

David I Roper

List of Publications by Year in descending order

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110
papers

3,668
citations

126907

33
h-index

155660

55
g-index

116
all docs

116
docs citations

116
times ranked

4855
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis of lipopolysaccharide maturation by the O-antigen ligase. <i>Nature</i> , 2022, 604, 371-376.	27.8	25
2	Characterization of secondary structure and thermal stability by biophysical methods of the D-alanyl,D-alanine ligase B protein from <i>Escherichia coli</i> . <i>Protein and Peptide Letters</i> , 2022, 29, .	0.9	0
3	Plant peptidoglycan precursor biosynthesis: Conservation between moss chloroplasts and Gram-negative bacteria. <i>Plant Physiology</i> , 2022, 190, 165-179.	4.8	6
4	Structure-based modeling and dynamics of MurM, a <i>Streptococcus pneumoniae</i> penicillin resistance determinant present at the cytoplasmic membrane. <i>Structure</i> , 2021, 29, 731-742.e6.	3.3	7
5	A molecular link between cell wall biosynthesis, translation fidelity, and stringent response in <i>Streptococcus pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
6	The Pneumococcal Divisome: Dynamic Control of <i>Streptococcus pneumoniae</i> Cell Division. <i>Frontiers in Microbiology</i> , 2021, 12, 737396.	3.5	22
7	A Dynamic Network of Proteins Facilitate Cell Envelope Biogenesis in Gram-Negative Bacteria. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12831.	4.1	13
8	Synthetic Sansanmycin Analogues as Potent <i>Mycobacterium tuberculosis</i> Translocase I Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17326-17345.	6.4	8
9	Substrate and Stereochemical Control of Peptidoglycan Cross-Linking by Transpeptidation by <i>Escherichia coli</i> PBP1B. <i>Journal of the American Chemical Society</i> , 2020, 142, 5034-5048.	13.7	21
10	The Extracellular Domain of Two-component System Sensor Kinase VanS from <i>Streptomyces coelicolor</i> Binds Vancomycin at a Newly Identified Binding Site. <i>Scientific Reports</i> , 2020, 10, 5727.	3.3	27
11	Insights into bacterial cell division from a structure of EnvC bound to the FtsX periplasmic domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28355-28365.	7.1	32
12	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. <i>ELife</i> , 2020, 9, .	6.0	25
13	Structure-Guided Enhancement of Selectivity of Chemical Probe Inhibitors Targeting Bacterial Seryl-tRNA Synthetase. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9703-9717.	6.4	5
14	Metallohelices that kill Gram-negative pathogens using intracellular antimicrobial peptide pathways. <i>Chemical Science</i> , 2019, 10, 9708-9720.	7.4	22
15	SMA-PAGE: A new method to examine complexes of membrane proteins using SMALP nano-encapsulation and native gel electrophoresis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 1437-1445.	2.6	22
16	Bacterial Lipid II Analogs: Novel In Vitro Substrates for Mammalian Oligosaccharyl Diphosphodolichol Diphosphatase (DLODP) Activities. <i>Molecules</i> , 2019, 24, 2135.	3.8	1
17	Analysis of SMALP co-extracted phospholipids shows distinct membrane environments for three classes of bacterial membrane protein. <i>Scientific Reports</i> , 2019, 9, 1813.	3.3	61
18	Mechanisms of Incorporation for D -Amino Acid Probes That Target Peptidoglycan Biosynthesis. <i>ACS Chemical Biology</i> , 2019, 14, 2745-2756.	3.4	101

