

Brian J Bender

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

1,275
citations

933447

10
h-index

1125743

13
g-index

15
all docs

15
docs citations

15
times ranked

1841
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	A practical guide to large-scale docking. <i>Nature Protocols</i> , 2021, 16, 4799-4832.	12.0	206
3	Protocols for Molecular Modeling with Rosetta3 and RosettaScripts. <i>Biochemistry</i> , 2016, 55, 4748-4763.	2.5	182
4	Structure, function and pharmacology of human itch GPCRs. <i>Nature</i> , 2021, 600, 170-175.	27.8	101
5	Structural basis of ligand binding modes at the neuropeptide Y Y1 receptor. <i>Nature</i> , 2018, 556, 520-524.	27.8	100
6	Human Cytomegalovirus UL97 Phosphorylates the Viral Nuclear Egress Complex. <i>Journal of Virology</i> , 2015, 89, 523-534.	3.4	56
7	Dynamic and Nucleolin-Dependent Localization of Human Cytomegalovirus UL84 to the Periphery of Viral Replication Compartments and Nucleoli. <i>Journal of Virology</i> , 2014, 88, 11738-11747.	3.4	31
8	Rosetta and the Design of Ligand Binding Sites. <i>Methods in Molecular Biology</i> , 2016, 1414, 47-62.	0.9	26
9	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. <i>Biochemistry</i> , 2021, 60, 825-846.	2.5	24
10	A Mutation Deleting Sequences Encoding the Amino Terminus of Human Cytomegalovirus UL84 Impairs Interaction with UL44 and Capsid Localization. <i>Journal of Virology</i> , 2012, 86, 11066-11077.	3.4	20
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	Viewpoints on the First Transatlantic GPCR Symposium for Early-Career Investigators. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 1705-1711.	4.9	1
14	Computational redesign of a fluorogen activating protein with Rosetta. <i>PLoS Computational Biology</i> , 2021, 17, e1009555.	3.2	0