

Anthony J Wilkinson

List of Publications by Year in descending order

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173
papers

11,951
citations

31976

53
h-index

30087

103
g-index

180
all docs

180
docs citations

180
times ranked

11017
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen bonding and biological specificity analysed by protein engineering. <i>Nature</i> , 1985, 314, 235-238.	27.8	1,143
2	AAA+superfamily ATPases: common structure-diverse function. <i>Genes To Cells</i> , 2001, 6, 575-597.	1.2	864
3	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012, 335, 1103-1106.	12.6	809
4	The use of double mutants to detect structural changes in the active site of the tyrosyl-tRNA synthetase (<i>Bacillus stearothermophilus</i>). <i>Cell</i> , 1984, 38, 835-840.	28.9	604
5	Redesigning enzyme structure by site-directed mutagenesis: tyrosyl tRNA synthetase and ATP binding. <i>Nature</i> , 1982, 299, 756-758.	27.8	342
6	Site-directed mutagenesis as a probe of enzyme structure and catalysis: tyrosyl-tRNA synthetase cysteine-35 to glycine-35 mutation. <i>Biochemistry</i> , 1983, 22, 3581-3586.	2.5	296
7	N-myristoyltransferase inhibitors as new leads to treat sleeping sickness. <i>Nature</i> , 2010, 464, 728-732.	27.8	272
8	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> . <i>Metabolism</i> . <i>Science</i> , 2012, 335, 1099-1103.	12.6	255
9	Conserved arginine residues implicated in ATP hydrolysis, nucleotide-sensing, and inter-subunit interactions in AAA and AAA+ ATPases. <i>Journal of Structural Biology</i> , 2004, 146, 106-112.	2.8	233
10	Global profiling of co- and post-translationally N-myristoylated proteomes in human cells. <i>Nature Communications</i> , 2014, 5, 4919.	12.8	199
11	Validation of N-myristoyltransferase as an antimalarial drug target using an integrated chemical biology approach. <i>Nature Chemistry</i> , 2014, 6, 112-121.	13.6	196
12	Dissecting the Role of a Conserved Motif (the Second Region of Homology) in the AAA Family of ATPases. <i>Journal of Biological Chemistry</i> , 1999, 274, 26225-26232.	3.4	179
13	A large increase in enzyme's substrate affinity by protein engineering. <i>Nature</i> , 1984, 307, 187-188.	27.8	154
14	Structural Factors Governing Hemin Dissociation from Metmyoglobin. <i>Biochemistry</i> , 1996, 35, 11300-11309.	2.5	150
15	Phosphorylated aspartate in the structure of a response regulator protein 1. Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 294, 9-15.	4.2	150
16	Stability of Myoglobin: A Model for the Folding of Heme Proteins. <i>Biochemistry</i> , 1994, 33, 11767-11775.	2.5	139
17	The Crystal Structure of the AAA Domain of the ATP-Dependent Protease FtsH of <i>Escherichia coli</i> at 1.5 Å... Resolution. <i>Structure</i> , 2002, 10, 1073-1083.	3.3	127
18	Protein engineering 20 years on. <i>Nature Reviews Molecular Cell Biology</i> , 2002, 3, 964-970.	37.0	123

