Mihai Pop

List of Publications by Year in descending order

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143 papers	57,664 citations	29994 54 h-index	15683 125 g-index
155 all docs	155 docs citations	155 times ranked	80317 citing authors

#	Article	IF	Citations
1	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biology, 2009, 10, R25.	13.9	19,212
2	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	13.7	9,614
3	Metagenomic Analysis of the Human Distal Gut Microbiome. Science, 2006, 312, 1355-1359.	6.0	3,964
4	A framework for human microbiome research. Nature, 2012, 486, 215-221.	13.7	2,249
5	Differential abundance analysis for microbial marker-gene surveys. Nature Methods, 2013, 10, 1200-1202.	9.0	1,921
6	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
7	Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. PLoS Computational Biology, 2009, 5, e1000352.	1.5	1,495
8	The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas Disease. Science, 2005, 309, 409-415.	6.0	1,273
9	Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440. Environmental Microbiology, 2002, 4, 799-808.	1.8	1,218
10	ARDB--Antibiotic Resistance Genes Database. Nucleic Acids Research, 2009, 37, D443-D447.	6.5	1,089
11	The genome of the protist parasite Entamoeba histolytica. Nature, 2005, 433, 865-868.	13.7	783
12	The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria. Nature, 2003, 423, 81-86.	13.7	760
13	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. Nature, 2002, 419, 512-519.	13.7	666
14	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	9.0	635
15	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	2.4	597
16	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i>. Science, 2007, 317, 1756-1760.	6.0	571
17	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. PLoS Computational Biology, 2019, 15, e1007273.	1.5	509
18	The Dog Genome: Survey Sequencing and Comparative Analysis. Science, 2003, 301, 1898-1903.	6.0	482

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19	Bioinformatics challenges of new sequencing technology. Trends in Genetics, 2008, 24, 142-149.	2.9	438
20	Searching for SNPs with cloud computing. Genome Biology, 2009, 10, R134.	13.9	437
21	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in Bacillus anthracis. Science, 2002, 296, 2028-2033.	6.0	413
22	Sequence assembly demystified. Nature Reviews Genetics, 2013, 14, 157-167.	7.7	396
23	Minimus: a fast, lightweight genome assembler. BMC Bioinformatics, 2007, 8, 64.	1.2	354
24	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. PLoS ONE, 2012, 7, e37919.	1.1	329
25	Genome assembly reborn: recent computational challenges. Briefings in Bioinformatics, 2009, 10, 354-366.	3.2	291
26	Exploiting sparseness in de novo genome assembly. BMC Bioinformatics, 2012, 13, S1.	1.2	279
27	Genome assembly forensics: finding the elusive mis-assembly. Genome Biology, 2008, 9, R55.	13.9	248
28	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. Genome Biology, 2014, 15, R76.	13.9	219
29	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. Npj Biofilms and Microbiomes, 2016, 2, 16004.	2.9	208
30	Next Generation Sequence Assembly with AMOS. Current Protocols in Bioinformatics, 2011, 33, Unit 11.8.	25.8	200
31	Scaffolding and validation of bacterial genome assemblies using optical restriction maps. Bioinformatics, 2008, 24, 1229-1235.	1.8	195
32	Scaffolding of long read assemblies using long range contact information. BMC Genomics, 2017, 18, 527.	1.2	194
33	Comparative genome assembly. Briefings in Bioinformatics, 2004, 5, 237-248.	3.2	193
34	MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. Genome Biology, 2013, 14, R2.	13.9	174
35	Hierarchical Scaffolding With Bambus. Genome Research, 2003, 14, 149-159.	2.4	172
36	Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences. BMC Genomics, 2011, 12, S4.	1.2	167

