

Laurent Maveyraud

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,218
citations

218677

26
h-index

289244

40
g-index

48
all docs

48
docs citations

48
times ranked

2081
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical involvement of a carbamylated lysine in catalytic function of class D β -lactamases. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14280-14285.	7.1	213
2	The structure of a Staphylococcus aureus leucocidin component (LukF-PV) reveals the fold of the water-soluble species of a family of transmembrane pore-forming toxins. Structure, 1999, 7, 277-287.	3.3	200
3	Structural Basis for Clinical Longevity of Carbapenem Antibiotics in the Face of Challenge by the Common Class A β -Lactamases from the Antibiotic-Resistant Bacteria. Journal of the American Chemical Society, 1998, 120, 9748-9752.	13.7	138
4	Insights into Class D β -Lactamases Are Revealed by the Crystal Structure of the OXA10 Enzyme from Pseudomonas aeruginosa. Structure, 2000, 8, 1289-1298.	3.3	135
5	Crystal Structure of β -(Hydroxymethyl)penicillanate Complexed to the TEM-1 β -Lactamase from Escherichia coli: A Evidence on the Mechanism of Action of a Novel Inhibitor Designed by a Computer-Aided Process. Journal of the American Chemical Society, 1996, 118, 7435-7440.	13.7	120
6	Protein X-ray Crystallography and Drug Discovery. Molecules, 2020, 25, 1030.	3.8	115
7	Crystal structure of Escherichia coli methionyl-tRNA synthetase highlights species-specific features. Journal of Molecular Biology, 1999, 294, 1287-1297.	4.2	107
8	Crystal Structure of an Acylation Transition-State Analog of the TEM-1 β -Lactamase. Mechanistic Implications for Class A β -Lactamases. Biochemistry, 1998, 37, 2622-2628.	2.5	86
9	X-ray Analysis of the NMC-A β -Lactamase at 1.64-Å... Resolution, a Class A Carbapenemase with Broad Substrate Specificity. Journal of Biological Chemistry, 1998, 273, 26714-26721.	3.4	79
10	Endogenous phosphatidylcholine and a long spacer ligand stabilize the lipid-binding groove of CD1b. EMBO Journal, 2006, 25, 3684-3692.	7.8	75
11	High-Resolution X-ray Structure of an Acyl-Enzyme Species for the Class D OXA-10 β -Lactamase. Journal of the American Chemical Society, 2002, 124, 2461-2465.	13.7	73
12	X-ray Structure of the Asn276Asp Variant of the Escherichia coli TEM-1 β -Lactamase: A Direct Observation of Electrostatic Modulation in Resistance to Inactivation by Clavulanic Acid. Biochemistry, 1999, 38, 9570-9576.	2.5	69
13	Electrostatic analysis of TEM1 β -lactamase: effect of substrate binding, steep potential gradients and consequences of site-directed mutations. Structure, 1995, 3, 603-613.	3.3	60
14	The High Resolution Crystal Structure for Class A β -Lactamase PER-1 Reveals the Bases for Its Increase in Breadth of Activity. Journal of Biological Chemistry, 2000, 275, 28075-28082.	3.4	60
15	Mass Spectral Kinetic Study of Acylation and Deacylation During the Hydrolysis of Penicillins and Cefotaxime by β -Lactamase TEM-1 and the G238S Mutant. Biochemistry, 1995, 34, 11660-11667.	2.5	54
16	Molecular Dynamics at the Root of Expansion of Function in the M69L Inhibitor-Resistant TEM β -Lactamase from Escherichia coli. Journal of the American Chemical Society, 2002, 124, 9422-9430.	13.7	54
17	Structural reorganization of the antigen-binding groove of human CD1b for presentation of mycobacterial sulfoglycolipids. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17755-17760.	7.1	52
18	The First Structural and Mechanistic Insights for Class D β -Lactamases: A Evidence for a Novel Catalytic Process for Turnover of β -Lactam Antibiotics. Journal of the American Chemical Society, 2000, 122, 6132-6133.	13.7	51