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19	The role of water in sequence-independent ligand binding by an oligopeptide transporter protein. <i>Nature Structural Biology</i> , 1996, 3, 998-1001.	9.7	119
20	The substrate-binding protein in bacterial ABC transporters: dissecting roles in the evolution of substrate specificity. <i>Biochemical Society Transactions</i> , 2015, 43, 1011-1017.	3.4	115
21	The structure of the cofactor-binding fragment of the LysR family member, CysB: a familiar fold with a surprising subunit arrangement. <i>Structure</i> , 1997, 5, 1017-1032.	3.3	111
22	Lipid spirals in <i>Bacillus subtilis</i> and their role in cell division. <i>Molecular Microbiology</i> , 2008, 68, 1315-1327.	2.5	110
23	Peptide Binding in OppA, the Crystal Structures of the Periplasmic Oligopeptide Binding Protein in the Unliganded Form and in Complex with Lysyllysine. <i>Biochemistry</i> , 1997, 36, 9747-9758.	2.5	99
24	An evolutionary link between sporulation and prophage induction in the structure of a repressor:anti-repressor complex. <i>Journal of Molecular Biology</i> , 1998, 283, 907-912.	4.2	99
25	N-Myristoyltransferase from <i>Leishmania donovani</i> : Structural and Functional Characterisation of a Potential Drug Target for Visceral Leishmaniasis. <i>Journal of Molecular Biology</i> , 2010, 396, 985-999.	4.2	98
26	Analysis of Enzyme Structure and Activity by Protein Engineering. <i>Angewandte Chemie International Edition in English</i> , 1984, 23, 467-473.	4.4	96
27	Probing histidine-substrate interactions in tyrosyl-tRNA synthetase using asparagine and glutamine replacements. <i>Biochemistry</i> , 1985, 24, 5106-5109.	2.5	96
28	Tetramerization and interdomain flexibility of the replication initiation controller YabA enables simultaneous binding to multiple partners. <i>Nucleic Acids Research</i> , 2016, 44, 449-463.	14.5	96
29	Fragment-derived inhibitors of human N-myristoyltransferase block capsid assembly and replication of the common cold virus. <i>Nature Chemistry</i> , 2018, 10, 599-606.	13.6	96
30	Distal pocket polarity in ligand binding to myoglobin: structural and functional characterization of a threonine68 (E11) mutant. <i>Biochemistry</i> , 1991, 30, 6252-6260.	2.5	94
31	The crystal structures of the oligopeptide-binding protein OppA complexed with tripeptide and tetrapeptide ligands. <i>Structure</i> , 1995, 3, 1395-1406.	3.3	91
32	Crystal structure of GerE, the ultimate transcriptional regulator of spore formation in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2001, 306, 759-771.	4.2	90
33	The Crystal Structures of Human S100A12 in Apo Form and in Complex with Zinc: New Insights into S100A12 Oligomerisation. <i>Journal of Molecular Biology</i> , 2009, 391, 536-551.	4.2	90
34	Serine92 (F7) contributes to the control of heme reactivity and stability in myoglobin. <i>Biochemistry</i> , 1993, 32, 5132-5138.	2.5	85
35	Gankyrin: a new oncoprotein and regulator of pRb and p53. <i>Trends in Cell Biology</i> , 2006, 16, 229-233.	7.9	84
36	The Structure of CodY, a GTP- and Isoleucine-responsive Regulator of Stationary Phase and Virulence in Gram-positive Bacteria. <i>Journal of Biological Chemistry</i> , 2006, 281, 11366-11373.	3.4	82

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37	The Crystal Structure of Gankyrin, an Oncoprotein Found in Complexes with Cyclin-dependent Kinase 4, a 19 S Proteasomal ATPase Regulator, and the Tumor Suppressors Rb and p53. <i>Journal of Biological Chemistry</i> , 2004, 279, 1541-1545.	3.4	81
38	dUTPase as a Platform for Antimalarial Drug Design: Structural Basis for the Selectivity of a Class of Nucleoside Inhibitors. <i>Structure</i> , 2005, 13, 329-338.	3.3	81
39	Conservation of Structure and Mechanism in Primary and Secondary Transporters Exemplified by SiaP, a Sialic Acid Binding Virulence Factor from <i>Haemophilus influenzae</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 22212-22222.	3.4	81
40	Selective Inhibitors of Protozoan Protein N-myristoyltransferases as Starting Points for Tropical Disease Medicinal Chemistry Programs. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1625.	3.0	79
41	Distal pocket polarity in ligand binding to myoglobin: Deoxy and carbonmonoxy forms of a threonine68(E11) mutant investigated by x-ray crystallography and infrared spectroscopy. <i>Biochemistry</i> , 1993, 32, 13061-13070.	2.5	74
42	Contributions of residue 45(CD3) and heme-6-propionate to the bimolecular and geminate recombination reactions of myoglobin. <i>Biochemistry</i> , 1991, 30, 4697-4705.	2.5	72
43	An ATP-binding cassette-type cysteine transporter in <i>Campylobacter jejuni</i> inferred from the structure of an extracytoplasmic solute receptor protein. <i>Molecular Microbiology</i> , 2005, 57, 143-155.	2.5	72
44	A fluorescence-based assay for N-myristoyltransferase activity. <i>Analytical Biochemistry</i> , 2012, 421, 342-344.	2.4	69
45	Dimer formation and transcription activation in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2002, 316, 235-245.	4.2	68
46	Domain swapping in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2000, 297, 757-770.	4.2	67
47	Mechanism of Hydrogen Cyanide Binding to Myoglobin. <i>Biochemistry</i> , 1996, 35, 7107-7113.	2.5	66
48	The Structure of the Oligopeptide-binding Protein, AppA, from <i>Bacillus subtilis</i> in Complex with a Nonapeptide. <i>Journal of Molecular Biology</i> , 2005, 345, 879-892.	4.2	66
49	Discovery of Plasmodium vivax N-Myristoyltransferase Inhibitors: Screening, Synthesis, and Structural Characterization of their Binding Mode. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 3578-3582.	6.4	65
50	Expression of HIV-1 gp120 and Human Soluble CD4 by Recombinant Baculoviruses and their Interaction In Vitro. <i>AIDS Research and Human Retroviruses</i> , 1990, 6, 765-773.	1.1	64
51	Alteration of Axial Coordination by Protein Engineering in Myoglobin. <i>Journal of Biological Chemistry</i> , 1995, 270, 15993-16001.	3.4	63
52	Design and Synthesis of High Affinity Inhibitors of Plasmodium falciparum and Plasmodium vivax N-Myristoyltransferases Directed by Ligand Efficiency Dependent Lipophilicity (LELP). <i>Journal of Medicinal Chemistry</i> , 2014, 57, 2773-2788.	6.4	63
53	Higher-throughput approaches to crystallization and crystal structure determination. <i>Biochemical Society Transactions</i> , 2008, 36, 771-775.	3.4	59
54	Discovery of Novel and Ligand-Efficient Inhibitors of Plasmodium falciparum and Plasmodium vivax N-Myristoyltransferase. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 371-375.	6.4	58

