Claude Thermes

List of Publications by Year in descending order

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CLAUDE THEDMES

#	Article	IF	CITATIONS
1	GC content, but not nucleosome positioning, directly contributes to intron splicing efficiency in <i>Paramecium</i> . Genome Research, 2022, 32, 699-709.	5.5	6
2	Transcriptome architecture and regulation at environmental transitions in flavobacteria: the case of an important fish pathogen. ISME Communications, 2021, 1, .	4.2	7
3	A Small RNA-Seq Protocol with Less Bias and Improved Capture of 2′-O-Methyl RNAs. Methods in Molecular Biology, 2021, 2298, 153-167.	0.9	1
4	Improving Small RNA-seq: Less Bias and Better Detection of 2'-O-Methyl RNAs. Journal of Visualized Experiments, 2019, , .	0.3	3
5	Transcription-mediated organization of the replication initiation program across large genes sets common fragile sites genome-wide. Nature Communications, 2019, 10, 5693.	12.8	73
6	Evidence for late Pleistocene origin of Astyanax mexicanus cavefish. BMC Evolutionary Biology, 2018, 18, 43.	3.2	117
7	The evolution of the temporal program of genome replication. Nature Communications, 2018, 9, 2199.	12.8	19
8	The Third Revolution in Sequencing Technology. Trends in Genetics, 2018, 34, 666-681.	6.7	759
9	Systematic comparison of small RNA library preparation protocols for next-generation sequencing. BMC Genomics, 2018, 19, 118.	2.8	93
10	Replication landscape of the human genome. Nature Communications, 2016, 7, 10208.	12.8	259
11	From the chromatin interaction network to the organization of the human genome into replication N/U-domains. New Journal of Physics, 2014, 16, 115014.	2.9	12
12	Large replication skew domains delimit GC-poor gene deserts in human. Computational Biology and Chemistry, 2014, 53, 153-165.	2.3	5
13	Megabase Replication Domains Along the Human Genome: Relation to Chromatin Structure and Genome Organisation. Sub-Cellular Biochemistry, 2013, 61, 57-80.	2.4	15
14	Replication Fork Polarity Gradients Revealed by Megabase-Sized U-Shaped Replication Timing Domains in Human Cell Lines. PLoS Computational Biology, 2012, 8, e1002443.	3.2	70
15	Multi-scale coding of genomic information: From DNA sequence to genome structure and function. Physics Reports, 2011, 498, 45-188.	25.6	108
16	Replication-Associated Mutational Asymmetry in the Human Genome. Molecular Biology and Evolution, 2011, 28, 2327-2337.	8.9	66
17	Wavelet-based method to disentangle transcription- and replication-associated strand asymmetries in mammalian genomes. Applied and Computational Harmonic Analysis, 2010, 28, 150-170.	2.2	22
18	A novel strategy of transcription regulation by intragenic nucleosome ordering. Genome Research, 2010, 20, 59-67.	5.5	64

CLAUDE THERMES

#	Article	IF	CITATIONS
19	Impact of replication timing on non-CpG and CpG substitution rates in mammalian genomes. Genome Research, 2010, 20, 447-457.	5.5	187
20	Open chromatin encoded in DNA sequence is the signature of â€~master' replication origins in human cells. Nucleic Acids Research, 2009, 37, 6064-6075.	14.5	52
21	DNA physical properties determine nucleosome occupancy from yeast to fly. Nucleic Acids Research, 2008, 36, 3746-3756.	14.5	125
22	The Dogfish <i>Scyliorhinus canicula:</i> A Reference in Jawed Vertebrates. Cold Spring Harbor Protocols, 2008, 2008, pdb.emo111.	0.3	60
23	Human gene organization driven by the coordination of replication and transcription. Genome Research, 2007, 17, 1278-1285.	5.5	147
24	Replication-associated strand asymmetries in mammalian genomes: Toward detection of replication origins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9836-9841.	7.1	133
25	Transcription-coupled and splicing-coupled strand asymmetries in eukaryotic genomes. Nucleic Acids Research, 2004, 32, 4969-4978.	14.5	73