

Brahm Yachnin

List of Publications by Year in descending order

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17
papers

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citations

1040056

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docs citations

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627
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Crystal Structures of Cyclohexanone Monooxygenase Reveal Complex Domain Movements and a Sliding Cofactor. <i>Journal of the American Chemical Society</i> , 2009, 131, 8848-8854. | 13.7 | 151 |
| 2 | The Substrate-Bound Crystal Structure of a Baeyer-Villiger Monooxygenase Exhibits a Criegee-like Conformation. <i>Journal of the American Chemical Society</i> , 2012, 134, 7788-7795. | 13.7 | 81 |
| 3 | Lactone-Bound Structures of Cyclohexanone Monooxygenase Provide Insight into the Stereochemistry of Catalysis. <i>ACS Chemical Biology</i> , 2014, 9, 2843-2851. | 3.4 | 39 |
| 4 | Multiple Conformers in Active Site of Human Dihydrofolate Reductase F31R/Q35E Double Mutant Suggest Structural Basis for Methotrexate Resistance. <i>Journal of Biological Chemistry</i> , 2009, 284, 20079-20089. | 3.4 | 33 |
| 5 | Characterization of the Redox and Metal Binding Activity of BsSco, a Protein Implicated in the Assembly of Cytochrome c Oxidase. <i>Biochemistry</i> , 2005, 44, 16949-16956. | 2.5 | 32 |
| 6 | Computational Design of a Photocontrolled Cytosine Deaminase. <i>Journal of the American Chemical Society</i> , 2018, 140, 14-17. | 13.7 | 26 |
| 7 | Identification and characterization of hippuristanol-resistant mutants reveals eIF4A1 dependencies within mRNA 5' leader regions. <i>Nucleic Acids Research</i> , 2020, 48, 9521-9537. | 14.5 | 22 |
| 8 | The role of conformational flexibility in Baeyer-Villiger monooxygenase catalysis and structure. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1641-1648. | 2.3 | 21 |
| 9 | Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947. | 12.8 | 16 |
| 10 | MHCEpitopeEnergy, a Flexible Rosetta-Based Biotherapeutic Deimmunization Platform. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2368-2382. | 5.4 | 12 |
| 11 | Novel crystallization conditions for tandem variant R67 DHFR yield a wild-type crystal structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1316-1322. | 0.7 | 8 |
| 12 | Engineering carboxypeptidase G2 circular permutations for the design of an autoinhibited enzyme. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 321-331. | 2.1 | 7 |
| 13 | Structure-Based Design of Dimeric Bisbenzimidazole Inhibitors to an Emergent Trimethoprim-Resistant Type II Dihydrofolate Reductase Guides the Design of Monomeric Analogues. <i>ACS Omega</i> , 2019, 4, 10056-10069. | 3.5 | 7 |
| 14 | Sustained Development in Baeyer-Villiger Biooxidation Technology. <i>ACS Symposium Series</i> , 2010, , 343-372. | 0.5 | 6 |
| 15 | Massively parallel, computationally guided design of a proenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116097119. | 7.1 | 6 |
| 16 | Comprehensive characterization of ligand-induced plasticity changes in a dimeric enzyme. <i>FEBS Journal</i> , 2016, 283, 3029-3038. | 4.7 | 4 |
| 17 | Massively Parallel Protein Design to Develop Enzymes for Next-Generation Chemotherapy. <i>FASEB Journal</i> , 2019, 33, 472.13. | 0.5 | 0 |