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55	Control of Initiation of DNA Replication in <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>Genes</i> , 2017, 8, 22.	2.4	58
56	pBaSysBioII: an integrative plasmid generating GFP transcriptional fusions for high-throughput analysis of gene expression in <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 1600-1608.	1.8	56
57	Design and Synthesis of Inhibitors of <i>Plasmodium falciparum</i> N-Myristoyltransferase, A Promising Target for Antimalarial Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 8879-8890.	6.4	56
58	Structure-Based Design of Potent and Selective <i>Leishmania</i> N-Myristoyltransferase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 8664-8670.	6.4	56
59	Residues in the Distal Heme Pocket of Neuroglobin. <i>Journal of Biological Chemistry</i> , 2004, 279, 5886-5893.	3.4	55
60	Division site recognition in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . <i>FEMS Microbiology Reviews</i> , 2007, 31, 311-326.	8.6	55
61	Structure of components of an intercellular channel complex in sporulating <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5441-5445.	7.1	54
62	Probing the mechanism of ATP hydrolysis and substrate translocation in the AAA protease FtsH by modelling and mutagenesis. <i>Molecular Microbiology</i> , 2001, 39, 890-903.	2.5	53
63	An [Fe(mecam)] ₂ 6 ⁺ Bridge in the Crystal Structure of a Ferric Enterobactin Binding Protein. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 5132-5136.	13.8	51
64	The Crystal Structure of YloQ, a Circularly Permuted GTPase Essential for <i>Bacillus subtilis</i> Viability. <i>Journal of Molecular Biology</i> , 2004, 340, 767-782.	4.2	50
65	Structural and biochemical characterization of a mitochondrial peroxiredoxin from <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2006, 61, 948-959.	2.5	48
66	Crystal structure of dihydrodipicolinate synthase (BA3935) from <i>Bacillus anthracis</i> at 1.94 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 297-301.	2.6	47
67	Tension in haemoglobin revealed by Fe-His(F8) bond rupture in the fully liganded T-state. <i>Journal of Molecular Biology</i> , 1997, 271, 161-167.	4.2	45
68	Structural Basis of the Sulphate Starvation Response in <i>E. coli</i> : Crystal Structure and Mutational Analysis of the Cofactor-binding Domain of the Cbl Transcriptional Regulator. <i>Journal of Molecular Biology</i> , 2006, 364, 309-322.	4.2	45
69	Structure of the catalytic domain of the human mitochondrial Lon protease: Proposed relation of oligomer formation and activity. <i>Protein Science</i> , 2010, 19, 987-999.	7.6	45
70	Fine structure-activity analysis of mutations at position 51 of tyrosyl-tRNA synthetase. <i>Biochemistry</i> , 1985, 24, 5858-5861.	2.5	43
71	Reduction in CD4 binding affinity associated with removal of a single glycosylation site in the external glycoprotein of HIV-2. <i>Virology</i> , 1991, 180, 853-856.	2.4	43
72	Genetic and Biochemical Analysis of the Interaction of <i>Bacillus subtilis</i> CodY with Branched-Chain Amino Acids. <i>Journal of Bacteriology</i> , 2009, 191, 6865-6876.	2.2	42

