

Julia Arand

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3524042/publications.pdf>

Version: 2024-02-01

25
papers

3,822
citations

567281

15
h-index

642732

23
g-index

27
all docs

27
docs citations

27
times ranked

5688
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive approach for genome-wide efficiency profiling of DNA modifying enzymes. <i>Cell Reports Methods</i> , 2022, 2, 100187.	2.9	4
2	Tet enzymes are essential for early embryogenesis and completion of embryonic genome activation. <i>EMBO Reports</i> , 2022, 23, e53968.	4.5	20
3	Reprogramming of DNA methylation is linked to successful human preimplantation development. <i>Histochemistry and Cell Biology</i> , 2021, 156, 197-207.	1.7	11
4	DNA hypomethylation leads to cGAS-induced autoinflammation in the epidermis. <i>EMBO Journal</i> , 2021, 40, e108234.	7.8	17
5	RB depletion is required for the continuous growth of tumors initiated by loss of RB. <i>PLoS Genetics</i> , 2021, 17, e1009941.	3.5	6
6	Unbiased Proteomic Profiling Uncovers a Targetable GNAS/PKA/PP2A Axis in Small Cell Lung Cancer Stem Cells. <i>Cancer Cell</i> , 2020, 38, 129-143.e7.	16.8	57
7	The MEK5-ERK5 Kinase Axis Controls Lipid Metabolism in Small-Cell Lung Cancer. <i>Cancer Research</i> , 2020, 80, 1293-1303.	0.9	49
8	E2F4 regulates transcriptional activation in mouse embryonic stem cells independently of the RB family. <i>Nature Communications</i> , 2019, 10, 2939.	12.8	59
9	G1 cyclins protect pluripotency. <i>Nature Cell Biology</i> , 2017, 19, 149-150.	10.3	6
10	Blockage of the Epithelial-to-Mesenchymal Transition Is Required for Embryonic Stem Cell Derivation. <i>Stem Cell Reports</i> , 2017, 9, 1275-1290.	4.8	12
11	Selective impairment of methylation maintenance is the major cause of DNA methylation reprogramming in the early embryo. <i>Epigenetics and Chromatin</i> , 2015, 8, 1.	3.9	149
12	DNA Methylation Reprogramming in Preimplantation Development. <i>Epigenetics and Human Health</i> , 2015, , 69-99.	0.2	0
13	Suv39h-Dependent H3K9me3 Marks Intact Retrotransposons and Silences LINE Elements in Mouse Embryonic Stem Cells. <i>Molecular Cell</i> , 2014, 55, 277-290.	9.7	278
14	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 360-369.	11.1	424
15	The <i>Polycomb</i> group protein <i>MEDEA</i> and the DNA methyltransferase <i>MET1</i> interact to repress autonomous endosperm development in <i>A. rabidopsis</i> . <i>Plant Journal</i> , 2013, 73, 776-787.	5.7	49
16	FGF Signaling Inhibition in ESCs Drives Rapid Genome-wide Demethylation to the Epigenetic Ground State of Pluripotency. <i>Cell Stem Cell</i> , 2013, 13, 351-359.	11.1	371
17	Bi-PROF. <i>Epigenetics</i> , 2013, 8, 765-771.	2.7	34
18	In Vivo Control of CpG and Non-CpG DNA Methylation by DNA Methyltransferases. <i>PLoS Genetics</i> , 2012, 8, e1002750.	3.5	337

#	ARTICLE	IF	CITATIONS
19	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. <i>Molecular Cell</i> , 2012, 48, 849-862.	9.7	837
20	Identification of a DNA methylation-independent imprinting control region at the <i>Arabidopsis</i> MEDEA locus. <i>Genes and Development</i> , 2012, 26, 1837-1850.	5.9	48
21	5-Hydroxymethylcytosine in the mammalian zygote is linked with epigenetic reprogramming. <i>Nature Communications</i> , 2011, 2, 241.	12.8	674
22	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <i>Nucleic Acids Research</i> , 2011, 39, W551-W556.	14.5	114
23	Dynamic link of DNA demethylation, DNA strand breaks and repair in mouse zygotes. <i>EMBO Journal</i> , 2010, 29, 1877-1888.	7.8	221
24	DNA methylation reprogramming and DNA repair in the mouse zygote. <i>International Journal of Developmental Biology</i> , 2010, 54, 1565-1574.	0.6	16
25	Active DNA demethylation. , 0, , 91-103.		0