

Laxmi Parida

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

2,908
citations

279798

23
h-index

214800

47
g-index

120
all docs

120
docs citations

120
times ranked

4907
citing authors

#	ARTICLE	IF	CITATIONS
1	Variant analysis of SARS-CoV-2 genomes. Bulletin of the World Health Organization, 2020, 98, 495-504.	3.3	451
2	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. Nature Medicine, 2019, 25, 1415-1421.	30.7	359
3	Emergence of Drift Variants That May Affect COVID-19 Vaccine Development and Antibody Treatment. Pathogens, 2020, 9, 324.	2.8	184
4	Malware phylogeny generation using permutations of code. Journal in Computer Virology, 2005, 1, 13-23.	1.9	155
5	The Lipogenic Regulator SREBP2 Induces Transferrin in Circulating Melanoma Cells and Suppresses Ferroptosis. Cancer Discovery, 2021, 11, 678-695.	9.4	114
6	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. MSystems, 2020, 5, .	3.8	80
7	Enhancing Next-Generation Sequencing-Guided Cancer Care Through Cognitive Computing. Oncologist, 2018, 23, 179-185.	3.7	78
8	The Emergence of Pattern Discovery Techniques in Computational Biology. Metabolic Engineering, 2000, 2, 159-177.	7.0	71
9	Parallel Genomic Alterations of Antigen and Payload Targets Mediate Polyclonal Acquired Clinical Resistance to Sacituzumab Govitecan in Triple-Negative Breast Cancer. Cancer Discovery, 2021, 11, 2436-2445.	9.4	69
10	Challenges in benchmarking metagenomic profilers. Nature Methods, 2021, 18, 618-626.	19.0	63
11	Paralog knockout profiling identifies DUSP4 and DUSP6 as a digenic dependence in MAPK pathway-driven cancers. Nature Genetics, 2021, 53, 1664-1672.	21.4	61
12	Incremental Paradigms of Motif Discovery. Journal of Computational Biology, 2004, 11, 15-25.	1.6	58
13	In Silico Pattern-Based Analysis of the Human Cytomegalovirus Genome. Journal of Virology, 2003, 77, 4326-4344.	3.4	54
14	Application of Genome Wide Association and Genomic Prediction for Improvement of Cacao Productivity and Resistance to Black and Frosty Pod Diseases. Frontiers in Plant Science, 2017, 8, 1905.	3.6	50
15	Dictionary building via unsupervised hierarchical motif discovery in the sequence space of natural proteins. , 1999, 37, 264-277.		45
16	Population Differentiation of Southern Indian Male Lineages Correlates with Agricultural Expansions Predating the Caste System. PLoS ONE, 2012, 7, e50269.	2.5	40
17	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. Microbiome, 2021, 9, 132.	11.1	37
18	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. MSystems, 2021, 6, .	3.8	36

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19	Recombination Gives a New Insight in the Effective Population Size and the History of the Old World Human Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 25-30.	8.9	31
20	Food authentication from shotgun sequencing reads with an application on high protein powders. <i>Npj Science of Food</i> , 2019, 3, 24.	5.5	31
21	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. <i>Cancer Discovery</i> , 2021, 11, 3048-3063.	9.4	31
22	Gene Proximity Analysis across Whole Genomes via PQ Trees1. <i>Journal of Computational Biology</i> , 2005, 12, 1289-1306.	1.6	30
23	Evaluation of Methods for De Novo Genome Assembly from High-Throughput Sequencing Reads Reveals Dependencies That Affect the Quality of the Results. <i>PLoS ONE</i> , 2011, 6, e24182.	2.5	29
24	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. <i>Journal of Computational Biology</i> , 2008, 15, 1133-1153.	1.6	27
25	Permutation Pattern Discovery in Biosequences. <i>Journal of Computational Biology</i> , 2004, 11, 1050-1060.	1.6	26
26	Efficient algorithms for polyploid haplotype phasing. <i>BMC Genomics</i> , 2018, 19, 110.	2.8	25
27	Dictionary-driven protein annotation. <i>Nucleic Acids Research</i> , 2002, 30, 3901-3916.	14.5	24
28	Functional profiling of COVID-19 respiratory tract microbiomes. <i>Scientific Reports</i> , 2021, 11, 6433.	3.3	24
29	iXora: exact haplotype inferencing and trait association. <i>BMC Genetics</i> , 2013, 14, 48.	2.7	23
30	Watson for Genomics: Moving Personalized Medicine Forward. <i>Trends in Cancer</i> , 2016, 2, 392-395.	7.4	23
31	Discovering Topological Motifs Using a Compact Notation. <i>Journal of Computational Biology</i> , 2007, 14, 300-323.	1.6	22
32	Monitoring the microbiome for food safety and quality using deep shotgun sequencing. <i>Npj Science of Food</i> , 2021, 5, 3.	5.5	22
33	Conservative extraction of over-represented extensible motifs. <i>Bioinformatics</i> , 2005, 21, i9-i18.	4.1	20
34	Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis. <i>Nature Communications</i> , 2022, 13, 898.	12.8	19
35	Using PQ Trees for Comparative Genomics. <i>Lecture Notes in Computer Science</i> , 2005, , 128-143.	1.3	17
36	Computational methods for evaluating swept object boundaries. <i>Visual Computer</i> , 1994, 10, 266-276.	3.5	16

