

Gabriella Ficz

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

5,577
citations

393982

19
h-index

525886

27
g-index

31
all docs

31
docs citations

31
times ranked

8780
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.	1.4	4
2	An shRNA kinase screen identifies regulators of UHRF1 stability and activity in mouse embryonic stem cells. <i>Epigenetics</i> , 2022, , 1-18.	1.3	1
3	Corrupted devolution: How normal cells are reborn as cancer precursors. <i>International Journal of Biochemistry and Cell Biology</i> , 2022, 149, 106263.	1.2	0
4	Genomic alterations in high-risk chronic lymphocytic leukemia frequently affect cell cycle key regulators and NOTCH1-regulated transcription. <i>Haematologica</i> , 2020, 105, 1379-1390.	1.7	24
5	A novel use of random priming-based single-strand library preparation for whole genome sequencing of formalin-fixed paraffin-embedded tissue samples. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz017.	1.5	4
6	Transition to naïve human pluripotency mirrors pan-cancer DNA hypermethylation. <i>Nature Communications</i> , 2020, 11, 3671.	5.8	17
7	CRISPR/Cas9-Targeted De Novo DNA Methylation Is Maintained and Impacts the Colony Forming Potential of Human Hematopoietic CD34+ Cells. <i>Blood</i> , 2019, 134, 2517-2517.	0.6	1
8	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. <i>Genome Biology</i> , 2017, 18, 56.	3.8	164
9	Hit-and-run epigenetic editing prevents senescence entry in primary breast cells from healthy donors. <i>Nature Communications</i> , 2017, 8, 1450.	5.8	86
10	The Ageing Brain: Effects on DNA Repair and DNA Methylation in Mice. <i>Genes</i> , 2017, 8, 75.	1.0	28
11	The Influence of Hydroxylation on Maintaining CpG Methylation Patterns: A Hidden Markov Model Approach. <i>PLoS Computational Biology</i> , 2016, 12, e1004905.	1.5	18
12	Retinol and ascorbate drive erasure of epigenetic memory and enhance reprogramming to naïve pluripotency by complementary mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12202-12207.	3.3	139
13	New insights into mechanisms that regulate DNA methylation patterning. <i>Journal of Experimental Biology</i> , 2015, 218, 14-20.	0.8	49
14	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). <i>International Journal of Epidemiology</i> , 2015, 44, 1181-1190.	0.9	238
15	The Biology and Genomic Localization of Cytosine Modifications. <i>Epigenetics and Human Health</i> , 2015, , 167-191.	0.2	1
16	Resetting Transcription Factor Control Circuitry toward Ground-State Pluripotency in Human. <i>Cell</i> , 2014, 158, 1254-1269.	13.5	784
17	Loss of 5-hydroxymethylcytosine in cancer: Cause or consequence?. <i>Genomics</i> , 2014, 104, 352-357.	1.3	100
18	Breaking the Resolution Limit in Light Microscopy. <i>Methods in Cell Biology</i> , 2013, 114, 525-544.	0.5	23

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19	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.	5.2	371
20	Reprogramming by Cell Fusion: Boosted by Tets. <i>Molecular Cell</i> , 2013, 49, 1017-1018.	4.5	7
21	A screen for hydroxymethylcytosine and formylcytosine binding proteins suggests functions in transcription and chromatin regulation. <i>Genome Biology</i> , 2013, 14, R119.	13.9	269
22	Genome-wide distribution of 5-formylcytosine in embryonic stem cells is associated with transcription and depends on thymine DNA glycosylase. <i>Genome Biology</i> , 2012, 13, R69.	13.9	205
23	Quantitative Sequencing of 5-Methylcytosine and 5-Hydroxymethylcytosine at Single-Base Resolution. <i>Science</i> , 2012, 336, 934-937.	6.0	850
24	Uncovering the role of 5-hydroxymethylcytosine in the epigenome. <i>Nature Reviews Genetics</i> , 2012, 13, 7-13.	7.7	658
25	Dynamic regulation of 5-hydroxymethylcytosine in mouse ES cells and during differentiation. <i>Nature</i> , 2011, 473, 398-402.	13.7	1,035
26	The Epigenomic Landscape of Reprogramming in Mammals. , 2009, , 259-282.		3
27	Global Mapping of DNA Methylation in Mouse Promoters Reveals Epigenetic Reprogramming of Pluripotency Genes. <i>PLoS Genetics</i> , 2008, 4, e1000116.	1.5	317
28	Breaking the Resolution Limit in Light Microscopy. <i>Methods in Cell Biology</i> , 2007, 81, 561-580.	0.5	39
29	Breaking the resolution limit in light microscopy. <i>Briefings in Functional Genomics & Proteomics</i> , 2006, 5, 289-301.	3.8	142