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List of Publications by Year
in descending order

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Version: 2024-02-01

78 papers	3,706 citations	136950 32 h-index	133252 59 g-index

80 all docs	80 docs citations	80 times ranked	3853 citing authors

#	Article	IF	Citations
1	Structural Characterization of the D179N and D179Y Variants of KPC-2 Î²-Lactamase: Î©-Loop Destabilization as a Mechanism of Resistance to Ceftazidime-Avibactam. Antimicrobial Agents and Chemotherapy, 2022, 66, e0241421.	3.2	22
2	Different Conformations Revealed by NMR Underlie Resistance to Ceftazidime/Avibactam and Susceptibility to Meropenem and Imipenem among D179Y Variants of KPC Î²-Lactamase. Antimicrobial Agents and Chemotherapy, 2022, 66, e0212421.	3.2	11
3	Structural Characterization of Diazabicyclooctane Î²-Lactam â€œEnhancersâ€• in Complex with Penicillin-Binding Proteins PBP2 and PBP3 of Pseudomonas aeruginosa. MBio, 2021, 12, .	4.1	19
4	Turnover Chemistry and Structural Characterization of the Cj0843c Lytic Transglycosylase of Campylobacter jejuni. Biochemistry, 2021, 60, 1133-1144.	2.5	3
5	Discovery of the Soluble Guanylate Cyclase Activator Runcaciguat (BAY 1101042). Journal of Medicinal Chemistry, 2021, 64, 5323-5344.	6.4	38
6	Exploring a novel Class A Î²â€Łactamase Inhibitor against the Class C Î²â€Łactamase Pseudomonas â€Derived Cephalosporinase (PDC). FASEB Journal, 2021, 35, .	0.5	0
7	Turnover chemistry and structural characterization of the Cj0843c lytic transglycosylase of Campylobacter jejuni. FASEB Journal, 2021, 35, .	0.5	0
8	A Î³-lactam siderophore antibiotic effective against multidrug-resistant Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter spp.. European Journal of Medicinal Chemistry, 2021, 220, 113436.	5.5	14
9	Structural analysis of the boronic acid Î²-lactamase inhibitor vaborbactam binding to Pseudomonas aeruginosa penicillin-binding protein 3. PLoS ONE, 2021, 16, e0258359.	2.5	9
10	A Standard Numbering Scheme for Class C Î²-Lactamases. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	50
11	Structural Insights into Ceftobiprole Inhibition of Pseudomonas aeruginosa Penicillin-Binding Protein 3. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	9
12	A Î³-Lactam Siderophore Antibiotic Effective against Multidrug-Resistant Gram-Negative Bacilli. Journal of Medicinal Chemistry, 2020, 63, 5990-6002.	6.4	20
13	1256. In Vivo Activity and Structural Characterization of a New Generation Î³-Lactam Siderophore Antibiotic Against Multidrug-Resistant Gram-Negative Bacteria and Acinetobacter spp. Open Forum Infectious Diseases, 2020, 7, S645-S645.	0.9	0
14	1445. Deciphering the Role of the Y221H Î©-loop Substitution in Pseudomonas-derived Cephalosporinase (PDC) in Cephalosporin Resistance. Open Forum Infectious Diseases, 2020, 7, S725-S726.	0.9	0
15	Structural Analysis of The OXA-48 Carbapenemase Bound to A â€œPoorâ€• Carbapenem Substrate, Doripenem. Antibiotics, 2019, 8, 145.	3.7	9
16	Progestin therapy to prevent preterm birth: History and effectiveness of current strategies and development of novel approaches. Placenta, 2019, 79, 46-52.	1.5	14
17	Targeting Multidrug-Resistant Acinetobacter spp.: Sulbactam and the Diazabicyclooctenone Î²-Lactamase Inhibitor ETX2514 as a Novel Therapeutic Agent. MBio, 2019, 10, .	4.1	64
18	Molecular recognition of S-nitrosothiol substrate by its cognate protein denitrosylase. Journal of Biological Chemistry, 2019, 294, 1568-1578.	3.4	24