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37	An Approximation Algorithm for Alignment of Multiple Sequences using Motif Discovery. <i>Journal of Combinatorial Optimization</i> , 1999, 3, 247-275.	1.3	16
38	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.5	16
39	Variable-Selection Emerges on Top in Empirical Comparison of Whole-Genome Complex-Trait Prediction Methods. <i>PLoS ONE</i> , 2015, 10, e0138903.	2.5	15
40	Evaluating Clinical Genome Sequence Analysis by Watson for Genomics. <i>Frontiers in Medicine</i> , 2018, 5, 305.	2.6	15
41	Ancestral Recombinations Graph: A Reconstructability Perspective Using Random-Graphs Framework. <i>Journal of Computational Biology</i> , 2010, 17, 1345-1370.	1.6	14
42	A New Method to Reconstruct Recombination Events at a Genomic Scale. <i>PLoS Computational Biology</i> , 2010, 6, e1001010.	3.2	14
43	IRiS: Construction of ARG networks at genomic scales. <i>Bioinformatics</i> , 2011, 27, 2448-2450.	4.1	14
44	Irredundant tandem motifs. <i>Theoretical Computer Science</i> , 2014, 525, 89-102.	0.9	14
45	An inexact-suffix-tree-based algorithm for detecting extensible patterns. <i>Theoretical Computer Science</i> , 2005, 335, 3-14.	0.9	13
46	Detection of subtle variations as consensus motifs. <i>Theoretical Computer Science</i> , 2008, 395, 158-170.	0.9	13
47	IPED: Inheritance Path-based Pedigree Reconstruction Algorithm Using Genotype Data. <i>Journal of Computational Biology</i> , 2013, 20, 780-791.	1.6	13
48	Comparative exomics of Phalariscultivars under salt stress. <i>BMC Genomics</i> , 2014, 15, S18.	2.8	13
49	Minimizing recombinations in consensus networks for phylogeographic studies. <i>BMC Bioinformatics</i> , 2009, 10, S72.	2.6	12
50	A Topological Data Analysis Approach on Predicting Phenotypes from Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2020, , 178-187.	1.3	11
51	Haplotype assembly of autotetraploid potato using integer linear programming. <i>Bioinformatics</i> , 2019, 35, 3279-3286.	4.1	10
52	ARG-based genome-wide analysis of cacao cultivars. <i>BMC Bioinformatics</i> , 2012, 13, S17.	2.6	8
53	Gapped Permutation Patterns for Comparative Genomics. <i>Lecture Notes in Computer Science</i> , 2006, , 376-387.	1.3	8
54	A minimal descriptor of an ancestral recombinations graph. <i>BMC Bioinformatics</i> , 2011, 12, S6.	2.6	7