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37	DNACLUST: accurate and efficient clustering of phylogenetic marker genes. BMC Bioinformatics, 2011, 12, 271.	1.2	167
38	<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.	3.3	152
39	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. Nucleic Acids Research, 2012, 40, e9-e9.	6.5	150
40	Serendipitous discovery of Wolbachia genomes in multiple Drosophila species. Genome Biology, 2005, 6, R23.	13.9	126
41	Bambus 2: scaffolding metagenomes. Bioinformatics, 2011, 27, 2964-2971.	1.8	124
42	Assembly complexity of prokaryotic genomes using short reads. BMC Bioinformatics, 2010, 11, 21.	1.2	120
43	An optimized system for expression and purification of secreted bacterial proteins. Protein Expression and Purification, 2006, 46, 23-32.	0.6	113
44	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.	3.2	113
45	Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1.	13.9	103
46	Parametric Complexity of Sequence Assembly: Theory and Applications to Next Generation Sequencing. Journal of Computational Biology, 2009, 16, 897-908.	0.8	96
47	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.	1.8	96
48	TIPP: taxonomic identification and phylogenetic profiling. Bioinformatics, 2014, 30, 3548-3555.	1.8	93
49	The Theory and Practice of Genome Sequence Assembly. Annual Review of Genomics and Human Genetics, 2015, 16, 153-172.	2.5	87
50	Characterization of Ehp, a Secreted Complement Inhibitory Protein from Staphylococcus aureus. Journal of Biological Chemistry, 2007, 282, 30051-30061.	1.6	84
51	Metastats: an improved statistical method for analysis of metagenomic data. Genome Biology, 2011, 12, .	3.8	75
52	Bioinformatics for the Human Microbiome Project. PLoS Computational Biology, 2012, 8, e1002779.	1.5	73
53	Metagenomic Assembly: Overview, Challenges and Applications. Yale Journal of Biology and Medicine, 2016, 89, 353-362.	0.2	71
54	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.	3.8	66

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55	Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. Bioinformatics, 2019, 35, 1613-1614.	1.8	65
56	Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products. BMC Genomics, 2014, 15, 1101.	1.2	64
57	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. BMC Bioinformatics, 2010, 11, 152.	1.2	63
58	Genome sequence assembly: algorithms and issues. Computer, 2002, 35, 47-54.	1.2	60
59	Automated ensemble assembly and validation of microbial genomes. BMC Bioinformatics, 2014, 15, 126.	1.2	60
60	Modern technologies and algorithms for scaffolding assembled genomes. PLoS Computational Biology, 2019, 15, e1006994.	1.5	56
61	Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic Escherichia coli and subsequent ciprofloxacin treatment. BMC Genomics, 2016, 17, 440.	1.2	55
62	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. Briefings in Bioinformatics, 2013, 14, 213-224.	3.2	54
63	Assessing the benefits of using mate-pairs to resolve repeats in de novo short-read prokaryotic assemblies. BMC Bioinformatics, 2011, 12, 95.	1.2	53
64	Sequencing and Genome Assembly Using Next-Generation Technologies. Methods in Molecular Biology, 2010, 673, 1-17.	0.4	47
65	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. BMC Genomics, 2010, 11, 242.	1.2	46
66	MetaPhyler: Taxonomic profiling for metagenomic sequences. , 2010, , .		46
67	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.	1.5	45
68	MetaPath: identifying differentially abundant metabolic pathways in metagenomic datasets. BMC Proceedings, 2011, 5, S9.	1.8	44
69	De novo likelihood-based measures for comparing genome assemblies. BMC Research Notes, 2013, 6, 334.	0.6	43
70	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. Microbiome, 2016, 4, 38.	4.9	43
71	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.	3.9	43
72	Identification of Coli Surface Antigen 23, a Novel Adhesin of Enterotoxigenic Escherichia coli. Infection and Immunity, 2012, 80, 2791-2801.	1.0	42

