

# Lavanya Rishishwar

## List of Publications by Year in descending order

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49  
papers

1,249  
citations

430874

18  
h-index

414414

32  
g-index

57  
all docs

57  
docs citations

57  
times ranked

2326  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of Genetic Ancestry and Molecular Signatures with Cancer Survival Disparities: A Pan-Cancer Analysis. <i>Cancer Research</i> , 2022, 82, 1222-1233.	0.9	11
2	Effects of genetic ancestry and socioeconomic deprivation on ethnic differences in serum creatinine. <i>Gene</i> , 2022, 837, 146709.	2.2	4
3	Genomic characterization and computational phenotyping of nitrogen-fixing bacteria isolated from Colombian sugarcane fields. <i>Scientific Reports</i> , 2021, 11, 9187.	3.3	10
4	The Impact of Ethnicity and Genetic Ancestry on Disease Prevalence and Risk in Colombia. <i>Frontiers in Genetics</i> , 2021, 12, 690366.	2.3	8
5	Genetic ancestry and ethnic identity in Ecuador. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100050.	1.7	4
6	Genome-Enabled Molecular Subtyping and Serotyping for Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	3.9	1
7	Comparing Genetic and Socioenvironmental Contributions to Ethnic Differences in C-Reactive Protein. <i>Frontiers in Genetics</i> , 2021, 12, 738485.	2.3	7
8	The Phenotypic Consequences of Genetic Divergence between Admixed Latin American Populations: Antioquia and Chocó <sup>3</sup> , Colombia. <i>Genome Biology and Evolution</i> , 2020, 12, 1516-1527.	2.5	3
9	STing: accurate and ultrafast genomic profiling with exact sequence matches. <i>Nucleic Acids Research</i> , 2020, 48, 7681-7689.	14.5	5
10	Ancestry effects on type 2 diabetes genetic risk inference in Hispanic/Latino populations. <i>BMC Medical Genetics</i> , 2020, 21, 132.	2.1	17
11	Admixture-enabled selection for rapid adaptive evolution in the Americas. <i>Genome Biology</i> , 2020, 21, 29.	8.8	36
12	An atlas of transposable element-derived alternative splicing in cancer. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190342.	4.0	26
13	Analysis of <i>Vibrio cholerae</i> genomes identifies new type VI secretion system gene clusters. <i>Genome Biology</i> , 2019, 20, 163.	8.8	45
14	Native American admixture recapitulates population-specific migration and settlement of the continental United States. <i>PLoS Genetics</i> , 2019, 15, e1008225.	3.5	25
15	Assortative Mating on Ancestry-Variant Traits in Admixed Latin American Populations. <i>Frontiers in Genetics</i> , 2019, 10, 359.	2.3	12
16	Population Pharmacogenomics for Precision Public Health in Colombia. <i>Frontiers in Genetics</i> , 2019, 10, 241.	2.3	29
17	Genome Sequences of 15 <i>Klebsiella</i> sp. Isolates from Sugarcane Fields in Colombia's Cauca Valley. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
18	Diazotroph Community Characterization via a High-Throughput <i>nifH</i> Amplicon Sequencing and Analysis Pipeline. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	78

