Ho-Leung Ng

List of Publications by Year
in descending order

46 papers	3,815 citations	304743 22 h-index	315739 38 g-index
57 all docs	57 docs citations	57 times ranked	5199 citing authors

#	Article	IF	Citations
1	Recent Biophysical Advances in Drug Discovery. Biophysica, 2022, 2, 121-122.	1.4	0
2	Structural studies of full-length receptor tyrosine kinases and their implications for drug design. Advances in Protein Chemistry and Structural Biology, 2021, 124, 311-336.	2.3	2
3	Editorial: Mechanisms of Fluorescent Proteins. Frontiers in Molecular Biosciences, 2021, 8, 701523.	3.5	2
4	Locating ligand binding sites in G-protein coupled receptors using combined information from docking and sequence conservation. PeerJ, 2021, 9, e12219.	2.0	1
5	Mechanisms of allosteric and mixed mode aromatase inhibitors. RSC Chemical Biology, 2021, 2, 892-905.	4.1	5
6	Generative AI Models for Drug Discovery. Topics in Medicinal Chemistry, 2021, , 221-243.	0.8	5
7	An Open Drug Discovery Competition: Experimental Validation of Predictive Models in a Series of Novel Antimalarials. Journal of Medicinal Chemistry, 2021, 64, 16450-16463.	6.4	8
8	Deep neural network affinity model for BACE inhibitors in D3R Grand Challenge 4. Journal of Computer-Aided Molecular Design, 2020, 34, 201-217.	2.9	7
9	In-silico design of peptide inhibitors of K-Ras target in cancer disease. Journal of Biomolecular Structure and Dynamics, 2020, 38, 5488-5499.	3.5	31
10	RORÎ³ Structural Plasticity and Druggability. International Journal of Molecular Sciences, 2020, 21, 5329.	4.1	17
11	Decoding allosteric communication pathways in protein lysine acetyltransferase. International Journal of Biological Macromolecules, 2020, 149, 70-80.	7.5	26
12	Computerâ€Aided Discovery of Novel Human RORÎ³ Inverse Agonists. FASEB Journal, 2020, 34, 1-1.	0.5	0
13	G Proteinâ€“Coupled Estrogen Receptor Production Using an Escherichia coli Cellâ€Free Expression System. Current Protocols in Protein Science, 2019, 97, e88.	2.8	2
14	Recent Insights from Molecular Dynamics Simulations for G Protein-Coupled Receptor Drug Discovery. International Journal of Molecular Sciences, 2019, 20, 4237.	4.1	22
15	A Detailed Protocol for Large-scale Recombinant Expression and Validation of Human FGFR2 with Its Transmembrane and Extracellular Domains in Escherichia coli. Bio-protocol, 2019, 9, e3261.	0.4	0
16	Mutation of Phenylalanine-223 to Leucine Enhances Transformation of Benzo[a]pyrene by Ring-Hydroxylating Dioxygenase of Sphingobium sp. FB3 by increasing Accessibility of the Catalytic Site. Journal of Agricultural and Food Chemistry, 2018, 66, 1206-1213.	5.2	10
17	Protection against Î²â€amyloid neurotoxicity by a nonâ€toxic endogenous Nâ€terminal Î²â€amyloid fragment and its active hexapeptide core sequence. Journal of Neurochemistry, 2018, 144, 201-217.	3.9	23
18	Screening and Identifying Membrane Proteins Favorable for Crystallization. Current Protocols in Protein Science, 2017, 90, 29.19.1-29.19.10.	2.8	0

