

Matthew J O meara

List of Publications by Citations

Source: <https://exaly.com/author-pdf/3893572/matthew-j-omeara-publications-by-citations.pdf>
Version: 2024-04-11

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

26 papers	4,172 citations	18 h-index	30 g-index
30 ext. papers	5,933 ext. citations	15.5 avg, IF	4.7 L-index

#	Paper	IF	Citations
26	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020 , 583, 459-468	50.4	2142
25	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. <i>Journal of Chemical Theory and Computation</i> , 2017 , 13, 3031-3048	6.4	486
24	Ultra-large library docking for discovering new chemotypes. <i>Nature</i> , 2019 , 566, 224-229	50.4	309
23	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020 , 370,	33.3	261
22	Scientific benchmarks for guiding macromolecular energy function improvement. <i>Methods in Enzymology</i> , 2013 , 523, 109-43	1.7	164
21	Combined covalent-electrostatic model of hydrogen bonding improves structure prediction with Rosetta. <i>Journal of Chemical Theory and Computation</i> , 2015 , 11, 609-22	6.4	163
20	A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing 2020 ,		133
19	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021 , 373, 541-547	33.3	64
18	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, 673-84	4.8	62
17	A Web Resource for Standardized Benchmark Datasets, Metrics, and Rosetta Protocols for Macromolecular Modeling and Design. <i>PLoS ONE</i> , 2015 , 10, e0130433	3.7	58
16	The Recognition of Identical Ligands by Unrelated Proteins. <i>ACS Chemical Biology</i> , 2015 , 10, 2772-84	4.9	52
15	Morphological Cell Profiling of SARS-CoV-2 Infection Identifies Drug Repurposing Candidates for COVID-19 2020 ,		46
14	Role of electrostatic repulsion in controlling pH-dependent conformational changes of viral fusion proteins. <i>Structure</i> , 2013 , 21, 1085-96	5.2	41
13	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,	11.5	39
12	High-Throughput Screening Identifies Genes Required for Induction of Macrophage Pyroptosis. <i>MBio</i> , 2018 , 9,	7.8	36
11	Structures of the β receptor enable docking for bioactive ligand discovery. <i>Nature</i> , 2021 ,	50.4	24
10	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	11.7	23

9	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018 , 7,	8.9	22
8	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	9.7	18
7	Reengineering biocatalysts: Computational redesign of chondroitinase ABC improves efficacy and stability. <i>Science Advances</i> , 2020 , 6, eabc6378	14.3	7
6	Ligand Similarity Complements Sequence, Physical Interaction, and Co-Expression for Gene Function Prediction. <i>PLoS ONE</i> , 2016 , 11, e0160098	3.7	6
5	Crystal structures of the μ receptor template large-library docking for selective chemotypes active in vivo		5
4	DeORFanizing <i>Candida albicans</i> Genes using Coexpression. <i>MSphere</i> , 2021 , 6,	5	5
3	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. <i>Nature Communications</i> , 2021 , 12, 6497	17.4	4
2	Valproic Acid-Induced Changes of 4D Nuclear Morphology in Astrocyte Cells		1
1	Phospholipidosis is a shared mechanism underlying the antiviral activity of many repurposed drugs against SARS-CoV-2 2021 ,		1