Giancarlo Bonora

List of Publications by Citations

22 papers	1,107 citations	14 h-index	25 g-index
25 ext. papers	1,496 ext. citations	14.4 avg, IF	4.22 L-index

#	Paper	IF	Citations
22	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. *Cell*, **2017**, 168, 442-459.e20	56.2	274
21	Long-range chromatin contacts in embryonic stem cells reveal a role for pluripotency factors and polycomb proteins in genome organization. *Cell Stem Cell*, **2013**, 13, 602-16	18	197
20	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. *ELife*, **2015**, 4, e06205	8.9	107
19	X chromosome reactivation dynamics reveal stages of reprogramming to pluripotency. *Cell*, **2014**, 159, 1681-97	56.2	77
18	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. *Cell Reports*, **2017**, 18, 54-67	10.6	72
17	A Genome-Wide Chronological Study of Gene Expression and Two Histone Modifications, H3K4me3 and H3K9ac, during Developmental Leaf Senescence. *Plant Physiology*, **2015**, 168, 1246-61	6.6	53
16	Dynamics of genome reorganization during human cardiogenesis reveal an RBM20-dependent splicing factory. *Nature Communications*, **2019**, 10, 1538	17.4	52
15	The Mbd1-Atf7ip-Setdb1 pathway contributes to the maintenance of X chromosome inactivation. *Epigenetics and Chromatin*, **2014**, 7, 12	5.8	50
14	Orientation-dependent Dxz4 contacts shape the 3D structure of the inactive X chromosome. *Nature Communications*, **2018**, 9, 1445	17.4	38
13	A mechanistic link between gene regulation and genome architecture in mammalian development. *Current Opinion in Genetics and Development*, **2014**, 27, 92-101	4.9	34
12	A high-throughput screen of inactive X chromosome reactivation identifies the enhancement of DNA demethylation by 5-aza-2ɑdC upon inhibition of ribonucleotide reductase. *Epigenetics and Chromatin*, **2015**, 8, 42	5.8	29
11	X Chromosome Dosage Influences DNA Methylation Dynamics during Reprogramming to Mouse iPSCs. *Stem Cell Reports*, **2018**, 10, 1537-1550	8	24
10	Capturing cell type-specific chromatin compartment patterns by applying topic modeling to single-cell Hi-C data. *PLoS Computational Biology*, **2020**, 16, e1008173	5	20
9	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. *Nature Communications*, **2020**, 11, 6053	17.4	15
8	Novel features of telomere biology revealed by the absence of telomeric DNA methylation. *Genome Research*, **2016**, 26, 1047-56	9.7	14
7	Structural aspects of the inactive X chromosome. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2017**, 372,	5.8	13
6	Interactions between core histone marks and DNA methyltransferases predict DNA methylation patterns observed in human cells and tissues. *Epigenetics*, **2020**, 15, 272-282	5.7	12

List of Publications

5	DNA methylation estimation using methylation-sensitive restriction enzyme bisulfite sequencing (MREBS). *PLoS ONE*, **2019**, 14, e0214368	3.7	10
4	Trans- and cis-acting effects of the lncRNA Firre on epigenetic and structural features of the inactive X chromosome		7
3	Unsupervised manifold alignment for single-cell multi-omics data		4
2	Orientation-dependent Dxz4 contacts shape the 3D structure of the inactive X chromosome		3
1	Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation. *Genome Biology*, **2021**, 22, 279	18.3	2