

Jerome Baudry

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

871
citations

15
h-index

29
g-index

39
ext. papers

1,114
ext. citations

4.6
avg, IF

4.25
L-index

#	Paper	IF	Citations
35	Cross-reactive immunogenicity of group A streptococcal vaccines designed using a recurrent neural network to identify conserved M protein linear epitopes. <i>Vaccine</i> , 2021 , 39, 1773-1779	4.1	1
34	The carboxylation status of osteocalcin has important consequences for its structure and dynamics. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021 , 1865, 129809	4	2
33	Supercomputer-Based Ensemble Docking Drug Discovery Pipeline with Application to Covid-19. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 5832-5852	6.1	71
32	Structure-based group A streptococcal vaccine design: Helical wheel homology predicts antibody cross-reactivity among streptococcal M protein-derived peptides. <i>Journal of Biological Chemistry</i> , 2020 , 295, 3826-3836	5.4	3
31	Supercomputer-Based Ensemble Docking Drug Discovery Pipeline with Application to Covid-19. <i>ChemRxiv</i> , 2020 ,	4.4	7
30	Structure based virtual screening identifies small molecule effectors for the sialoglycan binding protein Hsa. <i>Biochemical Journal</i> , 2020 , 477, 3695-3707	3.8	4
29	Ligand-Dependent Sodium Ion Dynamics within the A Adenosine Receptor: A Molecular Dynamics Study. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 7947-7954	3.4	2
28	Ensemble Docking in Drug Discovery: How Many Protein Configurations from Molecular Dynamics Simulations are Needed To Reproduce Known Ligand Binding?. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 5189-5195	3.4	42
27	GPCR6A Is a Molecular Target for the Natural Products Gallate and EGCG in Green Tea. <i>Molecular Nutrition and Food Research</i> , 2018 , 62, e1700770	5.9	14
26	Ensemble Docking in Drug Discovery. <i>Biophysical Journal</i> , 2018 , 114, 2271-2278	2.9	203
25	Ensemble docking to difficult targets in early-stage drug discovery: Methodology and application to fibroblast growth factor 23. <i>Chemical Biology and Drug Design</i> , 2018 , 91, 491-504	2.9	15
24	Computationally identified novel agonists for GPCR6A. <i>PLoS ONE</i> , 2018 , 13, e0195980	3.7	12
23	Polycystin-1 interacts with TAZ to stimulate osteoblastogenesis and inhibit adipogenesis. <i>Journal of Clinical Investigation</i> , 2018 , 128, 157-174	15.9	32
22	Binding Mechanisms of Electron Transport Proteins with Cyanobacterial Photosystem I: An Integrated Computational and Experimental Model. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 1026-1036	3.4	3
21	Small Molecule Condensin Inhibitors. <i>ACS Infectious Diseases</i> , 2018 , 4, 1737-1745	5.5	4
20	Novel Small Molecule JP-153 Targets the Src-FAK-Paxillin Signaling Complex to Inhibit VEGF-Induced Retinal Angiogenesis. <i>Molecular Pharmacology</i> , 2017 , 91, 1-13	4.3	15
19	Structure-based design of broadly protective group a streptococcal M protein-based vaccines. <i>Vaccine</i> , 2017 , 35, 19-26	4.1	31

18	Identification and Structure-Activity Relationships of Novel Compounds that Potentiate the Activities of Antibiotics in <i>Escherichia coli</i> . <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 6205-6219	8.3	33
17	Thermophilic Enzyme or Mesophilic Enzyme with Enhanced Thermostability: Can We Draw a Line?. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 7086-7094	3.4	2
16	Reviving Antibiotics: Efflux Pump Inhibitors That Interact with AcrA, a Membrane Fusion Protein of the AcrAB-TolC Multidrug Efflux Pump. <i>ACS Infectious Diseases</i> , 2017 , 3, 89-98	5.5	48
15	The quinic acid derivative KZ-41 prevents glucose-induced caspase-3 activation in retinal endothelial cells through an IGF-1 receptor dependent mechanism. <i>PLoS ONE</i> , 2017 , 12, e0180808	3.7	7
14	A computationally identified compound antagonizes excess FGF-23 signaling in renal tubules and a mouse model of hypophosphatemia. <i>Science Signaling</i> , 2016 , 9, ra113	8.8	19
13	Highly Dynamic Anion-Quadrupole Networks in Proteins. <i>Biochemistry</i> , 2016 , 55, 6056-6069	3.2	9
12	Discovery of Novel Nonactive Site Inhibitors of the Prothrombinase Enzyme Complex. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 535-47	6.1	12
11	General trends of dihedral conformational transitions in a globular protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 501-14	4.2	6
10	Evidence for Osteocalcin Binding and Activation of GPRC6A in ECells. <i>Endocrinology</i> , 2016 , 157, 1866-80	4.8	78
9	Ensemble-based docking: From hit discovery to metabolism and toxicity predictions. <i>Bioorganic and Medicinal Chemistry</i> , 2016 , 24, 4928-4935	3.4	30
8	Structural and Functional Evidence for Testosterone Activation of GPRC6A in Peripheral Tissues. <i>Molecular Endocrinology</i> , 2015 , 29, 1759-73		43
7	Discovery of an inhibitor of Z-alpha1 antitrypsin polymerization. <i>PLoS ONE</i> , 2015 , 10, e0126256	3.7	6
6	Polypharmacology and supercomputer-based docking: opportunities and challenges. <i>Molecular Simulation</i> , 2014 , 40, 848-854	2	10
5	Molecular interactions between photosystem I and ferredoxin: an integrated energy frustration and experimental model. <i>Journal of Molecular Recognition</i> , 2014 , 27, 597-608	2.6	11
4	Accelerating Virtual High-Throughput Ligand Docking: current technology and case study on a petascale supercomputer. <i>Concurrency Computation Practice and Experience</i> , 2014 , 26, 1268-1277	1.4	4
3	High-throughput virtual molecular docking with AutoDockCloud. <i>Concurrency Computation Practice and Experience</i> , 2014 , 26, 907-916	1.4	18
2	A phenylalanine rotameric switch for signal-state control in bacterial chemoreceptors. <i>Nature Communications</i> , 2013 , 4, 2881	17.4	29
1	VinaMPI: facilitating multiple receptor high-throughput virtual docking on high-performance computers. <i>Journal of Computational Chemistry</i> , 2013 , 34, 2212-21	3.5	45

