Stephanie Petrella

List of Publications by Year
in descending order

28	1,319	430874 18	526287 27
papers	citations	h-index	g-index

28	28	28	1865
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Crystal structure and activity of Bacillus subtilis YoaJ (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
2	Genetic Basis for Natural and Acquired Resistance to the Diarylquinoline R207910 in Mycobacteria. Antimicrobial Agents and Chemotherapy, 2006, 50, 2853-2856.	3.2	125
3	Structural Insights into the Quinolone Resistance Mechanism of Mycobacterium tuberculosis DNA Gyrase. PLoS ONE, 2010, 5, e12245.	2.5	118
4	Crystal Structure of the Pyrazinamidase of Mycobacterium tuberculosis: Insights into Natural and Acquired Resistance to Pyrazinamide. PLoS ONE, 2011, 6, e15785.	2.5	116
5	New Mutations in the Mycobacterial ATP Synthase: New Insights into the Binding of the Diarylquinoline TMC207 to the ATP Synthase C-Ring Structure. Antimicrobial Agents and Chemotherapy, 2012, 56, 2326-2334.	3.2	99
6	Genetic and Structural Insights into the Dissemination Potential of the Extremely Broad-Spectrum Class A Î²-Lactamase KPC-2 Identified in an Escherichia coli Strain and an Enterobacter cloacae Strain Isolated from the Same Patient in France. Antimicrobial Agents and Chemotherapy, 2008, 52, 3725-3736.	3.2	89
7	Extending the Definition of the GyrB Quinolone Resistance-Determining Region in Mycobacterium tuberculosis DNA Gyrase for Assessing Fluoroquinolone Resistance in M. tuberculosis. Antimicrobial Agents and Chemotherapy, 2012, 56, 1990-1996.	3.2	65
8	Crystal structures of the class D Î²-lactamase OXA-13 in the native form and in complex with meropenem. Journal of Molecular Biology, 2001, 310, 859-874.	4.2	64
9	Novel Class A Î²-Lactamase Sed-1 from Citrobacter sedlakii : Genetic Diversity of Î²-Lactamases within the Citrobacter Genus. Antimicrobial Agents and Chemotherapy, 2001, 45, 2287-2298.	3.2	52
10	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
11	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
12	Specific Structural Features of the N-Acetylmuramoyl-l-Alanine Amidase AmiD from Escherichia coli and Mechanistic Implications for Enzymes of This Family. Journal of Molecular Biology, 2010, 397, 249-259.	4.2	45
13	Mycobacterium tuberculosis DNA gyrase ATPase domain structures suggest a dissociative mechanism that explains how ATP hydrolysis is coupled to domain motion. Biochemical Journal, 2013, 456, 263-273.	3.7	38
14	Different Mutations in the HHV-6 DNA Polymerase Gene Accounting for Resistance to Foscarnet. Antiviral Therapy, 2007, 12, 877-888.	1.0	35
15	DNA Gyrase Inhibition Assays Are Necessary To Demonstrate Fluoroquinolone Resistance Secondary to gyrB Mutations in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2011, 55, 4524-4529.	3.2	33
16	Mycobacterium tuberculosis DNA gyrase possesses two functional GyrA-boxes. Biochemical Journal, 2013, 455, 285-294.	3.7	29
17	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
18	Overall Structures of Mycobacterium tuberculosis DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. Structure, 2019, 27, 579-589.e5.	3.3	24

#	Article	IF	Citations
19	Comparative study of enzymatic activities of new KatG mutants from low- and high-level isoniazid-resistant clinical isolates of Mycobacterium tuberculosis. Tuberculosis, 2016, 100, 15-24.	1.9	17
20	Characterization of the chromosomal class A ÃŽÂ²-lactamase CKO fromCitrobacter koseri. FEMS Microbiology Letters, 2006, 254, 285-292.	1.8	13
21	A systematic review of Mycobacterium leprae DNA gyrase mutations and their impact on fluoroquinolone resistance. Clinical Microbiology and Infection, 2021, 27, 1601-1612.	6.0	11
22	Topoisomerase I (TOP1) dynamics: conformational transition from open to closed states. Nature Communications, 2022, 13, 59.	12.8	11
23	Purification, crystallization and preliminary X-ray diffraction experiments on the breakage-reunion domain of the DNA gyrase fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1182-1186.	0.7	10
24	Description of compensatorygyrAmutations restoring fluoroquinolone susceptibility inMycobacterium tuberculosis. Journal of Antimicrobial Chemotherapy, 2016, 71, 2428-2431.	3.0	9
25	Structure-Based Drug Design for Tuberculosis: Challenges Still Ahead. Applied Sciences (Switzerland), 2020, 10, 4248.	2.5	9
26	Purification, crystallization and preliminary X-ray crystallographic studies of theMycobacterium tuberculosisDNA gyrase CTD. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 178-180.	0.7	8
27	Conservation of HHV-6 DNA polymerase processivity factor sequence and predicted structure suggests it as a target for antiviral development. Antiviral Research, 2010, 86, 316-319.	4.1	2
28	Synthesis and evaluation of original bioisosteres of bacterial type IIA topoisomerases inhibitors. Canadian Journal of Chemistry, 2016, 94, 240-250.	1.1	0