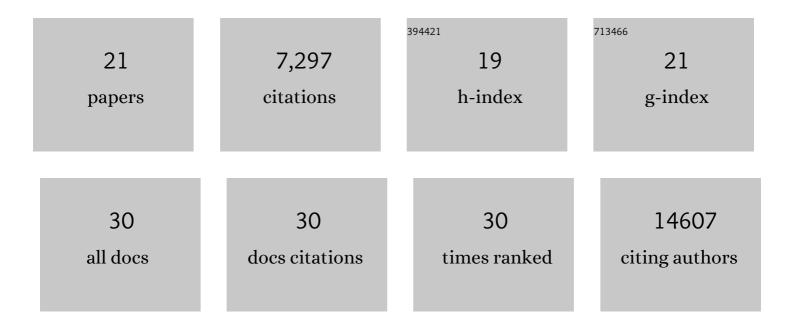
Matthew J O'meara

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
2	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
3	Ultra-large library docking for discovering new chemotypes. Nature, 2019, 566, 224-229.	27.8	595
4	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
5	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
6	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	1.0	195
7	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. Science, 2021, 373, 541-547.	12.6	148
8	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
9	Structures of the if 2 receptor enable docking for bioactive ligand discovery. Nature, 2021, 600, 759-764.	27.8	113
10	A Web Resource for Standardized Benchmark Datasets, Metrics, and Rosetta Protocols for Macromolecular Modeling and Design. PLoS ONE, 2015, 10, e0130433.	2.5	85
11	The <i>Cryptococcus neoformans</i> Rim101 Transcription Factor Directly Regulates Genes Required for Adaptation to the Host. Molecular and Cellular Biology, 2014, 34, 673-684.	2.3	73
12	The Recognition of Identical Ligands by Unrelated Proteins. ACS Chemical Biology, 2015, 10, 2772-2784.	3.4	70
13	High-Throughput Screening Identifies Genes Required for <i>Candida albicans</i> Induction of Macrophage Pyroptosis. MBio, 2018, 9, .	4.1	58
14	Role of Electrostatic Repulsion in Controlling pH-Dependent Conformational Changes of Viral Fusion Proteins. Structure, 2013, 21, 1085-1096.	3.3	53
15	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
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. PLoS Biology, 2019, 17, e3000358.	5.6	34
17	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. Nature Communications, 2021, 12, 6497.	12.8	33
18	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	6.0	30

#	Article	IF	CITATIONS
19	Reengineering biocatalysts: Computational redesign of chondroitinase ABC improves efficacy and stability. Science Advances, 2020, 6, eabc6378.	10.3	28
20	DeORFanizing Candida albicans Genes using Coexpression. MSphere, 2021, 6, .	2.9	11
21	Ligand Similarity Complements Sequence, Physical Interaction, and Co-Expression for Gene Function Prediction. PLoS ONE, 2016, 11, e0160098.	2.5	10