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19	Nano-encapsulated Escherichia coli Divisome Anchor ZipA, and in Complex with FtsZ. Scientific Reports, 2019, 9, 18712.	3.3	16
20	The crystal structure and oligomeric form of Escherichia coli I, d -carboxypeptidase A. Biochemical and Biophysical Research Communications, 2018, 499, 594-599.	2.1	6
21	In silico identification, synthesis and biological evaluation of novel tetrazole inhibitors of MurB. Chemical Biology and Drug Design, 2018, 91, 1101-1112.	3.2	10
22	A road map for prioritizing warheads for cysteine targeting covalent inhibitors. European Journal of Medicinal Chemistry, 2018, 160, 94-107.	5.5	80
23	The role of the jaw subdomain of peptidoglycan glycosyltransferases for lipid II polymerization. Cell Surface, 2018, 2, 54-66.	3.0	8
24	Substitutions in PBP2b from β -Lactam-resistant Streptococcus pneumoniae Have Different Effects on Enzymatic Activity and Drug Reactivity. Journal of Biological Chemistry, 2017, 292, 2854-2865.	3.4	14
25	Sansanmycin natural product analogues as potent and selective anti-mycobacterials that inhibit lipid I biosynthesis. Nature Communications, 2017, 8, 14414.	12.8	43
26	Diaryltriazenes as antibacterial agents against methicillin resistant Staphylococcus aureus (MRSA) and Mycobacterium smegmatis. European Journal of Medicinal Chemistry, 2017, 127, 223-234.	5.5	13
27	Inhibition of D-Ala:D-Ala ligase through a phosphorylated form of the antibiotic D-cycloserine. Nature Communications, 2017, 8, 1939.	12.8	59
28	In vitro characterization of the antivirulence target of Gram-positive pathogens, peptidoglycan O-acetyltransferase A (OatA). PLoS Pathogens, 2017, 13, e1006667.	4.7	35
29	Reconstruction of diaminopimelic acid biosynthesis allows characterisation of Mycobacterium tuberculosis N-succinyl-L,L-diaminopimelic acid desuccinylase. Scientific Reports, 2016, 6, 23191.	3.3	10
30	Beyond the Discovery Void: New Targets for Antibacterial Compounds. Science Progress, 2016, 99, 153-182.	1.9	7
31	Anticancer metallohelices: nanomolar potency and high selectivity. Chemical Science, 2016, 7, 951-958.	7.4	53
32	Core Steps of Membrane-Bound Peptidoglycan Biosynthesis: Recent Advances, Insight and Opportunities. Antibiotics, 2015, 4, 495-520.	3.7	35
33	Full-length structure of the major autolysin LytA. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1373-1381.	2.5	22
34	Bacterial Cell Division: Experimental and Theoretical Approaches to the Divisome. Science Progress, 2015, 98, 313-345.	1.9	6
35	Carbohydrate scaffolds as glycosyltransferase inhibitors with in vivo antibacterial activity. Nature Communications, 2015, 6, 7719.	12.8	34
36	Biological Insights from a Simulation Model of the Critical FtsZ Accumulation Required for Prokaryotic Cell Division. Biochemistry, 2015, 54, 3803-3813.	2.5	6

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37	Identification of a Novel Inhibition Site in Translocase MraY Based upon the Site of Interaction with Lysis Protein E from Bacteriophage ϕ X174. <i>ChemBioChem</i> , 2014, 15, 1300-1308.	2.6	26
38	Surfactant-free purification of membrane protein complexes from bacteria: application to the staphylococcal penicillin-binding protein complex PBP2/PBP2a. <i>Nanotechnology</i> , 2014, 25, 285101.	2.6	53
39	Observation of the time-course for peptidoglycan lipid intermediate II polymerization by <i>Staphylococcus aureus</i> monofunctional transglycosylase. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1628-1636.	1.8	3
40	Asymmetric triplex metallohelices with high and selective activity against cancer cells. <i>Nature Chemistry</i> , 2014, 6, 797-803.	13.6	115
41	Prospects for novel inhibitors of peptidoglycan transglycosylases. <i>Bioorganic Chemistry</i> , 2014, 55, 16-26.	4.1	26
42	Adenosine Tetraphosphoadenosine Drives a Continuous ATP-Release Assay for Aminoacyl-tRNA Synthetases and Other Adenylate-Forming Enzymes. <i>ACS Chemical Biology</i> , 2013, 8, 2157-2163.	3.4	10
43	Structural and mechanistic studies of theorf12gene product from the clavulanic acid biosynthesis pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1567-1579.	2.5	8
44	A model of membrane contraction predicting initiation and completion of bacterial cell division. <i>Integrative Biology (United Kingdom)</i> , 2013, 5, 778.	1.3	11
45	<i>In vitro</i> Reconstitution of Peptidoglycan Assembly from the Gram-Positive Pathogen <i>Streptococcus pneumoniae</i> . <i>ACS Chemical Biology</i> , 2013, 8, 2688-2696.	3.4	74
46	Tetramerization of ZapA is required for FtsZ bundling. <i>Biochemical Journal</i> , 2013, 449, 795-802.	3.7	37
47	Specificity Determinants for Lysine Incorporation in <i>Staphylococcus aureus</i> Peptidoglycan as Revealed by the Structure of a MurE Enzyme Ternary Complex. <i>Journal of Biological Chemistry</i> , 2013, 288, 33439-33448.	3.4	33
48	Crystallization and preliminary X-ray analysis of a UDP-MurNAc-tripeptide-D-alanyl-D-alanine-adding enzyme (PaMurF) from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 503-505.	0.7	3
49	Penicillin-Binding Protein 4. , 2013, , 3470-3473.		0
50	CO2 directly modulates connexin 26 by formation of carbamate bridges between subunits. <i>ELife</i> , 2013, 2, e01213.	6.0	103
51	Specificity determinants for lysine revealed by the <i>S. aureus</i> MurE structure. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s332-s332.	0.3	0
52	Structure and functional study of tRNA dependent Fem ligases in <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s336-s336.	0.3	0
53	The Mechanics of FtsZ Fibers. <i>Biophysical Journal</i> , 2012, 102, 731-738.	0.5	29
54	Crystal Structures of Penicillin-Binding Protein 3 (PBP3) from Methicillin-Resistant <i>Staphylococcus aureus</i> in the Apo and Cefotaxime-Bound Forms. <i>Journal of Molecular Biology</i> , 2012, 423, 351-364.	4.2	48

