Ian F Thorpe

List of Publications by Year
in descending order

11 papers	230 citations	1307594 7 h-index	1372567 10 g-index
12 all docs	12 docs citations	12 times ranked	401 citing authors

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