

Ian F Thorpe

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

230
citations

1307594

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1372567

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12
docs citations

12
times ranked

401
citing authors

#	ARTICLE	IF	CITATIONS
1	Using Structural Kinetic Modeling To Identify Key Determinants of Stability in Reaction Networks. <i>Journal of Physical Chemistry A</i> , 2017, 121, 4982-4992.	2.5	3
2	Molecular simulations to delineate functional conformational transitions in the HCV polymerase. <i>Journal of Computational Chemistry</i> , 2017, 38, 1125-1137.	3.3	3
3	Computational predictions suggest that structural similarity in viral polymerases may lead to comparable allosteric binding sites. <i>Virus Research</i> , 2016, 222, 80-93.	2.2	8
4	Current advances in molecular, biochemical, and computational modeling analysis of microalgal triacylglycerol biosynthesis. <i>Biotechnology Advances</i> , 2016, 34, 1046-1063.	11.7	79
5	Using the Hepatitis C Virus RNA-Dependent RNA Polymerase as a Model to Understand Viral Polymerase Structure, Function and Dynamics. <i>Viruses</i> , 2015, 7, 3974-3994.	3.3	44
6	Dual Allosteric Inhibitors Jointly Modulate Protein Structure and Dynamics in the Hepatitis C Virus Polymerase. <i>Biochemistry</i> , 2015, 54, 4131-4141.	2.5	8
7	Allosteric Inhibitors Have Distinct Effects, but Also Common Modes of Action, in the HCV Polymerase. <i>Biophysical Journal</i> , 2015, 108, 1785-1795.	0.5	12
8	Efficiently Refining a Transition Path Using Clustering. <i>Biophysical Journal</i> , 2013, 105, 545-546.	0.5	0
9	Inhibitors for the hepatitis C virus RNA polymerase explored by SAR with advanced machine learning methods. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 3127-3137.	3.0	21
10	Molecular Simulations Illuminate the Role of Regulatory Components of the RNA Polymerase from the Hepatitis C Virus in Influencing Protein Structure and Dynamics. <i>Biochemistry</i> , 2013, 52, 4541-4552.	2.5	14
11	Thumb inhibitor binding eliminates functionally important dynamics in the hepatitis C virus RNA polymerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 40-52.	2.6	38