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55	The pH Dependence of Polymerization and Bundling by the Essential Bacterial Cytoskeletal Protein FtsZ. PLoS ONE, 2011, 6, e19369.	2.5	23
56	Bacterial cell wall assembly: still an attractive antibacterial target. Trends in Biotechnology, 2011, 29, 167-173.	9.3	230
57	Indistinguishability and identifiability of kinetic models for the MurC reaction in peptidoglycan biosynthesis. Computer Methods and Programs in Biomedicine, 2011, 104, 70-80.	4.7	7
58	Crystallization and preliminary X-ray analysis of a <i>D</i> -alanyl- <i>D</i> -alanine ligase (EcDdlB) from <i>Escherichia coli</i> . Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 405-408.	0.7	8
59	Crystal Structures of Penicillin-Binding Proteins 4 and 5 from <i>Haemophilus influenzae</i> . Journal of Molecular Biology, 2010, 396, 634-645.	4.2	26
60	Structure of the diaminopimelate epimerase DapF from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 383-387.	2.5	21
61	Inhibition of tRNA-dependent ligase MurM from <i>Streptococcus pneumoniae</i> by phosphonate and sulfonamide inhibitors. Bioorganic and Medicinal Chemistry, 2009, 17, 3443-3455.	3.0	13
62	Design and synthesis of new hydroxyethylamines as inhibitors of <i>D</i> -alanyl- <i>D</i> -lactate ligase (VanA) and <i>D</i> -alanyl- <i>D</i> -alanine ligase (DdlB). Bioorganic and Medicinal Chemistry Letters, 2009, 19, 1376-1379.	2.2	41
63	Mutational Analysis of the Substrate Specificity of <i>Escherichia coli</i> Penicillin Binding Protein 4. Biochemistry, 2009, 48, 2675-2683.	2.5	35
64	<i>Pseudomonas aeruginosa</i> MurE amide ligase: enzyme kinetics and peptide inhibitor. Biochemical Journal, 2009, 421, 263-272.	3.7	25
65	Expression, purification and characterisation of soluble GlfT and the identification of a novel galactofuranosyltransferase Rv3782 involved in priming GlfT-mediated galactan polymerisation in <i>Mycobacterium tuberculosis</i> . Protein Expression and Purification, 2008, 58, 332-341.	1.3	37
66	Crystal Structure and Functional Assignment of YfaU, a Metal Ion Dependent Class II Aldolase from <i>Escherichia coli</i> K12. Biochemistry, 2008, 47, 9955-9965.	2.5	38
67	Kinetic Characterization of Lipid II-Ala:Alanyl-tRNA Ligase (MurN) from <i>Streptococcus pneumoniae</i> using Semisynthetic Aminoacyl-lipid II Substrates. Journal of Biological Chemistry, 2008, 283, 34571-34579.	3.4	14
68	Characterization of tRNA-dependent Peptide Bond Formation by MurM in the Synthesis of <i>Streptococcus pneumoniae</i> Peptidoglycan. Journal of Biological Chemistry, 2008, 283, 6402-6417.	3.4	70
69	Nod1 Signaling Overcomes Resistance of <i>S. pneumoniae</i> to Opsonophagocytic Killing. PLoS Pathogens, 2007, 3, e118.	4.7	72
70	Structural Characterisation of the Insecticidal Toxin XptA1, Reveals a 1.15 ÅMDa Tetramer with a Cage-like Structure. Journal of Molecular Biology, 2007, 366, 1558-1568.	4.2	37
71	FtsZ Polymer-bundling by the <i>Escherichia coli</i> ZapA Orthologue, YgfE, Involves a Conformational Change in Bound GTP. Journal of Molecular Biology, 2007, 369, 210-221.	4.2	83
72	Structure and Mechanism of HpcG, a Hydratase in the Homoprotocatechuate Degradation Pathway of <i>Escherichia coli</i> . Journal of Molecular Biology, 2007, 370, 899-911.	4.2	17