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19	Genetic ancestry, admixture and health determinants in Latin America. <i>BMC Genomics</i> , 2018, 19, 861.	2.8	78
20	Global Distribution of Genetic Traits (GADGET) web server: polygenic trait scores worldwide. <i>Nucleic Acids Research</i> , 2018, 46, W121-W126.	14.5	8
21	Evidence for positive selection on recent human transposable element insertions. <i>Gene</i> , 2018, 675, 69-79.	2.2	30
22	Benchmarking computational tools for polymorphic transposable element detection. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw072.	6.5	64
23	Population and clinical genetics of human transposable elements in the (post) genomic era. <i>Mobile Genetic Elements</i> , 2017, 7, 1-20.	1.8	22
24	Implications of human evolution and admixture for mitochondrial replacement therapy. <i>BMC Genomics</i> , 2017, 18, 140.	2.8	44
25	A Comparative Analysis of Genetic Ancestry and Admixture in the Colombian Populations of Chocó <sup>3</sup> and Medellín. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3435-3447.	1.8	39
26	Influence of genetic ancestry and socioeconomic status on type 2 diabetes in the diverse Colombian populations of Chocó <sup>3</sup> and Antioquia. <i>Scientific Reports</i> , 2017, 7, 17127.	3.3	17
27	stringMLST: a fast k-mer based tool for multilocus sequence typing. <i>Bioinformatics</i> , 2017, 33, 119-121.	4.1	72
28	A decade of viral mutations and associated drug resistance in a population of HIV-1+ Puerto Ricans: 2002–2011. <i>PLoS ONE</i> , 2017, 12, e0177452.	2.5	4
29	Patterns of Transposable Element Expression and Insertion in Cancer. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 76.	3.5	21
30	El Chocó <sup>3</sup> , Colombia: un hotspot de la biodiversidad humana. <i>Revista Biodiversidad Neotropical</i> , 2016, 6, 45.	0.2	15
31	Human population-specific gene expression and transcriptional network modification with polymorphic transposable elements. <i>Nucleic Acids Research</i> , 2016, 45, gkw1286.	14.5	45
32	Whole-Genome Sequences of 26 <i>Vibrio cholerae</i> Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
33	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	4.1	105
34	Comparative Genomic Analysis of <i>Haemophilus haemolyticus</i> and Nontypeable <i>Haemophilus influenzae</i> and a New Testing Scheme for Their Discrimination. <i>Journal of Clinical Microbiology</i> , 2016, 54, 3010-3017.	3.9	12
35	Population Genomics of Reduced Vancomycin Susceptibility in <i>Staphylococcus aureus</i> . <i>MSphere</i> , 2016, 1, .	2.9	16
36	Characterization of clinical and environmental isolates of <i>Vibrio cidicii</i> sp. nov., a close relative of <i>Vibrio navarrensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4148-4155.	1.7	21

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37	Transposable element polymorphisms recapitulate human evolution. <i>Mobile DNA</i> , 2015, 6, 21.	3.6	58
38	Ancestry, admixture and fitness in Colombian genomes. <i>Scientific Reports</i> , 2015, 5, 12376.	3.3	85
39	A combined evidence Bayesian method for human ancestry inference applied to Afro-Colombians. <i>Gene</i> , 2015, 574, 345-351.	2.2	7
40	Insights into Environmental Microbial Denitrification from Integrated Metagenomic, Cultivation, and Genomic Analyses. , 2015, , 293-303.		1
41	Genome Sequence-Based Discriminator for Vancomycin-Intermediate <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2014, 196, 940-948.	2.2	29
42	Genome Sequences of <i>Vibrio navarrensis</i> , a Potential Human Pathogen. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
43	Origin and evolution of the cystic fibrosis transmembrane regulator protein R domain. <i>Gene</i> , 2013, 523, 137-146.	2.2	25
44	Insights into Environmental Microbial Denitrification from Integrated Metagenomic, Cultivation, and Genomic Analyses. , 2013, , 1-12.		0
45	Genomic Basis of a Polyagglutinating Isolate of <i>Neisseria meningitidis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 5649-5656.	2.2	9
46	Genome Sequences for Six <i>Rhodanobacter</i> Strains, Isolated from Soils and the Terrestrial Subsurface, with Variable Denitrification Capabilities. <i>Journal of Bacteriology</i> , 2012, 194, 4461-4462.	2.2	62
47	Relating the Disease Mutation Spectrum to the Evolution of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR). <i>PLoS ONE</i> , 2012, 7, e42336.	2.5	12
48	Mining Genomic Patterns in <i>Mycobacterium tuberculosis</i> H37Rv Using a Web Server Tuber-Gene. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 171-178.	6.9	0
49	ProCoS: Protein composition server. <i>Bioinformatics</i> , 2010, 5, 227-227.	0.5	3