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55	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012, 131, 601-613.	3.8	7
56	Transcriptome characterization and differentially expressed genes under flooding and drought stress in the biomass grasses <i>Phalaris arundinacea</i> and <i>Dactylis glomerata</i> . <i>Annals of Botany</i> , 2019, 124, 717-730.	2.9	7
57	Dark-matter matters: Discriminating subtle blood cancers using the darkest DNA. <i>PLoS Computational Biology</i> , 2019, 15, e1007332.	3.2	7
58	Hierarchically Labeled Database Indexing Allows Scalable Characterization of Microbiomes. <i>IScience</i> , 2020, 23, 100988.	4.1	7
59	Re-purposing software for functional characterization of the microbiome. <i>Microbiome</i> , 2021, 9, 4.	11.1	7
60	K-Mer Analyses Reveal Different Evolutionary Histories of Alpha, Beta, and Gamma Papillomaviruses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9657.	4.1	7
61	SUBTLE MOTIF DISCOVERY FOR DETECTION OF DNA REGULATORY SITES. , 2007, , .		7
62	Using PQ Structures for Genomic Rearrangement Phylogeny. <i>Journal of Computational Biology</i> , 2006, 13, 1685-1700.	1.6	6
63	Characterizing redescrptions using persistent homology to isolate genetic pathways contributing to pathogenesis. <i>BMC Systems Biology</i> , 2016, 10, 10.	3.0	6
64	Some Results on Flexible-Pattern Discovery. <i>Lecture Notes in Computer Science</i> , 2000, , 33-45.	1.3	6
65	Bridging Lossy and Lossless Compression by Motif Pattern Discovery. <i>Electronic Notes in Discrete Mathematics</i> , 2005, 21, 219-225.	0.4	5
66	Gapped Permutation Pattern Discovery for Gene Order Comparisons. <i>Journal of Computational Biology</i> , 2007, 14, 45-55.	1.6	5
67	Sum of parts is greater than the whole: inference of common genetic history of populations. <i>BMC Genomics</i> , 2013, 14, S10.	2.8	5
68	Efficient in silico Chromosomal Representation of Populations via Indexing Ancestral Genomes. <i>Algorithms</i> , 2013, 6, 430-441.	2.1	5
69	Partitioning single-molecule maps into multiple populations: algorithms and probabilistic analysis. <i>Discrete Applied Mathematics</i> , 2000, 104, 203-227.	0.9	4
70	The web server of IBM's Bioinformatics and Pattern Discovery group. <i>Nucleic Acids Research</i> , 2003, 31, 3645-3650.	14.5	4
71	Statistical Significance of Large Gene Clusters. <i>Journal of Computational Biology</i> , 2007, 14, 1145-1159.	1.6	4
72	Sampling ARG of multiple populations under complex configurations of subdivision and admixture. <i>Bioinformatics</i> , 2016, 32, 1048-1056.	4.1	4

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73	Linear Time Algorithms to Construct Populations Fitting Multiple Constraint Distributions at Genomic Scales. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1132-1142.	3.0	4
74	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. Biometrics, 2022, 78, 1155-1167.	1.4	4
75	Graph Model of Coalescence with Recombinations. , 2010, , 85-100.		4
76	Combinatorial Pattern Discovery Approach for the Folding Trajectory Analysis of a \hat{I}^2 -Hairpin. PLoS Computational Biology, 2005, 1, e8.	3.2	4
77	A common methodological phylogenomics framework for intra-patient heteroplasmies to infer SARS-CoV-2 sublineages and tumor clones. BMC Genomics, 2021, 22, 518.	2.8	4
78	Nonredundant Representation of Ancestral Recombinations Graphs. Methods in Molecular Biology, 2012, 856, 315-332.	0.9	3
79	SimBA: simulation algorithm to fit extant-population distributions. BMC Bioinformatics, 2015, 16, 82.	2.6	3
80	Topological Signatures for Population Admixture. Lecture Notes in Computer Science, 2015, , 261-275.	1.3	3
81	A Uniform Framework for Ordered Restriction Map Problems. Journal of Computational Biology, 1998, 5, 725-739.	1.6	2
82	Signal enrichment with strain-level resolution in metagenomes using topological data analysis. BMC Genomics, 2019, 20, 194.	2.8	2
83	A closed form solution to the problem of tangential circles, lines, points with extension to 3D. Computers and Graphics, 1991, 15, 49-55.	2.5	1
84	A computational technique for general shape deformations for use in font design. Computers and Graphics, 1993, 17, 349-356.	2.5	1
85	Scalable Algorithms at Genomic Resolution to fit LD Distributions. , 2016, , .		1
86	A Quantitative and Qualitative Characterization of k-mer Based Alignment-Free Phylogeny Construction. Lecture Notes in Computer Science, 2019, , 19-31.	1.3	1
87	APBC 2010. The Eighth Asia Pacific Bioinformatics Conference Bangalore, India, 18-21 January 2010. BMC Bioinformatics, 2010, 11, 11.	2.6	0
88	Discovering Patterns in Gene Order. Methods in Molecular Biology, 2012, 855, 431-455.	0.9	0
89	Using Random Graphs in Population Genomics. Lecture Notes in Computer Science, 2013, , 340-341.	1.3	0
90	Effect of sampling on the extent and accuracy of the inferred genetic history of recombining genome. Computational Biology and Chemistry, 2014, 50, 68-74.	2.3	0

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91	Multiple Loci Selection with Multi-Way Epistasis in Coalescence with Recombination. Algorithms, 2021, 14, 136.	2.1	0
92	Combinatorics in Recombinational Population Genomics. Lecture Notes in Computer Science, 2010, , 126-127.	1.3	0
93	Genetic History of Populations: Limits to Inference. Computational Biology, 2013, , 309-323.	0.2	0
94	Simultaneous Phasing of Multiple Polyploids. Lecture Notes in Computer Science, 2020, , 50-68.	1.3	0