

# Christopher Davies

## List of Publications by Year in descending order

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45  
papers

1,555  
citations

304368

22  
h-index

315357

38  
g-index

45  
all docs

45  
docs citations

45  
times ranked

1720  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tetracyclines and bone: Unclear actions with potentially lasting effects. <i>Bone</i> , 2022, 159, 116377.	1.4	22
2	Molecular Features of Cephalosporins Important for Activity against Antimicrobial-Resistant <i>Neisseria gonorrhoeae</i> . <i>ACS Infectious Diseases</i> , 2021, 7, 293-308.	1.8	7
3	High-resolution crystal structure of the <i>Borrelia burgdorferi</i> PlzA protein in complex with c-di-GMP: new insights into the interaction of c-di-GMP with the novel xPilZ domain. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	7
4	Mutations in PBP2 from ceftriaxone-resistant <i>Neisseria gonorrhoeae</i> alter the dynamics of the $\beta$ 3 $\alpha$ 24 loop to favor a low-affinity drug-binding state. <i>Journal of Biological Chemistry</i> , 2021, 297, 101188.	1.6	7
5	Development and optimization of OspC chimeritope vaccinogens for Lyme disease. <i>Vaccine</i> , 2020, 38, 1915-1924.	1.7	23
6	Mutations in penicillin-binding protein 2 from cephalosporin-resistant <i>Neisseria gonorrhoeae</i> hinder ceftriaxone acylation by restricting protein dynamics. <i>Journal of Biological Chemistry</i> , 2020, 295, 7529-7543.	1.6	20
7	Editorial: Bacterial Mechanisms of Antibiotic Resistance: A Structural Perspective. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 71.	1.6	6
8	Recognition of the $\beta$ -lactam carboxylate triggers acylation of <i>Neisseria gonorrhoeae</i> penicillin-binding protein 2. <i>Journal of Biological Chemistry</i> , 2019, 294, 14020-14032.	1.6	18
9	New views on an old enzyme: allosteric regulation and evolution of archaeal pyruvate kinases. <i>FEBS Journal</i> , 2019, 286, 2471-2489.	2.2	17
10	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments of N-acetylmuramyl-l-alanine amidase (AmiC) N-terminal domain (NTD) from <i>Neisseria gonorrhoeae</i> . <i>Biomolecular NMR Assignments</i> , 2019, 13, 63-66.	0.4	0
11	The Structure of the Biofilm-controlling Response Regulator BfmR from <i>Acinetobacter baumannii</i> Reveals Details of Its DNA-binding Mechanism. <i>Journal of Molecular Biology</i> , 2018, 430, 806-821.	2.0	47
12	Molecular mechanism of a covalent allosteric inhibitor of SUMO E1 activating enzyme. <i>Nature Communications</i> , 2018, 9, 5145.	5.8	46
13	Acyl Carrier Protein 3 Is Involved in Oxidative Stress Response in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2244.	1.5	8
14	Alanine 501 Mutations in Penicillin-Binding Protein 2 from <i>Neisseria gonorrhoeae</i> : Structure, Mechanism, and Effects on Cephalosporin Resistance and Biological Fitness. <i>Biochemistry</i> , 2017, 56, 1140-1150.	1.2	39
15	Penicillin-Binding Protein 3 Is Essential for Growth of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	36
16	CNPY2 is a key initiator of the PERK $\alpha$ -CHOP pathway of the unfolded protein response. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 834-839.	3.6	42
17	Amidase Activity of AmiC Controls Cell Separation and Stem Peptide Release and Is Enhanced by NlpD in <i>Neisseria gonorrhoeae</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 10916-10933.	1.6	26
18	A computational model to monitor and predict trends in bacterial resistance. <i>Journal of Global Antimicrobial Resistance</i> , 2015, 3, 174-183.	0.9	9