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73	AGORA: Assembly Guided by Optical Restriction Alignment. BMC Bioinformatics, 2012, 13, 189.	1.2	42
74	The Capacity to Produce Hydrogen Sulfide (H2S) via Cysteine Degradation Is Ubiquitous in the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, 705583.	1.5	37
75	Use and mis-use of supplementary material in science publications. BMC Bioinformatics, 2015, 16, 237.	1.2	36
76	Computational methods for optical mapping. GigaScience, 2014, 3, 33.	3.3	33
77	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. Microbiome, 2017, 5, 22.	4.9	33
78	Pharmaceuticals, herbicides, and disinfectants in agricultural water sources. Environmental Research, 2019, 174, 1-8.	3.7	33
79	Figaro: a novel statistical method for vector sequence removal. Bioinformatics, 2008, 24, 462-467.	1.8	31
80	Microbiota That Affect Risk for Shigellosis in Children in Low-Income Countries. Emerging Infectious Diseases, 2015, 21, 242-250.	2.0	30
81	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Journal of Computational Biology, 2010, 17, 503-516.	0.8	29
82	Exploring variation-aware contig graphs for (comparative) metagenomics using MaryGold. Bioinformatics, 2013, 29, 2826-2834.	1.8	29
83	Complete Genome Sequence of<i>Aggregatibacter</i>(<i>Haemophilus</i>)<i>aphrophilus</i>NJ8700. Journal of Bacteriology, 2009, 191, 4693-4694.	1.0	28
84	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	3.8	26
85	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.	1.8	25
86	Genome-Wide Analysis of Repetitive Elements in Papaya. Tropical Plant Biology, 2008, 1, 191-201.	1.0	24
87	Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications. Water Research, 2020, 169, 115250.	5.3	21
88	Efficient perspective-accurate silhouette computation and applications. , 2001, , .		20
89	Shotgun Sequence Assembly. Advances in Computers, 2004, 60, 193-248.	1.2	20
90	Maligner: a fast ordered restriction map aligner. Bioinformatics, 2016, 32, 1016-1022.	1.8	19

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91	Incidence of fecal indicator and pathogenic bacteria in reclaimed and return flow waters in Arizona, USA. Environmental Research, 2019, 170, 122-127.	3.7	19
92	Genomic Drivers of Multidrug-Resistant <i>Shigella</i> Affecting Vulnerable Patient Populations in the United States and Abroad. MBio, 2021, 12, .	1.8	19
93	Metastats: an improved statistical method for analysis of metagenomic data. Genome Biology, 2011, 12, .	13.9	18
94	We are what we eat: how the diet of infants affects their gut microbiome. Genome Biology, 2012, 13, 152.	13.9	18
95	TIPP2: metagenomic taxonomic profiling using phylogenetic markers. Bioinformatics, 2021, 37, 1839-1845.	1.8	18
96	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
97	Diversity in a Polymicrobial Community Revealed by Analysis of Viromes, Endolysins and CRISPR Spacers. PLoS ONE, 2016, 11, e0160574.	1.1	17
98	Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond. Environmental Microbiomes, 2020, 15, 18.	2.2	16
99	Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic Escherichia coli. Frontiers in Cellular and Infection Microbiology, 2016, 6, 200.	1.8	15
100	A critical assessment of gene catalogs for metagenomic analysis. Bioinformatics, 2021, 37, 2848-2857.	1.8	15
101	Reply to: "A fair comparison". Nature Methods, 2014, 11, 359-360.	9.0	14
102	Outlier detection in BLAST hits. Algorithms for Molecular Biology, 2018, 13, 7.	0.3	14
103	MetaCarvel: linking assembly graph motifs to biological variants. Genome Biology, 2019, 20, 174.	3.8	14
104	SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning. Genome Biology, 2022, 23, .	3.8	13
105	Identification of microbiota dynamics using robust parameter estimation methods. Mathematical Biosciences, 2017, 294, 71-84.	0.9	12
106	MetAMOS: a metagenomic assembly and analysis pipeline for AMOS. Genome Biology, 2011, 12, .	13.9	11
107	Characterization of Two Cryptic Plasmids Isolated in Haiti from Clinical Vibrio cholerae Non-O1/Non-O139. Frontiers in Microbiology, 2017, 8, 2283.	1.5	11
108	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.	3.9	11

