

# Giri Narasimhan

## List of Publications by Citations

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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.

135  
papers

2,303  
citations

26  
h-index

45  
g-index

169  
ext. papers

2,908  
ext. citations

2.9  
avg, IF

4.81  
L-index

#	Paper	IF	Citations
135	Dynamics of <i>Pseudomonas aeruginosa</i> genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 3100-5	11.5	367
134	Geometric Spanner Networks <b>2007</b> ,		173
133	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. <i>Evolutionary Bioinformatics</i> , <b>2016</b> , 12, 5-16	1.9	140
132	Alginate production affects <i>Pseudomonas aeruginosa</i> biofilm development and architecture, but is not essential for biofilm formation. <i>Journal of Medical Microbiology</i> , <b>2004</b> , 53, 679-690	3.2	125
131	Current concepts in the pathogenesis and treatment of chronic suppurative otitis media. <i>Journal of Medical Microbiology</i> , <b>2015</b> , 64, 1103-1116	3.2	96
130	Distinct transcriptional profiles characterize oral epithelium-microbiota interactions. <i>Cellular Microbiology</i> , <b>2005</b> , 7, 811-23	3.9	89
129	The regulatory repertoire of <i>Pseudomonas aeruginosa</i> AmpC $\beta$ -lactamase regulator AmpR includes virulence genes. <i>PLoS ONE</i> , <b>2012</b> , 7, e34067	3.7	82
128	Fast Greedy Algorithms for Constructing Sparse Geometric Spanners. <i>SIAM Journal on Computing</i> , <b>2002</b> , 31, 1479-1500	1.1	71
127	Mining protein sequences for motifs. <i>Journal of Computational Biology</i> , <b>2002</b> , 9, 707-20	1.7	55
126	Approximating the Stretch Factor of Euclidean Graphs. <i>SIAM Journal on Computing</i> , <b>2000</b> , 30, 978-989	1.1	52
125	NEW SPARSENESS RESULTS ON GRAPH SPANNERS. <i>International Journal of Computational Geometry and Applications</i> , <b>1995</b> , 05, 125-144	0.3	51
124	New sparseness results on graph spanners <b>1992</b> ,		49
123	A Fast Algorithm for Constructing Sparse Euclidean Spanners. <i>International Journal of Computational Geometry and Applications</i> , <b>1997</b> , 07, 297-315	0.3	46
122	Deep sequencing analyses expands the <i>Pseudomonas aeruginosa</i> AmpR regulon to include small RNA-mediated regulation of iron acquisition, heat shock and oxidative stress response. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 979-98	20.1	45
121	So you think you can PLS-DA?. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 2	3.6	44
120	Resource-constrained geometric network optimization <b>1998</b> ,		38
119	Optimally sparse spanners in 3-dimensional Euclidean space <b>1993</b> ,		38

118	Improved Algorithms for Constructing Fault-Tolerant Spanners. <i>Algorithmica</i> , <b>2002</b> , 32, 144-156	0.9	33
117	LR-visibility in polygons. <i>Computational Geometry: Theory and Applications</i> , <b>1997</b> , 7, 37-57	0.4	31
116	Rational design of thermally stable proteins: relevance to bionanotechnology. <i>Journal of Nanoscience and Nanotechnology</i> , <b>2005</b> , 5, 1759-67	1.3	31
115	Transcriptional response of mucoid <i>Pseudomonas aeruginosa</i> to human respiratory mucus. <i>MBio</i> , <b>2013</b> , 3, e00410-12	7.8	30
114	Dynamic interaction network inference from longitudinal microbiome data. <i>Microbiome</i> , <b>2019</b> , 7, 54	16.6	29
113	Approximating geometric bottleneck shortest paths. <i>Computational Geometry: Theory and Applications</i> , <b>2004</b> , 29, 233-249	0.4	29
112	Automatic Construction of 3-D Building Model From Airborne LIDAR Data Through 2-D Snake Algorithm. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , <b>2015</b> , 53, 3-14	8.1	28
111	Structural and functional characterization of <i>Pseudomonas aeruginosa</i> global regulator AmpR. <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 3890-902	3.5	26
110	Microbial "social networks". <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 11, S6	4.5	26
109	Influence of irrigated agriculture on soil microbial diversity. <i>Applied Soil Ecology</i> , <b>2008</b> , 40, 146-154	5	26
108	Efficient algorithms for constructing fault-tolerant geometric spanners <b>1998</b> ,		23
107	Mutation-induced changes in the receptor-binding interface of the SARS-CoV-2 Delta variant B.1.617.2 and implications for immune evasion. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 574, 14-19	3.4	23
106	The gut microbiome and neuropsychiatric disorders: implications for attention deficit hyperactivity disorder (ADHD). <i>Journal of Medical Microbiology</i> , <b>2020</b> , 69, 14-24	3.2	19
105	An eco-informatics tool for microbial community studies: supervised classification of Amplicon Length Heterogeneity (ALH) profiles of 16S rRNA. <i>Journal of Microbiological Methods</i> , <b>2006</b> , 65, 49-62	2.8	18
104	Approximate Distance Oracles Revisited. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 357-368	0.9	17
103	Bioinformatics Approach to Assess the Biogeographical Patterns of Soil Communities: The Utility for Soil Provenance. <i>Journal of Forensic Sciences</i> , <b>2018</b> , 63, 1033-1042	1.8	14
102	Optimal Algorithms for Two-Guard Walkability of Simple Polygons. <i>Lecture Notes in Computer Science</i> , <b>2001</b> , 438-449	0.9	13
101	Improved Greedy Algorithms for Constructing Sparse Geometric Spanners. <i>Lecture Notes in Computer Science</i> , <b>2000</b> , 314-328	0.9	13

