

Rafael Galupa

List of Publications by Year in Descending Order

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Version: 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

12
papers

846
citations

10
h-index

19
g-index

19
ext. papers

1,104
ext. citations

17.1
avg, IF

4.57
L-index

#	Paper	IF	Citations
12	Parental-to-embryo switch of chromosome organization in early embryogenesis. <i>Nature</i> , 2020 , 580, 142-146	14.6	55
11	Enhancer-Promoter Communication: Thinking Outside the TAD. <i>Trends in Genetics</i> , 2020 , 36, 459-461	8.5	2
10	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. <i>Molecular Cell</i> , 2020 , 77, 352-367.e8	17.6	23
9	Robust and efficient gene regulation through localized nuclear microenvironments. <i>Development (Cambridge)</i> , 2020 , 147,	6.6	3
8	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. <i>Nature Genetics</i> , 2019 , 51, 1024-1034	36.3	37
7	The Ftx Noncoding Locus Controls X Chromosome Inactivation Independently of Its RNA Products. <i>Molecular Cell</i> , 2018 , 70, 462-472.e8	17.6	52
6	X-Chromosome Inactivation: A Crossroads Between Chromosome Architecture and Gene Regulation. <i>Annual Review of Genetics</i> , 2018 , 52, 535-566	14.5	113
5	Xist-dependent imprinted X inactivation and the early developmental consequences of its failure. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 226-233	17.6	79
4	Contribution of epigenetic landscapes and transcription factors to X-chromosome reactivation in the inner cell mass. <i>Nature Communications</i> , 2017 , 8, 1297	17.4	33
3	Topologically Associating Domains in Chromosome Architecture and Gene Regulatory Landscapes during Development, Disease, and Evolution. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017 , 82, 267-278	3.9	18
2	X-chromosome inactivation: new insights into cis and trans regulation. <i>Current Opinion in Genetics and Development</i> , 2015 , 31, 57-66	4.9	108
1	Predictive polymer modeling reveals coupled fluctuations in chromosome conformation and transcription. <i>Cell</i> , 2014 , 157, 950-63	56.2	321