

Anthony J Wilkinson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9373113/publications.pdf>

Version: 2024-02-01

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	Bromodomain factor 5 is an essential regulator of transcription in Leishmania. Nature Communications, 2022, 13, .	12.8	8
2	EARLY FLOWERING3 sub-nuclear localization responds to changes in ambient temperature. Plant Physiology, 2021, 187, 2352-2355.	4.8	21
3	Alanine-scanning mutagenesis of protein mannosyl-transferase from Streptomyces coelicolor reveals strong activity-stability correlation. Microbiology (United Kingdom), 2021, 167, .	1.8	5
4	Drug discovery in leishmaniasis using protein lipidation as a target. Biophysical Reviews, 2021, 13, 1139-1146.	3.2	6
5	The molecular basis of thioalcohol production in human body odour. Scientific Reports, 2020, 10, 12500.	3.3	16
6	Single-molecule optical microscopy of protein dynamics and computational analysis of images to determine cell structure development in differentiating Bacillus subtilis. Computational and Structural Biotechnology Journal, 2020, 18, 1474-1486.	4.1	8
7	Novel Thienopyrimidine Inhibitors of <i>Leishmania N</i> -Myristoyltransferase with On-Target Activity in Intracellular Amastigotes. Journal of Medicinal Chemistry, 2020, 63, 7740-7765.	6.4	15
8	Leishmania differentiation requires ubiquitin conjugation mediated by a UBC2-UEV1 E2 complex. PLoS Pathogens, 2020, 16, e1008784.	4.7	15
9	Crystal structures of the GH18 domain of the bifunctional peroxiredoxin-chitinase CotE from <i>Clostridium difficile</i> . Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 241-249.	0.8	1
10	Impact of CodY protein on metabolism, sporulation and virulence in Clostridioides difficile ribotype 027. PLoS ONE, 2019, 14, e0206896.	2.5	24
11	Crystal structure of the putative peptide-binding protein AppA from <i>Clostridium difficile</i> . Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 246-253.	0.8	10
12	Identification of essential residues for polyprenol phosphate mannose synthase and protein O-mannosyl transferase activities required for protein glycosylation in Streptomyces. Access Microbiology, 2019, 1, .	0.5	0
13	A rapid introduction to neurological biochemistry using Drosophila melanogaster. Invertebrate Neuroscience, 2018, 18, 15.	1.8	0
14	Site-selective C ¹³ modification of proteins at neutral pH using organocatalyst-mediated cross aldol ligations. Chemical Science, 2018, 9, 5585-5593.	7.4	33
15	Fragment-derived inhibitors of human N-myristoyltransferase block capsid assembly and replication of the common cold virus. Nature Chemistry, 2018, 10, 599-606.	13.6	96
16	Mucosal Antibodies to the C Terminus of Toxin A Prevent Colonization of Clostridium difficile. Infection and Immunity, 2017, 85, .	2.2	27
17	Structure of the Branched-chain Amino Acid and GTP-sensing Global Regulator, CodY, from Bacillus subtilis. Journal of Biological Chemistry, 2017, 292, 2714-2728.	3.4	34
18	Structure-guided optimization of quinoline inhibitors of Plasmodium N-myristoyltransferase. MedChemComm, 2017, 8, 191-197.	3.4	14

