

Lionel Mourey

List of Publications by Year in descending order

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94
papers

4,943
citations

87888

38
h-index

98798

67
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all docs

98
docs citations

98
times ranked

5224
citing authors

#	ARTICLE	IF	CITATIONS
1	Microtubule nucleation by β -tubulin complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 709-721.	37.0	616
2	Crystal structure of <i>Escherichia coli</i> TEM1 β -lactamase at 1.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 364-383.	2.6	364
3	Assistance of Microbial Glycolipid Antigen Processing by CD1e. <i>Science</i> , 2005, 310, 1321-1324.	12.6	229
4	The structure of a <i>Staphylococcus aureus</i> leucocidin component (LukF-PV) reveals the fold of the water-soluble species of a family of transmembrane pore-forming toxins. <i>Structure</i> , 1999, 7, 277-287.	3.3	200
5	Conformational changes induced by phosphorylation of the FixJ receiver domain. <i>Structure</i> , 1999, 7, 1505-1515.	3.3	187
6	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. <i>Journal of the American Chemical Society</i> , 1998, 120, 9748-9752.	13.7	138
7	Structure of the CheY-binding domain of histidine kinase CheA in complex with CheY. <i>Nature Structural Biology</i> , 1998, 5, 25-29.	9.7	117
8	Protein X-ray Crystallography and Drug Discovery. <i>Molecules</i> , 2020, 25, 1030.	3.8	115
9	Crystal Structure of Cleaved Bovine Antithrombin III at 3.2 Å... Resolution. <i>Journal of Molecular Biology</i> , 1993, 232, 223-241.	4.2	110
10	Crystal Structure of Leucotoxin S Component. <i>Journal of Biological Chemistry</i> , 2004, 279, 41028-41037.	3.4	99
11	Exploring the Conformational States and Rearrangements of <i>Yarrowia lipolytica</i> Lipase. <i>Biophysical Journal</i> , 2010, 99, 2225-2234.	0.5	96
12	The Polyketide Synthase Pks13 Catalyzes a Novel Mechanism of Lipid Transfer in <i>Mycobacteria</i> . <i>Chemistry and Biology</i> , 2014, 21, 1660-1669.	6.0	91
13	The structure of <i>Staphylococcus aureus</i> epidermolytic toxin A, an atypic serine protease, at 1.7 Å... resolution. <i>Structure</i> , 1997, 5, 813-824.	3.3	88
14	Protein-protein interactions within the Fatty Acid Synthase-II system of <i>Mycobacterium tuberculosis</i> are essential for mycobacterial viability. <i>Molecular Microbiology</i> , 2004, 54, 1161-1172.	2.5	88
15	X-ray Analysis of the NMC-A β -Lactamase at 1.64-Å... Resolution, a Class A Carbapenemase with Broad Substrate Specificity. <i>Journal of Biological Chemistry</i> , 1998, 273, 26714-26721.	3.4	79
16	Crystal structure of β -tubulin complex protein GCP4 provides insight into microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 915-919.	8.2	79
17	Functional and Structural Characterization of β -1,4-Glucanase Derived from DSR-E Glucanase. <i>Journal of Biological Chemistry</i> , 2012, 287, 7915-7924.	3.4	78
18	Structure-Function Analysis of the THAP Zinc Finger of THAP1, a Large C2CH DNA-binding Module Linked to Rb/E2F Pathways. <i>Journal of Biological Chemistry</i> , 2008, 283, 4352-4363.	3.4	76

