# Robin M Betz

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 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 | 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 |
| 15 | How Effectively Can Adaptive Sampling Methods Capture Spontaneous Ligand Binding?. *Journal of Chemical Theory and Computation*, **2019**, 15, 2053-2063 | 6.4 | 21 |
| 14 | 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 |
| 13 | Structure-inspired design of β-arrestin-biased ligands for aminergic GPCRs. *Nature Chemical Biology* , **2018**, 14, 126-134 | 11.7 | 96 |
| 12 | Exploring the Structural Mechanism of Covalently Bound E3 Ubiquitin Ligase: Catalytic or Allosteric Inhibition?. *Protein Journal*, **2018**, 37, 500-509 | 3.9 | 7 |
| 11 | Structural basis for β-receptor ligand recognition. *Nature Structural and Molecular Biology*, **2018**, 25, 981-987 | 13.6 | 63 |
| 10 | Crystal Structure of an LSD-Bound Human Serotonin Receptor. *Cell*, **2017**, 168, 377-389.e12 | 56.2 | 214 |
| 9 | Structural and Functional Analysis of a β-Adrenergic Receptor Complex with GRK5. *Cell*, **2017**, 169, 407-421.e16 | 56.2 | 99 |
| 8 | D dopamine receptor high-resolution structures enable the discovery of selective agonists. *Science*, **2017**, 358, 381-386 | 33.3 | 128 |
| 7 | Paramfit: automated optimization of force field parameters for molecular dynamics simulations. *Journal of Computational Chemistry*, **2015**, 36, 79-87 | 3.5 | 67 |
| 6 | Lipid14: The Amber Lipid Force Field. *Journal of Chemical Theory and Computation*, **2014**, 10, 865-879 | 6.4 | 725 |
| 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 | Implementing continuous integration software in an established computational chemistry software package **2013**, | | 2 |
| 3 | An investigation of the effects of error correcting code on GPU-accelerated molecular dynamics simulations **2013**, | | 2 |
| 2 | GAFFlipid: a General Amber Force Field for the accurate molecular dynamics simulation of phospholipid. *Soft Matter*, **2012**, 8, 9617 | 3.6 | 151 |
| 1 | Stable networks of water-mediated interactions are conserved in activation of diverse GPCRs | | 2 |