# Michael Joseph Robertson

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 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 | Plasticity in ligand recognition at somatostatin receptors.. *Nature Structural and Molecular Biology*, **2022**, | 17.6 | 2 |
| 35 | The oxytocin signaling complex reveals a molecular switch for cation dependence.. *Nature Structural and Molecular Biology*, **2022**, | 17.6 | 4 |
| 34 | The tethered peptide activation mechanism of adhesion GPCRs.. *Nature*, **2022**, | 50.4 | 4 |
| 33 | Structure and mechanism of the SGLT family of glucose transporters. *Nature*, **2021**, | 50.4 | 6 |
| 32 | Isolating Conformers to Assess Dynamics of Peptidic Catalysts Using Computationally Designed Macrocyclic Peptides. *ACS Catalysis*, **2021**, 11, 4395-4400 | 13.1 | 4 |
| 31 | Asymmetric activation of the calcium-sensing receptor homodimer. *Nature*, **2021**, 595, 455-459 | 50.4 | 14 |
| 30 | G-protein activation by a metabotropic glutamate receptor. *Nature*, **2021**, 595, 450-454 | 50.4 | 24 |
| 29 | Drug discovery in the era of cryo-electron microscopy. *Trends in Biochemical Sciences*, **2021**, | 10.3 | 7 |
| 28 | Structural insights into GIRK2 channel modulation by cholesterol and PIP. *Cell Reports*, **2021**, 36, 109619 | 10.6 | 8 |
| 27 | GemSpot: A Pipeline for Robust Modeling of Ligands into Cryo-EM Maps. *Structure*, **2020**, 28, 707-716.e3 | 5.2 | 28 |
| 26 | Structure of the neurotensin receptor 1 in complex with β-arrestin 1. *Nature*, **2020**, 579, 303-308 | 50.4 | 124 |
| 25 | Structure of the M2 muscarinic receptor-β-arrestin complex in a lipid nanodisc. *Nature*, **2020**, 579, 297-302 | 50.4 | 123 |
| 24 | Assessment of Biased Agonism among Distinct Synthetic Cannabinoid Receptor Agonist Scaffolds. *ACS Pharmacology and Translational Science*, **2020**, 3, 285-295 | 5.9 | 28 |
| 23 | Structures of metabotropic GABA receptor. *Nature*, **2020**, 584, 310-314 | 50.4 | 34 |
| 22 | Structure of a Hallucinogen-Activated Gq-Coupled 5-HT Serotonin Receptor. *Cell*, **2020**, 182, 1574-1588.e19 | 36.2 | 101 |
| 21 | Development and Validation of the Quantum Mechanical Bespoke Protein Force Field. *ACS Omega*, **2019**, 4, 14537-14550 | 3.9 | 13 |
| 20 | Structural insights into the activation of metabotropic glutamate receptors. *Nature*, **2019**, 566, 79-84 | 50.4 | 148 |

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| 19 | Structures of the M1 and M2 muscarinic acetylcholine receptor/G-protein complexes. *Science*, **2019**, 364, 552-557 | 33.3 | 130 |
| 18 | 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 |
| 17 | Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. *Cell*, **2019**, 176, 448-458.e12 | 56.2 | 196 |
| 16 | Optimization of Pyrazoles as Phenol Surrogates to Yield Potent Inhibitors of Macrophage Migration Inhibitory Factor. *ChemMedChem*, **2018**, 13, 1092-1097 | 3.7 | 12 |
| 15 | Molecular Dynamics Simulations of a Conformationally Mobile Peptide-Based Catalyst for Atroposelective Bromination. *ACS Catalysis*, **2018**, 8, 9968-9979 | 13.1 | 21 |
| 14 | Improved Treatment of Nucleosides and Nucleotides in the OPLS-AA Force Field. *Chemical Physics Letters*, **2017**, 683, 276-280 | 2.5 | 13 |
| 13 | 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 |
| 12 | 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 |
| 11 | 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 |
| 10 | Performance of Protein-Ligand Force Fields for the Flavodoxin-Flavin Mononucleotide System. *Journal of Physical Chemistry Letters*, **2016**, 7, 3032-6 | 6.4 | 12 |
| 9 | 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 |
| 8 | Irregularities in enzyme assays: The case of macrophage migration inhibitory factor. *Bioorganic and Medicinal Chemistry Letters*, **2016**, 26, 2764-2767 | 2.9 | 22 |
| 7 | 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 |
| 6 | Improved Peptide and Protein Torsional Energetics with the OPLSAA Force Field. *Journal of Chemical Theory and Computation*, **2015**, 11, 3499-509 | 6.4 | 391 |
| 5 | Illustrating Concepts in Physical Organic Chemistry with 3D Printed Orbitals. *Journal of Chemical Education*, **2015**, 92, 2113-2116 | 2.4 | 44 |
| 4 | Development of OPLS-AA/M Parameters for Simulations of G Protein-Coupled Receptors and Other Membrane Proteins | | 1 |
| 3 | Structure Determination of Inactive-State GPCRs with a Universal Nanobody | | 2 |
| 2 | Plasticity in Ligand Recognition at Somatostatin Receptors | | 3 |