Mihai Pop

List of Publications by Year
in descending order

143 papers	57,664 citations	30070 54 h-index	15732 125 g-index
155 all docs	155 docs citations	155 times ranked	80317 citing authors

#	Article	IF	Citations
1	SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning. Genome Biology, 2022, 23, .	8.8	13
2	TIPP2: metagenomic taxonomic profiling using phylogenetic markers. Bioinformatics, 2021, 37, 1839-1845.	4.1	18
3	Binnacle: Using Scaffolds to Improve the Contiguity and Quality of Metagenomic Bins. Frontiers in Microbiology, 2021, 12, 638561.	3.5	2
4	A critical assessment of gene catalogs for metagenomic analysis. Bioinformatics, 2021, 37, 2848-2857.	4.1	15
5	Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads. BMC Genomics, 2021, 22, 389.	2.8	9
6	What do Eulerian and Hamiltonian cycles have to do with genome assembly?. PLoS Computational Biology, 2021, 17, e1008928.	3.2	7
7	Whole-Genome Assessment of Clinical Acinetobacter baumannii Isolates Uncovers Potentially Novel Factors Influencing Carbapenem Resistance. Frontiers in Microbiology, 2021, 12, 714284.	3.5	3
8	Genomic Drivers of Multidrug-Resistant <i>Shigella</i> Affecting Vulnerable Patient Populations in the United States and Abroad. MBio, 2021, 12, .	4.1	19
9	The Capacity to Produce Hydrogen Sulfide (H2S) via Cysteine Degradation Is Ubiquitous in the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, 705583.	3.5	37
10	Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications. Water Research, 2020, 169, 115250.	11.3	21
11	Metagenomic analysis of bacterial and viral assemblages from a freshwater creek and irrigated field reveals temporal and spatial dynamics. Science of the Total Environment, 2020, 706, 135395.	8.0	11
12	Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water. Frontiers in Environmental Science, 2020, 8, .	3.3	7
13	Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond. Environmental Microbiomes, 2020, 15, 18.	5.0	16
14	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	8.8	26
15	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0
16	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. Genome Biology, 2019, 20, 153.	8.8	66
17	Modern technologies and algorithms for scaffolding assembled genomes. PLoS Computational Biology, 2019, 15, e1006994.	3.2	56
18	MetaCarvel: linking assembly graph motifs to biological variants. Genome Biology, 2019, 20, 174.	8.8	14

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19	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. PLoS Computational Biology, 2019, 15, e1007273.	3.2	509
20	Pharmaceuticals, herbicides, and disinfectants in agricultural water sources. Environmental Research, 2019, 174, 1-8.	7.5	33
21	Microbiota of the Hickey Run Tributary of the Anacostia River. Microbiology Resource Announcements, 2019, 8, .	0.6	8
22	SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest. , 2019, , .		7
23	Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. MSystems, 2019, 4, .	3.8	6
24	Embracing Ambiguity in the Taxonomic Classification of Microbiome Sequencing Data. Frontiers in Genetics, 2019, 10, 1022.	2.3	6
25	Incidence of fecal indicator and pathogenic bacteria in reclaimed and return flow waters in Arizona, USA. Environmental Research, 2019, 170, 122-127.	7.5	19
26	Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. Bioinformatics, 2019, 35, 1613-1614.	4.1	65
27	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. Briefings in Bioinformatics, 2019, 20, 1140-1150.	6.5	113
28	You can't always sequence your way out of a tight spot. EMBO Reports, 2018, 19, .	4.5	3
29	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. Science of the Total Environment, 2018, 639, 1126-1137.	8.0	43
30	Outlier detection in BLAST hits. Algorithms for Molecular Biology, 2018, 13, 7.	1.2	14
31	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. Microbiome, 2017, 5, 22.	11.1	33
32	Critical Assessment of Metagenome Interpretationâ€"a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
33	Identification of microbiota dynamics using robust parameter estimation methods. Mathematical Biosciences, 2017, 294, 71-84.	1.9	12
34	Temporal Variations in Cigarette Tobacco Bacterial Community Composition and Tobacco-Specific Nitrosamine Content Are Influenced by Brand and Storage Conditions. Frontiers in Microbiology, 2017, 08, 358.	3.5	45
35	Characterization of Two Cryptic Plasmids Isolated in Haiti from Clinical Vibrio cholerae Non-O1/Non-O139. Frontiers in Microbiology, 2017, 8, 2283.	3.5	11
36	Scaffolding of long read assemblies using long range contact information. BMC Genomics, 2017, 18, 527.	2.8	194

