Thomas Abeel

List of Publications by Year
in descending order

63 papers	11,286 citations	159358 30 h-index	110170 64 g-index
75 all docs	75 docs citations	75 times ranked	18665 citing authors

#	Article	IF	Citations
1	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. PLoS ONE, 2014, 9, e112963.	1.1	6,781
2	Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. Bioinformatics, 2010, 26, 392-398.	1.8	494
3	The Mycobacterium tuberculosis regulatory network and hypoxia. Nature, 2013, 499, 178-183.	13.7	416
4	Robust Feature Selection Using Ensemble Feature Selection Techniques. Lecture Notes in Computer Science, 2008, , 313-325.	1.0	411
5	Genomic analysis of globally diverse Mycobacterium tuberculosis strains provides insights into the emergence and spread of multidrug resistance. Nature Genetics, 2017, 49, 395-402.	9.4	258
6	Evolution of Extensively Drug-Resistant Tuberculosis over Four Decades: Whole Genome Sequencing and Dating Analysis of Mycobacterium tuberculosis Isolates from KwaZulu-Natal. PLoS Medicine, 2015, 12, e1001880.	3.9	236
7	ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during *Arabidopsis* Leaf Development. Plant Cell, 2014, 26, 210-229.	3.1	219
8	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	3.2	207
9	Generic eukaryotic core promoter prediction using structural features of DNA. Genome Research, 2008, 18, 310-323.	2.4	181
10	ORCAE: online resource for community annotation of eukaryotes. Nature Methods, 2012, 9, 1041-1041.	9.0	176
11	Genomic and functional analyses of Mycobacterium tuberculosis strains implicate ald in D-cycloserine resistance. Nature Genetics, 2016, 48, 544-551.	9.4	145
12	GenomeView: a next-generation genome browser. Nucleic Acids Research, 2012, 40, e12-e12.	6.5	126
13	Comparative and Functional Genomics of Rhodococcus opacus PD630 for Biofuels Development. PLoS Genetics, 2011, 7, e1002219.	1.5	109
14	Deciphering drug resistance in Mycobacterium tuberculosis using whole-genome sequencing: progress, promise, and challenges. Genome Medicine, 2019, 11, 45.	3.6	88
15	Nanopore sequencing enables near-complete de novo assembly of Saccharomyces cerevisiae reference strain CEN.PK113-7D. FEMS Yeast Research, 2017, 17, .	1.1	84
16	Evolution of Invasion in a Diverse Set of *Fusobacterium* Species. MBio, 2014, 5, e01864.	1.8	82
17	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. BMC Genomics, 2012, 13, 120.	1.2	80
18	Mycobacterium tuberculosis Whole Genome Sequences From Southern India Suggest Novel Resistance Mechanisms and the Need for Region-Specific Diagnostics. Clinical Infectious Diseases, 2017, 64, 1494-1501.	2.9	76

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19	ProSOM: core promoter prediction based on unsupervised clustering of DNA physical profiles. Bioinformatics, 2008, 24, i24-i31.	1.8	75
20	Free-floating extracellular DNA: Systematic profiling of mobile genetic elements and antibiotic resistance from wastewater. Water Research, 2021, 189, 116592.	5.3	67
21	Computational Methods for Strain-Level Microbial Detection in Colony and Metagenome Sequencing Data. Frontiers in Microbiology, 2020, 11, 1925.	1.5	66
22	Toward a gold standard for promoter prediction evaluation. Bioinformatics, 2009, 25, i313-i320.	1.8	63
23	Spatially distinct physiology of Bacteroides fragilis within the proximal colon of gnotobiotic mice. Nature Microbiology, 2020, 5, 746-756.	5.9	57
24	Translation initiation site prediction on a genomic scale: beauty in simplicity. Bioinformatics, 2007, 23, i418-i423.	1.8	48
25	Nucleus-specific expression in the multinuclear mushroom-forming fungus *Agaricus bisporus* reveals different nuclear regulatory programs. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4429-4434.	3.3	48
26	Whole-Genome Sequencing of Mycobacterium tuberculosis Provides Insight into the Evolution and Genetic Composition of Drug-Resistant Tuberculosis in Belarus. Journal of Clinical Microbiology, 2017, 55, 457-469.	1.8	47
27	A Generic Tool for Transcription Factor Target Gene Discovery in Arabidopsis Cell Suspension Cultures Based on Tandem Chromatin Affinity Purification. Plant Physiology, 2014, 164, 1122-1133.	2.3	43
28	Chromosome level assembly and comparative genome analysis confirm lager-brewing yeasts originated from a single hybridization. BMC Genomics, 2019, 20, 916.	1.2	43
29	Whole Genome Sequencing of Mycobacterium africanum Strains from Mali Provides Insights into the Mechanisms of Geographic Restriction. PLoS Neglected Tropical Diseases, 2016, 10, e0004332.	1.3	41
30	Laboratory Evolution of a Saccharomyces cerevisiae Ã— S. eubayanus Hybrid Under Simulated Lager-Brewing Conditions. Frontiers in Genetics, 2019, 10, 242.	1.1	35
31	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. Genome Biology, 2022, 23, 74.	3.8	35
32	Metagenomic profiling and transfer dynamics of antibiotic resistance determinants in a full-scale granular sludge wastewater treatment plant. Water Research, 2022, 219, 118571.	5.3	34
33	QuantTB â€" a method to classify mixed Mycobacterium tuberculosis infections within whole genome sequencing data. BMC Genomics, 2020, 21, 80.	1.2	30
34	Discriminative and informative features for biomolecular text mining with ensemble feature selection. Bioinformatics, 2010, 26, i554-i560.	1.8	29
35	Populations of latent Mycobacterium tuberculosis lack a cell wall: Isolation, visualization, and whole-genome characterization. International Journal of Mycobacteriology, 2016, 5, 66-73.	0.3	26
36	Extensive global movement of multidrug-resistant *M. tuberculosis* strains revealed by whole-genome analysis. Thorax, 2019, 74, 882-889.	2.7	24

