

Darwin Y Fu

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

415
citations

8
h-index

14
g-index

14
ext. papers

681
ext. citations

6.3
avg, IF

3.8
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 12 | Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020 , 17, 665-680 | 21.6 | 165 |
| 11 | Protocols for Molecular Modeling with Rosetta3 and RosettaScripts. <i>Biochemistry</i> , 2016 , 55, 4748-63 | 3.2 | 118 |
| 10 | Releasing a preprint is associated with more attention and citations for the peer-reviewed article. <i>ELife</i> , 2019 , 8, | 8.9 | 59 |
| 9 | Development of Erasin: a chromone-based STAT3 inhibitor which induces apoptosis in Erlotinib-resistant lung cancer cells. <i>Scientific Reports</i> , 2017 , 7, 17390 | 4.9 | 15 |
| 8 | Predictive Power of Different Types of Experimental Restraints in Small Molecule Docking: A Review. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 225-233 | 6.1 | 13 |
| 7 | RosettaLigandEnsemble: A Small-Molecule Ensemble-Driven Docking Approach. <i>ACS Omega</i> , 2018 , 3, 3655-3664 | 3.9 | 11 |
| 6 | Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record. <i>BMC Genomics</i> , 2019 , 20, 805 | 4.5 | 10 |
| 5 | The STAT5b Linker Domain Mediates the Selectivity of Catechol Bisphosphates for STAT5b over STAT5a. <i>ACS Chemical Biology</i> , 2019 , 14, 796-805 | 4.9 | 8 |
| 4 | Commonly used fluoroquinolones cross-react with urine drug screens for opiates, buprenorphine, and amphetamines. <i>Clinical Biochemistry</i> , 2019 , 68, 50-54 | 3.5 | 7 |
| 3 | Simphony: simulating large-scale, rhythmic data. <i>PeerJ</i> , 2019 , 7, e6985 | 3.1 | 5 |
| 2 | Releasing a preprint is associated with more attention and citations for the peer-reviewed article | | 2 |
| 1 | Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record | | 1 |