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19	Strategic Approaches to Overcome Resistance against Gram-Negative Pathogens Using Î²-Lactamase Inhibitors and Î²-Lactam Enhancers: Activity of Three Novel Diazabicyclooctanes WCK 5153, Zidebactam (WCK 5107), and WCK 4234. Journal of Medicinal Chemistry, 2018, 61, 4067-4086.	6.4	117
20	Mutations in the mitochondrial ribosomal protein MRPS22 lead to primary ovarian insufficiency. Human Molecular Genetics, 2018, 27, 1913-1926.	2.9	39
21	Exploring Additional Dimensions of Complexity in Inhibitor Design for Serine Î²-Lactamases: Mechanistic and Intra- and Inter-molecular Chemistry Approaches. Frontiers in Microbiology, 2018, 9, 622.	3.5	28
22	Structural studies and molecular dynamics simulations suggest a processive mechanism of exolytic lytic transglycosylase from Campylobacter jejuni. PLoS ONE, 2018, 13, e0197136.	2.5	11
23	Structural and Mechanistic Insights into the Doughnutâ€Shaped Lytic Transglycosylase from Campylobacter jejuni. FASEB Journal, 2018, 32, 527.5.	0.5	0
24	The Novel Î²-Lactamase Inhibitor, ETX-2514, in Combination with Sulbactam Effectively Inhibits Acinetobacter baumannii. Open Forum Infectious Diseases, 2017, 4, S368-S368.	0.9	4
25	Inhibition of soluble guanylyl cyclase by small molecules targeting the catalytic domain. FEBS Letters, 2016, 590, 3669-3680.	2.8	7
26	Crystal Structures of KPC-2 and SHV-1 Î²-Lactamases in Complex with the Boronic Acid Transition State Analog S02030. Antimicrobial Agents and Chemotherapy, 2016, 60, 1760-1766.	3.2	36
27	Identification of new inhibitors of soluble guanylyl cyclase activity. BMC Pharmacology & Toxicology, 2015, 16, .	2.4	0
28	Inhibition of Klebsiella Î²-Lactamases (SHV-1 and KPC-2) by Avibactam: A Structural Study. PLoS ONE, 2015, 10, e0136813.	2.5	67
29	Detecting a Quasi-stable Imine Species on the Reaction Pathway of SHV-1 Î²-Lactamase and 6Î²-(Hydroxymethyl)penicillanic Acid Sulfone. Biochemistry, 2015, 54, 734-743.	2.5	7
30	Penam Sulfones and Î²-Lactamase Inhibition: SA2-13 and the Importance of the C2 Side Chain Length and Composition. PLoS ONE, 2014, 9, e85892.	2.5	9
31	Insights into Soluble Guanylyl Cyclase Activation Derived from Improved Heme-Mimetics. Journal of Medicinal Chemistry, 2013, 56, 8948-8952.	6.4	18
32	Insights into BAY 60-2770 Activation and S-Nitrosylation-Dependent Desensitization of Soluble Guanylyl Cyclase via Crystal Structures of Homologous Nostoc H-NOX Domain Complexes. Biochemistry, 2013, 52, 3601-3608.	2.5	52
33	Design and Exploration of Novel Boronic Acid Inhibitors Reveals Important Interactions with a Clavulanic Acid-Resistant Sulfhydryl-Variable (SHV) Î²-Lactamase. Journal of Medicinal Chemistry, 2013, 56, 1084-1097.	6.4	40
34	Î²-Lactamase Inhibition by 7-Alkylidenecephalosporin Sulfones: Allylic Transposition and Formation of an Unprecedented Stabilized Acyl-Enzyme. Journal of the American Chemical Society, 2013, 135, 18358-18369.	13.7	18
35	Crystal Structures of KPC-2 Î²-Lactamase in Complex with 3-Nitrophenyl Boronic Acid and the Penam Sulfone PSR-3-226. Antimicrobial Agents and Chemotherapy, 2012, 56, 2713-2718.	3.2	46
36	Crystal Structure of a Preacylation Complex of the Î²-Lactamase Inhibitor Sulbactam Bound to a Sulfenamide Bond-Containing Thiol-Î²-lactamase. Journal of the American Chemical Society, 2012, 134, 16798-16804.	13.7	27

