

Maxim V C Greenberg

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

2,715
citations

687363

13
h-index

839539

18
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23
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docs citations

23
times ranked

4260
citing authors

#	ARTICLE	IF	CITATIONS
1	Divergent transcriptional and transforming properties of PAX3-FOXO1 and PAX7-FOXO1 paralogs. <i>PLoS Genetics</i> , 2022, 18, e1009782.	3.5	4
2	The Polycomb landscape in mouse development. <i>Nature Genetics</i> , 2021, 53, 427-429.	21.4	2
3	Get Out and Stay Out: New Insights Into DNA Methylation Reprogramming in Mammals. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 629068.	3.7	12
4	The diverse roles of DNA methylation in mammalian development and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 590-607.	37.0	1,269
5	Dynamic enhancer partitioning instructs activation of a growth-related gene during exit from naïve pluripotency. <i>ELife</i> , 2019, 8, .	6.0	11
6	Transient transcription in the early embryo sets an epigenetic state that programs postnatal growth. <i>Nature Genetics</i> , 2017, 49, 110-118.	21.4	76
7	Cultural relativism: maintenance of genomic imprints in pluripotent stem cell culture systems. <i>Current Opinion in Genetics and Development</i> , 2015, 31, 42-49.	3.3	16
8	C-terminal domains of histone demethylase JMJ14 interact with a pair of NAC transcription factors to mediate specific chromatin association. <i>Cell Discovery</i> , 2015, 1, .	6.7	47
9	The Gpr1/Zdbf2 locus provides new paradigms for transient and dynamic genomic imprinting in mammals. <i>Genes and Development</i> , 2014, 28, 463-478.	5.9	63
10	SNF2 chromatin remodeler-family proteins FRG1 and -2 are required for RNA-directed DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17666-17671.	7.1	27
11	Comprehensive Analysis of Silencing Mutants Reveals Complex Regulation of the Arabidopsis Methylome. <i>Cell</i> , 2013, 152, 352-364.	28.9	748
12	Interplay between Active Chromatin Marks and RNA-Directed DNA Methylation in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2013, 9, e1003946.	3.5	70
13	The splicing factor SR45 affects the RNA-directed DNA methylation pathway in Arabidopsis. <i>Epigenetics</i> , 2012, 7, 29-33.	2.7	68
14	The SET-Domain Protein SUV5 Mediates H3K9me2 Deposition and Silencing at Stimulus Response Genes in a DNA Methylation-Independent Manner. <i>PLoS Genetics</i> , 2012, 8, e1002995.	3.5	54
15	INVOLVED IN DE NOVO 2-containing complex involved in RNA-directed DNA methylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8374-8381.	7.1	85
16	Identification of genes required for de novo DNA methylation in Arabidopsis. <i>Epigenetics</i> , 2011, 6, 344-354.	2.7	64
17	Involvement of a Jumonji domain-containing histone demethylase in DRM2-mediated maintenance of DNA methylation. <i>EMBO Reports</i> , 2010, 11, 950-955.	4.5	78
18	Cytotoxic Activity of 2,2-Difluorodeoxycytidine (Gemcitabine) in Poorly Differentiated Thyroid Carcinoma Cells. <i>Thyroid</i> , 2000, 10, 865-869.	4.5	17