# Carles Corbi-Verge

List of Publications by Year
in descending order



| 20 | 546 | 687363 13 | 752698 20 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 21 | 21 | 21 | 957 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | 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 |
| 2 | Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. STAR Protocols, 2021, 2, 100505. | 1.2 | 5 |
| 3 | Fast and Flexible Protein Design Using Deep Graph Neural Networks. Cell Systems, 2020, 11, 402-411.e4. | 6.2 | 121 |
| 4 | The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. Nucleic Acids Research, 2020, 48, 6382-6402. | 14.5 | 4 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domainâ€“Peptide Interactions. ACS Synthetic Biology, 2019, 8, 918-928. | 3.8 | 6 |
| 9 | Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. Journal of Molecular Biology, 2019, 431, 336-350. | 4.2 | 20 |
| 10 | 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 |
| 11 | Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. Methods in Molecular Biology, 2019, 1851, 1-17. | 0.9 | 12 |
| 12 | 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 |
| 13 | 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 |
| 14 | Protein engineering by highly parallel screening of computationally designed variants. Science Advances, 2016, 2, e1600692. | 10.3 | 32 |
| 15 | Motif mediated protein-protein interactions as drug targets. Cell Communication and Signaling, 2016, 14, 8. | 6.5 | 76 |
| 16 | Pooled screening for antiproliferative inhibitors of protein-protein interactions. Nature Chemical Biology, 2016, 12, 275-281. | 8.0 | 37 |
| 17 | Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189. | 6.4 | 22 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Two-state dynamics of the SH3â€“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 |
| 20 | 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 |