

Jean-Karim Hrich

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.

19
papers

415
citations

13
h-index

20
g-index

25
ext. papers

574
ext. citations

8.6
avg, IF

3.21
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 19 | 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 | 9.7 | 63 |
| 18 | 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 |
| 17 | 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 |
| 16 | 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 |
| 15 | A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 841-5 | 17.6 | 33 |
| 14 | Profiling DNA damage response following mitotic perturbations. <i>Nature Communications</i> , 2016 , 7, 13887 | 7.4 | 33 |
| 13 | The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. <i>EMBO Journal</i> , 2018 , 37, | 13 | 26 |
| 12 | An Open Science Peer Review Oath. <i>F1000Research</i> , 2014 , 3, 271 | 3.6 | 21 |
| 11 | Integrating Imaging and Omics: Computational Methods and Challenges. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 175-197 | 5.6 | 17 |
| 10 | The cellular microscopy phenotype ontology. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 28 | 2.2 | 17 |
| 9 | Tracking cells in epithelial acini by light sheet microscopy reveals proximity effects in breast cancer initiation. <i>ELife</i> , 2020 , 9, | 8.9 | 17 |
| 8 | REMBI: Recommended Metadata for Biological Images-enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021 , 18, 1418-1422 | 21.6 | 16 |
| 7 | 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 |
| 6 | The open science peer review oath. <i>F1000Research</i> , 2014 , 3, 271 | 3.6 | 11 |
| 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 | How can functional annotations be derived from profiles of phenotypic annotations?. <i>BMC Bioinformatics</i> , 2017 , 18, 96 | 3.6 | 4 |
| 3 | 3D super-resolution fluorescence microscopy maps the variable molecular architecture of the Nuclear Pore Complex | | 1 |

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|---|--|-------|
| 2 | Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data | 1 |
| 1 | Bioimage analysis workflows: community resources to navigate through a complex ecosystem. <i>F1000Research</i> , 2021, 10, 320 | 3.6 0 |