

Ho-Leung Ng

List of Publications by Year in descending order

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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	Detecting Protein Function and Protein-Protein Interactions from Genome Sequences. <i>Science</i> , 1999, 285, 751-753.	12.6	1,595
2	<i>Saccharomyces cerevisiae</i> septins: Supramolecular organization of heterooligomers and the mechanism of filament assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8274-8279.	7.1	268
3	Autofluorescent Proteins with Excitation in the Optical Window for Intravital Imaging in Mammals. <i>Chemistry and Biology</i> , 2009, 16, 1169-1179.	6.0	244
4	A bright cyan-excitable orange fluorescent protein facilitates dual-emission microscopy and enhances bioluminescence imaging in vivo. <i>Nature Biotechnology</i> , 2016, 34, 760-767.	17.5	221
5	Non-invasive intravital imaging of cellular differentiation with a bright red-excitable fluorescent protein. <i>Nature Methods</i> , 2014, 11, 572-578.	19.0	196
6	Automated electron density sampling reveals widespread conformational polymorphism in proteins. <i>Protein Science</i> , 2010, 19, 1420-1431.	7.6	155
7	Moving Metal Ions through Ferritin Protein Nanocages from Three-Fold Pores to Catalytic Sites. <i>Journal of the American Chemical Society</i> , 2010, 132, 14562-14569.	13.7	117
8	The structure of a stable intermediate in the A to B DNA helix transition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 2035-2039.	7.1	104
9	An Alternate Conformation and a Third Metal in PstP/Ppp, the <i>M. tuberculosis</i> PP2C-Family Ser/Thr Protein Phosphatase. <i>Structure</i> , 2004, 12, 1947-1954.	3.3	96
10	DNA structure from A to B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 6986-6988.	7.1	75
11	<i>Mycobacterium tuberculosis</i> Protein Tyrosine Phosphatase PtpB Structure Reveals a Diverged Fold and a Buried Active Site. <i>Structure</i> , 2005, 13, 1625-1634.	3.3	72
12	Sensor Domain of the <i>Mycobacterium tuberculosis</i> Receptor Ser/Thr Protein Kinase, PknD, forms a Highly Symmetric β^2 Propeller. <i>Journal of Molecular Biology</i> , 2004, 339, 459-469.	4.2	65
13	Ferritin Protein Nanocage Ion Channels. <i>Journal of Biological Chemistry</i> , 2012, 287, 13016-13025.	3.4	63
14	A Conserved Dimer and Global Conformational Changes in the Structure of apo-PknE Ser/Thr Protein Kinase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2006, 360, 409-420.	4.2	57
15	Local conformational variations observed in B-DNA crystals do not improve base stacking: computational analysis of base stacking in a d(CATGGGCCCATG) ₂ B-DNA intermediate crystal structure. <i>Nucleic Acids Research</i> , 2000, 28, 4893-4902.	14.5	53
16	Allosteric Activation Mechanism of the <i>Mycobacterium tuberculosis</i> Receptor Ser/Thr Protein Kinase, PknB. <i>Structure</i> , 2010, 18, 1667-1677.	3.3	50
17	Structure of a TCR-Mimic Antibody with Target Predicts Pharmacogenetics. <i>Journal of Molecular Biology</i> , 2016, 428, 194-205.	4.2	48
18	Mediation of the A/B-DNA helix transition by G-tracts in the crystal structure of duplex CATGGGCCCATG. <i>Nucleic Acids Research</i> , 2002, 30, 4061-4067.	14.5	47

