Matthew J O'meara

List of Publications by Year
in descending order

21 papers	7,297 citations	394421 19 h-index	713466 21 g-index
30 all docs	30 docs citations	30 times ranked	14607 citing authors

#	Article	IF	Citations
1	DeORFanizing Candida albicans Genes using Coexpression. MSphere, 2021, 6, .	2.9	11
2	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. Science, 2021, 373, 541-547.	12.6	148
3	Morphological cell profiling of SARS-CoV-2 infection identifies drug repurposing candidates for COVID-19. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	124
4	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. Nature Communications, 2021, 12, 6497.	12.8	33
5	Structures of the Ïƒ2 receptor enable docking for bioactive ligand discovery. Nature, 2021, 600, 759-764.	27.8	113
6	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
7	Reengineering biocatalysts: Computational redesign of chondroitinase ABC improves efficacy and stability. Science Advances, 2020, 6, eabc6378.	10.3	28
8	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
9	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. PLoS Biology, 2019, 17, e3000358.	5.6	34
10	Local delivery of stabilized chondroitinase ABC degrades chondroitin sulfate proteoglycans in stroke-injured rat brains. Journal of Controlled Release, 2019, 297, 14-25.	9.9	41
11	Ultra-large library docking for discovering new chemotypes. Nature, 2019, 566, 224-229.	27.8	595
12	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	6.0	30
13	High-Throughput Screening Identifies Genes Required for Candida albicans Induction of Macrophage Pyroptosis. MBio, 2018, 9, .	4.1	58
14	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	5.3	1,032
15	Ligand Similarity Complements Sequence, Physical Interaction, and Co-Expression for Gene Function Prediction. PLoS ONE, 2016, 11, e0160098.	2.5	10
16	A Web Resource for Standardized Benchmark Datasets, Metrics, and Rosetta Protocols for Macromolecular Modeling and Design. PLoS ONE, 2015, 10, e0130433.	2.5	85
17	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. Journal of Chemical Theory and Computation, 2015, 11, 609-622.	5.3	204
18	The Recognition of Identical Ligands by Unrelated Proteins. ACS Chemical Biology, 2015, 10, 2772-2784.	3.4	70

#	Article	IF	Citations
19	The Cryptococcus neoformans Rim101 Transcription Factor Directly Regulates Genes Required for Adaptation to the Host. Molecular and Cellular Biology, 2014, 34, 673-684.	2.3	73
20	Role of Electrostatic Repulsion in Controlling pH-Dependent Conformational Changes of Viral Fusion Proteins. Structure, 2013, 21, 1085-1096.	3.3	53
21	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	1.0	195