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37	Structure of an Engineered Î²-Lactamase Maltose Binding Protein Fusion Protein: Insights into Heterotropic Allosteric Regulation. PLoS ONE, 2012, 7, e39168.	2.5	15
38	The Importance of the transâ€Enamine Intermediate as a Î²â€Lactamase Inhibition Strategy Probed in Inhibitorâ€Resistant SHV Î²â€Lactamase Variants. ChemMedChem, 2012, 7, 1002-1008.	3.2	7
39	Structures of SHV-1 Î²-Lactamase with Penem and Penam Sulfone Inhibitors That Form Cyclic Intermediates Stabilized by Carbonyl Conjugation. PLoS ONE, 2012, 7, e49035.	2.5	7
40	Aspartate 102 in the Heme Domain of Soluble Guanylyl Cyclase Has a Key Role in NO Activation. Biochemistry, 2011, 50, 4291-4297.	2.5	15
41	Novel Insights into the Mode of Inhibition of Class A SHV-1 Î²-Lactamases Revealed by Boronic Acid Transition State Inhibitors. Antimicrobial Agents and Chemotherapy, 2011, 55, 174-183.	3.2	23
42	Identification of Residues in the Heme Domain of Soluble Guanylyl Cyclase that are Important for Basal and Stimulated Catalytic Activity. PLoS ONE, 2011, 6, e26976.	2.5	15
43	Structural insights into sGC activation by different activators. BMC Pharmacology, 2011, 11, .	0.4	0
44	Modifications of the C6-substituent of penicillin sulfones with the goal of improving inhibitor recognition and efficacy. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 387-393.	2.2	19
45	Ligand-Dependent Disorder of the Î© Loop Observed in Extended-Spectrum SHV-Type Î²-Lactamase. Antimicrobial Agents and Chemotherapy, 2011, 55, 2303-2309.	3.2	24
46	Crystal structure of the signaling helix coiled-coil domain of the Î²1 subunit of the soluble guanylyl cyclase. BMC Structural Biology, 2010, 10, 2.	2.3	59
47	Structure of Cinaciguat (BAY 58â€“2667) Bound to Nostoc H-NOX Domain Reveals Insights into Heme-mimetic Activation of the Soluble Guanylyl Cyclase. Journal of Biological Chemistry, 2010, 285, 22651-22657.	3.4	90
48	Is Nostoc H-NOX a NO Sensor or Redox Switch?. Biochemistry, 2010, 49, 6587-6599.	2.5	41
49	Design, Synthesis, and Crystal Structures of 6-Alkylidene-2â€²-Substituted Penicillanic Acid Sulfones as Potent Inhibitors of Acinetobacter baumannii OXA-24 Carbapenemase. Journal of the American Chemical Society, 2010, 132, 13320-13331.	13.7	60
50	Structural insights into sGC. BMC Pharmacology, 2009, 9, .	0.4	1
51	Expression, purification, and characterization of the intra-cellular domain of the ANP receptor. Biochimie, 2009, 91, 888-893.	2.6	11
52	Strategic Design of an Effective Î²-Lactamase Inhibitor. Journal of Biological Chemistry, 2009, 284, 945-953.	3.4	45
53	PAS-mediated Dimerization of Soluble Guanylyl Cyclase Revealed by Signal Transduction Histidine Kinase Domain Crystal Structure. Journal of Biological Chemistry, 2008, 283, 1167-1178.	3.4	84
54	Desensitization of soluble guanylyl cyclase, the NO receptor, by S-nitrosylation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12312-12317.	7.1	201

