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	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. Cancer Cell, 2021, 39, 694-707.e7.	16.8	115
2	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. Science Advances, 2020, 6, eaay2078.	10.3	22
3	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. Nature Genetics, 2020, 52, 264-272.	21.4	104
4	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
5	Producing genome structure populations with the dynamic and automated PGS software. Nature Protocols, 2018, 13, 915-926.	12.0	67
6	Picky comprehensively detects high-resolution structural variants in nanopore long reads. Nature Methods, 2018, 15, 455-460.	19.0	80
7	Quantitative Methods to Investigate the 4D Dynamics of Heterochromatic Repair Sites in Drosophila Cells. Methods in Enzymology, 2018, 601, 359-389.	1.0	24
8	The three-dimensional genome organization of Drosophila melanogaster through data integration. Genome Biology, 2017, 18, 145.	8.8	86
9	Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. Nature Communications, 2016, 7, 11549.	12.8	36
10	Electrostatic effects on the folding stability of FKBP12. Protein Engineering, Design and Selection, 2016, 29, 301-308.	2.1	6
11	Global reorganization of budding yeast chromosome conformation in different physiological conditions. Journal of Cell Biology, 2016, 212, 321-334.	5.2	36
12	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
13	TopDom: an efficient and deterministic method for identifying topological domains in genomes. Nucleic Acids Research, 2016, 44, e70-e70.	14.5	246
14	Comparative 3D Genome Structure Analysis of the Fission and the Budding Yeast. PLoS ONE, 2015, 10, e0119672.	2.5	20
15	Physical tethering and volume exclusion determine higher-order genome organization in budding yeast. Genome Research, 2012, 22, 1295-1305.	5.5	190
16	Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. Nature Biotechnology, 2012, 30, 90-98.	17.5	524
17	Exploring the spatial and temporal organization of a cellâ€™s proteome. Journal of Structural Biology, 2011, 173, 483-496.	2.8	36
18	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

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19	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
20	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
21	Prediction of Protein Solubility from Calculation of Transfer Free Energy. Biophysical Journal, 2008, 95, 2601-2609.	0.5	50
22	On the Dielectric Boundary in Poissonâ^'Boltzmann Calculations. Journal of Chemical Theory and Computation, 2008, 4, 507-514.	5.3	30
23	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
24	Modeling Proteinâ€“Protein and Proteinâ€“Nucleic Acid Interactions: Structure, Thermodynamics, and Kinetics. Annual Reports in Computational Chemistry, 2008, , 67-87.	1.7	3
25	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
26	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
27	DISPLAR: an accurate method for predicting DNA-binding sites on protein surfaces. Nucleic Acids Research, 2007, 35, 1465-1477.	14.5	142
28	PI2PE: protein interface/interior prediction engine. Nucleic Acids Research, 2007, 35, W357-W362.	14.5	32
29	GBr6:Â A Parameterization-Free, Accurate, Analytical Generalized Born Method. Journal of Physical Chemistry B, 2007, 111, 3055-3061.	2.6	84
30	The dependence of electrostatic solvation energy on dielectric constants in Poisson-Boltzmann calculations. Journal of Chemical Physics, 2006, 125, 206101.	3.0	16
31	Modeling Protein Solubility in Implicit Solvent. , 0, , 191-207.		0