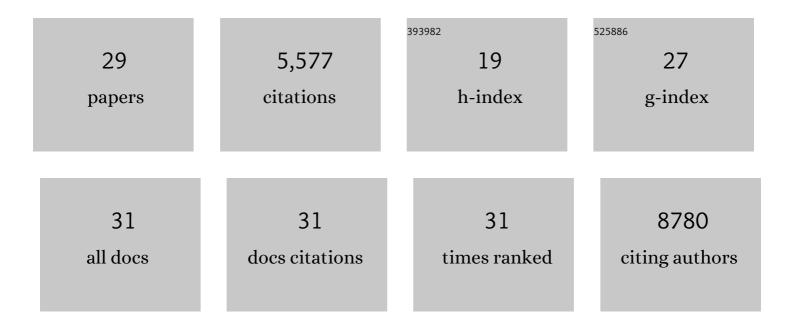
## Gabriella Ficz

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2066491/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A comprehensive approach for genome-wide efficiency profiling of DNA modifying enzymes. Cell Reports Methods, 2022, 2, 100187.	1.4	4
2	An shRNA kinase screen identifies regulators of UHRF1 stability and activity in mouse embryonic stem cells. Epigenetics, 2022, , 1-18.	1.3	1
3	Corrupted devolution: How normal cells are reborn as cancer precursors. International Journal of Biochemistry and Cell Biology, 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. Haematologica, 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. NAR Genomics and Bioinformatics, 2020, 2, lqz017.	1.5	4
6	Transition to na $\tilde{A}$ ve human pluripotency mirrors pan-cancer DNA hypermethylation. Nature Communications, 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. Blood, 2019, 134, 2517-2517.	0.6	1
8	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. Genome Biology, 2017, 18, 56.	3.8	164
9	Hit-and-run epigenetic editing prevents senescence entry in primary breast cells from healthy donors. Nature Communications, 2017, 8, 1450.	5.8	86
10	The Ageing Brain: Effects on DNA Repair and DNA Methylation in Mice. Genes, 2017, 8, 75.	1.0	28
11	The Influence of Hydroxylation on Maintaining CpG Methylation Patterns: A Hidden Markov Model Approach. PLoS Computational Biology, 2016, 12, e1004905.	1.5	18
12	Retinol and ascorbate drive erasure of epigenetic memory and enhance reprogramming to naÃ <sup>-</sup> ve pluripotency by complementary mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12202-12207.	3.3	139
13	New insights into mechanisms that regulate DNA methylation patterning. Journal of Experimental Biology, 2015, 218, 14-20.	0.8	49
14	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	0.9	238
15	The Biology and Genomic Localization of Cytosine Modifications. Epigenetics and Human Health, 2015, , 167-191.	0.2	1
16	Resetting Transcription Factor Control Circuitry toward Ground-State Pluripotency in Human. Cell, 2014, 158, 1254-1269.	13.5	784
17	Loss of 5-hydroxymethylcytosine in cancer: Cause or consequence?. Genomics, 2014, 104, 352-357.	1.3	100
18	Breaking the Resolution Limit in Light Microscopy. Methods in Cell Biology, 2013, 114, 525-544.	0.5	23

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#	Article	IF	CITATIONS
19	FGF Signaling Inhibition in ESCs Drives Rapid Genome-wide Demethylation to the Epigenetic Ground State of Pluripotency. Cell Stem Cell, 2013, 13, 351-359.	5.2	371
20	Reprogramming by Cell Fusion: Boosted by Tets. Molecular Cell, 2013, 49, 1017-1018.	4.5	7
21	A screen for hydroxymethylcytosine and formylcytosine binding proteins suggests functions in transcription and chromatin regulation. Genome Biology, 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. Genome Biology, 2012, 13, R69.	13.9	205
23	Quantitative Sequencing of 5-Methylcytosine and 5-Hydroxymethylcytosine at Single-Base Resolution. Science, 2012, 336, 934-937.	6.0	850
24	Uncovering the role of 5-hydroxymethylcytosine in the epigenome. Nature Reviews Genetics, 2012, 13, 7-13.	7.7	658
25	Dynamic regulation of 5-hydroxymethylcytosine in mouse ES cells and during differentiation. Nature, 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. PLoS Genetics, 2008, 4, e1000116.	1.5	317
28	Breaking the Resolution Limit in Light Microscopy. Methods in Cell Biology, 2007, 81, 561-580.	0.5	39
29	Breaking the resolution limit in light microscopy. Briefings in Functional Genomics & Proteomics, 2006, 5, 289-301.	3.8	142