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37	Diversity in a Polymicrobial Community Revealed by Analysis of Viromes, Endolysins and CRISPR Spacers. PLoS ONE, 2016, 11, e0160574.	2.5	17
38	Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic Escherichia coli and subsequent ciprofloxacin treatment. BMC Genomics, 2016, 17, 440.	2.8	55
39	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. Microbiome, 2016, 4, 38.	11.1	43
40	Limitations of Current Approaches for Reference-Free, Graph-Based Variant Detection. , 2016, , .		1
41	Better Identification of Repeats in Metagenomic Scaffolding. Lecture Notes in Computer Science, 2016, , 174-184.	1.3	2
42	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. Npj Biofilms and Microbiomes, 2016, 2, 16004.	6.4	208
43	Maligner: a fast ordered restriction map aligner. Bioinformatics, 2016, 32, 1016-1022.	4.1	19
44	Capturing the most wanted taxa through cross-sample correlations. ISME Journal, 2016, 10, 2459-2467.	9.8	9
45	Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic Escherichia coli. Frontiers in Cellular and Infection Microbiology, 2016, 6, 200.	3.9	15
46	Metagenomic Assembly: Overview, Challenges and Applications. Yale Journal of Biology and Medicine, 2016, 89, 353-362.	0.2	71
47	Use and mis-use of supplementary material in science publications. BMC Bioinformatics, 2015, 16, 237.	2.6	36
48	Computational challenges in microbiome research. , 2015, , .		0
49	High-Throughput Sequencing as a Tool for Exploring the Human Microbiome. , 2015, , 55-66.		3
50	The Theory and Practice of Genome Sequence Assembly. Annual Review of Genomics and Human Genetics, 2015, 16, 153-172.	6.2	87
51	Microbiota That Affect Risk for Shigellosis in Children in Low-Income Countries. Emerging Infectious Diseases, 2015, 21, 242-250.	4.3	30
52	TIPP: taxonomic identification and phylogenetic profiling. Bioinformatics, 2014, 30, 3548-3555.	4.1	93
53	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. Genome Biology, 2014, 15, R76.	9.6	219
54	Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products. BMC Genomics, 2014, 15, 1101.	2.8	64

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55	Computational methods for optical mapping. GigaScience, 2014, 3, 33.	6.4	33
56	Reply to: "A fair comparison". Nature Methods, 2014, 11, 359-360.	19.0	14
57	Automated ensemble assembly and validation of microbial genomes. BMC Bioinformatics, 2014, 15, 126.	2.6	60
58	K-mulus: Strategies for BLAST in the Cloud. Lecture Notes in Computer Science, 2014, , 237-246.	1.3	2
59	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. Genome Biology, 2013, 14, R2.	9.6	174
60	Exploring variation-aware contig graphs for (comparative) metagenomics using MaryGold. Bioinformatics, 2013, 29, 2826-2834.	4.1	29
61	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. Briefings in Bioinformatics, 2013, 14, 213-224.	6.5	54
62	De novo likelihood-based measures for comparing genome assemblies. BMC Research Notes, 2013, 6, 334.	1.4	43
63	Differential abundance analysis for microbial marker-gene surveys. Nature Methods, 2013, 10, 1200-1202.	19.0	1,921
64	De novo likelihood-based measures for comparing metagenomic assemblies. , 2013, , .		1
65	Sequence assembly demystified. Nature Reviews Genetics, 2013, 14, 157-167.	16.3	396
66	Quantitative PCR for Detection of Shigella Improves Ascertainment of Shigella Burden in Children with Moderate-to-Severe Diarrhea in Low-Income Countries. Journal of Clinical Microbiology, 2013, 51, 1740-1746.	3.9	96
67	Survey of Culture, GoldenGate Assay, Universal Biosensor Assay, and 16S rRNA Gene Sequencing as Alternative Methods of Bacterial Pathogen Detection. Journal of Clinical Microbiology, 2013, 51, 3263-3269.	3.9	25
68	Genome Sequencing of Four Strains of Rickettsia prowazekii, the Causative Agent of Epidemic Typhus, Including One Flying Squirrel Isolate. Genome Announcements, 2013, 1, .	0.8	17
69	Bioinformatics for the Human Microbiome Project. PLoS Computational Biology, 2012, 8, e1002779.	3.2	73
70	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. Nucleic Acids Research, 2012, 40, e9-e9.	14.5	150
71	Identification of Coli Surface Antigen 23, a Novel Adhesin of Enterotoxigenic Escherichia coli. Infection and Immunity, 2012, 80, 2791-2801.	2.2	42
72	We are what we eat: how the diet of infants affects their gut microbiome. Genome Biology, 2012, 13, 152.	9.6	18

