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List of Publications by Year in Descending Order

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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.

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	Structures of the Receptor enable docking for bioactive ligand discovery. <i>Nature</i> , 2021 ,	50.4	24
25	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. <i>Nature Communications</i> , 2021 , 12, 6497	17.4	4
24	Phospholipidosis is a shared mechanism underlying the antiviral activity of many repurposed drugs against SARS-CoV-2 2021 ,		1
23	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021 , 373, 541-547	33.3	64
22	DeORFanizing Candida albicans Genes using Coexpression. <i>MSphere</i> , 2021 , 6,	5	5
21	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
20	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020 , 583, 459-468	50.4	2142
19	A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing 2020 ,		133
18	Morphological Cell Profiling of SARS-CoV-2 Infection Identifies Drug Repurposing Candidates for COVID-19 2020 ,		46
17	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020 , 370,	33.3	261
16	Reengineering biocatalysts: Computational redesign of chondroitinase ABC improves efficacy and stability. <i>Science Advances</i> , 2020 , 6, eabc6378	14.3	7
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	11.7	23
14	Ultra-large library docking for discovering new chemotypes. <i>Nature</i> , 2019 , 566, 224-229	50.4	309
13	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
12	High-Throughput Screening Identifies Genes Required for Induction of Macrophage Pyroptosis. <i>MBio</i> , 2018 , 9,	7.8	36
11	Prediction of enzymatic pathways by integrative pathway mapping. <i>ELife</i> , 2018 , 7,	8.9	22
10	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

9	Ligand Similarity Complements Sequence, Physical Interaction, and Co-Expression for Gene Function Prediction. <i>PLoS ONE</i> , 2016 , 11, e0160098	3.7	6
8	The Recognition of Identical Ligands by Unrelated Proteins. <i>ACS Chemical Biology</i> , 2015 , 10, 2772-84	4.9	52
7	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
6	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
5	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
4	Role of electrostatic repulsion in controlling pH-dependent conformational changes of viral fusion proteins. <i>Structure</i> , 2013 , 21, 1085-96	5.2	41
3	Scientific benchmarks for guiding macromolecular energy function improvement. <i>Methods in Enzymology</i> , 2013 , 523, 109-43	1.7	164
2	Valproic Acid-Induced Changes of 4D Nuclear Morphology in Astrocyte Cells		1
1	Crystal structures of the μ receptor template large-library docking for selective chemotypes active in vivo		5