

Matthew J O'meara

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

7,297
citations

393982

19
h-index

713013

21
g-index

30
all docs

30
docs citations

30
times ranked

14607
citing authors

#	ARTICLE	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
2	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3031-3048.	2.3	1,032
3	Ultra-large library docking for discovering new chemotypes. <i>Nature</i> , 2019, 566, 224-229.	13.7	595
4	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
5	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 609-622.	2.3	204
6	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. <i>Methods in Enzymology</i> , 2013, 523, 109-143.	0.4	195
7	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021, 373, 541-547.	6.0	148
8	Morphological cell profiling of SARS-CoV-2 infection identifies drug repurposing candidates for COVID-19. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	124
9	Structures of the β 2 receptor enable docking for bioactive ligand discovery. <i>Nature</i> , 2021, 600, 759-764.	13.7	113
10	A Web Resource for Standardized Benchmark Datasets, Metrics, and Rosetta Protocols for Macromolecular Modeling and Design. <i>PLoS ONE</i> , 2015, 10, e0130433.	1.1	85
11	The <i>Cryptococcus neoformans</i> Rim101 Transcription Factor Directly Regulates Genes Required for Adaptation to the Host. <i>Molecular and Cellular Biology</i> , 2014, 34, 673-684.	1.1	73
12	The Recognition of Identical Ligands by Unrelated Proteins. <i>ACS Chemical Biology</i> , 2015, 10, 2772-2784.	1.6	70
13	High-Throughput Screening Identifies Genes Required for <i>Candida albicans</i> Induction of Macrophage Pyroptosis. <i>MBio</i> , 2018, 9, .	1.8	58
14	Role of Electrostatic Repulsion in Controlling pH-Dependent Conformational Changes of Viral Fusion Proteins. <i>Structure</i> , 2013, 21, 1085-1096.	1.6	53
15	Local delivery of stabilized chondroitinase ABC degrades chondroitin sulfate proteoglycans in stroke-injured rat brains. <i>Journal of Controlled Release</i> , 2019, 297, 14-25.	4.8	41
16	Global proteomic analyses define an environmentally contingent Hsp90 interactome and reveal chaperone-dependent regulation of stress granule proteins and the R2TP complex in a fungal pathogen. <i>PLoS Biology</i> , 2019, 17, e3000358.	2.6	34
17	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. <i>Nature Communications</i> , 2021, 12, 6497.	5.8	33
18	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018, 7, .	2.8	30

#	ARTICLE	IF	CITATIONS
19	Reengineering biocatalysts: Computational redesign of chondroitinase ABC improves efficacy and stability. Science Advances, 2020, 6, eabc6378.	4.7	28
20	DeORFanizing Candida albicans Genes using Coexpression. MSphere, 2021, 6, .	1.3	11
21	Ligand Similarity Complements Sequence, Physical Interaction, and Co-Expression for Gene Function Prediction. PLoS ONE, 2016, 11, e0160098.	1.1	10