Christopher A Lavender

List of Publications by Citations

20 papers	1,798 citations
14 h-index	21 g-index
21 ext. papers	2,349 ext. citations
9.7 avg, IF	4.18 L-index

#	Paper	IF	Citations
20	Opportunities and obstacles for deep learning in biology and medicine. *Journal of the Royal Society Interface*, **2018**, 15,	4.1	780
19	RNA-Puzzles: a CASP-like evaluation of RNA three-dimensional structure prediction. *Rna*, **2012**, 18, 610-25	5.8	181
18	Multiple Micellization and Dissociation Transitions of Thermo- and Light-Sensitive Poly(ethylene oxide)-b-poly(ethoxytri(ethylene glycol) acrylate-co-o-nitrobenzyl acrylate) in Water. *Macromolecules*, **2008**, 41, 2632-2643	5.5	178
17	Widespread transcriptional pausing and elongation control at enhancers. *Genes and Development*, **2018**, 32, 26-41	12.6	167
16	Single-molecule correlated chemical probing of RNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13858-63	11.5	95
15	Three-dimensional RNA structure refinement by hydroxyl radical probing. *Nature Methods*, **2012**, 9, 603-8	21.6	64
14	In-cell SHAPE reveals that free 30S ribosome subunits are in the inactive state. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 2425-30	11.5	51
13	Revealing a human p53 universe. *Nucleic Acids Research*, **2018**, 46, 8153-8167	20.1	47
12	Opportunities and obstacles for deep learning in biology and medicine		45
11	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. *PLoS Computational Biology*, **2015**, 11, e1004126	5	36
10	Structure-Based Alignment and Consensus Secondary Structures for Three HIV-Related RNA Genomes. *PLoS Computational Biology*, **2015**, 11, e1004230	5	28
9	Robust and generic RNA modeling using inferred constraints: a structure for the hepatitis C virus IRES pseudoknot domain. *Biochemistry*, **2010**, 49, 4931-3	3.2	26
8	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. *Nature Communications*, **2019**, 10, 3072	17.4	25
7	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. *ELife*, **2017**, 6,	8.9	20
6	Ultrasensitive deletion detection links mitochondrial DNA replication, disease, and aging. *Genome Biology*, **2020**, 21, 248	18.3	14
5	Downstream Antisense Transcription Predicts Genomic Features That Define the Specific Chromatin Environment at Mammalian Promoters. *PLoS Genetics*, **2016**, 12, e1006224	6	13
4	ORIO (Online Resource for Integrative Omics): a web-based platform for rapid integration of next generation sequencing data. *Nucleic Acids Research*, **2017**, 45, 5678-5690	20.1	9

LIST OF PUBLICATIONS

3	Muver, a computational framework for accurately calling accumulated mutations. *BMC Genomics*, **2018**, 19, 345	4.5	9
2	Increased Burden of Rare Sequence Variants in GnRH-Associated Genes in Women With Hypothalamic Amenorrhea. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, e1441-e1452	5.6	8
1	ORSO (Online Resource for Social Omics): A data-driven social network connecting scientists to genomics datasets. *PLoS Computational Biology*, **2020**, 16, e1007571	5	1