

Todd M Lowe

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

23,158
citations

201674

27
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330143

37
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45
all docs

45
docs citations

45
times ranked

23997
citing authors

#	ARTICLE	IF	CITATIONS
1	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. Nucleic Acids Research, 1997, 25, 955-964.	14.5	9,417
2	tRNAscan-SE: A Program for Improved Detection of Transfer RNA Genes in Genomic Sequence. Nucleic Acids Research, 1997, 25, 0955-964.	14.5	3,970
3	tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Research, 2016, 44, W54-W57.	14.5	2,219
4	The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. Nucleic Acids Research, 2005, 33, W686-W689.	14.5	2,090
5	tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods in Molecular Biology, 2019, 1962, 1-14.	0.9	1,023
6	GtRNAdb: a database of transfer RNA genes detected in genomic sequence. Nucleic Acids Research, 2009, 37, D93-D97.	14.5	782
7	GtRNAdb 2.0: an expanded database of transfer RNA genes identified in complete and draft genomes. Nucleic Acids Research, 2016, 44, D184-D189.	14.5	776
8	tRNAscan-SE 2.0: improved detection and functional classification of transfer RNA genes. Nucleic Acids Research, 2021, 49, 9077-9096.	14.5	569
9	ARM-seq: AlkB-facilitated RNA methylation sequencing reveals a complex landscape of modified tRNA fragments. Nature Methods, 2015, 12, 879-884.	19.0	350
10	Homologs of Small Nucleolar RNAs in Archaea. Science, 2000, 288, 517-522.	12.6	324
11	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	14.5	174
12	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
13	A guided tour: small RNA function in Archaea. Molecular Microbiology, 2001, 40, 509-519.	2.5	128
14	Matching tRNA modifications in humans to their known and predicted enzymes. Nucleic Acids Research, 2019, 47, 2143-2159.	14.5	116
15	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	14.5	103
16	Small RNA Modifications: Integral to Function and Disease. Trends in Molecular Medicine, 2016, 22, 1025-1034.	6.7	90
17	The UCSC Archaeal Genome Browser: 2012 update. Nucleic Acids Research, 2012, 40, D646-D652.	14.5	89
18	Stress response of a marine ammonia-oxidizing archaeon informs physiological status of environmental populations. ISME Journal, 2018, 12, 508-519.	9.8	82

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19	A guide to naming human non-coding RNA genes. EMBO Journal, 2020, 39, e103777.	7.8	77
20	Small nucleolar RNAs and RNA-guided post-transcriptional modification. Essays in Biochemistry, 2013, 54, 53-77.	4.7	69
21	Discovery of permuted and recently split transfer RNAs in Archaea. Genome Biology, 2011, 12, R38.	8.8	58
22	R2DT is a framework for predicting and visualising RNA secondary structure using templates. Nature Communications, 2021, 12, 3494.	12.8	58
23	IscR Is Essential for Yersinia pseudotuberculosis Type III Secretion and Virulence. PLoS Pathogens, 2014, 10, e1004194.	4.7	53
24	Diversity of Antisense and Other Non-Coding RNAs in Archaea Revealed by Comparative Small RNA Sequencing in Four Pyrobaculum Species. Frontiers in Microbiology, 2012, 3, 231.	3.5	46
25	Transfer RNA genes experience exceptionally elevated mutation rates. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8996-9001.	7.1	40
26	C/D box sRNA-guided 2'-O-methylation patterns of archaeal rRNA molecules. BMC Genomics, 2015, 16, 632.	2.8	35
27	Predicting transfer RNA gene activity from sequence and genome context. Genome Research, 2020, 30, 85-94.	5.5	22
28	Reclassification of Thermoproteus neutrophilus Stetter and Zillig 1989 as Pyrobaculum neutrophilum comb. nov. based on phylogenetic analysis. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 751-754.	1.7	21
29	Distinct Stress-Dependent Signatures of Cellular and Extracellular tRNA-Derived Small RNAs. Advanced Science, 2022, 9, e2200829.	11.2	19
30	Draft De Novo Transcriptome of the Rat Kangaroo Potorous tridactylus as a Tool for Cell Biology. PLoS ONE, 2015, 10, e0134738.	2.5	18
31	High-Throughput Small RNA Sequencing Enhanced by AlkB-Facilitated RNA de-Methylation (ARM-Seq). Methods in Molecular Biology, 2017, 1562, 231-243.	0.9	17
32	tRNAviz: explore and visualize tRNA sequence features. Nucleic Acids Research, 2019, 47, W542-W547.	14.5	17
33	Distinct Modified Nucleosides in tRNA ^{Trp} from the Hyperthermophilic Archaeon Thermococcus kodakarensis and Requirement of tRNA ^{m²} G10/m ² G10 Methytransferase (Archaeal Trm11) for Survival at High Temperatures. Journal of Bacteriology, 2019, 201, .	2.2	15
34	Complete genome sequence of Pyrobaculum oguniense. Standards in Genomic Sciences, 2012, 6, 336-345.	1.5	10
35	Methylation guide RNA evolution in archaea: structure, function and genomic organization of 110 C/D box sRNA families across six Pyrobaculum species. Nucleic Acids Research, 2018, 46, 5678-5691.	14.5	7
36	Eukaryotic tRNA sequences present conserved and amino acid-specific structural signatures. Nucleic Acids Research, 2022, 50, 4100-4112.	14.5	6