

# Renwick C J Dobson

## List of Publications by Year in descending order

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145  
papers

11,104  
citations

117453

34  
h-index

32761

100  
g-index

151  
all docs

151  
docs citations

151  
times ranked

20143  
citing authors

#	ARTICLE	IF	CITATIONS
1	How plants solubilise seed fats: revisiting oleosin structure and function to inform commercial applications. <i>Biophysical Reviews</i> , 2022, 14, 257-266.	1.5	8
2	The structure and function of modular <i>Escherichia coli</i> O157:H7 bacteriophage FTBEc1 endolysin, LysT84: defining a new endolysin catalytic subfamily. <i>Biochemical Journal</i> , 2022, 479, 207-223.	1.7	5
3	Capillary field effect transistors. <i>Microsystems and Nanoengineering</i> , 2022, 8, 33.	3.4	5
4	Fermentation of plant-based dairy alternatives by lactic acid bacteria. <i>Microbial Biotechnology</i> , 2022, 15, 1404-1421.	2.0	43
5	Structure of Reelin repeat 8 and the adjacent C-terminal region. <i>Biophysical Journal</i> , 2022, 121, 2526-2537.	0.2	0
6	Sialic Acid Derivatives Inhibit SiaT Transporters and Delay Bacterial Growth. <i>ACS Chemical Biology</i> , 2022, 17, 1890-1900.	1.6	7
7	New flow control systems in capillaries: off valves. <i>Lab on A Chip</i> , 2021, 21, 205-214.	3.1	11
8	Quaternary variations in the structural assembly of N-acetylglucosamine-6-phosphate deacetylase from <i>Pasteurella multocida</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 81-93.	1.5	5
9	Transistor off-Valve Based Feedback, Metering and Logic Operations in Capillary Microfluidics. , 2021, , .		4
10	Amino acid-derived defense metabolites from plants: A potential source to facilitate novel antimicrobial development. <i>Journal of Biological Chemistry</i> , 2021, 296, 100438.	1.6	31
11	Modifying the resolving cysteine affects the structure and hydrogen peroxide reactivity of peroxiredoxin 2. <i>Journal of Biological Chemistry</i> , 2021, 296, 100494.	1.6	14
12	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. <i>Nature Communications</i> , 2021, 12, 1988.	5.8	16
13	The structure-function relationship of a signaling-competent, dimeric Reelin fragment. <i>Structure</i> , 2021, 29, 1156-1170.e6.	1.6	6
14	The Molecular Basis for <i>Escherichia coli</i> O157:H7 Phage FAHEc1 Endolysin Function and Protein Engineering to Increase Thermal Stability. <i>Viruses</i> , 2021, 13, 1101.	1.5	10
15	Selective Nutrient Transport in Bacteria: Multicomponent Transporter Systems Reign Supreme. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 699222.	1.6	23
16	Synthesis of N-acetylmannosamine-6-phosphate derivatives to investigate the mechanism of N-acetylmannosamine-6-phosphate 2-epimerase. <i>Carbohydrate Research</i> , 2021, 510, 108445.	1.1	2
17	Molecular basis of a redox switch: molecular dynamics simulations and surface plasmon resonance provide insight into reduced and oxidised angiotensinogen. <i>Biochemical Journal</i> , 2021, 478, 3319-3330.	1.7	1
18	N-acetylmannosamine-6-phosphate 2-epimerase uses a novel substrate-assisted mechanism to catalyze amino sugar epimerization. <i>Journal of Biological Chemistry</i> , 2021, 297, 101113.	1.6	4

