Harianto Tjong

List of Publications by Year
in descending order

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31	2,351	331670 21	454955 30
papers	citations	h-index	g-index

34	34	34	3520
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. Nature Biotechnology, 2012, 30, 90-98.	17.5	524
2	TopDom: an efficient and deterministic method for identifying topological domains in genomes. Nucleic Acids Research, 2016, 44, e70-e70.	14.5	246
3	Physical tethering and volume exclusion determine higher-order genome organization in budding yeast. Genome Research, 2012, 22, 1295-1305.	5.5	190
4	Population-based 3D genome structure analysis reveals driving forces in spatial genome organization. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1663-72.	7.1	182
5	DISPLAR: an accurate method for predicting DNA-binding sites on protein surfaces. Nucleic Acids Research, 2007, 35, 1465-1477.	14.5	142
6	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. Cancer Cell, 2021, 39, 694-707.e7.	16.8	115
7	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. Nature Genetics, 2020, 52, 264-272.	21.4	104
8	The three-dimensional genome organization of Drosophila melanogaster through data integration. Genome Biology, 2017, 18, 145.	8.8	86
9	GBr6:Â A Parameterization-Free, Accurate, Analytical Generalized Born Method. Journal of Physical Chemistry B, 2007, 111, 3055-3061.	2.6	84
10	Picky comprehensively detects high-resolution structural variants in nanopore long reads. Nature Methods, 2018, 15, 455-460.	19.0	80
11	Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. Cell Stem Cell, 2019, 24, 462-476.e6.	11.1	72
12	Producing genome structure populations with the dynamic and automated PGS software. Nature Protocols, 2018, 13, 915-926.	12.0	67
13	Prediction of Protein Solubility from Calculation of Transfer Free Energy. Biophysical Journal, 2008, 95, 2601-2609.	0.5	50
14	Spontaneous conformational change and toxin binding in Î±7 acetylcholine receptor: Insight into channel activation and inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8280-8285.	7.1	46
15	GBr6NL: A generalized Born method for accurately reproducing solvation energy of the nonlinear Poisson-Boltzmann equation. Journal of Chemical Physics, 2007, 126, 195102.	3.0	41
16	Exploring the spatial and temporal organization of a cellâ€™s proteome. Journal of Structural Biology, 2011, 173, 483-496.	2.8	36
17	Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. Nature Communications, 2016, 7, 11549.	12.8	36
18	Global reorganization of budding yeast chromosome conformation in different physiological conditions. Journal of Cell Biology, 2016, 212, 321-334.	5.2	36

#	Article	IF	Citations
19	PI2PE: protein interface/interior prediction engine. Nucleic Acids Research, 2007, 35, W357-W362.	14.5	32
20	On the Dielectric Boundary in Poissonâ^'Boltzmann Calculations. Journal of Chemical Theory and Computation, 2008, 4, 507-514.	5.3	30
21	Quantitative Methods to Investigate the 4D Dynamics of Heterochromatic Repair Sites in Drosophila Cells. Methods in Enzymology, 2018, 601, 359-389.	1.0	24
22	The Folding Transition-State Ensemble of a Four-Helix Bundle Protein: Helix Propensity as a Determinant and Macromolecular Crowding as a Probe. Biophysical Journal, 2010, 98, 2273-2280.	0.5	22
23	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. Science Advances, 2020, 6, eaay2078.	10.3	22
24	Comparative 3D Genome Structure Analysis of the Fission and the Budding Yeast. PLoS ONE, 2015, 10, e0119672.	2.5	20
25	The dependence of electrostatic solvation energy on dielectric constants in Poisson-Boltzmann calculations. Journal of Chemical Physics, 2006, 125, 206101.	3.0	16
26	Rational design of a conformationâ€switchable Ca²⁺â€•and Tb³⁺â€binding protein without the use of multiple coupled metalâ€binding sites. FEBS Journal, 2008, 275, 5048-5061.	4.7	12
27	Inverse tuning of metal binding affinity and protein stability by altering charged coordination residues in designed calcium binding proteins. PMC Biophysics, 2009, 2, 11.	2.3	12
28	Accurate Calculations of Binding, Folding, and Transfer Free Energies by a Scaled Generalized Born Method. Journal of Chemical Theory and Computation, 2008, 4, 1733-1744.	5.3	10
29	Electrostatic effects on the folding stability of FKBP12. Protein Engineering, Design and Selection, 2016, 29, 301-308.	2.1	6
30	Modeling Proteinâ€“Protein and Proteinâ€“Nucleic Acid Interactions: Structure, Thermodynamics, and Kinetics. Annual Reports in Computational Chemistry, 2008, , 67-87.	1.7	3
31	Modeling Protein Solubility in Implicit Solvent. , 0, , 191-207.		0