#	ARTICLE	IF	CITATIONS
19	The <i>Rhodococcus equi</i> virulence protein VapA disrupts endolysosome function and stimulates lysosome biogenesis. <i>MicrobiologyOpen</i> , 2017, 6, e00416.	3.0	17
20	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
21	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
22	A widespread family of serine/threonine protein phosphatases shares a common regulatory switch with proteasomal proteases. <i>ELife</i> , 2017, 6, .	6.0	28
23	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
24	Morphogenic Protein RodZ Interacts with Sporulation Specific SpoII ϵ in <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2016, 11, e0159076.	2.5	17
25	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
26	Structure mediation in substrate binding and post-translational processing of penicillin acylases: Information from mutant structures of <i>Kluyvera citrophila</i> penicillin G acylase. <i>Protein Science</i> , 2015, 24, 1660-1670.	7.6	10
27	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
28	Discovery of pyridyl-based inhibitors of <i>Plasmodium falciparum</i> N-myristoyltransferase. <i>MedChemComm</i> , 2015, 6, 1767-1772.	3.4	13
29	Discovery of high affinity inhibitors of <i>Leishmania donovani</i> N-myristoyltransferase. <i>MedChemComm</i> , 2015, 6, 1761-1766.	3.4	30
30	Structure and interactions of the <i>Bacillus subtilis</i> sporulation inhibitor of DNA replication, SirA, with domain I of DnaA. <i>Molecular Microbiology</i> , 2014, 93, 975-991.	2.5	38
31	Global profiling of co- and post-translationally N-myristoylated proteomes in human cells. <i>Nature Communications</i> , 2014, 5, 4919.	12.8	199
32	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
33	Design and Synthesis of High Affinity Inhibitors of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> N-Myristoyltransferases Directed by Ligand Efficiency Dependent Lipophilicity (LELP). <i>Journal of Medicinal Chemistry</i> , 2014, 57, 2773-2788.	6.4	63
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Peptidomimetic inhibitors of N-myristoyltransferase from human malaria and leishmaniasis parasites. <i>Organic and Biomolecular Chemistry</i> , 2014, 12, 8132-8137.	2.8	30
38	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
39	Crystal and Solution Studies Reveal That the Transcriptional Regulator AcnR of Corynebacterium glutamicum 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
40	Cloning, overexpression, crystallization and preliminary X-ray crystallographic analysis of a slow-processing mutant of penicillin G acylase from <i>Kluyvera citrophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 925-929.	0.7	6
41	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
42	MpaA is a murein-tripeptide-specific zinc carboxypeptidase that functions as part of a catabolic pathway for peptidoglycan-derived peptides in <i>I³-proteobacteria</i> . <i>Biochemical Journal</i> , 2012, 448, 329-341.	3.7	12
43	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
44	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. <i>Science</i> , 2012, 335, 1099-1103.	12.6	255
45	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
46	Structure of the Phosphatase Domain of the Cell Fate Determinant SpoII E from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2012, 415, 343-358.	4.2	27
47	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012, 335, 1103-1106.	12.6	809
48	Design and Synthesis of Inhibitors of Plasmodium falciparum N-Myristoyltransferase, A Promising Target for Antimalarial Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 8879-8890.	6.4	56
49	High-resolution temporal analysis of global promoter activity in <i>Bacillus subtilis</i> . <i>Methods in Microbiology</i> , 2012, 39, 1-26.	0.8	2
50	A fluorescence-based assay for N-myristoyltransferase activity. <i>Analytical Biochemistry</i> , 2012, 421, 342-344.	2.4	69
51	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
52	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
53	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
54	The Selected Papers of Sir Alan Fersht: Development of Protein Engineering. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 225-227.	2.1	0

#	ARTICLE	IF	CITATIONS
55	The Structure and Interactions of SpoIIISA and SpoIIISB, a Toxin-Antitoxin System in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 6808-6819.	3.4	12
56	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
57	Structural basis for the efficient phosphorylation of AZT-MP (3-azido-3-deoxythymidine) Tj ETQq1 1 0.784314 rgBT /Overlock I <i>Journal</i> , 2010, 428, 499-509.	3.7	38
58	The <i>Corynebacterium glutamicum</i> aconitase repressor: scratching around for crystals. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1074-1077.	0.7	3
59	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
60	N-myristoyltransferase inhibitors as new leads to treat sleeping sickness. <i>Nature</i> , 2010, 464, 728-732.	27.8	272
61	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
62	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
63	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
64	Expression and localization of SpoIIISA toxin during the life cycle of <i>Bacillus subtilis</i> . <i>Research in Microbiology</i> , 2010, 161, 750-756.	2.1	5
65	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
66	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
67	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
68	The structure of Rph, an exoribonuclease from <i>Bacillus anthracis</i> , at 1.7 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 2-7.	0.7	0
69	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
70	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
71	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
72	Lipid spirals in <i>Bacillus subtilis</i> and their role in cell division. <i>Molecular Microbiology</i> , 2008, 68, 1315-1327.	2.5	110