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55	Crystal Structure of KPC-2:â€‰ Insights into Carbapenemase Activity in Class A Î²-Lactamases,. Biochemistry, 2007, 46, 5732-5740.	2.5	109
56	Raman Crystallographic Studies of the Intermediates Formed by Ser130Gly SHV, a Î²-Lactamase that Confers Resistance to Clinical Inhibitors. Biochemistry, 2007, 46, 8689-8699.	2.5	20
57	Desensitization of soluble guanylyl cyclase, the NO-receptor, by S-nitrosylation. BMC Pharmacology, 2007, 7, .	0.4	0
58	Structural insights into sGC. BMC Pharmacology, 2007, 7, S37.	0.4	0
59	NO and CO differentially activate soluble guanylyl cyclase via a heme pivot-bend mechanism. EMBO Journal, 2007, 26, 578-588.	7.8	208
60	Rational Design of a Î²-Lactamase Inhibitor Achieved via Stabilization of thetrans-Enamine Intermediate:Â 1.28 Ã... Crystal Structure ofwtSHV-1 Complex with a Penam Sulfone. Journal of the American Chemical Society, 2006, 128, 13235-13242.	13.7	51
61	Effect of the Inhibitor-Resistant M69V Substitution on the Structures and Populations oftrans-Enamine Î²-Lactamase Intermediatesâ€. Biochemistry, 2006, 45, 11895-11904.	2.5	52
62	High Resolution Crystal Structures of the trans-Enamine Intermediates Formed by Sulbactam and Clavulanic Acid and E166A SHV-1 Î²-Lactamase. Journal of Biological Chemistry, 2005, 280, 34900-34907.	3.4	66
63	Structural insights into the regulation and the activation mechanism of mammalian guanylyl cyclases. , 2004, 104, 83-99.		47
64	Expression and crystallization of several forms of thePropionibacterium shermaniitranscarboxylase 5S subunit. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 521-523.	2.5	3
65	Tazobactam Forms a Stoichiometric trans-Enamine Intermediate in the E166A Variant of SHV-1 Î²-Lactamase:â€‰ 1.63 Ã... Crystal Structure,. Biochemistry, 2004, 43, 843-848.	2.5	67
66	Mutations in the Transmembrane Natriuretic Peptide Receptor NPR-B Impair Skeletal Growth and Cause Acromesomelic Dysplasia, Type Maroteaux. American Journal of Human Genetics, 2004, 75, 27-34.	6.2	325
67	AIPL1, a protein implicated in Leber's congenital amaurosis, interacts with and aids in processing of farnesylated proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12630-12635.	7.1	78
68	Structural insights into the ligand binding domains of membrane bound guanylyl cyclases and natriuretic peptide receptors11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 311, 923-937.	4.2	61
69	Structure of the dimerized hormone-binding domain of a guanylyl- cyclase-coupled receptor. Nature, 2000, 406, 101-104.	27.8	164
70	Association of STATs with relatives and friends. Trends in Cell Biology, 2000, 10, 106-111.	7.9	100
71	Adenovirus E1A Down-regulates LMP2 Transcription by Interfering with the Binding of Stat1 to IRF1. Journal of Biological Chemistry, 2000, 275, 20406-20411.	3.4	38
72	Difference density quality (DDQ): a method to assess the global and local correctness of macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 206-218.	2.5	38

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73	Crystal structure of a nonâ€toxic mutant of heatâ€labile enterotoxin, which is a potent mucosal adjuvant. Protein Science, 1997, 6, 2650-2654.	7.6	22
74	Tumor marker disaccharide Dâ€Galâ€Î²1,3â€GalNAc complexed to heatâ€labile enterotoxin from Escherichia coli. Protein Science, 1996, 5, 1184-1188.	7.6	26
75	Crystal structure of a new heat-labile enterotoxin, LT-IIb. Structure, 1996, 4, 665-678.	3.3	74
76	Protein engineering studies of A-chain loop 47-56 of Escherichia coli heat-labile enterotoxin point to a prominent role of this loop for cytotoxicity. Molecular Microbiology, 1996, 20, 823-832.	2.5	26
77	Crystal structure of cholera toxin Bâ€pentamer bound to receptor G_{M1} pentasaccharide. Protein Science, 1994, 3, 166-175.	7.6	534
78	Protein crystallography and infectious diseases. Protein Science, 1994, 3, 1670-1686.	7.6	48