

Joseph Audie

List of Publications by Year in descending order

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Version: 2024-02-01

10
papers

193
citations

1478505

6
h-index

1372567

10
g-index

10
all docs

10
docs citations

10
times ranked

306
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | A novel empirical free energy function that explains and predicts protein-protein binding affinities. <i>Biophysical Chemistry</i> , 2007, 129, 198-211. | 2.8 | 57 |
| 2 | Rational, computer-enabled peptide drug design: principles, methods, applications and future directions. <i>Future Medicinal Chemistry</i> , 2015, 7, 2173-2193. | 2.3 | 35 |
| 3 | Development and validation of an empirical free energy function for calculating protein-protein binding free energy surfaces. <i>Biophysical Chemistry</i> , 2009, 139, 84-91. | 2.8 | 28 |
| 4 | Recent work in the development and application of protein-peptide docking. <i>Future Medicinal Chemistry</i> , 2012, 4, 1619-1644. | 2.3 | 28 |
| 5 | Advances in the Prediction of Protein-Peptide Binding Affinities: Implications for Peptide-Based Drug Discovery. <i>Chemical Biology and Drug Design</i> , 2013, 81, 50-60. | 3.2 | 21 |
| 6 | Continued development of an empirical function for predicting and rationalizing protein-protein binding affinities. <i>Biophysical Chemistry</i> , 2009, 143, 139-144. | 2.8 | 10 |
| 7 | Computational prediction and analysis of the DR6-NAPP interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1376-1395. | 2.6 | 6 |
| 8 | Rigorous Computational and Experimental Investigations on MDM2/MDMX-Targeted Linear and Macrocyclic Peptides. <i>Molecules</i> , 2019, 24, 4586. | 3.8 | 4 |
| 9 | An unexpected way forward: towards a more accurate and rigorous protein-protein binding affinity scoring function by eliminating terms from an already simple scoring function. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 83-97. | 3.5 | 2 |
| 10 | PeptideNavigator: An interactive tool for exploring large and complex data sets generated during peptide-based drug design projects. <i>Computers in Biology and Medicine</i> , 2018, 92, 176-187. | 7.0 | 2 |