

Carles Corbi-Verge

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

546
citations

687363

13
h-index

752698

20
g-index

21
all docs

21
docs citations

21
times ranked

957
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast and Flexible Protein Design Using Deep Graph Neural Networks. <i>Cell Systems</i> , 2020, 11, 402-411.e4.	6.2	121
2	Motif mediated protein-protein interactions as drug targets. <i>Cell Communication and Signaling</i> , 2016, 14, 8.	6.5	76
3	Pooled screening for antiproliferative inhibitors of protein-protein interactions. <i>Nature Chemical Biology</i> , 2016, 12, 275-281.	8.0	37
4	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.	9.4	37
5	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.	7.1	33
6	Protein engineering by highly parallel screening of computationally designed variants. <i>Science Advances</i> , 2016, 2, e1600692.	10.3	32
7	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 1093-1102.	8.2	31
8	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.	2.5	28
9	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015, 12, 183-189.	6.4	22
10	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. <i>Journal of Molecular Biology</i> , 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. <i>PLoS ONE</i> , 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. <i>Human Mutation</i> , 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. <i>Proteins: Structure, Function and Bioinformatics</i> , 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. <i>Scientific Reports</i> , 2019, 9, 15076.	3.3	12
15	Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2019, 1851, 1-17.	0.9	12
16	Rapid and accurate structure based therapeutic peptide design using GPU accelerated thermodynamic integration. <i>Proteins: Structure, Function and Bioinformatics</i> , 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. <i>ACS Synthetic Biology</i> , 2019, 8, 918-928.	3.8	6
18	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. <i>STAR Protocols</i> , 2021, 2, 100505.	1.2	5

#	ARTICLE	IF	CITATIONS
19	The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. <i>Nucleic Acids Research</i> , 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. <i>International Journal of Biological Macromolecules</i> , 2022, 207, 308-323.	7.5	3