

Chun-Long Chen

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

4,434
citations

304743

22
h-index

302126

39
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49
all docs

49
docs citations

49
times ranked

6340
citing authors

#	ARTICLE	IF	CITATIONS
1	Prospectively defined patterns of APOBEC3A mutagenesis are prevalent in human cancers. <i>Cell Reports</i> , 2022, 38, 110555.	6.4	25
2	GC content, but not nucleosome positioning, directly contributes to intron splicing efficiency in <i>Paramecium</i> . <i>Genome Research</i> , 2022, 32, 699-709.	5.5	6
3	Kronos scRT: a uniform framework for single-cell replication timing analysis. <i>Nature Communications</i> , 2022, 13, 2329.	12.8	9
4	Cohesin-mediated loop anchors confine the locations of human replication origins. <i>Nature</i> , 2022, 606, 812-819.	27.8	47
5	Topoisomerase I prevents transcription-replication conflicts at transcription termination sites. <i>Molecular and Cellular Oncology</i> , 2021, 8, 1843951.	0.7	8
6	DNA molecular combing-based replication fork directionality profiling. <i>Nucleic Acids Research</i> , 2021, 49, e69-e69.	14.5	7
7	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	12.8	9
8	Genome-wide mapping of human DNA replication by optical replication mapping supports a stochastic model of eukaryotic replication. <i>Molecular Cell</i> , 2021, 81, 2975-2988.e6.	9.7	57
9	Editorial: DNA Replication Stress and Cell Fate. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 778486.	3.7	0
10	Reply to Alexander Yang, Vincent L. Cannataro, Jeffrey P. Townsend's Letter to the Editor, re: Ming-Jun Shi, Xiang-Yu Meng, Philippe Lamy, et al. APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. <i>Eur Urol</i> 2019, 76:9-13. <i>European Urology</i> , 2020, 77, e26-e27.	1.9	3
11	Replication Stress Induces Global Chromosome Breakage in the Fragile X Genome. <i>Cell Reports</i> , 2020, 32, 108179.	6.4	33
12	Identification of new driver and passenger mutations within APOBEC-induced hotspot mutations in bladder cancer. <i>Genome Medicine</i> , 2020, 12, 85.	8.2	39
13	Exo1 recruits Cdc5 polo kinase to MutL ³ to ensure efficient meiotic crossover formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30577-30588.	7.1	28
14	Topoisomerase 1 prevents replication stress at R-loop-enriched transcription termination sites. <i>Nature Communications</i> , 2020, 11, 3940.	12.8	105
15	DNA polymerase δ interacts with H3-H4 and facilitates the transfer of parental histones to lagging strands. <i>Science Advances</i> , 2020, 6, eabb5820.	10.3	62
16	The impact of transcription-mediated replication stress on genome instability and human disease. <i>Genome Instability & Disease</i> , 2020, 1, 207-234.	1.1	8
17	APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. <i>European Urology</i> , 2019, 76, 9-13.	1.9	34
18	Transcription-mediated organization of the replication initiation program across large genes sets common fragile sites genome-wide. <i>Nature Communications</i> , 2019, 10, 5693.	12.8	73

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19	Replication landscape of the human genome. <i>Nature Communications</i> , 2016, 7, 10208.	12.8	259
20	From the chromatin interaction network to the organization of the human genome into replication N/U-domains. <i>New Journal of Physics</i> , 2014, 16, 115014.	2.9	12
21	From Simple Bacterial and Archaeal Replicons to Replication N/U-Domains. <i>Journal of Molecular Biology</i> , 2013, 425, 4673-4689.	4.2	32
22	Multiscale analysis of genome-wide replication timing profiles using a wavelet-based signal-processing algorithm. <i>Nature Protocols</i> , 2013, 8, 98-110.	12.0	50
23	Megabase Replication Domains Along the Human Genome: Relation to Chromatin Structure and Genome Organisation. <i>Sub-Cellular Biochemistry</i> , 2013, 61, 57-80.	2.4	15
24	Replication Fork Polarity Gradients Revealed by Megabase-Sized U-Shaped Replication Timing Domains in Human Cell Lines. <i>PLoS Computational Biology</i> , 2012, 8, e1002443.	3.2	70
25	Linking the DNA strand asymmetry to the spatio-temporal replication program. <i>European Physical Journal E</i> , 2012, 35, 92.	1.6	16
26	Linking the DNA strand asymmetry to the spatio-temporal replication program. <i>European Physical Journal E</i> , 2012, 35, 123.	1.6	13
27	XUTs are a class of Xrn1-sensitive antisense regulatory non-coding RNA in yeast. <i>Nature</i> , 2011, 475, 114-117.	27.8	329
28	Tight protein-DNA interactions favor gene silencing. <i>Genes and Development</i> , 2011, 25, 1365-1370.	5.9	71
29	Replication-Associated Mutational Asymmetry in the Human Genome. <i>Molecular Biology and Evolution</i> , 2011, 28, 2327-2337.	8.9	66
30	Evidence for Sequential and Increasing Activation of Replication Origins along Replication Timing Gradients in the Human Genome. <i>PLoS Computational Biology</i> , 2011, 7, e1002322.	3.2	124
31	Impact of replication timing on non-CpG and CpG substitution rates in mammalian genomes. <i>Genome Research</i> , 2010, 20, 447-457.	5.5	187
32	SnoRNAs from the filamentous fungus <i>Neurospora crassa</i> : structural, functional and evolutionary insights. <i>BMC Genomics</i> , 2009, 10, 515.	2.8	15
33	Genome-wide evolutionary analysis of the noncoding RNA genes and noncoding DNA of <i>Paramecium tetraurelia</i> . <i>Rna</i> , 2009, 15, 503-514.	3.5	11
34	Genomewide Analysis of Box C/D and Box H/ACA snoRNAs in <i>Chlamydomonas reinhardtii</i> Reveals an Extensive Organization Into Intronic Gene Clusters. <i>Genetics</i> , 2008, 179, 21-30.	2.9	27
35	Exploration of Pairing Constraints Identifies a 9 Base-pair Core within Box C/D snoRNA-rRNA Duplexes. <i>Journal of Molecular Biology</i> , 2007, 369, 771-783.	4.2	30
36	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354

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37	Genome-wide analyses of two families of snoRNA genes from <i>Drosophila melanogaster</i> , demonstrating the extensive utilization of introns for coding of snoRNAs. <i>Rna</i> , 2005, 11, 1303-1316.	3.5	69
38	Identification and functional analysis of 23 novel box C/D snoRNAs from <i>Oryza sativa</i> . <i>Science Bulletin</i> , 2003, 48, 2077.	1.7	0
39	The high diversity of snoRNAs in plants: identification and comparative study of 120 snoRNA genes from <i>Oryza sativa</i> . <i>Nucleic Acids Research</i> , 2003, 31, 2601-2613.	14.5	64
40	A novel gene organization: intronic snoRNA gene clusters from <i>Oryza sativa</i> . <i>Nucleic Acids Research</i> , 2002, 30, 3262-3272.	14.5	38