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37	Emergence of novel SARS-CoV-2 variants in the Netherlands. Scientific Reports, 2021, 11, 6625.	1.6	22
38	Decoding ChIP-seq with a double-binding signal refines binding peaks to single-nucleotides and predicts cooperative interaction. Genome Research, 2014, 24, 1686-1697.	2.4	21
39	An educational guide for nanopore sequencing in the classroom. PLoS Computational Biology, 2020, 16, e1007314.	1.5	20
40	Schizophyllum commune has an extensive and functional alternative splicing repertoire. Scientific Reports, 2016, 6, 33640.	1.6	19
41	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. Microbial Genomics, 2018, 4, .	1.0	18
42	Soft Skills: An Important Asset Acquired from Organizing Regional Student Group Activities. PLoS Computational Biology, 2014, 10, e1003708.	1.5	15
43	Patterns of Conservation and Diversification in the Fungal Polarization Network. Genome Biology and Evolution, 2018, 10, 1765-1782.	1.1	15
44	The Regional Student Group Program of the ISCB Student Council: Stories from the Road. PLoS Computational Biology, 2013, 9, e1003241.	1.5	13
45	Fatal Nosocomial MDR TB Identified through Routine Genetic Analysis and Whole-Genome Sequencing. Emerging Infectious Diseases, 2015, 21, 1082-1084.	2.0	12
46	Highlights from the Student Council Symposium 2011 at the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology. BMC Bioinformatics, 2011, 12, .	1.2	11
47	Semantically linking molecular entities in literature through entity relationships. BMC Bioinformatics, 2012, 13, S6.	1.2	11
48	Highlights from the 5th International Society for Computational Biology Student Council Symposium at the 17th Annual International Conference on Intelligent Systems for Molecular Biology and the 8th European Conference on Computational Biology. BMC Bioinformatics, 2009, 10, I1.	1.2	10
49	Ten Simple Rules for Starting a Regional Student Group. PLoS Computational Biology, 2013, 9, e1003340.	1.5	10
50	Explainable artificial intelligence in forensics: Realistic explanations for number of contributor predictions of DNA profiles. Forensic Science International: Genetics, 2022, 56, 102632.	1.6	10
51	Highlights from the 6th International Society for Computational Biology Student Council Symposium at the 18th Annual International Conference on Intelligent Systems for Molecular Biology. BMC Bioinformatics, 2010, 11, .	1.2	9
52	Highlights from the Eighth International Society for Computational Biology (ISCB) Student Council Symposium 2012. BMC Bioinformatics, 2012, 13, .	1.2	8
53	ISCB Computational Biology Wikipedia Competition. PLoS Computational Biology, 2013, 9, e1003242.	1.5	8
54	The Upside of Failure: How Regional Student Groups Learn from Their Mistakes. PLoS Computational Biology, 2014, 10, e1003768.	1.5	8

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55	Design and Experimental Evaluation of a Minimal, Innocuous Watermarking Strategy to Distinguish Near-Identical DNA and RNA Sequences. ACS Synthetic Biology, 2020, 9, 1361-1375.	1.9	8
56	Approximate, simultaneous comparison of microbial genome architectures via syntenic anchoring of quiver representations. Bioinformatics, 2018, 34, i732-i742.	1.8	7
57	Evidence for Highly Variable, Region-Specific Patterns of T-Cell Epitope Mutations Accumulating in Mycobacterium tuberculosis Strains. Frontiers in Immunology, 2019, 10, 195.	2.2	6
58	Normalizing alternate representations of large sequence variants across multiple bacterial genomes. BMC Bioinformatics, 2015, 16, .	1.2	5
59	A comparative study of pan-genome methods for microbial organisms: Acinetobacter baumannii pan-genome reveals structural variation in antimicrobial resistance-carrying plasmids. Microbial Genomics, 2021, 7, .	1.0	4
60	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. PLoS Computational Biology, 2013, 9, e1002834.	1.5	3
61	The Spirit of Competition: To Win or Not To Win. PLoS Computational Biology, 2013, 9, e1003413.	1.5	2
62	Draft Genome Sequences of Two Extensively Drug-Resistant Strains of Mycobacterium tuberculosis Belonging to the Euro-American S Lineage. Genome Announcements, 2016, 4, .	0.8	2
63	Reply to Lee and Howden. Clinical Infectious Diseases, 2018, 66, 160-161.	2.9	1