

Moritz Kueblbeck

List of Publications by Citations

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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

761
citations

7
h-index

13
g-index

13
ext. papers

1,146
ext. citations

17.1
avg, IF

3.68
L-index

#	Paper	IF	Citations
12	Topologically associating domains and chromatin loops depend on cohesin and are regulated by CTCF, WAPL, and PDS5 proteins. <i>EMBO Journal</i> , 2017 , 36, 3573-3599	13	360
11	Nuclear pores as versatile reference standards for quantitative superresolution microscopy. <i>Nature Methods</i> , 2019 , 16, 1045-1053	21.6	105
10	A quantitative map of human Condensins provides new insights into mitotic chromosome architecture. <i>Journal of Cell Biology</i> , 2018 , 217, 2309-2328	7.3	89
9	Experimental and computational framework for a dynamic protein atlas of human cell division. <i>Nature</i> , 2018 , 561, 411-415	50.4	65
8	Generation and validation of homozygous fluorescent knock-in cells using CRISPR-Cas9 genome editing. <i>Nature Protocols</i> , 2018 , 13, 1465-1487	18.8	58
7	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
6	Multivariate Control of Transcript to Protein Variability in Single Mammalian Cells. <i>Cell Systems</i> , 2018 , 7, 398-411.e6	10.6	17
5	Three-dimensional superresolution fluorescence microscopy maps the variable molecular architecture of the nuclear pore complex. <i>Molecular Biology of the Cell</i> , 2021 , 32, 1523-1533	3.5	7
4	Chemogenetic Control of Nanobodies		3
3	A quantitative map of nuclear pore assembly reveals two distinct mechanisms		2
2	3D super-resolution fluorescence microscopy maps the variable molecular architecture of the Nuclear Pore Complex		1
1	Rapid generation of homozygous fluorescent knock-in human cells using CRISPR/Cas9 genome editing and validation by automated imaging and digital PCR screening		1