

# Apurva Narechania

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

24,414  
citations

182225

30  
h-index

232693

48  
g-index

52  
all docs

52  
docs citations

52  
times ranked

36498  
citing authors

#	ARTICLE	IF	CITATIONS
1	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. <i>Systematic Biology</i> , 2021, 70, 360-375.	2.7	21
2	Adaptation by Ancient Horizontal Acquisition of Butyrate Metabolism Genes in <i>Aggregatibacter actinomycetemcomitans</i> . <i>MBio</i> , 2021, 12, .	1.8	2
3	Genetic variation of staphylococcal LukAB toxin determines receptor tropism. <i>Nature Microbiology</i> , 2021, 6, 731-745.	5.9	14
4	Multidrug-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> Associated with Bacteremia and Monocyte Evasion, Rio de Janeiro, Brazil. <i>Emerging Infectious Diseases</i> , 2021, 27, 2825-2835.	2.0	16
5	Genomic Epidemiology of Vancomycin-Resistant <i>Enterococcus faecium</i> (VREfm) in Latin America: Revisiting The Global VRE Population Structure. <i>Scientific Reports</i> , 2020, 10, 5636.	1.6	39
6	Genomic variant-identification methods may alter <i>Mycobacterium tuberculosis</i> transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
7	Strains of <i>Staphylococcus aureus</i> that Colonize and Infect Skin Harbor Mutations in Metabolic Genes. <i>IScience</i> , 2019, 19, 281-290.	1.9	22
8	CFTR-PTEN-dependent mitochondrial metabolic dysfunction promotes <i>Pseudomonas aeruginosa</i> airway infection. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	65
9	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.	3.3	23
10	Local Diversification of Methicillin- Resistant <i>Staphylococcus aureus</i> ST239 in South America After Its Rapid Worldwide Dissemination. <i>Frontiers in Microbiology</i> , 2019, 10, 82.	1.5	20
11	Antimicrobial sensing coupled with cell membrane remodeling mediates antibiotic resistance and virulence in <i>Enterococcus faecalis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26925-26932.	3.3	58
12	1232. Phylogenomics of <i>Enterococcus faecium</i> From South America: Revisiting Worldwide VRE Population Structure. <i>Open Forum Infectious Diseases</i> , 2018, 5, S374-S374.	0.4	0
13	Mobile-Genetic-Element-Encoded Hypertolerance to Copper Protects <i>Staphylococcus aureus</i> from Killing by Host Phagocytes. <i>MBio</i> , 2018, 9, .	1.8	33
14	Transmission of Extensively Drug-Resistant Tuberculosis in South Africa. <i>New England Journal of Medicine</i> , 2017, 376, 243-253.	13.9	230
15	A Prospective Cohort Multicenter Study of Molecular Epidemiology and Phylogenomics of <i>Staphylococcus aureus</i> Bacteremia in Nine Latin American Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	95
16	Architecture of a Species: Phylogenomics of <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , 2017, 25, 153-166.	3.5	91
17	Co-existence of <i>BRAF</i> and <i>NRAS</i> driver mutations in the same melanoma cells results in heterogeneity of targeted therapy resistance. <i>Oncotarget</i> , 2016, 7, 77163-77174.	0.8	73
18	Genomic Epidemiology of Lineage 4 <i>Mycobacterium tuberculosis</i> Subpopulations in New York City and New Jersey, 1999-2009. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.4	0

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19	Rickettsial endosymbiont in the "early" diverging streptophyte green alga <i>Mesostigma viride</i> . <i>Journal of Phycology</i> , 2016, 52, 219-229.	1.0	21
20	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
21	The mitogenome of the bed bug <i>Cimex lectularius</i> (Hemiptera: Cimicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 425-427.	0.2	5
22	Genomic epidemiology of Lineage 4 <i>Mycobacterium tuberculosis</i> subpopulations in New York City and New Jersey, 1999-2009. <i>BMC Genomics</i> , 2016, 17, 947.	1.2	13
23	Clusterflock: a flocking algorithm for isolating congruent phylogenomic datasets. <i>GigaScience</i> , 2016, 5, 44.	3.3	7
24	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
25	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.	1.1	9
26	Methicillin-Susceptible, Vancomycin-Resistant <i>Staphylococcus aureus</i> , Brazil. <i>Emerging Infectious Diseases</i> , 2015, 21, 1844-1848.	2.0	38
27	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, 1874-1882.	1.9	107
28	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, 3047-3061.	1.1	36
29	Complete Genome Sequence of <i>Streptococcus agalactiae</i> CNCTC 10/84, a Hypervirulent Sequence Type 26 Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
30	Induction of Type I Interferon Signaling Determines the Relative Pathogenicity of <i>Staphylococcus aureus</i> Strains. <i>PLoS Pathogens</i> , 2014, 10, e1003951.	2.1	84
31	Genome Sequence of Bacterial Interference Strain <i>Staphylococcus aureus</i> 502A. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
32	Transferable Vancomycin Resistance in a Community-Associated MRSA Lineage. <i>New England Journal of Medicine</i> , 2014, 370, 1524-1531.	13.9	136
33	Evolution of hypervirulence by a MRSA clone through acquisition of a transposable element. <i>Molecular Microbiology</i> , 2014, 93, 664-681.	1.2	93
34	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.	1.8	108
35	Insect Phylogenomics: Exploring the Source of Incongruence Using New Transcriptomic Data. <i>Genome Biology and Evolution</i> , 2012, 4, 1295-1309.	1.1	71
36	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, 2357-2375.	1.8	29

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37	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.	1.1	34
38	Catching the phylogenetic history through the ontogenic hourglass: a phylogenomic analysis of <i>Drosophila</i> body segmentation genes. <i>Evolution &amp; Development</i> , 2010, 12, 288-295.	1.1	8
39	A Genome-Wide Characterization of MicroRNA Genes in Maize. <i>PLoS Genetics</i> , 2009, 5, e1000716.	1.5	318
40	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
41	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
42	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
43	A new method to compute K-mer frequencies and its application to annotate large repetitive plant genomes. <i>BMC Genomics</i> , 2008, 9, 517.	1.2	214
44	Phylogenetic Incongruence among Oncogenic Genital Alpha Human Papillomaviruses. <i>Journal of Virology</i> , 2005, 79, 15503-15510.	1.5	94
45	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.	1.3	45
46	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.	1.3	56
47	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. <i>Genome Research</i> , 2003, 13, 2129-2141.	2.4	2,703
48	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40
49	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623