Robin M Betz

List of Publications by Citations

16 papers	1,683 citations	11 h-index	16 g-index
16 ext. papers	2,128 ext. citations	16.1 avg, IF	4.71 L-index

#	Paper	IF	Citations
16	Lipid14: The Amber Lipid Force Field. *Journal of Chemical Theory and Computation*, **2014**, 10, 865-879	6.4	725
15	Crystal Structure of an LSD-Bound Human Serotonin Receptor. *Cell*, **2017**, 168, 377-389.e12	56.2	214
14	GAFFlipid: a General Amber Force Field for the accurate molecular dynamics simulation of phospholipid. *Soft Matter*, **2012**, 8, 9617	3.6	151
13	D dopamine receptor high-resolution structures enable the discovery of selective agonists. *Science*, **2017**, 358, 381-386	33.3	128
12	Structural and Functional Analysis of a Adrenergic Receptor Complex with GRK5. *Cell*, **2017**, 169, 407-42[illegible]e16	[illegible]6	99
11	Structure-inspired design of arrestin-biased ligands for aminergic GPCRs. *Nature Chemical Biology* , **2018**, 14, 126-134	11.7	96
10	Diverse GPCRs exhibit conserved water networks for stabilization and activation. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 3288-3293	11.5	71
9	Paramfit: automated optimization of force field parameters for molecular dynamics simulations. *Journal of Computational Chemistry*, **2015**, 36, 79-87	3.5	67
8	Structural basis for receptor ligand recognition. *Nature Structural and Molecular Biology*, **2018**, 25, 981-987	13.6	63
7	Reversible versus irreversible inhibition modes of ERK2: a comparative analysis for ERK2 protein kinase in cancer therapy. *Future Medicinal Chemistry*, **2018**, 10, 1003-1015	4.1	28
6	How Effectively Can Adaptive Sampling Methods Capture Spontaneous Ligand Binding?. *Journal of Chemical Theory and Computation*, **2019**, 15, 2053-2063	6.4	21
5	An investigation of the effects of hard and soft errors on graphics processing unit-accelerated molecular dynamics simulations. *Concurrency Computation Practice and Experience*, **2014**, 26, 2134-2140	1.4	7
4	Exploring the Structural Mechanism of Covalently Bound E3 Ubiquitin Ligase: Catalytic or Allosteric Inhibition?. *Protein Journal*, **2018**, 37, 500-509	3.9	7
3	Implementing continuous integration software in an established computational chemistry software package **2013**,		2
2	An investigation of the effects of error correcting code on GPU-accelerated molecular dynamics simulations **2013**,		2
1	Stable networks of water-mediated interactions are conserved in activation of diverse GPCRs		2