

# Emiliano Dalla

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4639759/publications.pdf>

Version: 2024-02-01

32  
papers

7,698  
citations

516710  
16  
h-index

414414  
32  
g-index

36  
all docs

36  
docs citations

36  
times ranked

13695  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
2	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
3	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
4	p65/RelA Modulates <i>BECN1</i> Transcription and Autophagy. <i>Molecular and Cellular Biology</i> , 2009, 29, 2594-2608.	2.3	235
5	Proteasome machinery is instrumental in a common gain-of-function program of the p53 missense mutants in cancer. <i>Nature Cell Biology</i> , 2016, 18, 897-909.	10.3	205
6	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. <i>Nature Genetics</i> , 2019, 51, 138-150.	21.4	177
7	Mammalian APE1 controls miRNA processing and its interactome is linked to cancer RNA metabolism. <i>Nature Communications</i> , 2017, 8, 797.	12.8	107
8	Different class IIa HDACs repressive complexes regulate specific epigenetic responses related to cell survival in leiomyosarcoma cells. <i>Nucleic Acids Research</i> , 2020, 48, 646-664.	14.5	39
9	HDAC7-mediated control of tumour microenvironment maintains proliferative and stemness competence of human mammary epithelial cells. <i>Molecular Oncology</i> , 2019, 13, 1651-1668.	4.6	29
10	HDAC4 degradation during senescence unleashes an epigenetic program driven by AP-1/p300 at selected enhancers and super-enhancers. <i>Genome Biology</i> , 2021, 22, 129.	8.8	29
11	APE1 and NPM1 protect cancer cells from platinum compounds cytotoxicity and their expression pattern has a prognostic value in TNBC. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 309.	8.6	28
12	Integrated multi-omics analyses on patient-derived CRC organoids highlight altered molecular pathways in colorectal cancer progression involving PTEN. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 198.	8.6	27
13	Architecture of The Human Ape1 Interactome Defines Novel Cancers Signatures. <i>Scientific Reports</i> , 2020, 10, 28.	3.3	22
14	Heterogeneity Matters: Different Regions of Glioblastoma Are Characterized by Distinctive Tumor-Supporting Pathways. <i>Cancers</i> , 2020, 12, 2960.	3.7	22
15	New perspectives in cancer biology from a study of canonical and non-canonical functions of base excision repair proteins with a focus on early steps. <i>Mutagenesis</i> , 2020, 35, 129-149.	2.6	21
16	IL-10-producing B cells are characterized by a specific methylation signature. <i>European Journal of Immunology</i> , 2019, 49, 1213-1225.	2.9	19
17	Heart failure impairs the mechanotransduction properties of human cardiac pericytes. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 151, 15-30.	1.9	17
18	GTSE1: a novel TEAD4-E2F1 target gene involved in cell protrusions formation in triple-negative breast cancer cell models. <i>Oncotarget</i> , 2017, 8, 67422-67438.	1.8	17

#	ARTICLE	IF	CITATIONS
19	Role of phase partitioning in coordinating DNA damage response: focus on the Apurinic Apyrimidinic Endonuclease 1 interactome. <i>Biomolecular Concepts</i> , 2020, 11, 209-220.	2.2	15
20	Transcriptomic and genomic studies classify NKL54 as a histone deacetylase inhibitor with indirect influence on MEF2-dependent transcription. <i>Nucleic Acids Research</i> , 2022, 50, 2566-2586.	14.5	12
21	The miRNA Content of Exosomes Released from the Glioma Microenvironment Can Affect Malignant Progression. <i>Biomedicines</i> , 2020, 8, 564.	3.2	11
22	miRNA expression profiles in liver grafts of HCV and HIV/HCV-coinfected recipients, 6 months after liver transplantation. <i>Journal of Medical Virology</i> , 2021, 93, 4992-5000.	5.0	11
23	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
24	Cleavage of the APE1 N-Terminal Domain in Acute Myeloid Leukemia Cells Is Associated with Proteasomal Activity. <i>Biomolecules</i> , 2020, 10, 531.	4.0	6
25	Enhancing Proteotoxic Stress in Leiomyosarcoma Cells Triggers Mitochondrial Dysfunctions, Cell Death, and Antitumor Activity <i>in vivo</i> . <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1039-1051.	4.1	6
26	Discovery of 342 putative new genes from the analysis of 5' end-sequenced full-length-enriched cDNA human transcripts. <i>Genomics</i> , 2005, 85, 739-751.	2.9	5
27	A regulative epigenetic circuit supervised by HDAC7 represses IGFBP6 and IGFBP7 expression to sustain mammary stemness. <i>Epigenomics</i> , 2021, 13, 683-698.	2.1	4
28	Reinfection of Transplanted Livers in HCV- and HCV/HIV-Infected Patients Is Characterized by a Different MicroRNA Expression Profile. <i>Cells</i> , 2022, 11, 690.	4.1	4
29	LNCIB human full-length cDNAs collection: towards a better comprehension of the human transcriptome. <i>Comptes Rendus - Biologies</i> , 2003, 326, 967-970.	0.2	2
30	Identification of a Prognostic Microenvironment-Related Gene Signature in Glioblastoma Patients Treated with Carmustine Wafers. <i>Cancers</i> , 2022, 14, 3413.	3.7	2
31	Identification of a gene signature for the prediction of recurrence and progression in non-muscle-invasive bladder cancer. <i>Molecular Biomedicine</i> , 2022, 3, 9.	4.4	1
32	MOTIF DISCOVERY FIXING MISMATCH POSITIONS. , 2007, , .		0