

# Apurva Narechania

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

24,414  
citations

159525

30  
h-index

206029

48  
g-index

52  
all docs

52  
docs citations

52  
times ranked

32482  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
2	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
3	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. <i>Genome Research</i> , 2003, 13, 2129-2141.	2.4	2,703
4	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
5	A Genome-Wide Characterization of MicroRNA Genes in Maize. <i>PLoS Genetics</i> , 2009, 5, e1000716.	1.5	318
6	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
7	Transmission of Extensively Drug-Resistant Tuberculosis in South Africa. <i>New England Journal of Medicine</i> , 2017, 376, 243-253.	13.9	230
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.	1.2	214
9	Transferable Vancomycin Resistance in a Community-Associated MRSA Lineage. <i>New England Journal of Medicine</i> , 2014, 370, 1524-1531.	13.9	136
10	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
11	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
12	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
13	Phylogenetic Incongruence among Oncogenic Genital Alpha Human Papillomaviruses. <i>Journal of Virology</i> , 2005, 79, 15503-15510.	1.5	94
14	Evolution of hypervirulence by a MRSA clone through acquisition of a transposable element. <i>Molecular Microbiology</i> , 2014, 93, 664-681.	1.2	93
15	Architecture of a Species: Phylogenomics of <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , 2017, 25, 153-166.	3.5	91
16	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
17	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
18	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

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19	Insect Phylogenomics: Exploring the Source of Incongruence Using New Transcriptomic Data. <i>Genome Biology and Evolution</i> , 2012, 4, 1295-1309.	1.1	71
20	CFTR-PTEN-dependent mitochondrial metabolic dysfunction promotes <i>Pseudomonas aeruginosa</i> airway infection. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	65
21	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
22	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
23	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
24	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40
25	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
26	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
27	Methicillin-Susceptible, Vancomycin-Resistant <i>Staphylococcus aureus</i> , Brazil. <i>Emerging Infectious Diseases</i> , 2015, 21, 1844-1848.	2.0	38
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	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
30	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
31	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
32	Genomic variant-identification methods may alter <i>Mycobacterium tuberculosis</i> transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
33	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
34	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
35	Genome Sequence of Bacterial Interference Strain <i>Staphylococcus aureus</i> 502A. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
36	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

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37	Rickettsial endosymbiont in the "early"diverging"streptophyte green alga <i>Mesostigma viride</i> . Journal of Phycology, 2016, 52, 219-229.	1.0	21
38	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. Systematic Biology, 2021, 70, 360-375.	2.7	21
39	Local Diversification of Methicillin- Resistant Staphylococcus aureus ST239 in South America After Its Rapid Worldwide Dissemination. Frontiers in Microbiology, 2019, 10, 82.	1.5	20
40	Multidrug-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> Associated with Bacteremia and Monocyte Evasion, Rio de Janeiro, Brazil. Emerging Infectious Diseases, 2021, 27, 2825-2835.	2.0	16
41	Genetic variation of staphylococcal LukAB toxin determines receptor tropism. Nature Microbiology, 2021, 6, 731-745.	5.9	14
42	Genomic epidemiology of Lineage 4 Mycobacterium tuberculosis subpopulations in New York City and New Jersey, 1999"2009. BMC Genomics, 2016, 17, 947.	1.2	13
43	Spermatogenesis Drives Rapid Gene Creation and Masculinization of the X Chromosome in Stalk-Eyed Flies (Diopsidae). Genome Biology and Evolution, 2016, 8, 896-914.	1.1	9
44	Catching the phylogenetic history through the ontogenic hourglass: a phylogenomic analysis of <i>Drosophila</i> body segmentation genes. Evolution & Development, 2010, 12, 288-295.	1.1	8
45	Clusterflock: a flocking algorithm for isolating congruent phylogenomic datasets. GigaScience, 2016, 5, 44.	3.3	7
46	The mitogenome of the bed bug <i>Cimex lectularius</i> (Hemiptera: Cimicidae). Mitochondrial DNA Part B: Resources, 2016, 1, 425-427.	0.2	5
47	Adaptation by Ancient Horizontal Acquisition of Butyrate Metabolism Genes in <i>Aggregatibacter actinomycetemcomitans</i> . MBio, 2021, 12, .	1.8	2
48	Genomic Epidemiology of Lineage 4 Mycobacterium tuberculosis Subpopulations in New York City and New Jersey, 1999"2009. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
49	1232. Phylogenomics of <i>Enterococcus faecium</i> From South America: Revisiting Worldwide VRE Population Structure. Open Forum Infectious Diseases, 2018, 5, S374-S374.	0.4	0