

Patrick J Baker

List of Publications by Year in descending order

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112
papers

5,311
citations

109321

35
h-index

85541

71
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113
all docs

113
docs citations

113
times ranked

5054
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of specificity and deamidation of eIF4A by Burkholderia Lethal Factor 1. Communications Biology, 2022, 5, 272.	4.4	2
2	Characterisation of a tripartite Î±-pore forming toxin from Serratia marcescens. Scientific Reports, 2021, 11, 6447.	3.3	7
3	The structure of a major surface antigen SAG19 from Eimeria tenella unifies the Eimeria SAG family. Communications Biology, 2021, 4, 376.	4.4	9
4	The A component (SmhA) of a tripartite pore-forming toxin from <i>Serratia marcescens</i> : expression, purification and crystallographic analysis. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 577-582.	0.8	1
5	Identification and structural analysis of the tripartite Î±-pore forming toxin of Aeromonas hydrophila. Nature Communications, 2019, 10, 2900.	12.8	20
6	The molecular basis of endolytic activity of a multidomain alginate lyase from Defluviitalea phaphyphila, a representative of a new lyase family, PL39. Journal of Biological Chemistry, 2019, 294, 18077-18091.	3.4	37
7	Distant Non-Obvious Mutations Influence the Activity of a Hyperthermophilic Pyrococcus furiosus Phosphoglucose Isomerase. Biomolecules, 2019, 9, 212.	4.0	11
8	Elucidating the structural basis for differing enzyme inhibitor potency by cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1795-1800.	7.1	24
9	Structural insights into the function of type VI secretion system TssA subunits. Nature Communications, 2018, 9, 4765.	12.8	41
10	TssA from Aeromonas hydrophila: expression, purification and crystallographic studies. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 578-582.	0.8	1
11	Structural and functional studies of histidine biosynthesis in Acanthamoeba spp. demonstrates a novel molecular arrangement and target for antimicrobials. PLoS ONE, 2018, 13, e0198827.	2.5	12
12	TssA from Burkholderia cenocepacia: expression, purification, crystallization and crystallographic analysis. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 536-542.	0.8	1
13	Pnc1 piggy-back import into peroxisomes relies on Gpd1 homodimerisation. Scientific Reports, 2017, 7, 42579.	3.3	16
14	Conserved residues in Ycf54 are required for protochlorophyllide formation in Synechocystis sp. PCC 6803. Biochemical Journal, 2017, 474, 667-681.	3.7	12
15	The molecular basis of phosphite and hypophosphite recognition by ABC-transporters. Nature Communications, 2017, 8, 1746.	12.8	50
16	Mirrorâ€Image Packing Provides a Molecular Basis for the Nanomolar Equipotency of Enantiomers of an Experimental Herbicide. Angewandte Chemie, 2016, 128, 13683-13687.	2.0	1
17	The mechanism of a formaldehyde-sensing transcriptional regulator. Scientific Reports, 2016, 6, 38879.	3.3	46
18	Mirrorâ€Image Packing Provides a Molecular Basis for the Nanomolar Equipotency of Enantiomers of an Experimental Herbicide. Angewandte Chemie - International Edition, 2016, 55, 13485-13489.	13.8	13

