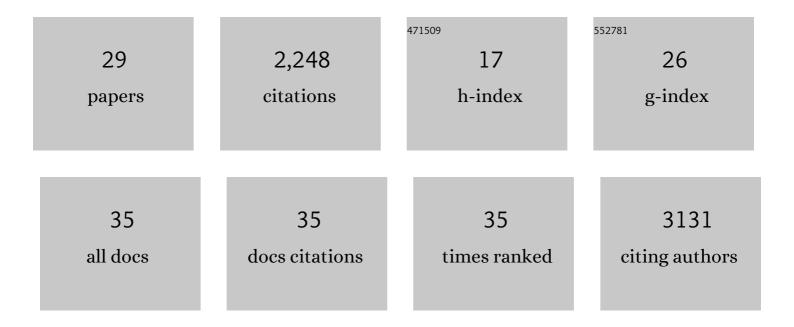
## David M Macalpine

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	27.8	363
2	Conserved nucleosome positioning defines replication origins. Genes and Development, 2010, 24, 748-753.	5.9	333
3	Epigenome characterization at single base-pair resolution. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18318-18323.	7.1	325
4	<i>Drosophila</i> ORC localizes to open chromatin and marks sites of cohesin complex loading. Genome Research, 2010, 20, 201-211.	5.5	248
5	Chromatin and DNA Replication. Cold Spring Harbor Perspectives in Biology, 2013, 5, a010207-a010207.	5.5	162
6	DNA replication origins—where do we begin?. Genes and Development, 2016, 30, 1683-1697.	5.9	153
7	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. Genome Research, 2014, 24, 1751-1764.	5.5	141
8	Genome-wide chromatin footprinting reveals changes in replication origin architecture induced by pre-RC assembly. Genes and Development, 2015, 29, 212-224.	5.9	82
9	DNA replication and transcription programs respond to the same chromatin cues. Genome Research, 2014, 24, 1102-1114.	5.5	74
10	Dynamic loading and redistribution of the Mcm2â€7 helicase complex through the cell cycle. EMBO Journal, 2015, 34, 531-543.	7.8	73
11	Nucleosomes influence multiple steps during replication initiation. ELife, 2017, 6, .	6.0	58
12	Noncoding Transcription Is a Driving Force for Nucleosome Instability in <i>spt16</i> Mutant Cells. Molecular and Cellular Biology, 2016, 36, 1856-1867.	2.3	39
13	Chromatin conformation and transcriptional activity are permissive regulators of DNA replication in <i>Drosophila</i> . Genome Research, 2018, 28, 1688-1700.	5.5	29
14	Nascent chromatin occupancy profiling reveals locus- and factor-specific chromatin maturation dynamics behind the DNA replication fork. Genome Research, 2019, 29, 1123-1133.	5.5	27
15	Sir2 suppresses transcription-mediated displacement of Mcm2-7 replicative helicases at the ribosomal DNA repeats. PLoS Genetics, 2019, 15, e1008138.	3.5	25
16	Capturing the primordial Kras mutation initiating urethane carcinogenesis. Nature Communications, 2020, 11, 1800.	12.8	25
17	Methylation of histone H4 lysine 20 by PR-Set7 ensures the integrity of late replicating sequence domains in <i>Drosophila</i> . Nucleic Acids Research, 2016, 44, gkw333.	14.5	24
18	Mcm2-7 Is an Active Player in the DNA Replication Checkpoint Signaling Cascade via Proposed Modulation of Its DNA Gate. Molecular and Cellular Biology, 2015, 35, 2131-2143.	2.3	14

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#	Article	IF	CITATIONS
19	Local nucleosome dynamics and eviction following a double-strand break are reversible by NHEJ-mediated repair in the absence of DNA replication. Genome Research, 2021, 31, 775-788.	5.5	10
20	SnapShot: Origins of DNA Replication. Cell, 2015, 161, 418-418.e1.	28.9	9
21	Linking the dynamics of chromatin occupancy and transcription with predictive models. Genome Research, 2021, 31, 1035-1046.	5.5	7
22	ORChestrating the human DNA replication program. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9136-9138.	7.1	4
23	Stochastic initiation of DNA replication across the human genome. Molecular Cell, 2021, 81, 2873-2874.	9.7	4
24	Disruption of origin chromatin structure by helicase activation in the absence of DNA replication. Genes and Development, 2021, 35, 1339-1355.	5.9	4
25	Chromatin Determinants of Origin Selection and Activation. , 2016, , 87-104.		4
26	RoboCOP: jointly computing chromatin occupancy profiles for numerous factors from chromatin accessibility data. Nucleic Acids Research, 2021, 49, 7925-7938.	14.5	3
27	Cell-Cycle–Dependent Chromatin Dynamics at Replication Origins. Genes, 2021, 12, 1998.	2.4	3
28	The role of local transcription and chromatin structure in establishing DNA replication origins. FASEB Journal, 2009, 23, 78.2.	0.5	0
29	RoboCOP: Multivariate State Space Model Integrating Epigenomic Accessibility Data to Elucidate Genome-Wide Chromatin Occupancy. Lecture Notes in Computer Science, 2020, 12074, 136-151.	1.3	0