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73	Crystallisation of the <i>Bacillus subtilis</i> sporulation inhibitor SinR, complexed with its antagonist, SinI. <i>FEBS Letters</i> , 1996, 378, 98-100.	2.8	41
74	Interactions among residues CD3, E7, E10, and E11 in myoglobins: Attempts to simulate the ligand-binding properties of <i>Aplysia</i> myoglobin. <i>Biochemistry</i> , 1995, 34, 8715-8725.	2.5	40
75	The trans-activation domain of the sporulation response regulator Spo0A revealed by X-ray crystallography. <i>Molecular Microbiology</i> , 2000, 38, 198-212.	2.5	40
76	Structural basis for the efficient phosphorylation of AZT-MP (3-azido-3-deoxythymidine) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Journal, 2010, 428, 499-509.	3.7	38
77	Structure and interactions of the <i>Bacillus subtilis</i> sporulation inhibitor of DNA replication, SirA, with domain I of DnaA.	2.5	38
78	Diverse modes of binding in structures of <i>Leishmania major</i> N-myristoyltransferase with selective inhibitors. <i>IUCr</i> , 2014, 1, 250-260.	2.2	38
79	Structural Rearrangement Accompanying Ligand Binding in the GAF Domain of CodY from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2009, 390, 1007-1018.	4.2	37
80	Structure and Organisation of SinR, the Master Regulator of Biofilm Formation in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2011, 411, 597-613.	4.2	37
81	The Spore Coat Protein CotE Facilitates Host Colonization by <i>Clostridium difficile</i> . <i>Journal of Infectious Diseases</i> , 2017, 216, 1452-1459.	4.0	37
82	Oligomerization of the <i>Bacillus subtilis</i> division protein DivIVA. <i>Microbiology (United Kingdom)</i> , 2002, 148, 807-813.	1.8	37
83	Structure of the <i>Bacillus</i> Cell Fate Determinant SpoIIAA in Phosphorylated and Unphosphorylated Forms. <i>Structure</i> , 2001, 9, 605-614.	3.3	36
84	Changes of lipid domains in <i>Bacillus subtilis</i> cells with disrupted cell wall peptidoglycan. <i>FEMS Microbiology Letters</i> , 2011, 325, 92-98.	1.8	36
85	Stabilizing Bound O ₂ in Myoglobin by Valine68(E11) to Asparagine Substitution. <i>Biochemistry</i> , 1998, 37, 15896-15907.	2.5	35
86	Crystallographic and Solution Studies of N-Lithocholyl Insulin: A New Generation of Prolonged-Acting Human Insulins. <i>Biochemistry</i> , 2004, 43, 5987-5995.	2.5	34
87	Small subunits of RNA polymerase: localization, levels and implications for core enzyme composition. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3532-3543.	1.8	34
88	Structure of the Branched-chain Amino Acid and GTP-sensing Global Regulator, CodY, from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 2714-2728.	3.4	34
89	Compensating Stereochemical Changes Allow Murein Tripeptide to Be Accommodated in a Conventional Peptide-binding Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 31512-31521.	3.4	33
90	Site-selective C ¹³ modification of proteins at neutral pH using organocatalyst-mediated cross aldol ligations. <i>Chemical Science</i> , 2018, 9, 5585-5593.	7.4	33