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19	The Dual Function of the Mycobacterium tuberculosis FadD32 Required for Mycolic Acid Biosynthesis. <i>Chemistry and Biology</i> , 2009, 16, 510-519.	6.0	76
20	Crystal Structure of the CheA Histidine Phosphotransfer Domain that Mediates Response Regulator Phosphorylation in Bacterial Chemotaxis. <i>Journal of Biological Chemistry</i> , 2001, 276, 31074-31082.	3.4	75
21	Endogenous phosphatidylcholine and a long spacer ligand stabilize the lipid-binding groove of CD1b. <i>EMBO Journal</i> , 2006, 25, 3684-3692.	7.8	75
22	Antithrombin III: structural and functional aspects. <i>Biochimie</i> , 1990, 72, 599-608.	2.6	72
23	Further Insight into S-Adenosylmethionine-dependent Methyltransferases. <i>Journal of Biological Chemistry</i> , 2006, 281, 4434-4445.	3.4	67
24	Fatty Acyl Structures of Mycobacterium tuberculosis Sulfoglycolipid Govern T Cell Response. <i>Journal of Immunology</i> , 2009, 182, 7030-7037.	0.8	63
25	4â€²-Phosphopantetheinyl Transferase PptT, a New Drug Target Required for Mycobacterium tuberculosis Growth and Persistence In Vivo. <i>PLoS Pathogens</i> , 2012, 8, e1003097.	4.7	63
26	Phosphorylation of KasB Regulates Virulence and Acid-Fastness in Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2014, 10, e1004115.	4.7	63
27	Characterization and sugar-binding properties of arcelin-1, an insecticidal lectin-like protein isolated from kidney bean (<i>Phaseolus vulgaris</i> L. cv. RAZ-2) seeds. <i>Biochemical Journal</i> , 1998, 329, 551-560.	3.7	62
28	Electrostatic analysis of TEM1 β -lactamase: effect of substrate binding, steep potential gradients and consequences of site-directed mutations. <i>Structure</i> , 1995, 3, 603-613.	3.3	60
29	Phosphorylation of Mycobacterial PcaA Inhibits Mycolic Acid Cyclopropanation. <i>Journal of Biological Chemistry</i> , 2012, 287, 26187-26199.	3.4	56
30	Structural Investigation of the Thermostability and Product Specificity of Amylosucrase from the Bacterium <i>Deinococcus geothermalis</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 6642-6654.	3.4	55
31	Structural reorganization of the antigen-binding groove of human CD1b for presentation of mycobacterial sulfoglycolipids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17755-17760.	7.1	52
32	Structural transitions in the FixJ receiver domain. <i>Structure</i> , 1999, 7, 1517-1526.	3.3	51
33	New Insights on the Mechanism of Quinoline-based DNA Methyltransferase Inhibitors. <i>Journal of Biological Chemistry</i> , 2015, 290, 6293-6302.	3.4	50
34	Applying Pairwise Combinations of Amino Acid Mutations for Sorting Out Highly Efficient Glucosylation Tools for Chemo-Enzymatic Synthesis of Bacterial Oligosaccharides. <i>Journal of the American Chemical Society</i> , 2012, 134, 18677-18688.	13.7	48
35	Inhibition of the NMC-A β -Lactamase by a Penicillanic Acid Derivative and the Structural Bases for the Increase in Substrate Profile of This Antibiotic Resistance Enzyme. <i>Journal of the American Chemical Society</i> , 1998, 120, 9382-9383.	13.7	47
36	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

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37	First Structural Insights into α -L-Arabinofuranosidases from the Two GH62 Glycoside Hydrolase Subfamilies. <i>Journal of Biological Chemistry</i> , 2014, 289, 5261-5273.	3.4	45
38	Discoupling the Ca ²⁺ -activation from the pore-forming function of the bi-component Panton-Valentine leucocidin in human PMNs. <i>FEBS Letters</i> , 1999, 461, 280-286.	2.8	39
39	The molecular puzzle of two-component signaling cascades. <i>Microbes and Infection</i> , 2001, 3, 417-424.	1.9	39
40	Biochemical and Structural Study of the Atypical Acyltransferase Domain from the Mycobacterial Polyketide Synthase Pks13. <i>Journal of Biological Chemistry</i> , 2012, 287, 33675-33690.	3.4	39
41	The Membrane-associated Form of the DNA Repair Protein Ku is Involved in Cell Adhesion to Fibronectin. <i>Journal of Molecular Biology</i> , 2004, 337, 503-511.	4.2	38
42	Chaperone addiction of toxin-antitoxin systems. <i>Nature Communications</i> , 2016, 7, 13339.	12.8	38
43	Crystal Structure of the Arcelin-1 Dimer from <i>Phaseolus vulgaris</i> at 1.9-Å Resolution. <i>Journal of Biological Chemistry</i> , 1998, 273, 12914-12922.	3.4	36
44	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
45	Natural disease history and characterisation of SUMF1 molecular defects in ten unrelated patients with multiple sulfatase deficiency. <i>Orphanet Journal of Rare Diseases</i> , 2015, 10, 31.	2.7	33
46	Structural Basis of Extended Spectrum TEM β -Lactamases. <i>Journal of Biological Chemistry</i> , 1996, 271, 10482-10489.	3.4	32
47	Assay Development for Identifying Inhibitors of the Mycobacterial FadD32 Activity. <i>Journal of Biomolecular Screening</i> , 2013, 18, 576-587.	2.6	31
48	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
49	Experimental mapping of soluble protein domains using a hierarchical approach. <i>Nucleic Acids Research</i> , 2011, 39, e125-e125.	14.5	29
50	Engineered covalent leucotoxin heterodimers form functional pores: insights into S-F interactions. <i>Biochemical Journal</i> , 2006, 396, 381-389.	3.7	28
51	A covalent S-F 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
52	S-Adenosyl-N-decyl-aminoethyl, a Potent Bisubstrate Inhibitor of <i>Mycobacterium tuberculosis</i> Mycolic Acid Methyltransferases. <i>Journal of Biological Chemistry</i> , 2009, 284, 19321-19330.	3.4	28
53	Insights into Substrate Modification by Dehydratases from Type I Polyketide Synthases. <i>Journal of Molecular Biology</i> , 2017, 429, 1554-1569.	4.2	24
54	Structural Insights into the Carbohydrate Binding Ability of an α -(1 \rightarrow 2) Branching Sucrase from Glycoside Hydrolase Family 70. <i>Journal of Biological Chemistry</i> , 2016, 291, 7527-7540.	3.4	23

