Lucile MoyniÃ©

List of Publications by Year
in descending order

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23
papers

1,323
citations

623734
14
h-index

642732
23
g-index

25
all docs

25
docs citations

25
times ranked

2816
citing authors

#	Article	IF	Citations
1	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
2	Porins and small-molecule translocation across the outer membrane of Gram-negative bacteria. Nature Reviews Microbiology, 2020, 18, 164-176.	28.6	225
3	Neutralizing nanobodies bind SARS-CoV-2 spike RBD and block interaction with ACE2. Nature Structural and Molecular Biology, 2020, 27, 846-854.	8.2	434
4	The complex of ferric-enterobactin with its transporter from Pseudomonas aeruginosa suggests a two-site model. Nature Communications, 2019, 10, 3673.	12.8	62
5	Complexes formed by the siderophore-based monosulfactam antibiotic BAL30072 and their interaction with the outer membrane receptor PiuA of P. aeruginosa. BioMetals, 2019, 32, 155-170.	4.1	8
6	Promysalin Elicits Species-Selective Inhibition of <i>Pseudomonas aeruginosa</i> by Targeting Succinate Dehydrogenase. Journal of the American Chemical Society, 2018, 140, 1774-1782.	13.7	63
7	TonB-Dependent Receptor Repertoire of Pseudomonas aeruginosa for Uptake of Siderophore-Drug Conjugates. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	95
8	A Key Role for the Periplasmic PfeE Esterase in Iron Acquisition <i>via</i> the Siderophore Enterobactin in <i>Pseudomonas aeruginosa</i>. ACS Chemical Biology, 2018, 13, 2603-2614.	3.4	30
9	Preacinetobactin not acinetobactin is essential for iron uptake by the BauA transporter of the pathogen Acinetobacter baumannii. ELife, 2018, 7, .	6.0	41
10	Structure and Function of the PiuA and PirA Siderophore-Drug Receptors from Pseudomonas aeruginosa and Acinetobacter baumannii. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	78
11	Investigation of Siderophore-Monobactam Antibiotic Derivatives: Their Iron(III)-Complexes and Binding to Receptors. Biophysical Journal, 2017, 112, 551a-552a.	0.5	1
12	Using the pimeloyl-CoA synthetase adenylation fold to synthesize fatty acid thioesters. Nature Chemical Biology, 2017, 13, 660-667.	8.0	21
13	MOMP from Campylobacter jejuni Is a Trimer of 18-Stranded Î²-Barrel Monomers with a Ca 2+ Ion Bound at the Constriction Zone. Journal of Molecular Biology, 2016, 428, 4528-4543.	4.2	36
14	A Substrate Mimic Allows High-Throughput Assay of the FabA Protein and Consequently the Identification of a Novel Inhibitor of Pseudomonas aeruginosa FabA. Journal of Molecular Biology, 2016, 428, 108-120.	4.2	8
15	Molecular Basis of Filtering Carbapenems by Porins from Î²-Lactam-resistant Clinical Strains of Escherichia coli. Journal of Biological Chemistry, 2016, 291, 2837-2847.	3.4	65
16	Structure of<i>Mycobacterium tuberculosis</i>nucleoside diphosphate kinase R80N mutant in complex with citrate. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 40-43.	0.8	6
17	Structural studies of proteins involved in the activity of novel antibiotics. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C710-C710.	0.1	0
18	Structural Insights into the Mechanism and Inhibition of the Î²-Hydroxydecanoyl-Acyl Carrier Protein Dehydratase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2013, 425, 365-377.	4.2	30

#	ARTICLE	IF	CITATIONS
19	Discovery of an Allosteric Inhibitor Binding Site in 3-Oxo-acyl-ACP Reductase from <i>Pseudomonas aeruginosa</i>. ACS Chemical Biology, 2013, 8, 2518-2527.	3.4	38
20	Intersubunit Ionic Interactions Stabilize the Nucleoside Diphosphate Kinase of Mycobacterium tuberculosis. PLoS ONE, 2013, 8, e57867.	2.5	12
21	Functional significance of four successive glycine residues in the pyrophosphate binding loop of fungal 6â€oxopurine phosphoribosyltransferases. Protein Science, 2012, 21, 1185-1196.	7.6	9
22	An intersubunit disulfide bridge stabilizes the tetrameric nucleoside diphosphate kinase of <i>Aquifex aeolicus</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1658-1668.	2.6	8
23	The structure of the Escherichia coli nucleoside diphosphate kinase reveals a new quaternary architecture for this enzyme family. Proteins: Structure, Function and Bioinformatics, 2007, 67, 755-765.	2.6	32