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List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

688
citations

623574

14
h-index

887953

17
g-index

25
all docs

25
docs citations

25
times ranked

1572
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. <i>PLoS Biology</i> , 2017, 15, e2001414.	2.6	97
2	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 21-28.	3.6	75
3	REMBI: Recommended Metadata for Biological Images enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021, 18, 1418-1422.	9.0	63
4	Correlative live and super-resolution imaging reveals the dynamic structure of replication domains. <i>Journal of Cell Biology</i> , 2018, 217, 1973-1984.	2.3	61
5	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. <i>EMBO Journal</i> , 2018, 37, .	3.5	50
6	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	3.6	47
7	Profiling DNA damage response following mitotic perturbations. <i>Nature Communications</i> , 2016, 7, 13887.	5.8	46
8	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, 2522-2536.	0.9	44
9	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.	0.9	37
10	Integrating Imaging and Omics: Computational Methods and Challenges. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 175-197.	2.8	33
11	Tracking cells in epithelial acini by light sheet microscopy reveals proximity effects in breast cancer initiation. <i>ELife</i> , 2020, 9, .	2.8	30
12	An Open Science Peer Review Oath. <i>F1000Research</i> , 2014, 3, 271.	0.8	25
13	The cellular microscopy phenotype ontology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 28.	0.9	24
14	ARHGEF17 is an essential spindle assembly checkpoint factor that targets Mps1 to kinetochores. <i>Journal of Cell Biology</i> , 2016, 212, 647-659.	2.3	20
15	The Open Science Peer Review Oath. <i>F1000Research</i> , 2014, 3, 271.	0.8	15
16	Bioimage analysis workflows: community resources to navigate through a complex ecosystem. <i>F1000Research</i> , 2021, 10, 320.	0.8	12
17	How can functional annotations be derived from profiles of phenotypic annotations?. <i>BMC Bioinformatics</i> , 2017, 18, 96.	1.2	5