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19	Reaction dynamics and residue identification of haemoglobin modification by acrolein, a lipid-peroxidation by-product. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 130013.	1.1	2
20	Guidelines for the use and interpretation of assays for monitoring autophagy (4th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (edition	4.3	1,430
21	Using cryo-EM to uncover mechanisms of bacterial transcriptional regulation. <i>Biochemical Society Transactions</i> , 2021, 49, 2711-2726.	1.6	6
22	On the structure and function of <i>Escherichia coli</i> YjhC: An oxidoreductase involved in bacterial sialic acid metabolism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 654-668.	1.5	13
23	On the catalytic mechanism of bacteriophage endolysins: Opportunities for engineering. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140302.	1.1	35
24	The lid domain is important, but not essential, for catalysis of <i>Escherichia coli</i> pyruvate kinase. <i>European Biophysics Journal</i> , 2020, 49, 761-772.	1.2	4
25	Cover Image, Volume 88, Issue 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, C1.	1.5	0
26	Multi-wavelength analytical ultracentrifugation as a tool to characterise protein-DNA interactions in solution. <i>European Biophysics Journal</i> , 2020, 49, 819-827.	1.2	10
27	G-quadruplex structures bind to EZ-Tn5 transposase. <i>Biochimie</i> , 2020, 177, 190-197.	1.3	2
28	Analytical ultracentrifugation: still the gold standard that offers multiple solutions. <i>European Biophysics Journal</i> , 2020, 49, 673-676.	1.2	5
29	On the utility of fluorescence-detection analytical ultracentrifugation in probing biomolecular interactions in complex solutions: a case study in milk. <i>European Biophysics Journal</i> , 2020, 49, 677-685.	1.2	4
30	Structure-Function Studies of the Antibiotic Target <i>l</i> -Diaminopimelate Aminotransferase from <i>Verrucomicrobium spinosum</i> Reveal an Unusual Oligomeric Structure. <i>Biochemistry</i> , 2020, 59, 2274-2288.	1.2	0
31	The structure of the extracellular domains of human interleukin 11± receptor reveals mechanisms of cytokine engagement. <i>Journal of Biological Chemistry</i> , 2020, 295, 8285-8301.	1.6	33
32	Sub-Ångstrom structure of collagen model peptide (GPO)10 shows a hydrated triple helix with pitch variation and two proline ring conformations. <i>Food Chemistry</i> , 2020, 319, 126598.	4.2	1
33	The basis for non-canonical ROK family function in the N-acetylmannosamine kinase from the pathogen <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 3301-3315.	1.6	13
34	Comparing the Conformational Stability of Pyruvate Kinase in the Gas Phase and in Solution. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 685-692.	1.2	8
35	Structure-function analyses of alkylhydroperoxidase D from <i>Streptococcus pneumoniae</i> reveal an unusual three-cysteine active site architecture. <i>Journal of Biological Chemistry</i> , 2020, 295, 2984-2999.	1.6	4
36	Comparative Molecular Dynamics Simulations Provide Insight Into Antibiotic Interactions: A Case Study Using the Enzyme <i>L,L</i> -Diaminopimelate Aminotransferase (DapL). <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 46.	1.6	1

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37	Structure-based mechanism of preferential complex formation by apoptosis signal-regulating kinases. <i>Science Signaling</i> , 2020, 13, .	1.6	18
38	Structure and Function of <i>N</i> -Acetylmannosamine Kinases from Pathogenic Bacteria. <i>ACS Omega</i> , 2020, 5, 30923-30936.	1.6	8
39	Stemming the tide of antibiotic resistance by exploiting bacteriophages. <i>Biochemist</i> , 2020, 42, 6-11.	0.2	1
40	The Quest for Novel Antimicrobial Compounds: Emerging Trends in Research, Development, and Technologies. <i>Antibiotics</i> , 2019, 8, 8.	1.5	67
41	Oxidative cross-linking of calprotectin occurs in vivo, altering its structure and susceptibility to proteolysis. <i>Redox Biology</i> , 2019, 24, 101202.	3.9	33
42	The First Purification of Functional Proteins from the Unculturable, Genome-Reduced, Bottlenecked <i>Î±-Proteobacterium</i> <i>Candidatus Liberibacter solanacearum</i> <sup>TM</sup> . <i>Phytopathology</i> , 2019, 109, 1141-1148.	1.1	1
43	Structure-function analyses of two plant meso-diaminopimelate decarboxylase isoforms reveal that active-site gating provides stereochemical control. <i>Journal of Biological Chemistry</i> , 2019, 294, 8505-8515.	1.6	6
44	Protein-protein crosslinking in food: Proteomic characterisation methods, consequences and applications. <i>Trends in Food Science and Technology</i> , 2019, 86, 217-229.	7.8	41
45	Functional and solution structure studies of amino sugar deacetylase and deaminase enzymes from <i>Staphylococcus Aureus</i> . <i>FEBS Letters</i> , 2019, 593, 52-66.	1.3	16
46	The fitness challenge of studying molecular adaptation. <i>Biochemical Society Transactions</i> , 2019, 47, 1533-1542.	1.6	5
47	Potential pathogenicity determinants in the genome of <i>Candidatus Liberibacter solanacearum</i> <sup>TM</sup> , the causal agent of zebra chip disease of potato. <i>Australasian Plant Pathology</i> , 2018, 47, 119-134.	0.5	5
48	The self-association and thermal denaturation of caprine and bovine $\beta$ -lactoglobulin. <i>European Biophysics Journal</i> , 2018, 47, 739-750.	1.2	4
49	Effects of Beneficial Mutations in <i>pykF</i> Gene Vary over Time and across Replicate Populations in a Long-Term Experiment with Bacteria. <i>Molecular Biology and Evolution</i> , 2018, 35, 202-210.	3.5	28
50	“Just a spoonful of sugar...” import of sialic acid across bacterial cell membranes. <i>Biophysical Reviews</i> , 2018, 10, 219-227.	1.5	29
51	Chromatic Bacteria – A Broad Host-Range Plasmid and Chromosomal Insertion Toolbox for Fluorescent Protein Expression in Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 3052.	1.5	65
52	A bidentate Polycomb Repressive-Deubiquitinase complex is required for efficient activity on nucleosomes. <i>Nature Communications</i> , 2018, 9, 3932.	5.8	25
53	The Sodium Sialic Acid Symporter From <i>Staphylococcus aureus</i> Has Altered Substrate Specificity. <i>Frontiers in Chemistry</i> , 2018, 6, 233.	1.8	24
54	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. <i>Structure</i> , 2018, 26, 948-959.e5.	1.6	5

