Michael Joseph Robertson

List of Publications by Citations

36 papers	1,674 citations	18 h-index	40 g-index
42 ext. papers	2,490 ext. citations	21 avg, IF	5.31 L-index

#	Paper	IF	Citations
36	Improved Peptide and Protein Torsional Energetics with the OPLSAA Force Field. *Journal of Chemical Theory and Computation*, **2015**, 11, 3499-509	6.4	391
35	Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. *Cell*, **2019**, 176, 448-458.e12	56.2	196
34	Structural insights into the activation of metabotropic glutamate receptors. *Nature*, **2019**, 566, 79-84	50.4	148
33	Structures of the M1 and M2 muscarinic acetylcholine receptor/G-protein complexes. *Science*, **2019**, 364, 552-557	33.3	130
32	Structure of the neurotensin receptor 1 in complex with β-arrestin 1. *Nature*, **2020**, 579, 303-308	50.4	124
31	Structure of the M2 muscarinic receptor-β-arrestin complex in a lipid nanodisc. *Nature*, **2020**, 579, 297-302	50.4	123
30	Structure of a Hallucinogen-Activated Gq-Coupled 5-HT Serotonin Receptor. *Cell*, **2020**, 182, 1574-1588.e19	56.2	101
29	Design, synthesis, and protein crystallography of biaryltriazoles as potent tautomerase inhibitors of macrophage migration inhibitory factor. *Journal of the American Chemical Society*, **2015**, 137, 2996-3003	16.4	51
28	Illustrating Concepts in Physical Organic Chemistry with 3D Printed Orbitals. *Journal of Chemical Education*, **2015**, 92, 2113-2116	2.4	44
27	Structures of metabotropic GABA receptor. *Nature*, **2020**, 584, 310-314	50.4	34
26	GemSpot: A Pipeline for Robust Modeling of Ligands into Cryo-EM Maps. *Structure*, **2020**, 28, 707-716.e3	5.2	28
25	Assessment of Biased Agonism among Distinct Synthetic Cannabinoid Receptor Agonist Scaffolds. *ACS Pharmacology and Translational Science*, **2020**, 3, 285-295	5.9	28
24	Development and Testing of the OPLS-AA/M Force Field for RNA. *Journal of Chemical Theory and Computation*, **2019**, 15, 2734-2742	6.4	26
23	A Fluorescence Polarization Assay for Binding to Macrophage Migration Inhibitory Factor and Crystal Structures for Complexes of Two Potent Inhibitors. *Journal of the American Chemical Society* , **2016**, 138, 8630-8	16.4	25
22	G-protein activation by a metabotropic glutamate receptor. *Nature*, **2021**, 595, 450-454	50.4	24
21	Irregularities in enzyme assays: The case of macrophage migration inhibitory factor. *Bioorganic and Medicinal Chemistry Letters*, **2016**, 26, 2764-2767	2.9	22
20	Systematic Study of Effects of Structural Modifications on the Aqueous Solubility of Drug-like Molecules. *ACS Medicinal Chemistry Letters*, **2017**, 8, 124-127	4.3	21

19	Molecular Dynamics Simulations of a Conformationally Mobile Peptide-Based Catalyst for Atroposelective Bromination. *ACS Catalysis*, **2018**, 8, 9968-9979	13.1	21
18	Improved Description of Sulfur Charge Anisotropy in OPLS Force Fields: Model Development and Parameterization. *Journal of Physical Chemistry B*, **2017**, 121, 6626-6636	3.4	18
17	Asymmetric activation of the calcium-sensing receptor homodimer. *Nature*, **2021**, 595, 455-459	50.4	14
16	Improved Treatment of Nucleosides and Nucleotides in the OPLS-AA Force Field. *Chemical Physics Letters*, **2017**, 683, 276-280	2.5	13
15	Development and Validation of the Quantum Mechanical Bespoke Protein Force Field. *ACS Omega*, **2019**, 4, 14537-14550	3.9	13
14	Optimization of Pyrazoles as Phenol Surrogates to Yield Potent Inhibitors of Macrophage Migration Inhibitory Factor. *ChemMedChem*, **2018**, 13, 1092-1097	3.7	12
13	Performance of Protein-Ligand Force Fields for the Flavodoxin-Flavin Mononucleotide System. *Journal of Physical Chemistry Letters*, **2016**, 7, 3032-6	6.4	12
12	Adding a Hydrogen Bond May Not Help: Naphthyridinone vs Quinoline Inhibitors of Macrophage Migration Inhibitory Factor. *ACS Medicinal Chemistry Letters*, **2017**, 8, 1287-1291	4.3	8
11	Structural insights into GIRK2 channel modulation by cholesterol and PIP. *Cell Reports*, **2021**, 36, 109619	10.6	8
10	Drug discovery in the era of cryo-electron microscopy. *Trends in Biochemical Sciences*, **2021**,	10.3	7
9	Structure and mechanism of the SGLT family of glucose transporters. *Nature*, **2021**,	50.4	6
8	GemSpot: A Pipeline for Robust Modeling of Ligands into CryoEM Maps		4
7	Isolating Conformers to Assess Dynamics of Peptidic Catalysts Using Computationally Designed Macrocyclic Peptides. *ACS Catalysis*, **2021**, 11, 4395-4400	13.1	4
6	The oxytocin signaling complex reveals a molecular switch for cation dependence.. *Nature Structural and Molecular Biology*, **2022**,	17.6	4
5	The tethered peptide activation mechanism of adhesion GPCRs.. *Nature*, **2022**,	50.4	4
4	Plasticity in Ligand Recognition at Somatostatin Receptors		3
3	Structure Determination of Inactive-State GPCRs with a Universal Nanobody		2
2	Plasticity in ligand recognition at somatostatin receptors.. *Nature Structural and Molecular Biology*, **2022**,	17.6	2

1 Development of OPLS-AA/M Parameters for Simulations of G Protein-Coupled Receptors and Other Membrane Proteins 1