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List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

2,276
citations

687363
13
h-index

940533
16
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17
all docs

17
docs citations

17
times ranked

3926
citing authors

#	ARTICLE	IF	CITATIONS
1	Promoter-bound METTL3 maintains myeloid leukaemia by m6A-dependent translation control. <i>Nature</i> , 2017, 552, 126-131.	27.8	833
2	Cytoplasmic 5'â€²-3'â€² exonuclease Xrn1p is also a genome-wide transcription factor in yeast. <i>Frontiers in Genetics</i> , 2014, 5, 1.	2.3	427
3	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. <i>Cell</i> , 2013, 153, 1000-1011.	28.9	311
4	Histone post-translational modifications " cause and consequence of genome function. <i>Nature Reviews Genetics</i> , 2022, 23, 563-580.	16.3	253
5	Nuclear functions of prefoldin. <i>Open Biology</i> , 2014, 4, 140085.	3.6	103
6	Genome architecture and stability in the <i>Saccharomyces cerevisiae</i> knockout collection. <i>Nature</i> , 2019, 573, 416-420.	27.8	72
7	Chromatin Reassembly Factors Are Involved in Transcriptional Interference Promoting HIV Latency. <i>Journal of Virology</i> , 2011, 85, 3187-3202.	3.4	71
8	The Prefoldin Complex Regulates Chromatin Dynamics during Transcription Elongation. <i>PLoS Genetics</i> , 2013, 9, e1003776.	3.5	45
9	H3K4 monomethylation dictates nucleosome dynamics and chromatin remodeling at stress-responsive genes. <i>Nucleic Acids Research</i> , 2015, 43, 4937-4949.	14.5	34
10	RNA Binding by Histone Methyltransferases Set1 and Set2. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	31
11	One step back before moving forward: Regulation of transcription elongation by arrest and backtracking. <i>FEBS Letters</i> , 2012, 586, 2820-2825.	2.8	25
12	Phosphorylation of Histone H4T80 Triggers DNA Damage Checkpoint Recovery. <i>Molecular Cell</i> , 2018, 72, 625-635.e4.	9.7	21
13	Methylation of histone H3 at lysine 37 by Set1 and Set2 prevents spurious DNA replication. <i>Molecular Cell</i> , 2021, 81, 2793-2807.e8.	9.7	18
14	Subtracting the sequence bias from partially digested MNase-seq data reveals a general contribution of TFIS to nucleosome positioning. <i>Epigenetics and Chromatin</i> , 2017, 10, 58.	3.9	17
15	The ribosome assembly gene network is controlled by the feedback regulation of transcription elongation. <i>Nucleic Acids Research</i> , 2017, 45, 9302-9318.	14.5	13
16	A Matter of Packaging: Influence of Nucleosome Positioning on Heterologous Gene Expression. <i>Methods in Molecular Biology</i> , 2012, 824, 51-64.	0.9	1