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55	Crystal structures and kinetic analyses of <i>N</i> -acetylmannosamine-6-phosphate 2-epimerases from <i>Fusobacterium nucleatum</i> and <i>Vibrio cholerae</i> . Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 431-440.	0.4	6
56	A Three-Ring Circus: Metabolism of the Three Proteogenic Aromatic Amino Acids and Their Role in the Health of Plants and Animals. Frontiers in Molecular Biosciences, 2018, 5, 29.	1.6	214
57	Potential for Bacteriophage Endolysins to Supplement or Replace Antibiotics in Food Production and Clinical Care. Antibiotics, 2018, 7, 17.	1.5	115
58	Substrate-bound outward-open structure of a Na <sup>+</sup> -coupled sialic acid symporter reveals a new Na <sup>+</sup> site. Nature Communications, 2018, 9, 1753.	5.8	62
59	Dihydrodipicolinate Synthase: Structure, Dynamics, Function, and Evolution. Sub-Cellular Biochemistry, 2017, 83, 271-289.	1.0	15
60	Synthesis and incorporation of an advanced lipid peroxidation end-product building block into collagen mimetic peptides. Chemical Communications, 2017, 53, 8459-8462.	2.2	2
61	Structural and functional analysis of the GABARAP interaction motif (GIM). EMBO Reports, 2017, 18, 1382-1396.	2.0	129
62	Cloning, expression, purification, crystallization and X-ray diffraction analysis of dihydrodipicolinate synthase from the human pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.1 Å resolution. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 2-9.	0.4	5
63	Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvylglucosamine Reductase/UDP-N-Acetylmuramate: l-Alanine Ligase Fusion Enzyme from <i>Verrucomicrobium spinosum</i> DSM 4136T. Frontiers in Microbiology, 2016, 7, 362.	1.5	6
64	Inhibition of <i>Arabidopsis</i> growth by the allelopathic compound azetidine-2-carboxylate is due to the low amino acid specificity of cytosolic prolyl-tRNA synthetase. Plant Journal, 2016, 88, 236-246.	2.8	11
65	Exploring the structure of glutamate racemase from <i>Mycobacterium tuberculosis</i> as a template for anti-mycobacterial drug discovery. Biochemical Journal, 2016, 473, 1267-1280.	1.7	17
66	Structure and inhibition of <i>N</i> -acetylneuraminase from methicillin-resistant <i>Staphylococcus aureus</i> . FEBS Letters, 2016, 590, 4414-4428.	1.3	18
67	The epigenetic regulator Smchd1 contains a functional GHKL-type ATPase domain. Biochemical Journal, 2016, 473, 1733-1744.	1.7	25
68	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
69	Grappling with anisotropic data, pseudo-merohedral twinning and pseudo-translational noncrystallographic symmetry: a case study involving pyruvate kinase. Acta Crystallographica Section D: Structural Biology, 2016, 72, 512-519.	1.1	10
70	Conformational Dynamics and Allostery in Pyruvate Kinase. Journal of Biological Chemistry, 2016, 291, 9244-9256.	1.6	29
71	The crystal structure of dihydrodipicolinate reductase from the human-pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.3 Å resolution. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 885-891.	0.4	4
72	Avoidance of stochastic RNA interactions can be harnessed to control protein expression levels in bacteria and archaea. ELife, 2016, 5, .	2.8	25