100	Degenerate primer design via clustering <b>2003</b> , 2, 75-83		13
99	Better primer design for metagenomics applications by increasing taxonomic distinguishability. <i>BMC Proceedings</i> , <b>2013</b> , 7, S4	2.3	11
98	Approximate distance oracles for geometric spanners. <i>ACM Transactions on Algorithms</i> , <b>2008</b> , 4, 1-34	1.2	11
97	Approaches to analyse dynamic microbial communities such as those seen in cystic fibrosis lung. <i>Human Genomics</i> , <b>2009</b> , 3, 246-56	6.8	10
96	Distance-preserving approximations of polygonal paths. <i>Computational Geometry: Theory and Applications</i> , <b>2007</b> , 36, 183-196	0.4	10
95	A Generalization of maximal independent sets. <i>Discrete Applied Mathematics</i> , <b>2001</b> , 109, 223-235	1	10
94	Dynamic Bayesian Networks for Integrating Multi-omics Time Series Microbiome Data. <i>MSystems</i> , <b>2021</b> , 6,	7.6	10
93	A note on the Hamiltonian Circuit Problem on directed path graphs. <i>Information Processing Letters</i> , <b>1989</b> , 32, 167-170	0.8	9
92	Multiple comparisons model-based clustering and ternary pattern tree numerical display of gene response to treatment: procedure and application to the preclinical evaluation of chemopreventive agents. <i>Molecular Cancer Therapeutics</i> , <b>2002</b> , 1, 1283-92	6.1	9
91	Degenerate primer design via clustering		8
90	Stability number and chromatic number of tolerance graphs. <i>Discrete Applied Mathematics</i> , <b>1992</b> , 36, 47-56	1	8
89	ATria: a novel centrality algorithm applied to biological networks. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 239	3.6	7
88	Fast Pruning of Geometric Spanners. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 508-520	0.9	7
87	ON HAMILTONIAN TRIANGULATIONS IN SIMPLE POLYGONS. <i>International Journal of Computational Geometry and Applications</i> , <b>1999</b> , 09, 261-275	0.3	7
86	Inferring Relationships in Microbiomes from Signed Bayesian Networks <b>2018</b> ,		7
85	Gene expression patterns in transgenic mouse models of hypertrophic cardiomyopathy caused by mutations in myosin regulatory light chain. <i>Archives of Biochemistry and Biophysics</i> , <b>2016</b> , 601, 121-32	4.1	6
84	Combination of 16S rRNA variable regions provides a detailed analysis of bacterial community dynamics in the lungs of cystic fibrosis patients. <i>Human Genomics</i> , <b>2010</b> , 4, 147-69	6.8	6
83	Serial NetEvolve: a flexible utility for generating serially-sampled sequences along a tree or recombinant network. <i>Bioinformatics</i> , <b>2006</b> , 22, 2313-4	7.2	6