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19	Crystallization and preliminary crystallographic analysis of the putative sugar-binding protein Msmeg_0515 (AgaE) from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 189-193.	0.8	0
20	Columnar Liquid Crystals in Cylindrical Nanoconfinement. <i>ACS Nano</i> , 2015, 9, 1759-1766.	14.6	51
21	Crystal Structures Reveal that the Reaction Mechanism of Imidazoleglycerol-Phosphate Dehydratase Is Controlled by Switching Mn(II) Coordination. <i>Structure</i> , 2015, 23, 1236-1245.	3.3	31
22	Crystallization and preliminary crystallographic analysis of a surface antigen glycoprotein, SAG19, from <i>Eimeria tenella</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1380-1383.	0.7	6
23	Crystallization and preliminary X-ray analysis of the receiver domain of a putative response regulator, BPSLO128, from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 917-922.	0.7	0
24	Cloning, purification, crystallization and preliminary X-ray analysis of the <i>Burkholderia pseudomallei</i> L1 ribosomal protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 347-350.	0.7	0
25	A <i>Burkholderia pseudomallei</i> Toxin Inhibits Helicase Activity of Translation Factor eIF4A. <i>Science</i> , 2011, 334, 821-824.	12.6	107
26	Cloning, purification and crystallographic analysis of a hypothetical protein, BPSL1549, from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1623-1626.	0.7	2
27	Structural origins of pH-dependent chemical shifts in the B1 domain of protein G. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3000-3016.	2.6	29
28	Active site dynamics in the zinc-dependent medium chain alcohol dehydrogenase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 779-784.	7.1	61
29	Cloning, purification and preliminary crystallographic analysis of a putative DNA-binding membrane protein, YmfM, from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 656-658.	0.7	0
30	An Inhibitor of FtsZ with Potent and Selective Anti-Staphylococcal Activity. <i>Science</i> , 2008, 321, 1673-1675.	12.6	389
31	Crystal structure of <i>S. aureus</i> YlaN, an essential leucine rich protein involved in the control of cell shape. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 438-445.	2.6	9
32	Analysis of protein solvent interactions in glucose dehydrogenase from the extreme halophile <i>Haloferax mediterranei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4846-4851.	7.1	134
33	Evidence Supporting a cis-enediol-based Mechanism for <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. <i>Journal of Molecular Biology</i> , 2006, 358, 1353-1366.	4.2	29
34	Cloning, purification and preliminary crystallographic analysis of a conserved hypothetical protein, SA0961 (YlaN), from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 778-780.	0.7	2
35	RusA Holliday junction resolvase: DNA complex structure—insights into selectivity and specificity. <i>Nucleic Acids Research</i> , 2006, 34, 5577-5584.	14.5	19
36	Substrate-Induced Conformational Changes in <i>Bacillus subtilis</i> Glutamate Racemase and Their Implications for Drug Discovery. <i>Structure</i> , 2005, 13, 1707-1713.	3.3	49

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37	Structure and Mechanism of Imidazoleglycerol-Phosphate Dehydratase. <i>Structure</i> , 2005, 13, 1809-1817.	3.3	31
38	Crystallization and preliminary X-ray analysis of binary and ternary complexes of Haloferax mediterranei glucose dehydrogenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 743-746.	0.7	8
39	Purification, crystallization and preliminary crystallographic analysis of Arabidopsis thaliana imidazoleglycerol-phosphate dehydratase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 776-778.	0.7	2
40	Expression, purification, crystallization and preliminary crystallographic analysis of a putative GTP-binding protein, YsxC, from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 166-168.	2.5	5
41	Expression, purification and preliminary X-ray analysis of crystals of <i>Bacillus subtilis</i> glutamate racemase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2031-2034.	2.5	14
42	Structure and Function of Amino Acid Ammonia-lyases. <i>Biocatalysis and Biotransformation</i> , 2004, 22, 133-140.	2.0	25
43	Substrate Specificity and Mechanism from the Structure of <i>Pyrococcus furiosus</i> Galactokinase. <i>Journal of Molecular Biology</i> , 2004, 337, 387-398.	4.2	53
44	Analysis of the Open and Closed Conformations of the GTP-binding Protein YsxC from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2004, 339, 265-278.	4.2	32
45	The Structures of Inhibitor Complexes of <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase Provide Insights into Substrate Binding and Catalysis. <i>Journal of Molecular Biology</i> , 2004, 343, 649-657.	4.2	19
46	From hyperthermophiles to psychrophiles: the structural basis of temperature stability of the amino acid dehydrogenases. <i>Biochemical Society Transactions</i> , 2004, 32, 264-268.	3.4	9
47	Alanine dehydrogenase from the psychrophilic bacterium strain PA-43: overexpression, molecular characterization, and sequence analysis. <i>Extremophiles</i> , 2003, 7, 135-143.	2.3	16
48	The Structure of <i>Escherichia coli</i> RusA Endonuclease Reveals a New Holliday Junction DNA Binding Fold. <i>Structure</i> , 2003, 11, 1557-1567.	3.3	24
49	The human granulocyte/macrophage colony-stimulating factor receptor $\hat{\pm}2$ isoform influences haemopoietic lineage commitment and divergence. <i>British Journal of Haematology</i> , 2003, 122, 150-158.	2.5	6
50	Cloning, purification, crystallization and preliminary crystallographic analysis of galactokinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1819-1821.	2.5	4
51	Purification, crystallization and preliminary crystallographic analysis of phosphoglucose isomerase from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1822-1823.	2.5	8
52	Optimization of selenium substructures as obtained from SHELXD. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1987-1994.	2.5	8
53	Crystal Structure of <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. <i>Journal of Biological Chemistry</i> , 2003, 278, 33290-33297.	3.4	32
54	Insights into Enzyme Evolution Revealed by the Structure of Methylaspartate Ammonia Lyase. <i>Structure</i> , 2002, 10, 105-113.	3.3	37