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73	Genome-wide binding and mechanistic analyses of SmcHd1-mediated epigenetic regulation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3535-44.	3.3	83
74	L,L-diaminopimelate aminotransferase (DapL): a putative target for the development of narrow-spectrum antibacterial compounds. Frontiers in Microbiology, 2014, 5, 509.	1.5	16
75	Ultra-high resolution crystal structure of recombinant caprine Î²-lactoglobulin. FEBS Letters, 2014, 588, 3816-3822.	1.3	16
76	Identification of the bona fide DHDPS from a common plant pathogen. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1869-1883.	1.5	14
77	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of N-acetylmannosamine-6-phosphate 2-epimerase from methicillin-resistant Staphylococcus aureus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 650-655.	0.4	8
78	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of N-acetylmannosamine kinase from methicillin-resistant Staphylococcus aureus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 643-649.	0.4	5
79	The purification, crystallization and preliminary X-ray diffraction analysis of two isoforms of meso-diaminopimelate decarboxylase from Arabidopsis thaliana. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 663-668.	0.4	2
80	Differential response of orthologous L,L-diaminopimelate aminotransferases (DapL) to enzyme inhibitory antibiotic lead compounds. Bioorganic and Medicinal Chemistry, 2014, 22, 523-530.	1.4	9
81	The structure of human interleukin-11 reveals receptor-binding site features and structural differences from interleukin-6. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2277-2285.	2.5	47
82	Activation of the pseudokinase MLKL unleashes the four-helix bundle domain to induce membrane localization and necroptotic cell death. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15072-15077.	3.3	484
83	Structural Basis of the Autophagy-Related LC3/Atg13 LIR Complex: Recognition and Interaction Mechanism. Structure, 2014, 22, 47-58.	1.6	93
84	Destabilization of the Homotetrameric Assembly of 3-Deoxy-d-Arabinose-7-Phosphate Synthase from the Hyperthermophile Pyrococcus furiosus Enhances Enzymatic Activity. Journal of Molecular Biology, 2014, 426, 656-673.	2.0	13
85	Structural, kinetic and computational investigation of Vitis vinifera DHDPS reveals new insight into the mechanism of lysine-mediated allosteric inhibition. Plant Molecular Biology, 2013, 81, 431-446.	2.0	30
86	The Pseudokinase MLKL Mediates Necroptosis via a Molecular Switch Mechanism. Immunity, 2013, 39, 443-453.	6.6	958
87	Discovery of a novel circular single-stranded DNA virus from porcine faeces. Archives of Virology, 2013, 158, 283-289.	0.9	36
88	Engineering allosteric control to an unregulated enzyme by transfer of a regulatory domain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2111-2116.	3.3	44
89	Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of N-acetylneuraminidase from methicillin-resistant Staphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 306-312.	0.7	11
90	Dimerization of Bacterial Diaminopimelate Epimerase Is Essential for Catalysis. Journal of Biological Chemistry, 2013, 288, 9238-9248.	1.6	41