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91	High-resolution x-ray structures of pig metmyoglobin and two CD3 mutants: Mb(Lys45 .fwdarw. Arg) and Mb(Lys45 .fwdarw. Ser). <i>Biochemistry</i> , 1992, 31, 8732-8739.	2.5	31
92	A Bacterial Virulence Factor with a Dual Role as an Adhesin and a Solute-binding Protein: The Crystal Structure at 1.5Å... Resolution of the PEB1a Protein from the Food-borne Human Pathogen <i>Campylobacter jejuni</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 160-171.	4.2	31
93	The crystal structures of macrophage migration inhibitory factor from <i>Plasmodium falciparum</i> and <i>Plasmodium berghei</i> . <i>Protein Science</i> , 2009, 18, 2578-2591.	7.6	30
94	Peptidomimetic inhibitors of <i>N</i> -myristoyltransferase from human malaria and leishmaniasis parasites. <i>Organic and Biomolecular Chemistry</i> , 2014, 12, 8132-8137.	2.8	30
95	Discovery of high affinity inhibitors of <i>Leishmania donovani</i> <i>N</i> -myristoyltransferase. <i>MedChemComm</i> , 2015, 6, 1761-1766.	3.4	30
96	Where asymmetry in gene expression originates. <i>Molecular Microbiology</i> , 2005, 57, 611-620.	2.5	29
97	Structures of <i>Plasmodium falciparum</i> purine nucleoside phosphorylase complexed with sulfate and its natural substrate inosine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1245-1254.	2.5	29
98	A widespread family of serine/threonine protein phosphatases shares a common regulatory switch with proteasomal proteases. <i>ELife</i> , 2017, 6, .	6.0	28
99	Functional Role for a Conserved Aspartate in the Spo0E Signature Motif Involved in the Dephosphorylation of the <i>Bacillus subtilis</i> Sporulation Regulator Spo0A. <i>Journal of Biological Chemistry</i> , 2008, 283, 2962-2972.	3.4	27
100	Structure and non-essential function of glycerol kinase in <i>Plasmodium falciparum</i> blood stages. <i>Molecular Microbiology</i> , 2009, 71, 533-545.	2.5	27
101	Structure of the Phosphatase Domain of the Cell Fate Determinant Spo0E from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2012, 415, 343-358.	4.2	27
102	Mucosal Antibodies to the C Terminus of Toxin A Prevent Colonization of <i>Clostridium difficile</i> . <i>Infection and Immunity</i> , 2017, 85, .	2.2	27
103	The crystal structure of superoxide dismutase from <i>Plasmodium falciparum</i> . <i>BMC Structural Biology</i> , 2006, 6, 20.	2.3	26
104	Apomyoglobin as a molecular recognition surface: expression, reconstitution and crystallization of recombinant porcine myoglobin in <i>Escherichia coli</i> . <i>Protein Engineering, Design and Selection</i> , 1988, 2, 233-237.	2.1	25
105	Quaternary re-arrangement analysed by spectral enhancement: the interaction of a sporulation repressor with its antagonist 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 293, 997-1004.	4.2	25
106	The response regulator Spo0A from <i>Bacillus subtilis</i> is efficiently phosphorylated in <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2003, 223, 153-157.	1.8	25
107	Dimer-induced signal propagation in Spo0A. <i>Molecular Microbiology</i> , 2004, 53, 829-842.	2.5	24
108	Application of high-throughput technologies to a structural proteomics-type analysis of <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1267-1275.	2.5	24

