Paul A Jensen

List of Publications by Year in descending order

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1163117 996975 17 606 8 15 citations h-index g-index papers 23 23 23 959 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	A reinforcement learning framework for pooled oligonucleotide design. Bioinformatics, 2022, 38, 2219-2225.	4.1	0
2	A Novel Competence Pathway in the Oral Pathogen <i>Streptococcus sobrinus</i> . Journal of Dental Research, 2021, 100, 542-548.	5.2	13
3	Laboratory Exercise to Measure Plasmid Copy Number by qPCR. Journal of Microbiology and Biology Education, 2021, 22, .	1.0	1
4	<scp>Gapsplit</scp> : efficient random sampling for non-convex constraint-based models. Bioinformatics, 2020, 36, 2623-2625.	4.1	11
5	The bare necessities: Uncovering essential and conditionâ€critical genes with transposon sequencing. Molecular Oral Microbiology, 2019, 34, 39-50.	2.7	10
6	Droplet Tn-Seq combines microfluidics with Tn-Seq for identifying complex single-cell phenotypes. Nature Communications, 2019, 10, 5729.	12.8	54
7	Metabolic Modeling of Streptococcus mutans Reveals Complex Nutrient Requirements of an Oral Pathogen. MSystems, 2019, 4, .	3.8	20
8	Designing Randomized DNA Sequences Free of Restriction Enzyme Recognition Sites. Biotechnology Journal, 2018, 13, 1700326.	3.5	5
9	Coupling Fluxes, Enzymes, and Regulation in Genome-Scale Metabolic Models. Methods in Molecular Biology, 2018, 1716, 337-351.	0.9	3
10	Complete Genome Sequences of Streptococcus sobrinus SL1 (ATCC 33478 = DSM 20742), NIDR 6715-7 (ATCC 27351), NIDR 6715-15 (ATCC 27352), and NCTC 10919 (ATCC 33402). Microbiology Resource Announcements, 2018, 7, .	0.6	4
11	Antibiotics Disrupt Coordination between Transcriptional and Phenotypic Stress Responses in Pathogenic Bacteria. Cell Reports, 2017, 20, 1705-1716.	6.4	65
12	Hands-On Assembly of DNA Sequencing Reads as a Gateway to Bioinformatics. Journal of Microbiology and Biology Education, 2017, 18, .	1.0	1
13	Miniaturized Plate Readers for Low-Cost, High-Throughput Phenotypic Screening. Journal of the Association for Laboratory Automation, 2015, 20, 51-55.	2.8	18
14	MetDraw: automated visualization of genome-scale metabolic network reconstructions and high-throughput data. Bioinformatics, 2014, 30, 1327-1328.	4.1	26
15	Functional integration of a metabolic network model and expression data without arbitrary thresholding. Bioinformatics, 2011, 27, 541-547.	4.1	266
16	TIGER: Toolbox for integrating genome-scale metabolic models, expression data, and transcriptional regulatory networks. BMC Systems Biology, 2011, 5, 147.	3.0	104
17	A scalable systems analysis approach for regulated metabolic networks. , 2009, 2009, 5464-5.		0