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91	Biochemical Characterization of UDP-N-acetylmuramoyl-L-alanyl-D-glutamate: meso-2,6-diaminopimelate ligase (MurE) from <i>Verrucomicrobium spinosum</i> DSM 4136T. <i>PLoS ONE</i> , 2013, 8, e66458.	1.1	9
92	Structural and Dynamic Requirements for Optimal Activity of the Essential Bacterial Enzyme Dihydrodipicolinate Synthase. <i>PLoS Computational Biology</i> , 2012, 8, e1002537.	1.5	16
93	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from <i>Agrobacterium tumefaciens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1040-1047.	0.7	8
94	Molecular characterisation of a novel cassava associated circular ssDNA virus. <i>Virus Research</i> , 2012, 166, 130-135.	1.1	62
95	Bovine $\beta$ -Lactoglobulin Is Dimeric Under Imitative Physiological Conditions: Dissociation Equilibrium and Rate Constants over the pH Range of 2.5-7.5. <i>Biophysical Journal</i> , 2012, 103, 303-312.	0.2	138
96	Characterisation of the First Enzymes Committed to Lysine Biosynthesis in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e40318.	1.1	45
97	Genomic and Biochemical Analysis of the Diaminopimelate and Lysine Biosynthesis Pathway in <i>Verrucomicrobium spinosum</i> : Identification and Partial Characterization of L,L-Diaminopimelate Aminotransferase and UDP-N-Acetylmuramoyl-L-alanyl-D-glutamyl-2,6-meso-Diaminopimelate Ligase. <i>Frontiers in Microbiology</i> , 2012, 3, 183.	1.5	14
98	The crystal structure of dihydrodipicolinate synthase from <i>Escherichia coli</i> with bound pyruvate and succinic acid semi-aldehyde: Unambiguous resolution of the stereochemistry of the condensation product. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, n/a-n/a.	1.5	5
99	Crystal, Solution and In silico Structural Studies of Dihydrodipicolinate Synthase from the Common Grapevine. <i>PLoS ONE</i> , 2012, 7, e38318.	1.1	32
100	A tetrameric structure is not essential for activity in dihydrodipicolinate synthase (DHDPS) from <i>Mycobacterium tuberculosis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2011, 512, 154-159.	1.4	16
101	Characterization of monomeric dihydrodipicolinate synthase variant reveals the importance of substrate binding in optimizing oligomerization. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1900-1909.	1.1	14
102	L,L-Diaminopimelate Aminotransferase from <i>Chlamydomonas reinhardtii</i> : A Target for Algaecide Development. <i>PLoS ONE</i> , 2011, 6, e20439.	1.1	24
103	In silico modeling of the Menkes copper-translocating P-type ATPase 3rd metal binding domain predicts that phosphorylation regulates copper-binding. <i>BioMetals</i> , 2011, 24, 477-487.	1.8	6
104	Crystallization and preliminary X-ray diffraction analysis of L,L-diaminopimelate aminotransferase (DapL) from <i>Chlamydomonas reinhardtii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 140-143.	0.7	7
105	Purification, crystallization, small-angle X-ray scattering and preliminary X-ray diffraction analysis of the SH2 domain of the Csk-homologous kinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 336-339.	0.7	17
106	Crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase 2 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1386-1390.	0.7	2
107	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the grapevine <i>Vitis vinifera</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1537-1541.	0.7	11
108	Dual diaminopimelate biosynthesis pathways in <i>Bacteroides fragilis</i> and <i>Clostridium thermocellum</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1162-1168.	1.1	17



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109	Tyrosine Latching of a Regulatory Gate Affords Allosteric Control of Aromatic Amino Acid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2011, 286, 10216-10224.	1.6	56
110	Crystallization and preliminary X-ray diffraction analysis of diaminopimelate epimerase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 37-40.	0.7	11
111	Cloning, expression and crystallization of dihydrodipicolinate reductase from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 57-60.	0.7	11
112	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the psychrophile <i>Shewanella benthica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1511-1516.	0.7	10
113	Substrate-mediated Stabilization of a Tetrameric Drug Target Reveals Achilles Heel in Anthrax. <i>Journal of Biological Chemistry</i> , 2010, 285, 5188-5195.	1.6	44
114	The quaternary structure of pyruvate kinase type 1 from <i>Escherichia coli</i> at low nanomolar concentrations. <i>Biochimie</i> , 2010, 92, 116-120.	1.3	17
115	Development of the procedures for high-yield expression and rapid purification of active recombinant Csk-homologous kinase (CHK): Comparison of the catalytic activities of CHK and CSK. <i>Protein Expression and Purification</i> , 2010, 74, 139-147.	0.6	10
116	Exploring the dihydrodipicolinate synthase tetramer: How resilient is the dimer-dimer interface?. <i>Archives of Biochemistry and Biophysics</i> , 2010, 494, 58-63.	1.4	30
117	Disruption of quaternary structure in <i>Escherichia coli</i> dihydrodipicolinate synthase (DHDPS) generates a functional monomer that is no longer inhibited by lysine. <i>Archives of Biochemistry and Biophysics</i> , 2010, 503, 202-206.	1.4	12
118	How essential is the "essential" active-site lysine in dihydrodipicolinate synthase?. <i>Biochimie</i> , 2010, 92, 837-845.	1.3	33
119	Aromatic residues in the C-terminal helix of human apoC-I mediate phospholipid interactions and particle morphology. <i>Journal of Lipid Research</i> , 2009, 50, 1384-1394.	2.0	13
120	Crystallization and preliminary X-ray analysis of dihydrodipicolinate synthase from <i>Clostridium botulinum</i> in the presence of its substrate pyruvate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 253-255.	0.7	14
121	Expression, purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase from <i>Bacillus anthracis</i> in the presence of pyruvate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 188-191.	0.7	17
122	Specificity versus catalytic potency: The role of threonine 44 in <i>Escherichia coli</i> dihydrodipicolinate synthase mediated catalysis. <i>Biochimie</i> , 2009, 91, 1036-1044.	1.3	12
123	The C-terminal domain of <i>Escherichia coli</i> dihydrodipicolinate synthase (DHDPS) is essential for maintenance of quaternary structure and efficient catalysis. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 802-806.	1.0	17
124	Federated repositories of X-ray diffraction images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 810-814.	2.5	42
125	The purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase from <i>Clostridium botulinum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 206-208.	0.7	14
126	Purification, crystallization and preliminary X-ray diffraction studies to near-atomic resolution of dihydrodipicolinate synthase from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 659-661.	0.7	20