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109	Impact of CodY protein on metabolism, sporulation and virulence in <i>Clostridioides difficile</i> ribotype 027. <i>PLoS ONE</i> , 2019, 14, e0206896.	2.5	24
110	CRYSTAL STRUCTURES OF PERIPLASMIC SOLUTE-BINDING PROTEINS IN ABC TRANSPORT COMPLEXES ILLUMINATE THEIR FUNCTION. , 2003, , 187-207.		23
111	EARLY FLOWERING3 sub-nuclear localization responds to changes in ambient temperature. <i>Plant Physiology</i> , 2021, 187, 2352-2355.	4.8	21
112	Engineering a Ligand Binding Pocket into a Four-Helix Bundle Protein Cytochrome b562. <i>Journal of the American Chemical Society</i> , 2001, 123, 512-513.	13.7	19
113	The GTPase, CpgA(YloQ), a putative translation factor, is implicated in morphogenesis in <i>Bacillus subtilis</i> . <i>Molecular Genetics and Genomics</i> , 2006, 275, 409-420.	2.1	19
114	Crystallization of the GTP-dependent transcriptional regulator CodY from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 155-157.	2.5	17
115	Structure of the virulence-associated protein VapD from the intracellular pathogen <i>Rhodococcus equi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2139-2151.	2.5	17
116	The <i>Rhodococcus equi</i> virulence protein VapA disrupts endolysosome function and stimulates lysosome biogenesis. <i>MicrobiologyOpen</i> , 2017, 6, e00416.	3.0	17
117	An oscillating Min system in <i>Bacillus subtilis</i> influences asymmetrical septation during sporulation. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1972-1981.	1.8	17
118	Morphogenic Protein RodZ Interacts with Sporulation Specific SpoII E in <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2016, 11, e0159076.	2.5	17
119	Raman and CD Spectroscopy of Recombinant 68-kDa DNA Human Topoisomerase I and Its Complex with Suicide DNA Substrate. <i>Biochemistry</i> , 1998, 37, 14630-14642.	2.5	16
120	Cysteine Thiolate Coordination in the Ferrous CO Complex of an Engineered Cytochrome b562. <i>Journal of the American Chemical Society</i> , 2001, 123, 2458-2459.	13.7	16
121	Structure of purine nucleoside phosphorylase (DeoD) from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 459-462.	0.7	16
122	The molecular basis of thioalcohol production in human body odour. <i>Scientific Reports</i> , 2020, 10, 12500.	3.3	16
123	Novel Thienopyrimidine Inhibitors of <i>Leishmania</i> N-Myristoyltransferase with On-Target Activity in Intracellular Amastigotes. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 7740-7765.	6.4	15
124	<i>Leishmania</i> differentiation requires ubiquitin conjugation mediated by a UBC2-UEV1 E2 complex. <i>PLoS Pathogens</i> , 2020, 16, e1008784.	4.7	15
125	A new mutation in Spo0A with intragenic suppressors in the effector domain. <i>FEMS Microbiology Letters</i> , 2000, 185, 123-128.	1.8	14
126	Structural Characterization of Spo0E-like Protein-aspartic Acid Phosphatases That Regulate Sporulation in Bacilli. <i>Journal of Biological Chemistry</i> , 2006, 281, 37993-38003.	3.4	14

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127	Structural characterisation of the virulence-associated protein VapG from the horse pathogen <i>Rhodococcus equi</i> . <i>Veterinary Microbiology</i> , 2015, 179, 42-52.	1.9	14
128	Structure-guided optimization of quinoline inhibitors of Plasmodium N-myristoyltransferase. <i>MedChemComm</i> , 2017, 8, 191-197.	3.4	14
129	Inversion of Axial Coordination in Myoglobin to Create a "Proximal" Ligand Binding Pocket. <i>Biochemistry</i> , 2003, 42, 10191-10199.	2.5	13
130	Discovery of pyridyl-based inhibitors of Plasmodium falciparum N-myristoyltransferase. <i>MedChemComm</i> , 2015, 6, 1767-1772.	3.4	13
131	Crystallization of the periplasmic oligopeptide-binding protein of <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 1988, 204, 493-494.	4.2	12
132	Crystallization of gankyrin, an oncoprotein that interacts with CDK4 and the S6b (rpt3) ATPase of the 19S regulator of the 26S proteasome. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1294-1295.	2.5	12
133	Crystal structure of PurE (BA0288) from <i>Bacillus anthracis</i> at 1.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 674-676.	2.6	12
134	The Structure and Interactions of SpoIIA and SpoIIB, a Toxin-Antitoxin System in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 6808-6819.	3.4	12
135	MpaA is a murein-tripeptide-specific zinc carboxypeptidase that functions as part of a catabolic pathway for peptidoglycan-derived peptides in <i>l³-proteobacteria</i> . <i>Biochemical Journal</i> , 2012, 448, 329-341.	3.7	12
136	Accommodating structurally diverse peptides in proteins. <i>Chemistry and Biology</i> , 1996, 3, 519-524.	6.0	11
137	Expression of soluble, active fragments of the morphogenetic protein SpoIIE from <i>Bacillus subtilis</i> using a library-based construct screen. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 817-825.	2.1	10
138	Crystal and Solution Studies Reveal That the Transcriptional Regulator AcnR of <i>Corynebacterium glutamicum</i> Is Regulated by Citrate-Mg ²⁺ Binding to a Non-canonical Pocket. <i>Journal of Biological Chemistry</i> , 2013, 288, 15800-15812.	3.4	10
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