

# Rocio G Urdinguio

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8491316/publications.pdf>

Version: 2024-02-01

38  
papers

2,345  
citations

304743

22  
h-index

377865

34  
g-index

40  
all docs

40  
docs citations

40  
times ranked

4963  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic Profiling and Response to CD19 Chimeric Antigen Receptor T-Cell Therapy in B-Cell Malignancies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 436-445.	6.3	29
2	Multi-omic rejuvenation of naturally aged tissues by a single cycle of transient reprogramming. <i>Aging Cell</i> , 2022, 21, e13578.	6.7	60
3	Conservation of Aging and Cancer Epigenetic Signatures across Human and Mouse. <i>Molecular Biology and Evolution</i> , 2021, 38, 3415-3435.	8.9	5
4	Stability of Imprinting and Differentiation Capacity in Naïve Human Cells Induced by Chemical Inhibition of CDK8 and CDK19. <i>Cells</i> , 2021, 10, 876.	4.1	0
5	Epigenetic Deregulation of the Histone Methyltransferase KMT5B Contributes to Malignant Transformation in Glioblastoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671838.	3.7	6
6	Physical exercise shapes the mouse brain epigenome. <i>Molecular Metabolism</i> , 2021, 54, 101398.	6.5	12
7	Epigenetic downregulation of TET3 reduces genome-wide 5hmC levels and promotes glioblastoma tumorigenesis. <i>International Journal of Cancer</i> , 2020, 146, 373-387.	5.1	45
8	Chromatin regulation by Histone H4 acetylation at Lysine 16 during cell death and differentiation in the myeloid compartment. <i>Nucleic Acids Research</i> , 2019, 47, 5016-5037.	14.5	23
9	Longitudinal genome-wide DNA methylation analysis uncovers persistent early-life DNA methylation changes. <i>Journal of Translational Medicine</i> , 2019, 17, 15.	4.4	44
10	Epigenome-wide analysis reveals specific DNA hypermethylation of T cells during human hematopoietic differentiation. <i>Epigenomics</i> , 2018, 10, 903-923.	2.1	11
11	Deregulation of the imprinted DLK1-DIO3 locus ncRNAs is associated with replicative senescence of human adipose-derived stem cells. <i>PLoS ONE</i> , 2018, 13, e0206534.	2.5	9
12	Loss of 5hmC identifies a new type of aberrant DNA hypermethylation in glioma. <i>Human Molecular Genetics</i> , 2018, 27, 3046-3059.	2.9	26
13	Epigenetic dysregulation of TET2 in human glioblastoma. <i>Oncotarget</i> , 2018, 9, 25922-25934.	1.8	29
14	DNA methylation changes in human lung epithelia cells exposed to multi-walled carbon nanotubes. <i>Nanotoxicology</i> , 2017, 11, 857-870.	3.0	36
15	Longitudinal study of DNA methylation during the first 5 years of life. <i>Journal of Translational Medicine</i> , 2016, 14, 160.	4.4	29
16	Age-associated hydroxymethylation in human bone-marrow mesenchymal stem cells. <i>Journal of Translational Medicine</i> , 2016, 14, 207.	4.4	33
17	HERG1A potassium channel is the predominant isoform in head and neck squamous cell carcinomas: evidence for regulation by epigenetic mechanisms. <i>Scientific Reports</i> , 2016, 6, 19666.	3.3	10
18	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	17.5	270

#	ARTICLE	IF	CITATIONS
19	Aberrant DNA methylation patterns of spermatozoa in men with unexplained infertility. <i>Human Reproduction</i> , 2015, 30, 1014-1028.	0.9	144
20	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	5.5	119
21	Epigenetics, Inflammation, and Aging. , 2014, , 85-101.		4
22	LINE-1 methylation in leukocyte DNA, interaction with phosphatidylethanolamine N-methyltransferase variants and bladder cancer risk. <i>British Journal of Cancer</i> , 2014, 110, 2123-2130.	6.4	17
23	Role of Epigenetics in Neural Differentiation: Implications for Health and Disease. , 2014, , 63-79.		2
24	The Epigenetic Basis of Adaptation and Responses to Environmental Change: Perspective on Human Reproduction. <i>Advances in Experimental Medicine and Biology</i> , 2014, 753, 97-117.	1.6	15
25	A DNA methylation signature associated with the epigenetic repression of glycine N-methyltransferase in human hepatocellular carcinoma. <i>Journal of Molecular Medicine</i> , 2013, 91, 939-950.	3.9	29
26	Immune-Dependent and Independent Antitumor Activity of GM-CSF Aberrantly Expressed by Mouse and Human Colorectal Tumors. <i>Cancer Research</i> , 2013, 73, 395-405.	0.9	69
27	DNA Methylation Signatures Identify Biologically Distinct Thyroid Cancer Subtypes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, 2811-2821.	3.6	100
28	DNA methylation map of mouse and human brain identifies target genes in Alzheimer's disease. <i>Brain</i> , 2013, 136, 3018-3027.	7.6	129
29	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	14.5	97
30	801 Frequent Aberrant Expression of the Human Ether a Go-go (hEAG1) Potassium Channel in Head and Neck Cancer – Pathobiological Mechanisms and Clinical Implications. <i>European Journal of Cancer</i> , 2012, 48, S191.	2.8	0
31	Frequent aberrant expression of the human ether A go-go (hEAG1) potassium channel in head and neck cancer: pathobiological mechanisms and clinical implications. <i>Journal of Molecular Medicine</i> , 2012, 90, 1173-1184.	3.9	43
32	A DNA methylation signature associated with aberrant promoter DNA hypermethylation of DNMT3B in human colorectal cancer. <i>European Journal of Cancer</i> , 2012, 48, 2270-2281.	2.8	23
33	Aberrant epigenetic regulation of bromodomain Brd4 in human colon cancer. <i>Journal of Molecular Medicine</i> , 2012, 90, 587-595.	3.9	50
34	Disrupted microRNA expression caused by Mecp2 loss in a mouse model of Rett syndrome. <i>Epigenetics</i> , 2010, 5, 656-663.	2.7	125
35	The RNA-binding protein HuR regulates DNA methylation through stabilization of DNMT3b mRNA. <i>Nucleic Acids Research</i> , 2009, 37, 2658-2671.	14.5	56
36	Epigenetic mechanisms in neurological diseases: genes, syndromes, and therapies. <i>Lancet Neurology</i> , The, 2009, 8, 1056-1072.	10.2	528

#	ARTICLE	IF	CITATIONS
37	Mecp2-Null Mice Provide New Neuronal Targets for Rett Syndrome. PLoS ONE, 2008, 3, e3669.	2.5	106
38	Histone H3 and H4 Modification Profiles in a Rett Syndrome Mouse Model. Epigenetics, 2007, 2, 11-14.	2.7	12