Laurent Maveyraud

List of Publications by Year
in descending order

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	Fragment-Based Ligand Discovery Applied to the Mycolic Acid Methyltransferase Hma (MmaA4) from Mycobacterium tuberculosis: A Crystallographic and Molecular Modelling Study. Pharmaceuticals, 2021, 14, 1282.	3.8	2
2	Molecular Basis for Extender Unit Specificity of Mycobacterial Polyketide Synthases. ACS Chemical Biology, 2020, 15, 3206-3216.	3.4	2
3	Protein X-ray Crystallography and Drug Discovery. Molecules, 2020, 25, 1030.	3.8	115
4	Occurrence and stability of hetero-hexamer associations formed by Î²-carboxysome CcmK shell components. PLoS ONE, 2019, 14, e0223877.	2.5	20
5	Structural insights into chaperone addiction of toxin-antitoxin systems. Nature Communications, 2019, 10, 782.	12.8	15
6	Title is missing!. , 2019, 14, e0223877.		0
7	Title is missing!. , 2019, 14, e0223877.		0
8	Title is missing!. , 2019, 14, e0223877.		0
9	Title is missing!. , 2019, 14, e0223877.		0
10	An overview on crystal structures of InhA protein: Apo-form, in complex with its natural ligands and inhibitors. European Journal of Medicinal Chemistry, 2018, 146, 318-343.	5.5	43
11	Molecular Dynamics as a Tool for Virtual Ligand Screening. Methods in Molecular Biology, 2018, 1762, 145-178.	0.9	16
12	Insights into Substrate Modification by Dehydratases from Type I Polyketide Synthases. Journal of Molecular Biology, 2017, 429, 1554-1569.	4.2	24
13	Strategies for Tackling Drug Resistance in Tuberculosis. , 2017, , 89-112.		1
14	The C-terminal region of the transcriptional regulator THAP11 forms a parallel coiled-coil domain involved in protein dimerization. Journal of Structural Biology, 2016, 194, 337-346.	2.8	10
15	Insight into Structure-Function Relationships and Inhibition of the Fatty Acyl-AMP Ligase (FadD32) Orthologs from Mycobacteria. Journal of Biological Chemistry, 2016, 291, 7973-7989.	3.4	22
16	Crystal structure of the enoyl-ACP reductase of Mycobacterium tuberculosis (InhA) in the apo-form and in complex with the active metabolite of isoniazid pre-formed by a biomimetic approach. Journal of Structural Biology, 2015, 190, 328-337.	2.8	31
17	Crystallographic studies of the structured core domain of Knr4 fromSaccharomyces cerevisiae. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1120-1124.	0.8	2
18	Residues Essential for Panton-Valentine Leukocidin S Component Binding to Its Cell Receptor Suggest Both Plasticity and Adaptability in Its Interaction Surface. PLoS ONE, 2014, 9, e92094.	2.5	20