#	ARTICLE	IF	CITATIONS
73	Higher-throughput approaches to crystallization and crystal structure determination. <i>Biochemical Society Transactions</i> , 2008, 36, 771-775.	3.4	59
74	Functional Role for a Conserved Aspartate in the SpoOE Signature Motif Involved in the Dephosphorylation of the <i>Bacillus subtilis</i> Sporulation Regulator SpoOA. <i>Journal of Biological Chemistry</i> , 2008, 283, 2962-2972.	3.4	27
75	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
76	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
77	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
78	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
79	The crystal structure of superoxide dismutase from <i>Plasmodium falciparum</i> . <i>BMC Structural Biology</i> , 2006, 6, 20.	2.3	26
80	Structural and biochemical characterization of a mitochondrial peroxiredoxin from <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2006, 61, 948-959.	2.5	48
81	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
82	Gankyrin: a new oncoprotein and regulator of pRb and p53. <i>Trends in Cell Biology</i> , 2006, 16, 229-233.	7.9	84
83	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
84	Structural Characterization of SpoOE-like Protein-aspartic Acid Phosphatases That Regulate Sporulation in Bacilli. <i>Journal of Biological Chemistry</i> , 2006, 281, 37993-38003.	3.4	14
85	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
86	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
87	Where asymmetry in gene expression originates. <i>Molecular Microbiology</i> , 2005, 57, 611-620.	2.5	29
88	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
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Structures of two superoxide dismutases from <i>Bacillus anthracis</i> reveal a novel active centre. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 621-624.	0.7	8
93	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
94	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
95	The Structure of Bypass of Forespore C, an Intercompartmental Signaling Factor during Sporulation in <i>Bacillus</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 36214-36220.	3.4	7
96	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
97	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
98	Residues in the Distal Heme Pocket of Neuroglobin. <i>Journal of Biological Chemistry</i> , 2004, 279, 5886-5893.	3.4	55
99	Dimer-induced signal propagation in Spo0A. <i>Molecular Microbiology</i> , 2004, 53, 829-842.	2.5	24
100	Crystallization of the oligopeptide-binding protein AppA from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 175-177.	2.5	2
101	Crystallization of YloQ, a GTPase of unknown function essential for <i>Bacillus subtilis</i> viability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 329-330.	2.5	2
102	Crystallization and preliminary crystallographic studies of the cofactor-binding domain of the LysR-type transcriptional regulator Cbl from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1654-1657.	2.5	7
103	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
104	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
105	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
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	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
108	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

#	ARTICLE	IF	CITATIONS
109	Inversion of Axial Coordination in Myoglobin to Create a "Proximal" Ligand Binding Pocket. <i>Biochemistry</i> , 2003, 42, 10191-10199.	2.5	13
110	CRYSTAL STRUCTURES OF PERIPLASMIC SOLUTE-BINDING PROTEINS IN ABC TRANSPORT COMPLEXES ILLUMINATE THEIR FUNCTION. , 2003, , 187-207.		23
111	Dimer formation and transcription activation in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2002, 316, 235-245.	4.2	68
112	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
113	Crystallization of the AAA domain of the ATP-dependent protease FtsH of <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1066-1067.	2.5	7
114	Bacillus subtilis division protein DivIVA " screen for stable oligomer state conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1542-1543.	2.5	8
115	Protein engineering 20 years on. <i>Nature Reviews Molecular Cell Biology</i> , 2002, 3, 964-970.	37.0	123
116	Oligomerization of the Bacillus subtilis division protein DivIVA. <i>Microbiology (United Kingdom)</i> , 2002, 148, 807-813.	1.8	37
117	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
118	Lessons and questions from the structure of the Spo0A activation domain: Response. <i>Trends in Microbiology</i> , 2001, 9, 150-151.	7.7	5
119	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
120	Crystallization of full-length CysB of <i>Klebsiella aerogenes</i> , a LysR-type transcriptional regulator. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 260-262.	2.5	7
121	Crystallization and preliminary X-ray analysis of the sporulation factor SpoIIAA in its native and phosphorylated forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 292-295.	2.5	1
122	AAA+superfamily ATPases: common structure-diverse function. <i>Genes To Cells</i> , 2001, 6, 575-597.	1.2	864
123	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
124	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
125	Structure of the Bacillus Cell Fate Determinant SpoIIAA in Phosphorylated and Unphosphorylated Forms. <i>Structure</i> , 2001, 9, 605-614.	3.3	36
126	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

