

Aaron A Best

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

13,534
citations

516215

16
h-index

525886

27
g-index

39
all docs

39
docs citations

39
times ranked

16716
citing authors

#	ARTICLE	IF	CITATIONS
1	The RAST Server: Rapid Annotations using Subsystems Technology. BMC Genomics, 2008, 9, 75.	1.2	9,977
2	High-throughput generation, optimization and analysis of genome-scale metabolic models. Nature Biotechnology, 2010, 28, 977-982.	9.4	974
3	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	9.4	955
4	Genomic Minimalism in the Early Diverging Intestinal Parasite <i>Giardia lamblia</i> . Science, 2007, 317, 1921-1926.	6.0	725
5	Expanding the Diversity of Mycobacteriophages: Insights into Genome Architecture and Evolution. PLoS ONE, 2011, 6, e16329.	1.1	133
6	Automated Genome Annotation and Metabolic Model Reconstruction in the SEED and Model SEED. Methods in Molecular Biology, 2013, 985, 17-45.	0.4	124
7	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. Nucleic Acids Research, 2021, 49, D575-D588.	6.5	119
8	Evolution of Eukaryotic Transcription: Insights From the Genome of <i>Giardia lamblia</i> . Genome Research, 2004, 14, 1537-1547.	2.4	87
9	Comparative genomics and functional analysis of rhamnose catabolic pathways and regulons in bacteria. Frontiers in Microbiology, 2013, 4, 407.	1.5	55
10	Characterization of Gut Microbiome Dynamics in Developing Pekin Ducks and Impact of Management System. Frontiers in Microbiology, 2016, 7, 2125.	1.5	46
11	Inference of the Transcriptional Regulatory Network in <i>Staphylococcus aureus</i> by Integration of Experimental and Genomics-Based Evidence. Journal of Bacteriology, 2011, 193, 3228-3240.	1.0	45
12	Diarrhea prevalence in a randomized, controlled prospective trial of point-of-use water filters in homes and schools in the Dominican Republic. Tropical Medicine and Health, 2021, 49, 1.	1.0	44
13	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. BMC Genomics, 2013, 14, 94.	1.2	38
14	Connecting genotype to phenotype in the era of high-throughput sequencing. Biochimica Et Biophysica Acta - General Subjects, 2011, 1810, 967-977.	1.1	28
15	Cluster J Mycobacteriophages: Intron Splicing in Capsid and Tail Genes. PLoS ONE, 2013, 8, e69273.	1.1	28
16	Diversity and Versatility of the <i>Thermotoga maritima</i> Sugar Kinome. Journal of Bacteriology, 2012, 194, 5552-5563.	1.0	25
17	Similar subunit architecture of archaeal and eukaryal RNA polymerases. FEMS Microbiology Letters, 2001, 195, 85-90.	0.7	14
18	Gene set analyses for interpreting microarray experiments on prokaryotic organisms. BMC Bioinformatics, 2008, 9, 469.	1.2	13

#	ARTICLE	IF	CITATIONS
19	Cautions about the reliability of pairwise gene correlations based on expression data. <i>Frontiers in Microbiology</i> , 2015, 6, 650.	1.5	11
20	Providing a Safe, In-Person, Residential College Experience During the COVID-19 Pandemic. <i>Frontiers in Public Health</i> , 2021, 9, 672344.	1.3	10
21	Evaluating the consistency of gene sets used in the analysis of bacterial gene expression data. <i>BMC Bioinformatics</i> , 2012, 13, 193.	1.2	8
22	Evaluating the efficacy of point-of-use water filtration units in Fiji. <i>Tropical Medicine and Health</i> , 2019, 47, 48.	1.0	8
23	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 1819.	1.5	7
24	Synthesis and antiprotozoal activity of 1,2,3,4-tetrahydro-2-thioxopyrimidine analogs of combretastatin A-4. <i>Medicinal Chemistry Research</i> , 2011, 20, 364-369.	1.1	5
25	A Bayesian Framework for the Classification of Microbial Gene Activity States. <i>Frontiers in Microbiology</i> , 2016, 7, 1191.	1.5	3
26	IDENTIFICATION AND ANALYSIS OF BACTERIAL GENOMIC METABOLIC SIGNATURES. , 2017, 22, 3-14.		1
27	Whole-Genome Shotgun Sequences of <i>Salmonella enterica</i> Serovar Typhimurium Lilleengen Type Strains LT1, LT18, LT19, LT20, LT21, and LT22. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
28	Genome Sequences of Mycobacteriophages Amgine, Amohnition, Bella96, Cain, DARTH, Hammy, Krueger, LastHope, Peanam, PhelpsODU, Phrank, SirPhilip, Slimphazie, and Unicorn. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
29	Virtual Laboratory Meets Case-Based Instruction Review of: <i>Case It!</i> website from the University of Wisconsin–River Falls, http://www.caseitproject.org/ . <i>Journal of Microbiology and Biology Education</i> , 2012, 13, 195-196.	0.5	0
30	A global reconnaissance of particulates and metals/metalloids in untreated drinking water sources. <i>Environmental Monitoring and Assessment</i> , 2021, 193, 307.	1.3	0
31	GLOBAL SURVEY OF SUSPENDED LOAD MINERALOGY, HEAVY METAL CONTENT, AND ANTIBIOTIC RESIDUES IN RURAL DRINKING WATER SOURCES USING POINT-OF-USE WATER FILTER KITS. , 2017, , .		0
32	DETERMINING SIZE DISTRIBUTION OF VERY FINE PARTICLES IN ENVIRONMENTAL SAMPLES VIA A SIMPLE SETTLING EXPERIMENT: A SPECTROSCOPIC RECONNAISSANCE METHOD. , 2018, , .		0
33	A GLOBAL RECONNAISSANCE SURVEY OF PARTICULATES IN UNTREATED DRINKING WATER SOURCES: POTENTIAL RELATIONSHIPS TO WORLDWIDE METADATA. , 2018, , .		0
34	GLOBAL SURVEY OF MICROBIAL POPULATIONS IN UNTREATED DRINKING WATER SOURCES. , 2018, , .		0
35	GLOBAL RECONNAISSANCE SURVEY OF METALS IN UNTREATED DRINKING WATER SOURCES. , 2018, , .		0