

Devin A King

List of Publications by Year in descending order

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12
papers

484
citations

1040056

9
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1199594

12
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13
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13
docs citations

13
times ranked

656
citing authors

#	ARTICLE	IF	CITATIONS
1	Retinoblastoma protein regulates carcinogen susceptibility at heterochromatic cancer driver loci. <i>Life Science Alliance</i> , 2022, 5, e202101134.	2.8	4
2	Endocardial/endothelial angiocrines regulate cardiomyocyte development and maturation and induce features of ventricular non-compaction. <i>European Heart Journal</i> , 2021, 42, 4264-4276.	2.2	41
3	Genome-wide profiles of UV lesion susceptibility, repair, and mutagenic potential in melanoma. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2021, 823, 111758.	1.0	4
4	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.	21.4	79
5	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. <i>Molecular Cell</i> , 2019, 76, 909-921.e3.	9.7	83
6	Endothelial deletion of Ino80 disrupts coronary angiogenesis and causes congenital heart disease. <i>Nature Communications</i> , 2018, 9, 368.	12.8	71
7	INO80 Chromatin Remodeling Coordinates Metabolic Homeostasis with Cell Division. <i>Cell Reports</i> , 2018, 22, 611-623.	6.4	28
8	The INO80 chromatin remodeler sustains metabolic stability by promoting TOR signaling and regulating histone acetylation. <i>PLoS Genetics</i> , 2018, 14, e1007216.	3.5	23
9	Carcinogen susceptibility is regulated by genome architecture and predicts cancer mutagenesis. <i>EMBO Journal</i> , 2017, 36, 2829-2843.	7.8	71
10	The INO80 Complex Requires the Arp5-Ies6 Subcomplex for Chromatin Remodeling and Metabolic Regulation. <i>Molecular and Cellular Biology</i> , 2016, 36, 979-991.	2.3	48
11	Set5 and Set1 cooperate to repress gene expression at telomeres and retrotransposons. <i>Epigenetics</i> , 2014, 9, 513-522.	2.7	28
12	Transcriptome profiling of Set5 and Set1 methyltransferases: Tools for visualization of gene expression. <i>Genomics Data</i> , 2014, 2, 216-218.	1.3	3