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55	Phthiocerol Dimycocerosates From Mycobacterium tuberculosis Increase the Membrane Activity of Bacterial Effectors and Host Receptors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 420.	3.9	23
56	Selectivity in substitution chemistry of mixed-metal, tetrahedral MCo ₃ (M = iron, ruthenium) carbonyl clusters: cobalt-59 NMR study and crystal structure of RuCo ₃ (.mu.3-H)(.mu.-CO) ₃ (CO) ₈ (NMe ₃). <i>Organometallics</i> , 1992, 11, 2628-2634.	2.3	22
57	Further insights into the mechanism of function of the response regulator CheY from crystallographic studies of the CheYâ€“CheA124â€“257 complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 44-51.	2.5	22
58	Insight into Structure-Function Relationships and Inhibition of the Fatty Acyl-AMP Ligase (FadD32) Orthologs from Mycobacteria. <i>Journal of Biological Chemistry</i> , 2016, 291, 7973-7989.	3.4	22
59	Inhibition of the Broad Spectrum Nonmetallo carbapenemase of Class A (NMC-A) Î²-Lactamase from <i>Enterobacter cloacae</i> by Monocyclic Î²-Lactams. <i>Journal of Biological Chemistry</i> , 1999, 274, 25260-25265.	3.4	20
60	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
61	Occurrence and stability of hetero-hexamers associations formed by Î²-carboxysome CcmK shell components. <i>PLoS ONE</i> , 2019, 14, e0223877.	2.5	20
62	6-(Hydroxyalkyl)penicillanates as Probes for Mechanisms of .BETA.-Lactamases.. <i>Journal of Antibiotics</i> , 2000, 53, 1022-1027.	2.0	19
63	Crystal structure of bovine antithrombin III. <i>Acta Crystallographica Section B: Structural Science</i> , 1990, 46, 550-556.	1.8	18
64	Structural bases for N-glycan processing by mannoside phosphorylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1335-1346.	2.5	18
65	Crystallization and preliminary crystallographic data for bovine antithrombin III. <i>Journal of Molecular Biology</i> , 1989, 210, 877-879.	4.2	17
66	Directed evolution of SecB chaperones toward toxin-antitoxin systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12584-12589.	7.1	15
67	Structural insights into chaperone addiction of toxin-antitoxin systems. <i>Nature Communications</i> , 2019, 10, 782.	12.8	15
68	Ser/Thr Phosphorylation Regulates the Fatty Acyl-AMP Ligase Activity of FadD32, an Essential Enzyme in Mycolic Acid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2016, 291, 22793-22805.	3.4	14
69	Small-Angle x-ray scattering and crystallographic studies of arcelin-1: An insecticidal lectin-like glycoprotein from <i>Phaseolus vulgaris</i> L. , 1997, 29, 433-442.		13
70	Distinction between Pore Assembly by Staphylococcal Î±-Toxin versus Leukotoxins. <i>Journal of Biomedicine and Biotechnology</i> , 2007, 2007, 1-13.	3.0	13
71	Virtual and Biophysical Screening Targeting the Î²-Tubulin Complex â€“ A New Target for the Inhibition of Microtubule Nucleation. <i>PLoS ONE</i> , 2013, 8, e63908.	2.5	13
72	Cell transfection of purified cytolethal distending toxin B subunits allows comparing their nuclease activity while plasmid degradation assay does not. <i>PLoS ONE</i> , 2019, 14, e0214313.	2.5	11

