Xiaodong Pang

List of Publications by Year
in descending order

34 papers	1,487 citations	567281 15 h-index	552781 26 g-index
34 all docs	34 docs citations	34 times ranked	2598 citing authors

#	Article	IF	Citations
1	Genetic factors associated with cancer racial disparity â€“ an integrative study across twentyâ€one cancer types. Molecular Oncology, 2020, 14, 2775-2786.	4.6	8
2	Maximizing the reusability of gene expression data by predicting missing metadata. PLoS Computational Biology, 2020, 16, e1007450.	3.2	4
3	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
4	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
5	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
6	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
7	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
8	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
9	The novel BETâ€CBP/p300 dual inhibitor NEO2734 is active in SPOP mutant and wildâ€type prostate cancer. EMBO Molecular Medicine, 2019, 11, e10659.	6.9	56
10	Influenza A M2 Channel Clustering at High Protein/Lipid Ratios: Viral Budding Implications. Biophysical Journal, 2019, 116, 1075-1084.	0.5	33
11	Electrostatic Interactions in Protein Structure, Folding, Binding, and Condensation. Chemical Reviews, 2018, 118, 1691-1741.	47.7	577
12	Rate Constants and Mechanisms of Proteinâ€“Ligand Binding. Annual Review of Biophysics, 2017, 46, 105-130.	10.0	49
13	The dockâ€andâ€coalesce mechanism for the association of a <scp>WASP</scp> disordered region with the Cdc42 <scp>GTP</scp>ase. FEBS Journal, 2017, 284, 3381-3391.	4.7	23
14	Structural modeling for the open state of an NMDA receptor. Journal of Structural Biology, 2017, 200, 369-375.	2.8	13
15	Mechanism and rate constants of the Cdc42 GTPase binding with intrinsically disordered effectors. Proteins: Structure, Function and Bioinformatics, 2016, 84, 674-685.	2.6	17
16	Computational full electron structure study of biological activity in Cyclophilin A. Journal of Biomolecular Structure and Dynamics, 2016, 34, 870-876.	3.5	0
17	Two Pathways Mediate Interdomain Allosteric Regulation in Pin1. Structure, 2015, 23, 237-247.	3.3	70
18	The full electron structure of the FKBP12/FK506 complex. Journal of Biomolecular Structure and Dynamics, 2015, 33, 388-394.	3.5	3

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19	Disorder-to-Order Transition of an Active-Site Loop Mediates the Allosteric Activation of Sortase A. Biophysical Journal, 2015, 109, 1706-1715.	0.5	26
20	Truncated ERG Oncoproteins from TMPRSS2-ERG Fusions Are Resistant to SPOP-Mediated Proteasome Degradation. Molecular Cell, 2015, 59, 904-916.	9.7	129
21	Distinct mechanisms of a phosphotyrosyl peptide binding to two SH2 domains. Journal of Theoretical and Computational Chemistry, 2014, 13, 1440003.	1.8	4
22	Design Rules for Selective Binding of Nuclear Localization Signals to Minor Site of Importin Î±. PLoS ONE, 2014, 9, e91025.	2.5	13
23	Molecular Structure of RADA16-I Designer Self-Assembling Peptide Nanofibers. ACS Nano, 2013, 7, 7562-7572.	14.6	124
24	Activation of signaling receptors: do ligands bind to receptor monomer, dimer, or both?. BMC Biophysics, 2013, 6, 7.	4.4	7
25	Solid-State NMR Evidence for Î²-Hairpin Structure within MAX8 Designer Peptide Nanofibers. Biophysical Journal, 2013, 105, 222-230.	0.5	24
26	Poisson-Boltzmann Calculations: van der Waals or Molecular Surface?. Communications in Computational Physics, 2013, 13, 1-12.	1.7	41
27	A Common Model for Cytokine Receptor Activation: Combined Scissor-Like Rotation and Self-Rotation of Receptor Dimer Induced by Class I Cytokine. PLoS Computational Biology, 2012, 8, e1002427.	3.2	24
28	Prediction and Dissection of Widely-Varying Association Rate Constants of Actin-Binding Proteins. PLoS Computational Biology, 2012, 8, e1002696.	3.2	13
29	Rate constants and mechanisms of intrinsically disordered proteins binding to structured targets. Physical Chemistry Chemical Physics, 2012, 14, 10466.	2.8	75
30	Rationalizing 5000-Fold Differences in Receptor-Binding Rate Constants ofÂFour Cytokines. Biophysical Journal, 2011, 101, 1175-1183.	0.5	20
31	Automated Prediction of Protein Association Rate Constants. Structure, 2011, 19, 1744-1751.	3.3	111
32	Discovery of a potent peptidic cyclophilin A inhibitor Trp-Gly-Pro. European Journal of Medicinal Chemistry, 2011, 46, 1701-1705.	5.5	10
33	A Mathematical Model for Peptide Inhibitor Design. Journal of Computational Biology, 2010, 17, 1081-1093.	1.6	4
34	Two Rules on the Protein-Ligand Interaction. Nature Precedings, 0, , .	0.1	9