

Carles Corbi-Verge

List of Publications by Citations

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Version: 2024-04-28

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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.

21
papers

324
citations

11
h-index

17
g-index

21
ext. papers

456
ext. citations

8.3
avg, IF

3.75
L-index

#	Paper	IF	Citations
21	Motif mediated protein-protein interactions as drug targets. <i>Cell Communication and Signaling</i> , 2016 , 14, 8	7.5	52
20	Fast and Flexible Protein Design Using Deep Graph Neural Networks. <i>Cell Systems</i> , 2020 , 11, 402-411.e4	10.6	37
19	Strategies to Develop Inhibitors of Motif-Mediated Protein-Protein Interactions as Drug Leads. <i>Annual Review of Pharmacology and Toxicology</i> , 2017 , 57, 39-60	17.9	27
18	Pooled screening for antiproliferative inhibitors of protein-protein interactions. <i>Nature Chemical Biology</i> , 2016 , 12, 275-81	11.7	26
17	Two-state dynamics of the SH3-SH2 tandem of Abl kinase and the allosteric role of the N-cap. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E3372-80	11.5	26
16	Protein engineering by highly parallel screening of computationally designed variants. <i>Science Advances</i> , 2016 , 2, e1600692	14.3	21
15	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 1093-1102	17.6	21
14	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015 , 12, 183-9	10.6	17
13	Post-translational modifications modulate ligand recognition by the third PDZ domain of the MAGUK protein PSD-95. <i>PLoS ONE</i> , 2014 , 9, e90030	3.7	16
12	Predicting changes in protein stability caused by mutation using sequence-and structure-based methods in a CAGI5 blind challenge. <i>Human Mutation</i> , 2019 , 40, 1414-1423	4.7	14
11	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. <i>Human Mutation</i> , 2019 , 40, 1392-1399	4.7	11
10	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. <i>Journal of Molecular Biology</i> , 2019 , 431, 336-350	6.5	11
9	The role of residue stability in transient protein-protein interactions involved in enzymatic phosphate hydrolysis. A computational study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 65-77	4.2	10
8	Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2019 , 1851, 1-17	1.4	9
7	Binding site plasticity in viral PPxY Late domain recognition by the third WW domain of human NEDD4. <i>Scientific Reports</i> , 2019 , 9, 15076	4.9	8
6	Fast and flexible design of novel proteins using graph neural networks		6
5	A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domain-Peptide Interactions. <i>ACS Synthetic Biology</i> , 2019 , 8, 918-928	5.7	5

4	Rapid and accurate structure-based therapeutic peptide design using GPU accelerated thermodynamic integration. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 236-244	4.2	5
3	The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. <i>Nucleic Acids Research</i> , 2020 , 48, 6382-6402	20.1	1
2	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. <i>STAR Protocols</i> , 2021 , 2, 100505	1.4	1
1	Phage display identification of nanomolar ligands for human NEDD4-WW3: Energetic and dynamic implications for the development of broad-spectrum antivirals.. <i>International Journal of Biological Macromolecules</i> , 2022 , 207, 308-323	7.9	