Brian Joseph Bender

List of Publications by Year
in descending order

14	1,007	1040056 9	1125743 13
papers	citations	h-index	g-index

16	16	16	1693
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Structural Basis of Peptide Binding at Class A G Protein-Coupled Receptors. Molecules, 2022, 27, 210.	3.8	10
2	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. Biochemistry, 2021, 60, 825-846.	2.5	24
3	Computational redesign of a fluorogen activating protein with Rosetta. PLoS Computational Biology, 2021, 17, e1009555.	3.2	0
4	Molecular basis for the evolved instability of a human G-protein coupled receptor. Cell Reports, 2021, 37, 110046.	6.4	5
5	Comparative modeling and docking of chemokine-receptor interactions with Rosetta. Biochemical and Biophysical Research Communications, 2020, 528, 389-397.	2.1	5
6	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
7	Improving homology modeling from low-sequence identity templates in Rosetta: A case study in GPCRs. PLoS Computational Biology, 2020, 16, e1007597.	3.2	37
8	Structural Model of Ghrelin Bound to its G Protein-Coupled Receptor. Structure, 2019, 27, 537-544.e4.	3.3	47
9	Modeling the complete chemokineâ€“receptor interaction. Methods in Cell Biology, 2019, 149, 289-314.	1.1	7
10	Structural basis of ligand binding modes at the neuropeptide Y Y1 receptor. Nature, 2018, 556, 520-524.	27.8	100
11	Î±2A- and Î±2C-Adrenoceptors as Potential Targets for Dopamine and Dopamine Receptor Ligands. Molecular Neurobiology, 2018, 55, 8438-8454.	4.0	26
12	Improved in Vitro Folding of the Y2 G Protein-Coupled Receptor into Bicelles. Frontiers in Molecular Biosciences, 2017, 4, 100.	3.5	22
13	Rosetta and the Design of Ligand Binding Sites. Methods in Molecular Biology, 2016, 1414, 47-62.	0.9	26
14	Protocols for Molecular Modeling with Rosetta3 and RosettaScripts. Biochemistry, 2016, 55, 4748-4763.	2.5	182