

# Brian Joseph Bender

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2036888/publications.pdf>

Version: 2024-02-01

14  
papers

1,007  
citations

1040056

9  
h-index

1125743

13  
g-index

16  
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16  
docs citations

16  
times ranked

1693  
citing authors

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