Boon Chong Goh

List of Publications by Year
in descending order

28 papers	907 citations	623734 14 h-index	677142 22 g-index
30 all docs	30 docs citations	30 times ranked	1716 citing authors

#	Article	IF	Citations
1	Crystal structure and functional analysis of mycobacterial erythromycin resistance methyltransferase Erm38 reveals its RNA-binding site. Journal of Biological Chemistry, 2022, 298, 101571.	3.4	2
2	Novel Phage Lysin Abp013 against Acinetobacter baumannii. Antibiotics, 2022, 11, 169.	3.7	11
3	inPhocus: Current State and Challenges of Phage Research in Singapore. Phage, 2022, 3, 6-11.	1.7	0
4	All-Atom MD Simulations of the HBV Capsid Complexed with AT130 Reveal Secondary and Tertiary Structural Changes and Mechanisms of Allostery. Viruses, 2021, 13, 564.	3.3	15
5	Cutibacterium acnes : Much ado about maybe nothing much. Experimental Dermatology, 2021, 30, 1471-1476.	2.9	6
6	Crystal structure of the periplasmic sensor domain of histidine kinase VbrK suggests indirect sensing of Î²-lactam antibiotics. Journal of Structural Biology, 2020, 212, 107610.	2.8	7
7	Turning an Asparaginyl Endopeptidase into a Peptide Ligase. ACS Catalysis, 2020, 10, 8825-8834.	11.2	29
8	Engineered Lysins With Customized Lytic Activities Against Enterococci and Staphylococci. Frontiers in Microbiology, 2020, 11, 574739.	3.5	18
9	The SiaABC threonine phosphorylation pathway controls biofilm formation in response to carbon availability in Pseudomonas aeruginosa. PLoS ONE, 2020, 15, e0241019.	2.5	6
10	Structural determinants for peptide-bond formation by asparaginyl ligases. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11737-11746.	7.1	81
11	Computational de novo design of antibodies binding to a peptide with high affinity. Biotechnology and Bioengineering, 2017, 114, 1331-1342.	3.3	25
12	Structural Mimicry of the Dengue Virus Envelope Glycoprotein Revealed by the Crystallographic Study of an Idiotypeâ€“Anti-idiotype Fab Complex. Journal of Virology, 2017, 91, .	3.4	6
13	Length of encapsidated cargo impacts stability and structure ofin vitroassembled alphavirus core-like particles. Journal of Physics Condensed Matter, 2017, 29, 484003.	1.8	19
14	Allosteric pyruvate kinase-based â€œlogic gateâ€•synergistically senses energy and sugar levels in Mycobacterium tuberculosis. Nature Communications, 2017, 8, 1986.	12.8	49
15	de novo Design and in silico Optimization of Antibody-Like Binders Targeting Ebola Viral Antigen. Biophysical Journal, 2016, 110, 537a.	0.5	0
16	Elucidating the Structure, Dynamics and Functions of an Immature Retrovirus in Atomistic Detail. Biophysical Journal, 2016, 110, 383a.	0.5	0
17	Contributions of Charged Residues in Structurally Dynamic Capsid Surface Loops to Rous Sarcoma Virus Assembly. Journal of Virology, 2016, 90, 5700-5714.	3.4	12
18	All-Atom Molecular Dynamics of Virus Capsids as Drug Targets. Journal of Physical Chemistry Letters, 2016, 7, 1836-1844.	4.6	73

#	Article	IF	Citations
19	Computational Methodologies for Real-Space Structural Refinement of Large Macromolecular Complexes. Annual Review of Biophysics, 2016, 45, 253-278.	10.0	67
20	Elucidation of Lipid Binding Sites on Lung Surfactant Protein A Using X-ray Crystallography, Mutagenesis, and Molecular Dynamics Simulations. Biochemistry, 2016, 55, 3692-3701.	2.5	25
21	Atomic detail visualization of photosynthetic membranes with GPU-accelerated ray tracing. Parallel Computing, 2016, 55, 17-27.	2.1	37
22	Unraveling the Dual Role of Surfactant Protein a at Atomistic Detail. Biophysical Journal, 2015, 108, 255a-256a.	0.5	0
23	Atomic Modeling of an Immature Retroviral Lattice Using Molecular Dynamics and Mutagenesis. Structure, 2015, 23, 1414-1425.	3.3	35
24	Molecular dynamics simulations of large macromolecular complexes. Current Opinion in Structural Biology, 2015, 31, 64-74.	5.7	347
25	Effect of Two Point Mutations in Lung Surfactant Protein-D on Enhancing its Inhibition Activity Against Influenza a Virus. Biophysical Journal, 2013, 104, 556a.	0.5	0
26	Molecular Mechanisms of Inhibition of Influenza by Surfactant Protein D Revealed by Large-Scale Molecular Dynamics Simulation. Biochemistry, 2013, 52, 8527-8538.	2.5	30
27	Mechanism of Interaction Between Lung Surfactant Protein-D and Influenza A Virus Hemagglutinin. Biophysical Journal, 2012, 102, 63a.	0.5	0
28	The mechanism of antiparallel Î²-sheet formation based on conditioned self-avoiding walk. European Physical Journal E, 2012, 35, 9704.	1.6	6