

Giancarlo Bonora

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1224884/publications.pdf>

Version: 2024-02-01

19
papers

1,701
citations

516710

16
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

3324
citing authors

#	ARTICLE	IF	CITATIONS
1	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. <i>Cell</i> , 2017, 168, 442-459.e20.	28.9	432
2	Long-Range Chromatin Contacts in Embryonic Stem Cells Reveal a Role for Pluripotency Factors and Polycomb Proteins in Genome Organization. <i>Cell Stem Cell</i> , 2013, 13, 602-616.	11.1	246
3	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. <i>ELife</i> , 2015, 4, e06205.	6.0	146
4	A Genome-Wide Chronological Study of Gene Expression and Two Histone Modifications, H3K4me3 and H3K9ac, during Developmental Leaf Senescence. <i>Plant Physiology</i> , 2015, 168, 1246-1261.	4.8	111
5	Dynamics of genome reorganization during human cardiogenesis reveal an RBM20-dependent splicing factory. <i>Nature Communications</i> , 2019, 10, 1538.	12.8	104
6	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. <i>Cell Reports</i> , 2017, 18, 54-67.	6.4	100
7	X Chromosome Reactivation Dynamics Reveal Stages of Reprogramming to Pluripotency. <i>Cell</i> , 2014, 159, 1681-1697.	28.9	97
8	The Mbd1-Atf7ip-Setdb1 pathway contributes to the maintenance of X chromosome inactivation. <i>Epigenetics and Chromatin</i> , 2014, 7, 12.	3.9	63
9	Orientation-dependent Dxz4 contacts shape the 3D structure of the inactive X chromosome. <i>Nature Communications</i> , 2018, 9, 1445.	12.8	63
10	Capturing cell type-specific chromatin compartment patterns by applying topic modeling to single-cell Hi-C data. <i>PLoS Computational Biology</i> , 2020, 16, e1008173.	3.2	59
11	A mechanistic link between gene regulation and genome architecture in mammalian development. <i>Current Opinion in Genetics and Development</i> , 2014, 27, 92-101.	3.3	51
12	X Chromosome Dosage Influences DNA Methylation Dynamics during Reprogramming to Mouse iPSCs. <i>Stem Cell Reports</i> , 2018, 10, 1537-1550.	4.8	39
13	A high-throughput screen of inactive X chromosome reactivation identifies the enhancement of DNA demethylation by 5-aza-2'-deoxycytidine upon inhibition of ribonucleotide reductase. <i>Epigenetics and Chromatin</i> , 2015, 8, 42.	3.9	38
14	Interactions between core histone marks and DNA methyltransferases predict DNA methylation patterns observed in human cells and tissues. <i>Epigenetics</i> , 2020, 15, 272-282.	2.7	35
15	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. <i>Nature Communications</i> , 2020, 11, 6053.	12.8	33
16	Structural aspects of the inactive X chromosome. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160357.	4.0	19
17	Novel features of telomere biology revealed by the absence of telomeric DNA methylation. <i>Genome Research</i> , 2016, 26, 1047-1056.	5.5	18
18	DNA methylation estimation using methylation-sensitive restriction enzyme bisulfite sequencing (MREBS). <i>PLoS ONE</i> , 2019, 14, e0214368.	2.5	14

#	ARTICLE	IF	CITATIONS
19	Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation. <i>Genome Biology</i> , 2021, 22, 279.	8.8	11