: a novel approach to the exploration of phylogenomic signal reveals strong agreement between core and shell genomic partitions in the cyanobacteria. <i>Genome Biology and Evolution</i> , 2012 , 4, 30-43	3.9	29
13	Catching the phylogenetic history through the ontogenic hourglass: a phylogenomic analysis of <i>Drosophila</i> body segmentation genes. <i>Evolution & Development</i> , 2010 , 12, 288-95	2.6	8
12	A genome-wide characterization of microRNA genes in maize. <i>PLoS Genetics</i> , 2009 , 5, e1000716	6	265
11	Detailed analysis of a contiguous 22-Mb region of the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000728	6	34
10	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009 , 457, 551-6	50.4	2200
9	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 2009 , 326, 1112-5	33.3	2949
8	A new method to compute K-mer frequencies and its application to annotate large repetitive plant genomes. <i>BMC Genomics</i> , 2008 , 9, 517	4.5	169
7	Overlapping reading frames in closely related human papillomaviruses result in modular rates of selection within E2. <i>Journal of General Virology</i> , 2005 , 86, 1307-1313	4.9	42
6	Phylogenetic incongruence among oncogenic genital alpha human papillomaviruses. <i>Journal of Virology</i> , 2005 , 79, 15503-10	6.6	86
5	Lack of the canonical pRB-binding domain in the E7 ORF of artiodactyl papillomaviruses is associated with the development of fibropapillomas. <i>Journal of General Virology</i> , 2004 , 85, 1243-1250	4.9	51
4	PANTHER: a library of protein families and subfamilies indexed by function. <i>Genome Research</i> , 2003 , 13, 2129-41	9.7	2102
3	Assessment of genome-wide protein function classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003 , 13, 2118-28	9.7	35
2	The sequence of the human genome. <i>Science</i> , 2001 , 291, 1304-51	33.3	10609
1	Genomic variant identification methods alter <i>Mycobacterium tuberculosis</i> transmission inference		3