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19	An Unusual Sugar Conformation in the Structure of an RNA/DNA Decamer of the Polypurine Tract May Affect Recognition by RNase H. <i>Journal of Molecular Biology</i> , 2003, 334, 653-665.	4.2	42
20	Structure of a dicationic monoimidazole lexitropsin bound to DNA. <i>Biochemistry</i> , 1995, 34, 16654-16661.	2.5	31
21	In-silico design of peptide inhibitors of K-Ras target in cancer disease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 5488-5499.	3.5	31
22	Decoding allosteric communication pathways in protein lysine acetyltransferase. <i>International Journal of Biological Macromolecules</i> , 2020, 149, 70-80.	7.5	26
23	Protection against β -amyloid neurotoxicity by a non-toxic endogenous N-terminal β -amyloid fragment and its active hexapeptide core sequence. <i>Journal of Neurochemistry</i> , 2018, 144, 201-217.	3.9	23
24	Recent Insights from Molecular Dynamics Simulations for G Protein-Coupled Receptor Drug Discovery. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4237.	4.1	22
25	ROR β Structural Plasticity and Druggability. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5329.	4.1	17
26	Structure-guided wavelength tuning in far-red fluorescent proteins. <i>Current Opinion in Structural Biology</i> , 2016, 39, 124-133.	5.7	14
27	Simulations reveal increased fluctuations in estrogen receptor-alpha conformation upon antagonist binding. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 69, 72-77.	2.4	13
28	Mutation of Phenylalanine-223 to Leucine Enhances Transformation of Benzo[<i>a</i>]pyrene by Ring-Hydroxylating Dioxygenase of <i>Sphingobium</i> sp. FB3 by increasing Accessibility of the Catalytic Site. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 1206-1213.	5.2	10
29	An Open Drug Discovery Competition: Experimental Validation of Predictive Models in a Series of Novel Antimalarials. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 16450-16463.	6.4	8
30	Deep neural network affinity model for BACE inhibitors in D3R Grand Challenge 4. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 201-217.	2.9	7
31	Mildly eccentric 'E-DNA'. , 2001, 8, 107-107.		6
32	Mechanisms of allosteric and mixed mode aromatase inhibitors. <i>RSC Chemical Biology</i> , 2021, 2, 892-905.	4.1	5
33	Generative AI Models for Drug Discovery. <i>Topics in Medicinal Chemistry</i> , 2021, , 221-243.	0.8	5
34	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. <i>Biochemistry</i> , 2017, 56, 4015-4027.	2.5	4
35	A Bright, Nontoxic, and Non-aggregating red Fluorescent Protein for Long-Term Labeling of Fine Structures in Neurons. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	3.7	4
36	Large-scale identification of membrane proteins with properties favorable for crystallization. <i>Protein Science</i> , 2015, 24, 1756-1763.	7.6	2

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37	G Protein–Coupled Estrogen Receptor Production Using an <i>Escherichia coli</i> Cell-Free Expression System. <i>Current Protocols in Protein Science</i> , 2019, 97, e88.	2.8	2
38	Structural studies of full-length receptor tyrosine kinases and their implications for drug design. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 124, 311-336.	2.3	2
39	Editorial: Mechanisms of Fluorescent Proteins. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 701523.	3.5	2
40	Recombinant expression in <i>E. coli</i> of human FGFR2 with its transmembrane and extracellular domains. <i>PeerJ</i> , 2017, 5, e3512.	2.0	2
41	Locating ligand binding sites in G-protein coupled receptors using combined information from docking and sequence conservation. <i>PeerJ</i> , 2021, 9, e12219.	2.0	1
42	Functional and Structural Characterization of A New Monomeric Far-Red Fluorescent Protein. <i>Biophysical Journal</i> , 2010, 98, 215a.	0.5	0
43	Screening and Identifying Membrane Proteins Favorable for Crystallization. <i>Current Protocols in Protein Science</i> , 2017, 90, 29.19.1-29.19.10.	2.8	0
44	A Detailed Protocol for Large-scale Recombinant Expression and Validation of Human FGFR2 with Its Transmembrane and Extracellular Domains in <i>Escherichia coli</i> . <i>Bio-protocol</i> , 2019, 9, e3261.	0.4	0
45	Computer-Aided Discovery of Novel Human ROR ¹ Inverse Agonists. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0
46	Recent Biophysical Advances in Drug Discovery. <i>Biophysica</i> , 2022, 2, 121-122.	1.4	0