

# Jean-Karim HÃ©richÃ©

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/893855/publications.pdf>

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	Bioimage analysis workflows: community resources to navigate through a complex ecosystem. F1000Research, 2021, 10, 320.	0.8	12
2	REMBI: Recommended Metadata for Biological Imagesâ€”enabling reuse of microscopy data in biology. Nature Methods, 2021, 18, 1418-1422.	9.0	63
3	Three-dimensional superresolution fluorescence microscopy maps the variable molecular architecture of the nuclear pore complex. Molecular Biology of the Cell, 2021, 32, 1523-1533.	0.9	37
4	Tracking cells in epithelial acini by light sheet microscopy reveals proximity effects in breast cancer initiation. ELife, 2020, 9, .	2.8	30
5	Integrating Imaging and Omics: Computational Methods and Challenges. Annual Review of Biomedical Data Science, 2019, 2, 175-197.	2.8	33
6	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. Nature Structural and Molecular Biology, 2018, 25, 21-28.	3.6	75
7	Correlative live and super-resolution imaging reveals the dynamic structure of replication domains. Journal of Cell Biology, 2018, 217, 1973-1984.	2.3	61
8	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. EMBO Journal, 2018, 37, .	3.5	50
9	How can functional annotations be derived from profiles of phenotypic annotations?. BMC Bioinformatics, 2017, 18, 96.	1.2	5
10	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	2.6	97
11	Profiling DNA damage response following mitotic perturbations. Nature Communications, 2016, 7, 13887.	5.8	46
12	The cellular microscopy phenotype ontology. Journal of Biomedical Semantics, 2016, 7, 28.	0.9	24
13	ARHGEF17 is an essential spindle assembly checkpoint factor that targets Mps1 to kinetochores. Journal of Cell Biology, 2016, 212, 647-659.	2.3	20
14	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. Molecular Biology of the Cell, 2014, 25, 2522-2536.	0.9	44
15	A 3D cellular context for the macromolecular world. Nature Structural and Molecular Biology, 2014, 21, 841-845.	3.6	47
16	The Open Science Peer Review Oath. F1000Research, 2014, 3, 271.	0.8	15
17	An Open Science Peer Review Oath. F1000Research, 2014, 3, 271.	0.8	25