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73	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
74	Workshop: Comparative assembly of metagenomic sequences. , 2012, , .		0
75	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
76	AGORA: Assembly Guided by Optical Restriction Alignment. BMC Bioinformatics, 2012, 13, 189.	2.6	42
77	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. PLoS ONE, 2012, 7, e37919.	2.5	329
78	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	5.5	597
79	Exploiting sparseness in de novo genome assembly. BMC Bioinformatics, 2012, 13, S1.	2.6	279
80	Human Microbiome, Assembly and Analysis Software, Project. , 2012, , 1-4.		0
81	Workshop: Can you assemble whole genomes from next generation sequencing data?. , 2011, , .		0
82	Next Generation Sequence Assembly with AMOS. Current Protocols in Bioinformatics, 2011, 33, Unit 11.8.	25.8	200
83	Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences. BMC Genomics, 2011, 12, S4.	2.8	167
84	Reconstructing microbial communities. Genome Biology, 2011, 12, .	9.6	0
85	Viral diversity in children with diarrhea in Gambia. Genome Biology, 2011, 12, .	9.6	1
86	Metastats: an improved statistical method for analysis of metagenomic data. Genome Biology, 2011, 12, .	9.6	18
87	Metastats: an improved statistical method for analysis of metagenomic data. Genome Biology, 2011, 12, .	8.8	75
88	On using optical maps for genome assembly. Genome Biology, 2011, 12, .	9.6	0
89	ScaffViz: visualizing metagenome assemblies. Genome Biology, 2011, 12, .	9.6	0
90	Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences. Genome Biology, 2011, 12, .	8.8	7

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91	MetAMOS: a metagenomic assembly and analysis pipeline for AMOS. Genome Biology, 2011, 12, .	9.6	11
92	MetaPath: identifying differentially abundant metabolic pathways in metagenomic datasets. BMC Proceedings, 2011, 5, S9.	1.6	44
93	DNACLUST: accurate and efficient clustering of phylogenetic marker genes. BMC Bioinformatics, 2011, 12, 271.	2.6	167
94	Assessing the benefits of using mate-pairs to resolve repeats in de novo short-read prokaryotic assemblies. BMC Bioinformatics, 2011, 12, 95.	2.6	53
95	Invited: Challenges in metagenomic assembly. , 2011, , .		0
96	Bambus 2: scaffolding metagenomes. Bioinformatics, 2011, 27, 2964-2971.	4.1	124
97	<i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5027-5032.	7.1	152
98	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. BMC Bioinformatics, 2010, 11, 152.	2.6	63
99	Assembly complexity of prokaryotic genomes using short reads. BMC Bioinformatics, 2010, 11, 21.	2.6	120
100	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. BMC Genomics, 2010, 11, 242.	2.8	46
101	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Journal of Computational Biology, 2010, 17, 503-516.	1.6	29
102	Sequencing and Genome Assembly Using Next-Generation Technologies. Methods in Molecular Biology, 2010, 673, 1-17.	0.9	47
103	Statistical methods for comparing the abundances of metabolic pathways in metagenomics. Genome Biology, 2010, 11, .	8.8	0
104	Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1.	9.6	103
105	MetaPhyler: Taxonomic profiling for metagenomic sequences. , 2010, , .		46
106	Identifying Differentially Abundant Metabolic Pathways in Metagenomic Datasets. Lecture Notes in Computer Science, 2010, , 101-112.	1.3	3
107	ARDB--Antibiotic Resistance Genes Database. Nucleic Acids Research, 2009, 37, D443-D447.	14.5	1,089
108	Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. PLoS Computational Biology, 2009, 5, e1000352.	3.2	1,495