82	Sliding MinPD: building evolutionary networks of serial samples via an automated recombination detection approach. <i>Bioinformatics</i> , <b>2007</b> , 23, 2993-3000	7.2	6
81	Optimal linear-time algorithm for the shortest illuminating line segment in a polygon <b>1994</b> ,		6
80	Geometric searching and link distance <b>1991</b> , 261-272		6
79	ESTIMATING SUPPORT FOR PROTEIN-PROTEIN INTERACTION DATA WITH APPLICATIONS TO FUNCTION PREDICTION <b>2008</b> ,		6
78	Region-Restricted Clustering for Geographic Data Mining. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 399-410	4.9	6
77	MinPD: distance-based phylogenetic analysis and recombination detection of serially-sampled HIV quasispecies <b>2004</b> , 110-9		5
76	Inferring directional relationships in microbial communities using signed Bayesian networks. <i>BMC Genomics</i> , <b>2020</b> , 21, 663	4.5	5
75	Can SLE classification rules be effectively applied to diagnose unclear SLE cases?. <i>Lupus</i> , <b>2017</b> , 26, 150-162	6.26	4
74	GPUDePiCt: A Parallel Implementation of a Clustering Algorithm for Computing Degenerate Primers on Graphics Processing Units. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2015</b> , 12, 445-54	3	4
73	Weighted Consensus Clustering for Identifying Functional Modules in Protein-Protein Interaction Networks <b>2009</b> ,		4
72	A Graph Reduction Method for 2D Snake Problems <b>2007</b> ,		4
71	Detection of DNA-binding helix-turn-helix motifs in proteins using the pattern dictionary method. <i>Methods in Enzymology</i> , <b>2003</b> , 370, 250-64	1.7	4
70	Microarray Data Analysis Using Neural Network Classifiers and Gene Selection Methods <b>2005</b> , 207-222		4
69	Identification of Cacao TIR-NBS-LRR Resistance Gene Homologues and Their Use as Genetic Markers. <i>Journal of the American Society for Horticultural Science</i> , <b>2006</b> , 131, 806-813	2.3	4
68	Distance-Preserving Approximations of Polygonal Paths. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 217-228	2.89	4
67	Causal effects in microbiomes using interventional calculus. <i>Scientific Reports</i> , <b>2021</b> , 11, 5724	4.9	4
66	IEM: an algorithm for iterative enhancement of motifs using comparative genomics data. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , <b>2007</b> , 6, 227-35		4
65	Large scale microbiome profiling in the cloud. <i>Bioinformatics</i> , <b>2019</b> , 35, i13-i22	7.2	3

64	CloG: A pipeline for closing gaps in a draft assembly using short reads <b>2011</b> ,		3
63	Serial evolutionary networks of within-patient HIV-1 sequences reveal patterns of evolution of X4 strains. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 62	3.5	3
62	Information capacity of binary weights associative memories. <i>Neurocomputing</i> , <b>1998</b> , 19, 35-58	5.4	3
61	Clustering genes using gene expression and text literature data <b>2005</b> , 329-40		3
60	Enhancement of protein thermal stability: toward the design of robust proteins for bionanotechnological applications <b>2006</b> , 117-139		3
59	Optimally computing a shortest weakly visible line segment inside a simple polygon. <i>Computational Geometry: Theory and Applications</i> , <b>2002</b> , 23, 1-29	0.4	3
58	Graph-theoretic techniques in D-optimal design problems. <i>Journal of Statistical Planning and Inference</i> , <b>2002</b> , 102, 377-387	0.8	3
57	Geometric Minimum Spanning Trees via Well-Separated Pair Decompositions. <i>Journal of Experimental Algorithmics</i> , <b>2001</b> , 6, 6	1.1	3
56	IEM: AN ALGORITHM FOR ITERATIVE ENHANCEMENT OF MOTIFS USING COMPARATIVE GENOMICS DATA <b>2007</b> ,		3
55	Causal Inference in Microbiomes Using Intervention Calculus		3
54	So you think you can PLS-DA?		3
53	Microbiome Analysis: State of the Art and Future Trends <b>2016</b> , 401-424		3
52	So you think you can PLS-DA? <b>2018</b> ,		3
51	On the dilation spectrum of paths, cycles, and trees. <i>Computational Geometry: Theory and Applications</i> , <b>2009</b> , 42, 923-933	0.4	2
50	On the Effectiveness of Constraints Sets in Clustering Genes <b>2007</b> ,		2
49	BALANCED PARTITION OF MINIMUM SPANNING TREES. <i>International Journal of Computational Geometry and Applications</i> , <b>2003</b> , 13, 303-316	0.3	2
48	Approximating Minimum Manhattan Networks. <i>Lecture Notes in Computer Science</i> , <b>1999</b> , 28-38	0.9	2
47	Inferring directional relationships in microbial communities using signed Bayesian networks		2