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19	Porin mutants with new channel properties. <i>Protein Science</i> , 1998, 7, 1603-1611.	7.6	47
20	Crystal structure of human CD1e reveals a groove suited for lipid-exchange processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13230-13235.	7.1	47
21	An overview on crystal structures of InhA protein: Apo-form, in complex with its natural ligands and inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2018, 146, 318-343.	5.5	43
22	Structural basis for sugar recognition, including the Tn carcinoma antigen, by the lectin SNA from <i>Sambucus nigra</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 89-103.	2.6	33
23	Structural Basis of Extended Spectrum TEM-1 β -Lactamases. <i>Journal of Biological Chemistry</i> , 1996, 271, 10482-10489.	3.4	32
24	Crystal structure of the enoyl-ACP reductase of <i>Mycobacterium tuberculosis</i> (InhA) in the apo-form and in complex with the active metabolite of isoniazid pre-formed by a biomimetic approach. <i>Journal of Structural Biology</i> , 2015, 190, 328-337.	2.8	31
25	Elucidation of Mechanism of Inhibition and X-ray Structure of the TEM-1 β -Lactamase from <i>Escherichia coli</i> Inhibited by a N-Sulfonyloxy- β -lactam. <i>Journal of the American Chemical Society</i> , 1999, 121, 5353-5359.	13.7	29
26	A covalent β heterodimer of leucotoxin reveals molecular plasticity of β -barrel pore-forming toxins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 485-496.	2.6	28
27	Site-directed mutagenesis of beta-lactamase TEM-1. Investigating the potential role of specific residues on the activity of <i>Pseudomonas</i> -specific enzymes. <i>FEBS Journal</i> , 1993, 217, 939-946.	0.2	26
28	Insights into Substrate Modification by Dehydratases from Type I Polyketide Synthases. <i>Journal of Molecular Biology</i> , 2017, 429, 1554-1569.	4.2	24
29	Insight into Structure-Function Relationships and Inhibition of the Fatty Acyl-AMP Ligase (FadD32) Orthologs from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 7973-7989.	3.4	22
30	Residues Essential for Panton-Valentine Leukocidin S Component Binding to Its Cell Receptor Suggest Both Plasticity and Adaptability in Its Interaction Surface. <i>PLoS ONE</i> , 2014, 9, e92094.	2.5	20
31	Occurrence and stability of hetero-hexamers formed by β -carboxysome CcmK shell components. <i>PLoS ONE</i> , 2019, 14, e0223877.	2.5	20
32	6-(Hydroxyalkyl)penicillanates as Probes for Mechanisms of β -Lactamases. <i>Journal of Antibiotics</i> , 2000, 53, 1022-1027.	2.0	19
33	Molecular Dynamics as a Tool for Virtual Ligand Screening. <i>Methods in Molecular Biology</i> , 2018, 1762, 145-178.	0.9	16
34	Structural insights into chaperone addiction of toxin-antitoxin systems. <i>Nature Communications</i> , 2019, 10, 782.	12.8	15
35	The C-terminal region of the transcriptional regulator THAP11 forms a parallel coiled-coil domain involved in protein dimerization. <i>Journal of Structural Biology</i> , 2016, 194, 337-346.	2.8	10
36	Crystallization and preliminary crystallographic studies of both components of the staphylococcal LukE-LukD leukotoxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 663-667.	0.7	5

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37	Molecular Basis for Extender Unit Specificity of Mycobacterial Polyketide Synthases. ACS Chemical Biology, 2020, 15, 3206-3216.	3.4	2
38	Crystallographic studies of the structured core domain of Knr4 from <i>Saccharomyces cerevisiae</i> . Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1120-1124.	0.8	2
39	Fragment-Based Ligand Discovery Applied to the Mycolic Acid Methyltransferase Hma (MmaA4) from <i>Mycobacterium tuberculosis</i> : A Crystallographic and Molecular Modelling Study. Pharmaceuticals, 2021, 14, 1282.	3.8	2
40	Strategies for Tackling Drug Resistance in Tuberculosis. , 2017, , 89-112.		1
41	Antibacterials as wonder drugs and how their effectiveness is being compromised. Pharmacotherapy Library, 2002, 32, 193-205.	0.1	0
42	Title is missing!. , 2019, 14, e0223877.		0
43	Title is missing!. , 2019, 14, e0223877.		0
44	Title is missing!. , 2019, 14, e0223877.		0
45	Title is missing!. , 2019, 14, e0223877.		0