## Lucile Moynié

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
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	TonB-Dependent Receptor Repertoire of Pseudomonas aeruginosa for Uptake of Siderophore-Drug Conjugates. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	95
4	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
5	Molecular Basis of Filtering Carbapenems by Porins from β-Lactam-resistant Clinical Strains of Escherichia coli. Journal of Biological Chemistry, 2016, 291, 2837-2847.	3.4	65
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	The complex of ferric-enterobactin with its transporter from Pseudomonas aeruginosa suggests a two-site model. Nature Communications, 2019, 10, 3673.	12.8	62
8	Preacinetobactin not acinetobactin is essential for iron uptake by the BauA transporter of the pathogen Acinetobacter baumannii. ELife, 2018, 7, .	6.0	41
9	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
10	MOMP from Campylobacter jejuni Is a Trimer of 18-Stranded β-Barrel Monomers with a Ca 2+ Ion Bound at the Constriction Zone. Journal of Molecular Biology, 2016, 428, 4528-4543.	4.2	36
11	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
12	Structural Insights into the Mechanism and Inhibition of the β-Hydroxydecanoyl-Acyl Carrier Protein Dehydratase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2013, 425, 365-377.	4.2	30
13	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
14	Using the pimeloyl-CoA synthetase adenylation fold to synthesize fatty acid thioesters. Nature Chemical Biology, 2017, 13, 660-667.	8.0	21
15	Intersubunit Ionic Interactions Stabilize the Nucleoside Diphosphate Kinase of Mycobacterium tuberculosis. PLoS ONE, 2013, 8, e57867.	2.5	12
16	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
17	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
18	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

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19	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
20	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
21	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
22	Investigation of Siderophore-Monobactam Antibiotic Derivatives: Their Iron(III)-Complexes and Binding to Receptors. Biophysical Journal, 2017, 112, 551a-552a.	0.5	1
23	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