46	Causal Inference Methods and their Challenges: The Case of 311 Data <b>2021</b> ,		2
45	MATria: a unified centrality algorithm. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 278	3.6	1
44	Constructing lightweight and flexible pipelines using Plugin-Based Microbiome Analysis (PluMA). <i>Bioinformatics</i> , <b>2018</b> , 34, 2881-2888	7.2	1
43	Comment on On the Uniqueness of Stable Marriage Matchings[Economic Letters 69(1):18, 2000]. <i>Economics Letters</i> , <b>2013</b> , 121, 468	1.3	1
42	Region-restricted clustering for geographic data mining. <i>Computational Geometry: Theory and Applications</i> , <b>2009</b> , 42, 231-240	0.4	1
41	The role of internal node sequences and the molecular clock in the analysis of serially-sampled data. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2008</b> , 4, 107-21	0.9	1
40	SBLAST: Structural Basic Local Alignment Searching Tools using Geometric Hashing <b>2007</b> ,		1
39	Clustering Using Adaptive Self-organizing Maps (ASOM) and Applications. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 944-951	0.9	1
38	Balanced Partition of Minimum Spanning Trees. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 26-35	0.9	1
37	Gene Function Prediction and Functional Network: The Role of Gene Ontology. <i>Intelligent Systems Reference Library</i> , <b>2012</b> , 123-162	0.8	1
36	Dynamic Bayesian networks for integrating multi-omics time-series microbiome data		1
35	Finding all weakly-visible chords of a polygon in linear time. <i>Lecture Notes in Computer Science</i> , <b>1994</b> , 119-130	0.9	1
34	On hamiltonian triangulations in simple polygons (Extended Abstract). <i>Lecture Notes in Computer Science</i> , <b>1997</b> , 321-330	0.9	1
33	Reconstructing Ancestor-Descendant Lineages from Serially-Sampled Data: A Comparison Study. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 807-814	0.9	0
32	Effect of metronidazole on vaginal microbiota associated with asymptomatic bacterial vaginosis. <i>Access Microbiology</i> , <b>2021</b> , 3, 000226	1	0
31	Computational Methods in Epigenetics <b>2015</b> , 153-180		
30	Fault-Tolerant Spanners427-442		
29	Discovering Sequence-Structure Patterns in Proteins with Variable Secondary Structure. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 702-709	0.9	

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| 10 | A Knowledge-Driven Method to Evaluate Multi-source Clustering. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 196-202   | 0.9 |
| 9  | Guest Editors—Introduction to the Special Section on Bioinformatics Research and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2022</b> , 19, 207-208 | 3   |
| 8  | Effects of Various Alpha-1 Antitrypsin Supplement Dosages on the Lung Microbiome and Metabolome. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 90-101                                    | 0.9 |
| 7  | PlasmoTFBM: An Intelligent Queriable Database for Predicted Transcription Factor Binding Motifs in <i>Plasmodium falciparum</i> <b>2007</b> , 121-136   |     |
| 6  | Searching for Recombinant Donors in a Phylogenetic Network of Serial Samples <b>2007</b> , 109-120  |     |
| 5  | Enhancing Motif Refinement by Incorporating Comparative Genomics Data <b>2007</b> , 329-337   |     |
| 4  | Approximation Algorithms for the Bottleneck Stretch Factor Problem. <i>Lecture Notes in Computer Science</i> , <b>2001</b> , 502-513  | 0.9 |
| 3  | Exact and Approximation Algorithms for Computing the Dilation Spectrum of Paths, Trees, and Cycles. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 849-858                                | 0.9 |
| 2  | Pooling Evidence to Identify Cell Cycle Regulated Genes. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 694-701   | 0.9 |
| 1  | Planar Geometric Spanners <b>2016</b> , 1570-1574   |     |