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127	The high-resolution structure of dihydrodipicolinate synthase from <i>Escherichia coli</i> bound to its first substrate, pyruvate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1092-1095.	0.7	20
128	Irreversible inhibition of dihydrodipicolinate synthase by 4-oxo-heptenedioic acid analogues. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 9975-9983.	1.4	31
129	Inhibiting dihydrodipicolinate synthase across species: Towards specificity for pathogens?. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 842-844.	1.0	42
130	Conformationally constrained diketopimelic acid analogues as inhibitors of dihydrodipicolinate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 460-463.	1.0	36
131	Conserved main-chain peptide distortions: A proposed role for Ile203 in catalysis by dihydrodipicolinate synthase. <i>Protein Science</i> , 2008, 17, 2080-2090.	3.1	31
132	Mutating the Tight-Dimer Interface of Dihydrodipicolinate Synthase Disrupts the Enzyme Quaternary Structure: Toward a Monomeric Enzyme. <i>Biochemistry</i> , 2008, 47, 12108-12117.	1.2	15
133	Evolution of Quaternary Structure in a Homotetrameric Enzyme. <i>Journal of Molecular Biology</i> , 2008, 380, 691-703.	2.0	77
134	Structure and Evolution of a Novel Dimeric Enzyme from a Clinically Important Bacterial Pathogen. <i>Journal of Biological Chemistry</i> , 2008, 283, 27598-27603.	1.6	85
135	Crystal structure and kinetic study of dihydrodipicolinate synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2008, 411, 351-360.	1.7	74
136	Two New Irreversible Inhibitors of Dihydrodipicolinate Synthase: Diethyl (E,E)-4-Oxo-2,5-heptadienedioate and Diethyl (E)-4-Oxo-2-heptenedioate.. <i>ChemInform</i> , 2005, 36, no.	0.1	0
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138	The crystal structures of native and (S)-lysine-bound dihydrodipicolinate synthase from <i>Escherichia coli</i> with improved resolution show new features of biological significance. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1116-1124.	2.5	77
139	Role of Arginine 138 in the Catalysis and Regulation of <i>Escherichia coli</i> Dihydrodipicolinate Synthase. <i>Biochemistry</i> , 2005, 44, 13007-13013.	1.2	51
140	Dihydrodipicolinate synthase (DHDPS) from <i>Escherichia coli</i> displays partial mixed inhibition with respect to its first substrate, pyruvate. <i>Biochimie</i> , 2004, 86, 311-315.	1.3	47
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142	Dihydrodipicolinate synthase is not inhibited by its substrate, (S)-aspartate beta-semialdehyde. <i>Biochemical Journal</i> , 2004, 377, 757-762.	1.7	39
143	Two complete syntheses of (S)-aspartate semi-aldehyde and demonstration that ̢ <sup>2</sup> -tetrahydroisophthalic acid is a non-competitive inhibitor of dihydrodipicolinate synthase. <i>Arkivoc</i> , 2004, 2004, 166-177.	0.3	10
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