

Stephanie Petrella

List of Publications by Year in descending order

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28
papers

1,319
citations

430874

18
h-index

526287

27
g-index

28
all docs

28
docs citations

28
times ranked

1865
citing authors

#	ARTICLE	IF	CITATIONS
1	Topoisomerase I (TOP1) dynamics: conformational transition from open to closed states. <i>Nature Communications</i> , 2022, 13, 59.	12.8	11
2	A systematic review of <i>Mycobacterium leprae</i> DNA gyrase mutations and their impact on fluoroquinolone resistance. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1601-1612.	6.0	11
3	Structure-Based Drug Design for Tuberculosis: Challenges Still Ahead. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 4248.	2.5	9
4	Overall Structures of <i>Mycobacterium tuberculosis</i> DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. <i>Structure</i> , 2019, 27, 579-589.e5.	3.3	24
5	Description of compensatorygyrA mutations restoring fluoroquinolone susceptibility in <i>Mycobacterium tuberculosis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2428-2431.	3.0	9
6	Comparative study of enzymatic activities of new KatG mutants from low- and high-level isoniazid-resistant clinical isolates of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2016, 100, 15-24.	1.9	17
7	Synthesis and evaluation of original bioisosteres of bacterial type IIA topoisomerases inhibitors. <i>Canadian Journal of Chemistry</i> , 2016, 94, 240-250.	1.1	0
8	<i>Mycobacterium tuberculosis</i> DNA gyrase possesses two functional GyrA-boxes. <i>Biochemical Journal</i> , 2013, 455, 285-294.	3.7	29
9	<i>Mycobacterium tuberculosis</i> DNA gyrase ATPase domain structures suggest a dissociative mechanism that explains how ATP hydrolysis is coupled to domain motion. <i>Biochemical Journal</i> , 2013, 456, 263-273.	3.7	38
10	Extending the Definition of the GyrB Quinolone Resistance-Determining Region in <i>Mycobacterium tuberculosis</i> DNA Gyrase for Assessing Fluoroquinolone Resistance in <i>M. tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1990-1996.	3.2	65
11	New Mutations in the <i>Mycobacterial</i> ATP Synthase: New Insights into the Binding of the Diarylquinoline TMC207 to the ATP Synthase C-Ring Structure. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2326-2334.	3.2	99
12	Purification, crystallization and preliminary X-ray crystallographic studies of the <i>Mycobacterium tuberculosis</i> DNA gyrase CTD. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 178-180.	0.7	8
13	DNA Gyrase Inhibition Assays Are Necessary To Demonstrate Fluoroquinolone Resistance Secondary to gyrB Mutations in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4524-4529.	3.2	33
14	Crystal Structure of the Pyrazinamidase of <i>Mycobacterium tuberculosis</i> : Insights into Natural and Acquired Resistance to Pyrazinamide. <i>PLoS ONE</i> , 2011, 6, e15785.	2.5	116
15	Conservation of HHV-6 DNA polymerase processivity factor sequence and predicted structure suggests it as a target for antiviral development. <i>Antiviral Research</i> , 2010, 86, 316-319.	4.1	2
16	Specific Structural Features of the N-Acetylmuramoyl-L-Alanine Amidase AmiD from <i>Escherichia coli</i> and Mechanistic Implications for Enzymes of This Family. <i>Journal of Molecular Biology</i> , 2010, 397, 249-259.	4.2	45
17	Structural Insights into the Quinolone Resistance Mechanism of <i>Mycobacterium tuberculosis</i> DNA Gyrase. <i>PLoS ONE</i> , 2010, 5, e12245.	2.5	118
18	Purification, crystallization and preliminary X-ray diffraction experiments on the breakage-reunion domain of the DNA gyrase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1182-1186.	0.7	10

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19	Crystal structure and activity of <i>Bacillus subtilis</i> Yoj (EXLX1), a bacterial expansin that promotes root colonization. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16876-16881.	7.1	175
20	Genetic and Structural Insights into the Dissemination Potential of the Extremely Broad-Spectrum Class A β -Lactamase KPC-2 Identified in an <i>Escherichia coli</i> Strain and an <i>Enterobacter cloacae</i> Strain Isolated from the Same Patient in France. Antimicrobial Agents and Chemotherapy, 2008, 52, 3725-3736.	3.2	89
21	Expression and Purification of an Active Form of the Mycobacterium leprae DNA Gyrase and Its Inhibition by Quinolones. Antimicrobial Agents and Chemotherapy, 2007, 51, 1643-1648.	3.2	25
22	Crystal Structure of the Bacillus subtilis Penicillin-binding Protein 4a, and its Complex with a Peptidoglycan Mimetic Peptide. Journal of Molecular Biology, 2007, 371, 528-539.	4.2	50
23	Different Mutations in the HHV-6 DNA Polymerase Gene Accounting for Resistance to Foscarnet. Antiviral Therapy, 2007, 12, 877-888.	1.0	35
24	Characterization of the chromosomal class A β -lactamase CKO from <i>Citrobacter koseri</i> . FEMS Microbiology Letters, 2006, 254, 285-292.	1.8	13
25	Genetic Basis for Natural and Acquired Resistance to the Diarylquinoline R207910 in Mycobacteria. Antimicrobial Agents and Chemotherapy, 2006, 50, 2853-2856.	3.2	125
26	Crystal Structure of the Actinomadura R39 DD-peptidase Reveals New Domains in Penicillin-binding Proteins. Journal of Biological Chemistry, 2005, 280, 31249-31256.	3.4	47
27	Crystal structures of the class D β -lactamase OXA-13 in the native form and in complex with meropenem. Journal of Molecular Biology, 2001, 310, 859-874.	4.2	64
28	Novel Class A β -Lactamase Sed-1 from <i>Citrobacter sedlakii</i> : Genetic Diversity of β -Lactamases within the <i>Citrobacter</i> Genus. Antimicrobial Agents and Chemotherapy, 2001, 45, 2287-2298.	3.2	52