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73	Structure and Mechanism of HpcH: A Metal Ion Dependent Class II Aldolase from the Homoprotocatechuate Degradation Pathway of Escherichia coli. <i>Journal of Molecular Biology</i> , 2007, 373, 866-876.	4.2	28
74	Adenosine phosphonate inhibitors of lipid II: Alanyl tRNA ligase MurM from Streptococcus pneumoniae. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 4654-4656.	2.2	15
75	Fluorescent reagents for in vitro studies of lipid-linked steps of bacterial peptidoglycan biosynthesis: derivatives of UDPMurNAc-pentapeptide containing d-cysteine at position 4 or 5. <i>Molecular BioSystems</i> , 2006, 2, 484.	2.9	32
76	Crystal Structure of Penicillin Binding Protein 4 (dacB) from Escherichia coli, both in the Native Form and Covalently Linked to Various Antibiotics. <i>Biochemistry</i> , 2006, 45, 783-792.	2.5	84
77	Expression, purification and crystallization of 2-oxo-hept-4-ene-1,7-dioate hydratase (HpcG) from Escherichia coli. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1010-1012.	0.7	2
78	Use of a codon alteration strategy in a novel approach to cloning the Mycobacterium tuberculosis diaminopimelic acid epimerase. <i>FEMS Microbiology Letters</i> , 2006, 262, 39-47.	1.8	6
79	Phospho-MurNAc-Pentapeptide Translocase (MraY) as a Target for Antibacterial Agents and Antibacterial Proteins. <i>Infectious Disorders - Drug Targets</i> , 2006, 6, 85-106.	0.8	119
80	IFN- γ Enhances Production of Nitric Oxide from Macrophages via a Mechanism That Depends on Nucleotide Oligomerization Domain-2. <i>Journal of Immunology</i> , 2006, 176, 4804-4810.	0.8	72
81	Active membrane transport and receptor proteins from bacteria. <i>Biochemical Society Transactions</i> , 2005, 33, 867-872.	3.4	22
82	A De Novo Designed Inhibitor of D-Ala-D-Ala Ligase from E. coli. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 6403-6406.	13.8	40
83	Expression, purification and crystallization of the cell-division protein YgfE from Escherichia coli. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 305-307.	0.7	0
84	Expression, purification and preliminary crystallographic analysis of 2,4-dihydroxy-hepta-2-ene-1,7-dioate aldolase (HpcH) from Escherichia coli. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 821-824.	0.7	6
85	Solution Structure and Interactions of the Escherichia coli Cell Division Activator Protein Ceda. <i>Biochemistry</i> , 2005, 44, 6738-6744.	2.5	8
86	Circular Dichroism Spectroscopy for the Study of Protein-Ligand Interactions. , 2005, 305, 343-364.		32
87	Expression, purification, crystallization and preliminary characterization of uridine 5'-diphospho-N-acetylmuramoyl-L-alanyl-D-glutamate:lysine ligase (MurE) from Streptococcus pneumoniae 110K/70. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 359-361.	2.5	6
88	Refinement of Haemophilus influenzae diaminopimelic acid epimerase (DapF) at 1.75 Å resolution suggests a mechanism for stereocontrol during catalysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 397-400.	2.5	23
89	Structure/Function Studies on a S-Adenosyl-L-methionine-dependent Uroporphyrinogen III C Methyltransferase (SUMT), a Key Regulatory Enzyme of Tetrapyrrole Biosynthesis. <i>Journal of Molecular Biology</i> , 2004, 344, 419-433.	4.2	56
90	The physico-chemical characterization of a boiling stable antifreeze protein from a perennial grass (Lolium perenne). <i>Archives of Biochemistry and Biophysics</i> , 2003, 410, 238-245.	3.0	70