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109	Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440. Environmental Microbiology, 2003, 5, 630-630.	1.8	10
110	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Lecture Notes in Computer Science, 2009, , 400-417.	1.0	10
111	Capturing the most wanted taxa through cross-sample correlations. ISME Journal, 2016, 10, 2459-2467.	4.4	9
112	Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads. BMC Genomics, 2021, 22, 389.	1.2	9
113	Efficient perspective-accurate silhouette computation. , 1999, , .		8
114	Microbiota of the Hickey Run Tributary of the Anacostia River. Microbiology Resource Announcements, 2019, 8, .	0.3	8
115	Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences. Genome Biology, 2011, 12, .	3.8	7
116	SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest. , 2019, , .		7
117	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, .	1.5	7
118	What do Eulerian and Hamiltonian cycles have to do with genome assembly?. PLoS Computational Biology, 2021, 17, e1008928.	1.5	7
119	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, .	1.7	6
120	Embracing Ambiguity in the Taxonomic Classification of Microbiome Sequencing Data. Frontiers in Genetics, 2019, 10, 1022.	1.1	6
121	Inexact Local Alignment Search over Suffix Arrays. , 2009, 2009, 83-97.		4
122	High-Throughput Sequencing as a Tool for Exploring the Human Microbiome. , 2015, , 55-66.		3
123	You can't always sequence your way out of a tight spot. EMBO Reports, 2018, 19, .	2.0	3
124	Whole-Genome Assessment of Clinical Acinetobacter baumannii Isolates Uncovers Potentially Novel Factors Influencing Carbapenem Resistance. Frontiers in Microbiology, 2021, 12, 714284.	1.5	3
125	Identifying Differentially Abundant Metabolic Pathways in Metagenomic Datasets. Lecture Notes in Computer Science, 2010, , 101-112.	1.0	3
126	Better Identification of Repeats in Metagenomic Scaffolding. Lecture Notes in Computer Science, 2016, , 174-184.	1.0	2

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127	Binnacle: Using Scaffolds to Improve the Contiguity and Quality of Metagenomic Bins. Frontiers in Microbiology, 2021, 12, 638561.	1.5	2
128	K-mulus: Strategies for BLAST in the Cloud. Lecture Notes in Computer Science, 2014, , 237-246.	1.0	2
129	Viral diversity in children with diarrhea in Gambia. Genome Biology, 2011, 12, .	13.9	1
130	De novo likelihood-based measures for comparing metagenomic assemblies. , 2013, , .		1
131	Limitations of Current Approaches for Reference-Free, Graph-Based Variant Detection. , 2016, , .		1
132	Suppression subtractive hybridization PCR isolation of cDNAs from a Caribbean soft coral. Electronic Journal of Biotechnology, 2001, 14, .	1.2	0
133	Microbial dynamics of human obesity. , 2009, , .		0
134	Statistical methods for comparing the abundances of metabolic pathways in metagenomics. Genome Biology, 2010, 11, .	3.8	0
135	Workshop: Can you assemble whole genomes from next generation sequencing data?. , 2011, , .		0
136	Reconstructing microbial communities. Genome Biology, 2011, 12, .	13.9	0
137	On using optical maps for genome assembly. Genome Biology, 2011, 12, .	13.9	0
138	ScaffViz: visualizing metagenome assemblies. Genome Biology, 2011, 12, .	13.9	0
139	Invited: Challenges in metagenomic assembly. , 2011, , .		0
140	Workshop: Comparative assembly of metagenomic sequences. , 2012, , .		0
141	Computational challenges in microbiome research. , 2015, , .		0
142	Human Microbiome, Assembly and Analysis Software, Project. , 2012, , 1-4.		0
143	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0