

Jean-Karim Heriche

List of Publications by Year in Descending Order

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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.

25
papers

2,794
citations

18
h-index

26
g-index

26
ext. papers

3,205
ext. citations

18.5
avg, IF

3.95
L-index

#	Paper	IF	Citations
25	Integrating Imaging and Omics: Computational Methods and Challenges. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 175-197	5.6	17
24	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 21-28	17.6	53
23	Correlative live and super-resolution imaging reveals the dynamic structure of replication domains. <i>Journal of Cell Biology</i> , 2018 , 217, 1973-1984	7.3	45
22	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. <i>EMBO Journal</i> , 2018 , 37,	13	26
21	Experimental and computational framework for a dynamic protein atlas of human cell division. <i>Nature</i> , 2018 , 561, 411-415	50.4	65
20	How can functional annotations be derived from profiles of phenotypic annotations?. <i>BMC Bioinformatics</i> , 2017 , 18, 96	3.6	4
19	The cellular microscopy phenotype ontology. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 28	2.2	17
18	ARHGEF17 is an essential spindle assembly checkpoint factor that targets Mps1 to kinetochores. <i>Journal of Cell Biology</i> , 2016 , 212, 647-59	7.3	14
17	Profiling DNA damage response following mitotic perturbations. <i>Nature Communications</i> , 2016 , 7, 13887	17.4	33
16	FUN-L: gene prioritization for RNAi screens. <i>Bioinformatics</i> , 2015 , 31, 2052-3	7.2	8
15	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. <i>Molecular Biology of the Cell</i> , 2014 , 25, 2522-36	3.5	36
14	High-content siRNA screen reveals global ENaC regulators and potential cystic fibrosis therapy targets. <i>Cell</i> , 2013 , 154, 1390-400	56.2	42
13	Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. <i>BMC Bioinformatics</i> , 2013 , 14, 308	3.6	10
12	Quantitative analysis of chromosome condensation in fission yeast. <i>Molecular and Cellular Biology</i> , 2013 , 33, 984-98	4.8	48
11	TRIP12 and UBR5 suppress spreading of chromatin ubiquitylation at damaged chromosomes. <i>Cell</i> , 2012 , 150, 697-709	56.2	224
10	Genome-wide RNAi screening identifies human proteins with a regulatory function in the early secretory pathway. <i>Nature Cell Biology</i> , 2012 , 14, 764-74	23.4	141
9	High-efficiency counterselection recombineering for site-directed mutagenesis in bacterial artificial chromosomes. <i>Nature Methods</i> , 2011 , 9, 103-9	21.6	44

8	Systematic phosphorylation analysis of human mitotic protein complexes. <i>Science Signaling</i> , 2011 , 4, rs12	8.8	74
7	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010 , 464, 721-7	50.4	668
6	Visualization of image data from cells to organisms. <i>Nature Methods</i> , 2010 , 7, S26-41	21.6	189
5	Visualizing biological data-now and in the future. <i>Nature Methods</i> , 2010 , 7, S2-4	21.6	85
4	Automatic identification and clustering of chromosome phenotypes in a genome wide RNAi screen by time-lapse imaging. <i>Journal of Structural Biology</i> , 2010 , 170, 1-9	3.4	42
3	Systematic analysis of human protein complexes identifies chromosome segregation proteins. <i>Science</i> , 2010 , 328, 593-9	33.3	419
2	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. <i>Nature Methods</i> , 2008 , 5, 409-15	21.6	484
1	Experimental and computational framework for a dynamic protein atlas of human cell division		3