#	Article	IF	Citations
19	Structural and Biophysical Characterization of the Mycobacterium tuberculosis Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent Tuberculosis Strains and Homologue of the Streptomyces coelicolor Protein KbpA. Biochemistry, 2017, 56, 4015-4027.	2.5	4
20	Recombinant expression in E. coli of human FGFR2 with its transmembrane and extracellular domains. PeerJ, 2017, 5, e3512.	2.0	2
21	Structure-guided wavelength tuning in far-red fluorescent proteins. Current Opinion in Structural Biology, 2016, 39, 124-133.	5.7	14
22	Simulations reveal increased fluctuations in estrogen receptor-alpha conformation upon antagonist binding. Journal of Molecular Graphics and Modelling, 2016, 69, 72-77.	2.4	13
23	A bright cyan-excitable orange fluorescent protein facilitates dual-emission microscopy and enhances bioluminescence imaging in vivo. Nature Biotechnology, 2016, 34, 760-767.	17.5	221
24	Structure of a TCR-Mimic Antibody with Target Predicts Pharmacogenetics. Journal of Molecular Biology, 2016, 428, 194-205.	4.2	48
25	Largeâ€scale identification of membrane proteins with properties favorable for crystallization. Protein Science, 2015, 24, 1756-1763.	7.6	2
26	Non-invasive intravital imaging of cellular differentiation with a bright red-excitable fluorescent protein. Nature Methods, 2014, 11, 572-578.	19.0	196
27	Ferritin Protein Nanocage Ion Channels. Journal of Biological Chemistry, 2012, 287, 13016-13025.	3.4	63
28	Allosteric Activation Mechanism of the Mycobacterium tuberculosis Receptor Ser/Thr Protein Kinase, PknB. Structure, 2010, 18, 1667-1677.	3.3	50
29	Automated electronâ€density sampling reveals widespread conformational polymorphism in proteins. Protein Science, 2010, 19, 1420-1431.	7.6	155
30	Functional and Structural Characterization of A New Monomeric Far-Red Fluorescent Protein. Biophysical Journal, 2010, 98, 215a.	0.5	0
31	Moving Metal Ions through Ferritinâ€'Protein Nanocages from Three-Fold Pores to Catalytic Sites. Journal of the American Chemical Society, 2010, 132, 14562-14569.	13.7	117
32	Autofluorescent Proteins with Excitation in the Optical Window for Intravital Imaging in Mammals. Chemistry and Biology, 2009, 16, 1169-1179.	6.0	244
33	Saccharomyces cerevisiae septins: Supramolecular organization of heterooligomers and the mechanism of filament assembly. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8274-8279.	7.1	268
34	A Conserved Dimer and Global Conformational Changes in the Structure of apo-PknE Ser/Thr Protein Kinase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2006, 360, 409-420.	4.2	57
35	Mycobacterium tuberculosis Protein Tyrosine Phosphatase PtpB Structure Reveals a Diverged Fold and a Buried Active Site. Structure, 2005, 13, 1625-1634.	3.3	72
36	An Alternate Conformation and a Third Metal in PstP/Ppp, the M. tuberculosis PP2C-Family Ser/Thr Protein Phosphatase. Structure, 2004, 12, 1947-1954.	3.3	96

#	Article	IF	Citations
37	Sensor Domain of the Mycobacterium tuberculosis Receptor Ser/Thr Protein Kinase, PknD, forms a Highly Symmetric Î² Propeller. Journal of Molecular Biology, 2004, 339, 459-469.	4.2	65
38	An Unusual Sugar Conformation in the Structure of an RNA/DNA Decamer of the Polypurine Tract May Affect Recognition by RNase H. Journal of Molecular Biology, 2003, 334, 653-665.	4.2	42
39	Mediation of the A/B-DNA helix transition by G-tracts in the crystal structure of duplex CATGGGCCCATG. Nucleic Acids Research, 2002, 30, 4061-4067.	14.5	47
40	Mildly eccentric 'E-DNA'. , 2001, 8, 107-107.		6
41	DNA structure from A to B. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 6986-6988.	7.1	75
42	The structure of a stable intermediate in the A left-right-arrow B DNA helix transition. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 2035-2039.	7.1	104
43	Local conformational variations observed in B-DNA crystals do not improve base stacking: computational analysis of base stacking in a d(CATGGGCCCATG)2 BleftrightarrowA intermediate crystal structure. Nucleic Acids Research, 2000, 28, 4893-4902.	14.5	53
44	Detecting Protein Function and Protein-Protein Interactions from Genome Sequences. Science, 1999, 285, 751-753.	12.6	1,595
45	Structure of a dicationic monoimidazole lexitropsin bound to DNA. Biochemistry, 1995, 34, 16654-16661.	2.5	31
46	A Bright, Nontoxic, and Non-aggregating red Fluorescent Protein for Long-Term Labeling of Fine Structures in Neurons. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	4