

Christopher A Lavender

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

2,702
citations

623574

14
h-index

752573

20
g-index

21
all docs

21
docs citations

21
times ranked

5001
citing authors

#	ARTICLE	IF	CITATIONS
1	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387.	1.5	1,282
2	Widespread transcriptional pausing and elongation control at enhancers. <i>Genes and Development</i> , 2018, 32, 26-41.	2.7	269
3	<i>RNA-Puzzles</i> : A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	1.6	241
4	Multiple Micellization and Dissociation Transitions of Thermo- and Light-Sensitive Poly(ethylene Terephthalate) Block Copolymers in Aqueous Solution. <i>Macromolecules</i> , 2008, 41, 2632-2643.	2.2	187
5	Single-molecule correlated chemical probing of RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13858-13863.	3.3	140
6	Three-dimensional RNA structure refinement by hydroxyl radical probing. <i>Nature Methods</i> , 2012, 9, 603-608.	9.0	77
7	Revealing a human p53 universe. <i>Nucleic Acids Research</i> , 2018, 46, 8153-8167.	6.5	75
8	In-cell SHAPE reveals that free 30S ribosome subunits are in the inactive state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2425-2430.	3.3	62
9	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. <i>Nature Communications</i> , 2019, 10, 3072.	5.8	53
10	Ultrasensitive deletion detection links mitochondrial DNA replication, disease, and aging. <i>Genome Biology</i> , 2020, 21, 248.	3.8	48
11	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. <i>PLoS Computational Biology</i> , 2015, 11, e1004126.	1.5	45
12	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. <i>ELife</i> , 2017, 6, .	2.8	42
13	Structure-Based Alignment and Consensus Secondary Structures for Three HIV-Related RNA Genomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004230.	1.5	34
14	Robust and Generic RNA Modeling Using Inferred Constraints: A Structure for the Hepatitis C Virus IRES Pseudoknot Domain. <i>Biochemistry</i> , 2010, 49, 4931-4933.	1.2	31
15	Downstream Antisense Transcription Predicts Genomic Features That Define the Specific Chromatin Environment at Mammalian Promoters. <i>PLoS Genetics</i> , 2016, 12, e1006224.	1.5	15
16	Increased Burden of Rare Sequence Variants in GnRH-Associated Genes in Women With Hypothalamic Amenorrhea. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e1441-e1452.	1.8	13
17	Muver, a computational framework for accurately calling accumulated mutations. <i>BMC Genomics</i> , 2018, 19, 345.	1.2	12
18	ORIO (Online Resource for Integrative Omics): a web-based platform for rapid integration of next generation sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 5678-5690.	6.5	11

#	ARTICLE	IF	CITATIONS
19	ORSO (Online Resource for Social Omics): A data-driven social network connecting scientists to genomics datasets. PLoS Computational Biology, 2020, 16, e1007571.	1.5	2