Hongchun Li

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4045754/publications.pdf

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		516710	526287
29	946	16	27
papers	citations	h-index	g-index

31	31	31	1216
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	DynOmics: dynamics of structural proteome and beyond. Nucleic Acids Research, 2017, 45, W374-W380.	14.5	135
2	Predicting Lipase Types by Improved Chous Pseudo-Amino Acid Composition. Protein and Peptide Letters, 2008, 15, 1132-1137.	0.9	98
3	ProDy 2.0: increased scale and scope after 10 years of protein dynamics modelling with Python. Bioinformatics, 2021, 37, 3657-3659.	4.1	93
4	Intrinsic dynamics is evolutionarily optimized to enable allosteric behavior. Current Opinion in Structural Biology, 2020, 62, 14-21.	5.7	85
5	iGNM 2.0: the Gaussian network model database for biomolecular structural dynamics. Nucleic Acids Research, 2016, 44, D415-D422.	14.5	71
6	Pharmacologic Suppression of B7-H4 Glycosylation Restores Antitumor Immunity in Immune-Cold Breast Cancers. Cancer Discovery, 2020, 10, 1872-1893.	9.4	66
7	Blocking the interaction between S100A9 and RAGE V domain using CHAPS molecule: A novel route to drug development against cell proliferation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1558-1569.	2.3	51
8	Shared Signature Dynamics Tempered by Local Fluctuations Enables Fold Adaptability and Specificity. Molecular Biology and Evolution, 2019, 36, 2053-2068.	8.9	45
9	Characterization of Differential Dynamics, Specificity, and Allostery of Lipoxygenase Family Members. Journal of Chemical Information and Modeling, 2019, 59, 2496-2508.	5.4	34
10	A novel strategy to block mitotic progression for targeted therapy. EBioMedicine, 2019, 49, 40-54.	6.1	33
11	Discriminating acidic and alkaline enzymes using a random forest model with secondary structure amino acid composition. Process Biochemistry, 2009, 44, 654-660.	3.7	25
12	Molecular Binding Sites Are Located Near the Interface of Intrinsic Dynamics Domains (IDDs). Journal of Chemical Information and Modeling, 2014, 54, 2275-2285.	5.4	23
13	QuartataWeb: Integrated Chemicalâ€“Protein-Pathway Mapping for Polypharmacology and Chemogenomics. Bioinformatics, 2020, 36, 3935-3937.	4.1	23
14	Connecting Neuronal Cell Protective Pathways and Drug Combinations in a Huntingtonâ€™s Disease Model through the Application of Quantitative Systems Pharmacology. Scientific Reports, 2017, 7, 17803.	3.3	22
15	Structural insights into the interaction of human S100B and basic fibroblast growth factor (FGF2): Effects on FGFR1 receptor signaling. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2606-2619.	2.3	21
16	Pharmmaker: Pharmacophore modeling and hit identification based on druggability simulations. Protein Science, 2020, 29, 76-86.	7.6	19
17	Coenzyme Coupling Boosts Charge Transport through Single Bioactive Enzyme Junctions. IScience, 2020, 23, 101001.	4.1	16
18	Dynamic Modulation of Binding Affinity as a Mechanism for Regulating Interferon Signaling. Journal of Molecular Biology, 2017, 429, 2571-2589.	4.2	14

#	Article	IF	Citations
19	Adaptability and specificity: how do proteins balance opposing needs to achieve function?. Current Opinion in Structural Biology, 2021, 67, 25-32.	5.7	11
20	Precise druggability of the PTH type 1 receptor. Nature Chemical Biology, 2022, 18, 272-280.	8.0	11
21	Quantitative Systems Pharmacological Analysis of Drugs of Abuse Reveals the Pleiotropy of Their Targets and the Effector Role of mTORC1. Frontiers in Pharmacology, 2019, 10, 191.	3.5	10
22	Helical structure motifs made searchable for functional peptide design. Nature Communications, 2022, 13, 102.	12.8	10
23	Modulation of Toroidal Proteins Dynamics in Favor of Functional Mechanisms upon Ligand Binding. Biophysical Journal, 2020, 118, 1782-1794.	0.5	9
24	An easily available lysosomal-targeted ratiometric fluorescent probe with aggregation induced emission characteristics for hydrogen polysulfide visualization in acute ulcerative colitis. Materials Chemistry Frontiers, 2021, 5, 7638-7644.	5.9	7
25	The N-terminal substrate-recognition domain of a LonC protease exhibits structural and functional similarity to cytosolic chaperones. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1789-1797.	2.5	6
26	Network-Based Target Prioritization and Drug Candidate Identification for Multiple Sclerosis: From Analyzing â€œOmics Dataâ€•to Druggability Simulations. ACS Chemical Neuroscience, 2021, 12, 917-929.	3.5	5
27	Editorial: Understanding Protein Dynamics, Binding and Allostery for Drug Design. Frontiers in Molecular Biosciences, 2021, 8, 681364.	3.5	2
28	Virtual substrates screening model of triacylglycerol lipase from Bacillus thermocatenulanatus. Wuhan University Journal of Natural Sciences, 2011, 16, 106-112.	0.4	1
29	Dynamic Modulation of Binding as a Mechanism for Regulating Interferon Signaling. Biophysical Journal, 2018, 114, 232a.	0.5	0