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109	Complete Genome Sequence of *Aggregatibacter* (*Haemophilus*) *aphrophilus* NJ8700. Journal of Bacteriology, 2009, 191, 4693-4694.	2.2	28
110	Microbial dynamics of human obesity. , 2009, , .		0
111	Searching for SNPs with cloud computing. Genome Biology, 2009, 10, R134.	9.6	437
112	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biology, 2009, 10, R25.	9.6	19,212
113	Genome assembly reborn: recent computational challenges. Briefings in Bioinformatics, 2009, 10, 354-366.	6.5	291
114	Inexact Local Alignment Search over Suffix Arrays. , 2009, 2009, 83-97.		4
115	Parametric Complexity of Sequence Assembly: Theory and Applications to Next Generation Sequencing. Journal of Computational Biology, 2009, 16, 897-908.	1.6	96
116	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Lecture Notes in Computer Science, 2009, , 400-417.	1.3	10
117	Genome-Wide Analysis of Repetitive Elements in Papaya. Tropical Plant Biology, 2008, 1, 191-201.	1.9	24
118	Bioinformatics challenges of new sequencing technology. Trends in Genetics, 2008, 24, 142-149.	6.7	438
119	Genome assembly forensics: finding the elusive mis-assembly. Genome Biology, 2008, 9, R55.	9.6	248
120	Figaro: a novel statistical method for vector sequence removal. Bioinformatics, 2008, 24, 462-467.	4.1	31
121	Scaffolding and validation of bacterial genome assemblies using optical restriction maps. Bioinformatics, 2008, 24, 1229-1235.	4.1	195
122	Characterization of Ehp, a Secreted Complement Inhibitory Protein from Staphylococcus aureus. Journal of Biological Chemistry, 2007, 282, 30051-30061.	3.4	84
123	Draft Genome of the Filarial Nematode Parasite *Brugia malayi*. Science, 2007, 317, 1756-1760.	12.6	571
124	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
125	Minimus: a fast, lightweight genome assembler. BMC Bioinformatics, 2007, 8, 64.	2.6	354
126	An optimized system for expression and purification of secreted bacterial proteins. Protein Expression and Purification, 2006, 46, 23-32.	1.3	113

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127	Metagenomic Analysis of the Human Distal Gut Microbiome. Science, 2006, 312, 1355-1359.	12.6	3,964
128	The genome of the protist parasite Entamoeba histolytica. Nature, 2005, 433, 865-868.	27.8	783
129	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. Science, 2005, 309, 409-415.	12.6	1,273
130	Serendipitous discovery of Wolbachia genomes in multiple Drosophila species. Genome Biology, 2005, 6, R23.	9.6	126
131	Comparative genome assembly. Briefings in Bioinformatics, 2004, 5, 237-248.	6.5	193
132	Shotgun Sequence Assembly. Advances in Computers, 2004, 60, 193-248.	1.6	20
133	Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440. Environmental Microbiology, 2003, 5, 630-630.	3.8	10
134	The Dog Genome: Survey Sequencing and Comparative Analysis. Science, 2003, 301, 1898-1903.	12.6	482
135	The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria. Nature, 2003, 423, 81-86.	27.8	760
136	Hierarchical Scaffolding With Bambus. Genome Research, 2003, 14, 149-159.	5.5	172
137	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in Bacillus anthracis. Science, 2002, 296, 2028-2033.	12.6	413
138	Genome sequence assembly: algorithms and issues. Computer, 2002, 35, 47-54.	1.1	60
139	Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440. Environmental Microbiology, 2002, 4, 799-808.	3.8	1,218
140	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. Nature, 2002, 419, 512-519.	27.8	666
141	Suppression subtractive hybridization PCR isolation of cDNAs from a Caribbean soft coral. Electronic Journal of Biotechnology, 2001, 14, .	2.2	0
142	Efficient perspective-accurate silhouette computation and applications. , 2001, , .		20
143	Efficient perspective-accurate silhouette computation. , 1999, , .		8