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91	Mutations in the DNA Mismatch Repair Proteins MutS and MutL of Oxazolidinone-Resistant or -Susceptible <i>Enterococcus faecium</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3061-3066.	3.2	34
92	The Crystal Structure of HpcE, a Bifunctional Decarboxylase/Isomerase with a Multifunctional Fold. <i>Biochemistry</i> , 2002, 41, 2982-2989.	2.5	26
93	Synthesis and in vitro enzyme activity of an oxa analogue of azi-DAP. <i>Journal of the Chemical Society, Perkin Transactions 1</i> , 2002, , 1029-1035.	1.3	14
94	Expression, purification, crystallization and preliminary characterization of an HHED aldolase homologue from <i>Escherichia coli</i> K12. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2191-2193.	2.5	3
95	Understanding the mechanism of ice binding by type III antifreeze proteins. <i>Journal of Molecular Biology</i> , 2001, 305, 875-889.	4.2	113
96	Vancomycin resistance in enterococci: reprogramming of the d-Ala-d-Ala ligases in bacterial peptidoglycan biosynthesis. <i>Chemistry and Biology</i> , 2000, 7, R109-R119.	6.0	127
97	The molecular basis of vancomycin resistance in clinically relevant <i>Enterococci</i> : Crystal structure of D-alanyl-D-lactate ligase (VanA). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 8921-8925.	7.1	63
98	Crystallization and preliminary X-ray characterization of VanA from <i>Enterococcus faecium</i> BM4147: towards the molecular basis of bacterial resistance to the glycopeptide antibiotic vancomycin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1481-1483.	2.5	5
99	The N-Terminal Domain of Human Topoisomerase III \pm Is a DNA-Dependent ATPase. <i>Biochemistry</i> , 1998, 37, 16997-17004.	2.5	32
100	Enzymatic Ketonization of 2-Hydroxymuconate: Specificity and Mechanism Investigated by the Crystal Structures of Two Isomerases. <i>Biochemistry</i> , 1996, 35, 792-802.	2.5	148
101	Crystallization and preliminary X-ray analysis of a bifunctional enzyme: HHDD isomerase/OPET decarboxylase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 1036-1038.	2.5	4
102	Sequence of the hpcC and hpcG genes of the meta-fission homoprotocatechuic acid pathway of <i>Escherichia coli</i> C: nearly 40% amino-acid identity with the analogous enzymes of the catechol pathway. <i>Gene</i> , 1995, 156, 47-51.	2.2	23
103	Allosteric Activation in <i>Bacillus stearothermophilus</i> Lactate Dehydrogenase Investigated by an X-ray Crystallographic Analysis of a Mutant Designed to Prevent Tetramerization of the Enzyme. <i>Journal of Molecular Biology</i> , 1994, 238, 615-625.	4.2	29
104	Preliminary crystallographic analysis of 4-oxalocrotonate tautomerase reveals the oligomeric structure of the enzyme. <i>Journal of Molecular Biology</i> , 1994, 243, 799-801.	4.2	17
105	The <i>Escherichia coli</i> C homoprotocatechuate degradative operon: hpc gene order, direction of transcription and control of expression. <i>Molecular Genetics and Genomics</i> , 1993, 237-237, 241-250.	2.4	72
106	Purification, nucleotide sequence and some properties of a bifunctional isomerase/decarboxylase from the homoprotocatechuate degradative pathway of <i>Escherichia coli</i> C. <i>FEBS Journal</i> , 1993, 217, 575-580.	0.2	21
107	The structural consequences of exchanging tryptophan and tyrosine residues in <i>B. stearothermophilus</i> lactate dehydrogenase. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 611-615.	2.1	5
108	Purification, some properties and nucleotide sequence of 5-carboxymethyl-2-hydroxymuconate isomerase of <i>Escherichia coli</i> C. <i>FEBS Letters</i> , 1990, 266, 63-66.	2.8	15

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109	Subcloning and nucleotide sequence of the 3,4-dihydroxyphenylacetate (homoprotocatechuate) 2,3-dioxygenase gene from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1990, 275, 53-57.	2.8	53
110	Preliminary crystallographic analysis of 5-carboxymethyl-2-hydroxymuconate isomerase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1989, 210, 881-882.	4.2	4