## George Hedger

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Lipid Interactions of a Ciliary Membrane TRP Channel: Simulation and Structural Studies of Polycystin-2. Structure, 2020, 28, 169-184.e5.	1.6	37
2	Cholesterol Interaction Sites on the Transmembrane Domain of the Hedgehog Signal Transducer and Class F G Protein-Coupled Receptor Smoothened. Structure, 2019, 27, 549-559.e2.	1.6	77
3	GPCRs: What Can We Learn from Molecular Dynamics Simulations?. Methods in Molecular Biology, 2018, 1705, 133-158.	0.4	13
4	PtdIns(4,5)P2 stabilizes active states of GPCRs and enhances selectivity of G-protein coupling. Nature, 2018, 559, 423-427.	13.7	236
5	Interactions of the EphA2 Kinase Domain with PIPs in Membranes: Implications for Receptor Function. Structure, 2018, 26, 1025-1034.e2.	1.6	33
6	Convergence and Sampling in Determining Free Energy Landscapes for Membrane Protein Association. Journal of Physical Chemistry B, 2017, 121, 3364-3375.	1.2	93
7	Free Energy Landscape of Lipid Interactions with Regulatory Binding Sites on the Transmembrane Domain of the EGF Receptor. Journal of Physical Chemistry B, 2016, 120, 8154-8163.	1.2	60
8	Structural basis of Smoothened regulation by its extracellular domains. Nature, 2016, 535, 517-522.	13.7	300
9	Lipid-Loving ANTs: Molecular Simulations of Cardiolipin Interactions and the Organization of the Adenine Nucleotide Translocase in Model Mitochondrial Membranes. Biochemistry, 2016, 55, 6238-6249.	1.2	63
10	Lipid interaction sites on channels, transporters and receptors: Recent insights from molecular dynamics simulations. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2390-2400.	1.4	143
11	Molecular simulations of glycolipids: Towards mammalian cell membrane models. Biochimie, 2016, 120, 105-109.	1.3	27
12	The juxtamembrane regions of human receptor tyrosine kinases exhibit conserved interaction sites with anionic lipids. Scientific Reports, 2015, 5, 9198.	1.6	89