# Andrew Leaver-Fay

List of Publications by Year
in descending order



| 16 | 4,617 | 687363 13 | 940533 16 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 16 | 16 | 16 | 6080 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Comparative Analysis of Sulfoniumâ˜Ï€, Ammoniumâ˜Ï€, and Sulfurâ˜Ï€ Interactions and Relevance to SAM-Dependent Methyltransferases. Journal of the American Chemical Society, 2022, 144, 2535-2545. | 13.7 | 2 |
| 2 | PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122. | 0.3 | 8 |
| 3 | Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947. | 12.8 | 16 |
| 4 | Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507. | 3.2 | 27 |
| 5 | Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680. | 19.0 | 513 |
| 6 | The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048. | 5.3 | 1,032 |
| 7 | Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. Bioinformatics, 2017, 33, 2765-2767. | 4.1 | 77 |
| 8 | A cyber-linked undergraduate research experience in computational biomolecular structure prediction and design. PLoS Computational Biology, 2017, 13, e1005837. | 3.2 | 12 |
| 9 | Computationally Designed Bispecific Antibodies using Negative State Repertoires. Structure, 2016, 24, 641-651. | 3.3 | 54 |
| 10 | SwiftLib: rapid degenerate-codon-library optimization through dynamic programming. Nucleic Acids Research, 2015, 43, e34-e34. | 14.5 | 53 |
| 11 | Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. Journal of Chemical Theory and Computation, 2015, 11, 609-622. | 5.3 | 204 |
| 12 | Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface. Nature Biotechnology, 2014, 32, 191-198. | 17.5 | 210 |
| 13 | Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143. | 1.0 | 195 |
| 14 | Rosetta3. Methods in Enzymology, 2011, 487, 545-574. | 1.0 | 1,620 |
| 15 | RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161. | 2.5 | 506 |
| 16 | A Generic Program for Multistate Protein Design. PLoS ONE, 2011, 6, e20937. | 2.5 | 88 |