

Michael F Lin

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

14,133
citations

394421

19
h-index

794594

19
g-index

20
all docs

20
docs citations

20
times ranked

22673
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	27.8	3,801
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
3	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
4	Extensive and coordinated transcription of noncoding RNAs within cell-cycle promoters. <i>Nature Genetics</i> , 2011, 43, 621-629.	21.4	1,080
5	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
6	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	27.8	963
7	PhyloCSF: a comparative genomics method to distinguish protein coding and non-coding regions. <i>Bioinformatics</i> , 2011, 27, i275-i282.	4.1	864
8	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012, 22, 577-591.	5.5	809
9	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	27.8	573
10	Distinguishing protein-coding and noncoding genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19428-19433.	7.1	503
11	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. <i>Genome Research</i> , 2009, 19, 1316-1323.	5.5	476
12	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	12.6	458
13	Evidence of abundant stop codon readthrough in <i>Drosophila</i> and other metazoa. <i>Genome Research</i> , 2011, 21, 2096-2113.	5.5	196
14	Revisiting the protein-coding gene catalog of <i>Drosophila melanogaster</i> using 12 fly genomes. <i>Genome Research</i> , 2007, 17, 1823-1836.	5.5	135
15	Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes. <i>Genome Research</i> , 2011, 21, 1916-1928.	5.5	83
16	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , 2016, 33, 3108-3132.	8.9	53
17	Performance and Scalability of Discriminative Metrics for Comparative Gene Identification in 12 <i>Drosophila</i> Genomes. <i>PLoS Computational Biology</i> , 2008, 4, e1000067.	3.2	45
18	FRESCO: finding regions of excess synonymous constraint in diverse viruses. <i>Genome Biology</i> , 2015, 16, 38.	8.8	35

#	ARTICLE	IF	CITATIONS
19	Error and Error Mitigation in Low-Coverage Genome Assemblies. PLoS ONE, 2011, 6, e17034.	2.5	33