Brian Tjaden

List of Publications by Year
in descending order

25 papers	3,278 citations	361045 20 h-index	610482 24 g-index
26 all docs	26 docs citations	26 times ranked	5383 citing authors

#	Article	IF	Citations
1	De novo assembly of bacterial transcriptomes from RNA-seq data. Genome Biology, 2015, 16, 1.	3.8	1,215
2	Computational analysis of bacterial RNA-Seq data. Nucleic Acids Research, 2013, 41, e140-e140.	6.5	573
3	Target prediction for small, noncoding RNAs in bacteria. Nucleic Acids Research, 2006, 34, 2791-2802.	6.5	219
4	TargetRNA2: identifying targets of small regulatory RNAs in bacteria. Nucleic Acids Research, 2014, 42, W124-W129.	6.5	177
5	Transcriptome analysis of Escherichia coli using high-density oligonucleotide probe arrays. Nucleic Acids Research, 2002, 30, 3732-3738.	6.5	167
6	A Novel Fur- and Iron-Regulated Small RNA, NrrF, Is Required for Indirect Fur-Mediated Regulation of the sdhA and sdhC Genes in Neisseria meningitidis. Journal of Bacteriology, 2007, 189, 3686-3694.	1.0	108
7	TargetRNA: a tool for predicting targets of small RNA action in bacteria. Nucleic Acids Research, 2008, 36, W109-W113.	6.5	108
8	Probing the sRNA regulatory landscape of P. aeruginosa: postâ€transcriptional control of determinants of pathogenicity and antibiotic susceptibility. Molecular Microbiology, 2017, 106, 919-937.	1.2	91
9	Small RNA profiling in Mycobacterium tuberculosis identifies MrsI as necessary for an anticipatory iron sparing response. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6464-6469.	3.3	83
10	GRIL-seq provides a method for identifying direct targets of bacterial small regulatory RNA by in vivo proximity ligation. Nature Microbiology, 2017, 2, 16239.	5.9	80
11	Small non-coding RNAs in Streptomyces coelicolor. Nucleic Acids Research, 2008, 36, 7240-7251.	6.5	79
12	The Gonococcal Transcriptome during Infection of the Lower Genital Tract in Women. PLoS ONE, 2015, 10, e0133982.	1.1	50
13	A computational system for identifying operons based on RNA-seq data. Methods, 2020, 176, 62-70.	1.9	47
14	Identifying operons and untranslated regions of transcripts using Escherichia coli RNA expression analysis. Bioinformatics, 2002, 18, S337-S344.	1.8	43
15	Bioinformatic prediction and experimental verification of sRNAs in the haloarchaeonHaloferax volcanii. RNA Biology, 2011, 8, 806-816.	1.5	37
16	Assessing computational tools for the discovery of small RNA genes in bacteria. Rna, 2011, 17, 1635-1647.	1.6	34
17	An approach for clustering gene expression data with error information. BMC Bioinformatics, 2006, 7, 17.	1.2	30
18	Transcriptome Analysis of Neisseria gonorrhoeae during Natural Infection Reveals Differential Expression of Antibiotic Resistance Determinants between Men and Women. MSphere, 2018, 3, .	1.3	26

#	Article	IF	Citations
19	Small RNAs of the halophilic archaeon Haloferax volcanii. Biochemical Society Transactions, 2009, 37, 133-136.	1.6	25
20	Prediction of small, noncoding RNAs in bacteria using heterogeneous data. Journal of Mathematical Biology, 2007, 56, 183-200.	0.8	24
21	Identification of sRNAs expressed by the human pathogen Neisseria gonorrhoeae under disparate growth conditions. Frontiers in Microbiology, 2014, 5, 456.	1.5	22
22	Identification and Characterization of Serotype-Specific Variation in Group A Streptococcus Pilus Expression. Infection and Immunity, 2018, 86, .	1.0	20
23	Computational Identification of sRNA Targets. Methods in Molecular Biology, 2012, 905, 227-234.	0.4	9
24	Computational prediction and transcriptional analysis of sRNAs in Nitrosomonas europaea. FEMS Microbiology Letters, 2010, 312, 46-54.	0.7	8
25	Biocomputational Identification of Bacterial Small RNAs and Their Target Binding Sites. , 2012, , 273-293.		3