Bian Li

List of Publications by Year
in descending order

20 papers	527 citations	932766 10 h-index	794141 19 g-index
27 all docs	27 docs citations	27 times ranked	884 citing authors

#	Article	IF	Citations
1	Micelleâ€Based Brainâ€Targeted Drug Delivery Enabled by a Nicotine Acetylcholine Receptor Ligand. Angewandte Chemie - International Edition, 2011, 50, 5482-5485.	7.2	124
2	High-Throughput Reclassification of SCN5A Variants. American Journal of Human Genetics, 2020, 107, 111-123.	2.6	88
3	Predicting changes in protein thermodynamic stability upon point mutation with deep 3D convolutional neural networks. PLoS Computational Biology, 2020, 16, e1008291.	1.5	76
4	Predicting the Functional Impact of KCNQ1 Variants of Unknown Significance. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	40
5	Finding the needle in the haystack: towards solving the protein-folding problem computationally. Critical Reviews in Biochemistry and Molecular Biology, 2018, 53, 1-28.	2.3	31
6	Contribution of Cotranslational Folding Defects to Membrane Protein Homeostasis. Journal of the American Chemical Society, 2019, 141, 204-215.	6.6	27
7	Distinct Features of Probands With Early Repolarization and Brugada Syndromes Carrying SCN5A Pathogenic Variants. Journal of the American College of Cardiology, 2021, 78, 1603-1617.	1.2	22
8	The 3D mutational constraint on amino acid sites in the human proteome. Nature Communications, 2022, 13, .	5.8	15
9	Molecular Insights into the D1R Agonist and D2R/D3R Antagonist Effects of the Natural Product (â^')-Stepholidine: Molecular Modeling and Dynamics Simulations. Journal of Physical Chemistry B, 2012, 116, 8121-8130.	1.2	13
10	CASP11 â€“ An Evaluation of a Modular BCL::Fold-Based Protein Structure Prediction Pipeline. PLoS ONE, 2016, 11, e0152517.	1.1	13
11	Structural determinants of cholesterol recognition in helical integral membrane proteins. Biophysical Journal, 2021, 120, 1592-1604.	0.2	12
12	Improving prediction of helixâ€“helix packing in membrane proteins using predicted contact numbers as restraints. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1212-1221.	1.5	9
13	Dominant negative effects of SCN5A missense variants. Genetics in Medicine, 2022, 24, 1238-1248.	1.1	9
14	Accurate Prediction of Contact Numbers for Multi-Spanning Helical Membrane Proteins. Journal of Chemical Information and Modeling, 2016, 56, 423-434.	2.5	7
15	Interfaces Between Alpha-helical Integral Membrane Proteins: Characterization, Prediction, and Docking. Computational and Structural Biotechnology Journal, 2019, 17, 699-711.	1.9	7
16	Building a Hybrid Physical-Statistical Classifier for Predicting the Effect of Variants Related to Protein-Drug Interactions. Structure, 2019, 27, 1469-1481.e3.	1.6	6
17	A Multitask Deep-Learning Method for Predicting Membrane Associations and Secondary Structures of Proteins. Journal of Proteome Research, 2021, 20, 4089-4100.	1.8	6
18	Discovery of novel small-molecule Src kinase inhibitors via a kinase-focused druglikeness rule and structure-based virtual screening. Molecular Simulation, 2014, 40, 341-348.	0.9	1

#	Article	IF	Citations
19	Clinical Characteristics and Electrophysiologic Properties of <i>SCN5A</i> Variants in Fever-Induced Brugada Syndrome. SSRN Electronic Journal, 0, , .	0.4	0
20	Integration of Protein Structure and Population-Scale DNA Sequence Data for Disease Gene Discovery and Variant Interpretation. Annual Review of Biomedical Data Science, 2022, 5, .	2.8	0