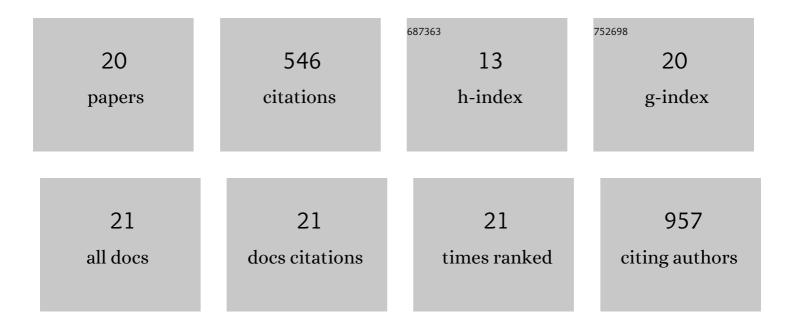
Carles Corbi-Verge

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6058600/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Fast and Flexible Protein Design Using Deep Graph Neural Networks. Cell Systems, 2020, 11, 402-411.e4.	6.2	121
2	Motif mediated protein-protein interactions as drug targets. Cell Communication and Signaling, 2016, 14, 8.	6.5	76
3	Pooled screening for antiproliferative inhibitors of protein-protein interactions. Nature Chemical Biology, 2016, 12, 275-281.	8.0	37
4	Strategies to Develop Inhibitors of Motif-Mediated Protein-Protein Interactions as Drug Leads. Annual Review of Pharmacology and Toxicology, 2017, 57, 39-60.	9.4	37
5	Two-state dynamics of the SH3–SH2 tandem of Abl kinase and the allosteric role of the N-cap. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3372-80.	7.1	33
6	Protein engineering by highly parallel screening of computationally designed variants. Science Advances, 2016, 2, e1600692.	10.3	32
7	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. Nature Structural and Molecular Biology, 2018, 25, 1093-1102.	8.2	31
8	Predicting changes in protein stability caused by mutation using sequenceâ€and structureâ€based methods in a CAGI5 blind challenge. Human Mutation, 2019, 40, 1414-1423.	2.5	28
9	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189.	6.4	22
10	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. Journal of Molecular Biology, 2019, 431, 336-350.	4.2	20
11	Post-Translational Modifications Modulate Ligand Recognition by the Third PDZ Domain of the MAGUK Protein PSD-95. PLoS ONE, 2014, 9, e90030.	2.5	19
12	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	2.5	16
13	The role of residue stability in transient protein-protein interactions involved in enzymatic phosphate hydrolysis. A computational study. Proteins: Structure, Function and Bioinformatics, 2005, 63, 65-77.	2.6	13
14	Binding site plasticity in viral PPxY Late domain recognition by the third WW domain of human NEDD4. Scientific Reports, 2019, 9, 15076.	3.3	12
15	Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. Methods in Molecular Biology, 2019, 1851, 1-17.	0.9	12
16	Rapid and accurate structureâ€based therapeutic peptide design using GPU accelerated thermodynamic integration. Proteins: Structure, Function and Bioinformatics, 2019, 87, 236-244.	2.6	7
17	A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domain–Peptide Interactions. ACS Synthetic Biology, 2019, 8, 918-928.	3.8	6
18	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. STAR Protocols, 2021, 2, 100505.	1.2	5

#	Article	IF	CITATIONS
19	The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. Nucleic Acids Research, 2020, 48, 6382-6402.	14.5	4
20	Phage display identification of nanomolar ligands for human NEDD4-WW3: Energetic and dynamic implications for the development of broad-spectrum antivirals. International Journal of Biological Macromolecules, 2022, 207, 308-323.	7.5	3