#	ARTICLE	IF	CITATIONS
127	A new mutation in spo0A with intragenic suppressors in the effector domain. FEMS Microbiology Letters, 2000, 185, 123-128.	1.8	14
128	Domain swapping in the sporulation response regulator Spo0A. Journal of Molecular Biology, 2000, 297, 757-770.	4.2	67
129	A new mutation in spo0A with intragenic suppressors in the effector domain. FEMS Microbiology Letters, 2000, 185, 123-128.	1.8	1
130	Dissecting the Role of a Conserved Motif (the Second Region of Homology) in the AAA Family of ATPases. Journal of Biological Chemistry, 1999, 274, 26225-26232.	3.4	179
131	Solution of the structure of the cofactor-binding fragment of CysB: a struggle against non-isomorphism. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 369-378.	2.5	7
132	Crystallization of the regulatory and effector domains of the key sporulation response regulator Spo0A. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 671-676.	2.5	7
133	Quaternary re-arrangement analysed by spectral enhancement: the interaction of a sporulation repressor with its antagonist 1 Edited by J. Karn. Journal of Molecular Biology, 1999, 293, 997-1004.	4.2	25
134	Phosphorylated aspartate in the structure of a response regulator protein 1 Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 294, 9-15.	4.2	150
135	Bacillus subtilis regulatory protein GerE. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1453-1455.	2.5	3
136	Stabilizing Bound O ₂ in Myoglobin by Valine68(E11) to Asparagine Substitution. Biochemistry, 1998, 37, 15896-15907.	2.5	35
137	Raman and CD Spectroscopy of Recombinant 68-kDa DNA Human Topoisomerase I and Its Complex with Suicide DNA Substrate. Biochemistry, 1998, 37, 14630-14642.	2.5	16
138	An evolutionary link between sporulation and prophage induction in the structure of a repressor:anti-repressor complex. Journal of Molecular Biology, 1998, 283, 907-912.	4.2	99
139	Peptide Binding in OppA, the Crystal Structures of the Periplasmic Oligopeptide Binding Protein in the Unliganded Form and in Complex with Lysyllysine. Biochemistry, 1997, 36, 9747-9758.	2.5	99
140	Tension in haemoglobin revealed by Fe-His(F8) bond rupture in the fully liganded T-state. Journal of Molecular Biology, 1997, 271, 161-167.	4.2	45
141	The structure of the cofactor-binding fragment of the LysR family member, CysB: a familiar fold with a surprising subunit arrangement. Structure, 1997, 5, 1017-1032.	3.3	111
142	Mechanism of Hydrogen Cyanide Binding to Myoglobin. Biochemistry, 1996, 35, 7107-7113.	2.5	66
143	Structural Factors Governing Hemin Dissociation from Metmyoglobin. Biochemistry, 1996, 35, 11300-11309.	2.5	150
144	Crystallisation of the Bacillus subtilis sporulation inhibitor SinR, complexed with its antagonist, SinI. FEBS Letters, 1996, 378, 98-100.	2.8	41

#	ARTICLE	IF	CITATIONS
145	Site-directed mutagenesis of the base recognition loop of ribonuclease from <i>Bacillus intermedius</i> (binase). <i>FEBS Letters</i> , 1996, 384, 143-146.	2.8	6
146	Crystallization and preliminary crystallographic analysis of the DNA gyrase B protein from <i>B. stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 1216-1218.	2.5	2
147	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
148	Accommodating structurally diverse peptides in proteins. <i>Chemistry and Biology</i> , 1996, 3, 519-524.	6.0	11
149	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
150	Alteration of Axial Coordination by Protein Engineering in Myoglobin. <i>Journal of Biological Chemistry</i> , 1995, 270, 15993-16001.	3.4	63
151	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
152	Crystallization of a DNA and N-acetylserine Binding Fragment (Residues 1 to 233) of <i>Klebsiella aerogenes</i> CysB Protein, a Member of the LysR Family. <i>Journal of Molecular Biology</i> , 1994, 235, 1159-1161.	4.2	6
153	Stability of Myoglobin: A Model for the Folding of Heme Proteins. <i>Biochemistry</i> , 1994, 33, 11767-11775.	2.5	139
154	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
155	Serine92 (F7) contributes to the control of heme reactivity and stability in myoglobin. <i>Biochemistry</i> , 1993, 32, 5132-5138.	2.5	85
156	High-resolution x-ray structures of pig metmyoglobin and two CD3 mutants: Mb(Lys45 → Arg) and Mb(Lys45 → Ser). <i>Biochemistry</i> , 1992, 31, 8732-8739.	2.5	31
157	Oxidation of residue 45 mutant forms of pig deoxymyoglobin with $[Fe(CN)_6]^{3-}$. <i>Journal of Inorganic Biochemistry</i> , 1992, 48, 79-84.	3.5	3
158	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
159	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
160	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
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	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
164	Hydrogen bonding and biological specificity analysed by protein engineering. <i>Nature</i> , 1985, 314, 235-238.	27.8	1,143
165	Engineering of tyrosyl tRNA synthetase. <i>Biochimie</i> , 1985, 67, 737-743.	2.6	2
166	Fine structure-activity analysis of mutations at position 51 of tyrosyl-tRNA synthetase. <i>Biochemistry</i> , 1985, 24, 5858-5861.	2.5	43
167	Probing histidine-substrate interactions in tyrosyl-tRNA synthetase using asparagine and glutamine replacements. <i>Biochemistry</i> , 1985, 24, 5106-5109.	2.5	96
168	A large increase in enzyme's substrate affinity by protein engineering. <i>Nature</i> , 1984, 307, 187-188.	27.8	154
169	Analysis of Enzyme Structure and Activity by Protein Engineering. <i>Angewandte Chemie International Edition in English</i> , 1984, 23, 467-473.	4.4	96
170	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
171	Genetic dissection of tyrosyl-tRNA synthetase. <i>Biochemical Society Transactions</i> , 1984, 12, 224-225.	3.4	4
172	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
173	Redesigning enzyme structure by site-directed mutagenesis: tyrosyl tRNA synthetase and ATP binding. <i>Nature</i> , 1982, 299, 756-758.	27.8	342