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73	Crystal structure of the F component of the Panton-Valentine leucocidin. <i>International Journal of Medical Microbiology</i> , 2000, 290, 395-401.	3.6	10
74	Crystallization and preliminary crystallographic data of a leucotoxin S component from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 310-313.	2.5	10
75	Detection of soluble co-factor dependent protein expression in vivo : Application to the 4â€²-phosphopantetheinyl transferase PptT from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural Biology</i> , 2013, 183, 320-328.	2.8	10
76	Oligomeric structure of the repressor of the bacteriophage Mu early operon. <i>FEBS Journal</i> , 1998, 252, 408-415.	0.2	9
77	NMR secondary structure and interactions of recombinant human MOZART1 protein, a component of the gammaâ€²-tubulin complex. <i>Protein Science</i> , 2017, 26, 2240-2248.	7.6	8
78	Fine-tuning of intrinsic N-Oct-3 POU domain allostery by regulatory DNA targets. <i>Nucleic Acids Research</i> , 2007, 35, 4420-4432.	14.5	7
79	Alpha-helix and beta-barrel pore-forming toxins (leucocidins, alpha-, gamma-, and delta-cytolysins) of <i>Staphylococcus aureus</i> . , 2006, , 590-607.		5
80	Crystallization and preliminary crystallographic studies of both components of the staphylococcal LukEâ€‘LukD leukotoxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 663-667.	0.7	5
81	Substrate recognition and cryo-EM structure of the ribosome-bound TAC toxin of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2022, 13, 2641.	12.8	5
82	Solution structure of the type I polyketide synthase Pks13 from <i>Mycobacterium tuberculosis</i> . <i>BMC Biology</i> , 2022, 20, .	3.8	5
83	Urea derivatives carrying a thiophenylthiazole moiety: Design, synthesis, and evaluation of antitubercular and InhA inhibitory activities. <i>Drug Development Research</i> , 2022, 83, 1292-1304.	2.9	5
84	Conformational flexibility of coenzyme A and its impact on the postâ€‘translational modification of acyl carrier proteins by 4â€²-phosphopantetheinyl transferases. <i>FEBS Journal</i> , 2020, 287, 4729-4746.	4.7	4
85	Molecular Basis for Extender Unit Specificity of Mycobacterial Polyketide Synthases. <i>ACS Chemical Biology</i> , 2020, 15, 3206-3216.	3.4	2
86	Phosphopantetheinyl transferase binding and inhibition by amidino-urea and hydroxypyrimidinethione compounds. <i>Scientific Reports</i> , 2021, 11, 18042.	3.3	2
87	Crystallographic studies of the structured core domain of Knr4 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1120-1124.	0.8	2
88	Bioinformatic Mining and Structure-Activity Profiling of Baeyer-Villiger Monooxygenases from <i>Mycobacterium tuberculosis</i> . <i>MSphere</i> , 2022, , e0048221.	2.9	2
89	Fragment-Based Ligand Discovery Applied to the Mycolic Acid Methyltransferase Hma (MmaA4) from <i>Mycobacterium tuberculosis</i> : A Crystallographic and Molecular Modelling Study. <i>Pharmaceuticals</i> , 2021, 14, 1282.	3.8	2
90	Antibacterials as wonder drugs and how their effectiveness is being compromised. <i>Pharmacochemistry Library</i> , 2002, 32, 193-205.	0.1	0

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91	Title is missing!. , 2019, 14, e0223877.		0
92	Title is missing!. , 2019, 14, e0223877.		0
93	Title is missing!.. , 2019, 14, e0223877.		0
94	Title is missing!.. , 2019, 14, e0223877.		0