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19	Structural Effect of the Asp345a Insertion in Penicillin-Binding Protein 2 from Penicillin-Resistant Strains of <i>Neisseria gonorrhoeae</i> . <i>Biochemistry</i> , 2014, 53, 7596-7603.	1.2	18
20	3-Phosphoglycerate Is an Allosteric Activator of Pyruvate Kinase from the Hyperthermophilic Archaeon <i>Pyrobaculum aerophilum</i> . <i>Biochemistry</i> , 2013, 52, 5865-5875.	1.2	11
21	Identification of Amino Acids Conferring High-Level Resistance to Expanded-Spectrum Cephalosporins in the <i>penA</i> Gene from <i>Neisseria gonorrhoeae</i> Strain H041. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3029-3036.	1.4	58
22	A Highly Conserved Interaction Involving the Middle Residue of the SXN Active-Site Motif Is Crucial for Function of Class B Penicillin-Binding Proteins: Mutational and Computational Analysis of PBP 2 from <i>N. gonorrhoeae</i> . <i>Biochemistry</i> , 2012, 51, 2775-2784.	1.2	16
23	The Role of the $\hat{I}^2\hat{A}^{\pm 11}$ Loop in the Active-Site Dynamics of Acylated Penicillin-Binding Protein A from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2012, 418, 316-330.	2.0	23
24	High-Throughput Screening for Novel Inhibitors of <i>Neisseria gonorrhoeae</i> Penicillin-Binding Protein 2. <i>PLoS ONE</i> , 2012, 7, e44918.	1.1	21
25	Structural Mechanisms of $\hat{I}^2$ -Lactam Antibiotic Resistance in Penicillin-Binding Proteins. , 2012, , 397-425.		7
26	Biochemical characterization of PqsD activity in alkylquinolone biosynthesis in <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , 2012, 26, 964.7.	0.2	1
27	Molecular and Structural Analysis of Mosaic Variants of Penicillin-Binding Protein 2 Conferring Decreased Susceptibility to Expanded-Spectrum Cephalosporins in <i>Neisseria gonorrhoeae</i> : Role of Epistatic Mutations. <i>Biochemistry</i> , 2010, 49, 8062-8070.	1.2	114
28	Unusual Conformation of the SxN Motif in the Crystal Structure of Penicillin-Binding Protein A from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2010, 398, 54-65.	2.0	26
29	Crystal Structures of Covalent Complexes of $\hat{I}^2$ -Lactam Antibiotics with <i>Escherichia coli</i> Penicillin-Binding Protein 5: Toward an Understanding of Antibiotic Specificity. <i>Biochemistry</i> , 2010, 49, 8094-8104.	1.2	46
30	Crystal Structures of Penicillin-binding Protein 2 from Penicillin-susceptible and -resistant Strains of <i>Neisseria gonorrhoeae</i> Reveal an Unexpectedly Subtle Mechanism for Antibiotic Resistance. <i>Journal of Biological Chemistry</i> , 2009, 284, 1202-1212.	1.6	76
31	Genetics of Chromosomally Mediated Intermediate Resistance to Ceftriaxone and Cefixime in <i>Neisseria gonorrhoeae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3744-3751.	1.4	139
32	Direct Binding of Glyceraldehyde 3-Phosphate Dehydrogenase to Telomeric DNA Protects Telomeres against Chemotherapy-Induced Rapid Degradation. <i>Journal of Molecular Biology</i> , 2009, 394, 789-803.	2.0	75
33	A large displacement of the SXN motif of Cys115-modified penicillin-binding protein 5 from <i>Escherichia coli</i> . <i>Biochemical Journal</i> , 2005, 392, 55-63.	1.7	15
34	Mutagenesis of catalytically important residues of cupin type phosphoglucose isomerase from <i>Archaeoglobus fulgidus</i> . <i>FEBS Journal</i> , 2005, 272, 6266-6275.	2.2	10
35	Crystal Structure of <i>Escherichia coli</i> Penicillin-Binding Protein 5 Bound to a Tripeptide Boronic Acid Inhibitor: A Role for Ser-110 in Deacylation. <i>Biochemistry</i> , 2005, 44, 8207-8217.	1.2	75
36	A Novel Phosphoglucose Isomerase (PGI)/Phosphomannose Isomerase from the Crenarchaeon <i>Pyrobaculum aerophilum</i> Is a Member of the PGI Superfamily. <i>Journal of Biological Chemistry</i> , 2004, 279, 39838-39845.	1.6	24

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37	Structural Basis for Phosphomannose Isomerase Activity in Phosphoglucose Isomerase from <i>Pyrobaculum aerophilum</i> : A Subtle Difference between Distantly Related Enzymes. <i>Biochemistry</i> , 2004, 43, 14088-14095.	1.2	22
38	The Crystal Structure of Mouse Phosphoglucose Isomerase at 1.6 Å Resolution and its Complex with Glucose 6-Phosphate Reveals the Catalytic Mechanism of Sugar Ring Opening. <i>Journal of Molecular Biology</i> , 2004, 342, 847-860.	2.0	44
39	Structure of native phosphoglucose isomerase from rabbit: conformational changes associated with catalytic function. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 453-465.	2.5	13
40	The structure of human phosphoglucose isomerase complexed with a transition-state analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1111-1113.	2.5	25
41	Structural Evidence for a Hydride Transfer Mechanism of Catalysis in Phosphoglucose Isomerase from <i>Pyrococcus furiosus</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 47261-47268.	1.6	37
42	Crystal Structure of Wild-type Penicillin-binding Protein 5 from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 52826-52833.	1.6	83
43	Crystal structure of phosphoglucose isomerase from pig muscle and its complex with 5-phosphoarabinonate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 577-579.	1.5	27
44	The crystal structure of human phosphoglucose isomerase at 1.6 Å resolution: implications for catalytic mechanism, cytokine activity and haemolytic anaemia. <i>Journal of Molecular Biology</i> , 2001, 309, 447-463.	2.0	98
45	Crystal Structure of a Deacylation-defective Mutant of Penicillin-binding Protein 5 at 2.3 Å Resolution. <i>Journal of Biological Chemistry</i> , 2001, 276, 616-623.	1.6	71