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19	Crystallization and preliminary crystallographic studies of both components of the staphylococcal LukEâ€“LukD leukotoxin. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 663-667.	0.7	5
20	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
21	Crystal structure of human CD1e reveals a groove suited for lipid-exchange processes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13230-13235.	7.1	47
22	Structural basis for sugar recognition, including the Tn carcinoma antigen, by the lectin SNAâ€‖ from Sambucus nigra. Proteins: Structure, Function and Bioinformatics, 2009, 75, 89-103.	2.6	33
23	A covalent Sâ€F heterodimer of leucotoxin reveals molecular plasticity of Î²â€barrel poreâ€forming toxins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 485-496.	2.6	28
24	Endogenous phosphatidylcholine and a long spacer ligand stabilize the lipid-binding groove of CD1b. EMBO Journal, 2006, 25, 3684-3692.	7.8	75
25	Antibacterials as wonder drugs and how their effectiveness is being compromised. Pharmacochemistry Library, 2002, 32, 193-205.	0.1	0
26	High-Resolution X-ray Structure of an Acyl-Enzyme Species for the Class D OXA-10 Î²-Lactamase. Journal of the American Chemical Society, 2002, 124, 2461-2465.	13.7	73
27	Molecular Dynamics at the Root of Expansion of Function in the M69L Inhibitor-Resistant TEM Î²-Lactamase fromEscherichiacoli. Journal of the American Chemical Society, 2002, 124, 9422-9430.	13.7	54
28	Critical involvement of a carbamylated lysine in catalytic function of class D Â-lactamases. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14280-14285.	7.1	213
29	6-(Hydroxyalkyl)penicillanates as Probes for Mechanisms of .BETA.-Lactamases.. Journal of Antibiotics, 2000, 53, 1022-1027.	2.0	19
30	Insights into Class D Î²-Lactamases Are Revealed by the Crystal Structure of the OXA10 Enzyme from Pseudomonas aeruginosa. Structure, 2000, 8, 1289-1298.	3.3	135
31	The High Resolution Crystal Structure for Class A Î²-Lactamase PER-1 Reveals the Bases for Its Increase in Breadth of Activity. Journal of Biological Chemistry, 2000, 275, 28075-28082.	3.4	60
32	The First Structural and Mechanistic Insights for Class D Î²-Lactamases:Â Evidence for a Novel Catalytic Process for Turnover of Î²-Lactam Antibiotics. Journal of the American Chemical Society, 2000, 122, 6132-6133.	13.7	51
33	Elucidation of Mechanism of Inhibition and X-ray Structure of the TEM-1 Î²-Lactamase from Escherichia coli Inhibited by a N-Sulfonyloxy-Î²-lactam. Journal of the American Chemical Society, 1999, 121, 5353-5359.	13.7	29
34	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
35	X-ray Structure of the Asn276Asp Variant of theEscherichia coliTEM-1 Î²-Lactamase:Â Direct Observation of Electrostatic Modulation in Resistance to Inactivation by Clavulanic Acidâ€,â€¡. Biochemistry, 1999, 38, 9570-9576.	2.5	69
36	Crystal structure of Escherichia coli methionyl-tRNA synthetase highlights species-specific features. Journal of Molecular Biology, 1999, 294, 1287-1297.	4.2	107

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37	Porin mutants with new channel properties. Protein Science, 1998, 7, 1603-1611.	7.6	47
38	Crystal Structure of an Acylation Transition-State Analog of the TEM-1 Î²-Lactamase. Mechanistic Implications for Class A Î²-Lactamasesâ€. Biochemistry, 1998, 37, 2622-2628.	2.5	86
39	Structural Basis for Clinical Longevity of Carbapenem Antibiotics in the Face of Challenge by the Common Class A Î²-Lactamases from the Antibiotic-Resistant Bacteria. Journal of the American Chemical Society, 1998, 120, 9748-9752.	13.7	138
40	X-ray Analysis of the NMC-A Î²-Lactamase at 1.64-Ã... Resolution, a Class A Carbapenemase with Broad Substrate Specificity. Journal of Biological Chemistry, 1998, 273, 26714-26721.	3.4	79
41	Crystal Structure of 6Î±-(Hydroxymethyl)penicillanate Complexed to the TEM-1 Î²-Lactamase fromEscherichia coli:Â 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
42	Structural Basis of Extended Spectrum TEM Î²-Lactamases. Journal of Biological Chemistry, 1996, 271, 10482-10489.	3.4	32
43	Electrostatic analysis of TEM1 Î²-lactamase: effect of substrate binding, steep potential gradients and consequences of site-directed mutations. Structure, 1995, 3, 603-613.	3.3	60
44	Mass Spectral Kinetic Study of Acylation and Deacylation During the Hydrolysis of Penicillins and Cefotaxime by .beta.-Lactamase TEM-1 and the G238S Mutant. Biochemistry, 1995, 34, 11660-11667.	2.5	54
45	Site-directed mutagenesis of beta-lactamase TEM-1. Investigating the potential role of specific residues on the activity of Pseudomonas-specific enzymes. FEBS Journal, 1993, 217, 939-946.	0.2	26