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55	The Crystal Structure of Diadenosine Tetraphosphate Hydrolase from <i>Caenorhabditis elegans</i> in Free and Binary Complex Forms. <i>Structure</i> , 2002, 10, 589-600.	3.3	57
56	X-Ray Crystallographic Studies on Butyryl-ACP Reveal Flexibility of the Structure around a Putative Acyl Chain Binding Site. <i>Structure</i> , 2002, 10, 825-835.	3.3	114
57	Crystallization and preliminary X-ray crystallographic studies on acyl-(acyl carrier protein) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 330-332.	2.5	11
58	Crystallization and preliminary X-ray analysis of substrate complexes of leucine dehydrogenase from <i>Thermoactinomyces intermedius</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1059-1062.	2.5	3
59	Crystallization and preliminary X-ray analysis of the ytxM gene product from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2138-2140.	2.5	0
60	Crystallization and preliminary X-ray crystallographic studies on the class II cholesterol oxidase from <i>Burkholderia cepacia</i> containing bound flavin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2182-2183.	2.5	2
61	The crystal structure of <i>Thermotoga maritima</i> maltosyltransferase and its implications for the molecular basis of the novel transfer specificity 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 312, 119-131.	4.2	14
62	The 1.2 Å... structure of a novel quorum-sensing protein, <i>Bacillus subtilis</i> LuxS 1. Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2001, 313, 111-122.	4.2	79
63	The structure and domain organization of <i>Escherichia coli</i> isocitrate lyase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1209-1218.	2.5	35
64	Crystallization and preliminary X-ray analysis of glucose dehydrogenase from <i>Haloferax mediterranei</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1887-1889.	2.5	11
65	Crystallization and preliminary X-ray analysis of <i>Citrobacter amalonaticus</i> methylaspartate ammonia lyase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1922-1924.	2.5	2
66	Purification, crystallization and quaternary structure analysis of a glycerol dehydrogenase S305C mutant from <i>Bacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 165-167.	2.5	3
67	Glycerol Dehydrogenase. <i>Structure</i> , 2001, 9, 789-802.	3.3	101
68	Antibiotic Activity and Characterization of BB-3497, a Novel Peptide Deformylase Inhibitor. <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 563-570.	3.2	224
69	The mechanism of the oxidation of glycerol to dihydroxyacetone in <i>Bacillus stearothermophilus</i> . <i>Biochemical Society Transactions</i> , 2000, 28, A331-A331.	3.4	0
70	Crystallization and preliminary X-ray crystallographic studies on maltosyltransferase from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1049-1050.	2.5	2
71	Crystallization of the dl component of transhydrogenase, a proton-translocating membrane protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1170-1172.	2.5	1
72	The crystal structure and active site location of isocitrate lyase from the fungus <i>Aspergillus nidulans</i> . <i>Structure</i> , 2000, 8, 349-362.	3.3	64

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73	Proteinâ€ protein recognition, hydride transfer and proton pumping in the transhydrogenase complex11Because Structure with Folding & Design operates a â€ Continuous Publication Systemâ€™™ For Research Papers, this paper has been published on the internet before being printed (accessed from) Tj ETQq1 1307843145gBT /Ove page... Structure, 2000, 8, 800-815.	13.7	45
74	Molecular basis of triclosan activity. Nature, 1999, 398, 383-384.	27.8	473
75	Insights into the mechanism of domain closure and substrate specificity of glutamate dehydrogenase from Clostridium symbiosum 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 285, 875-885.	4.2	41
76	Structure determination of the glutamate dehydrogenase from the hyperthermophile Thermococcus litoralis and its comparison with that from Pyrococcus furiosus 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 293, 1121-1132.	4.2	52
77	Crystallographic analysis of triclosan bound to enoyl reductase. Journal of Molecular Biology, 1999, 294, 527-535.	4.2	90
78	Analysis of the structure and substrate binding of Phormidium lapideum alanine dehydrogenase. Nature Structural Biology, 1998, 5, 561-567.	9.7	78
79	Crystallization of NAD+dependent phenylalanine dehydrogenase from Nocardia sp239. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 269-272.	2.5	6
80	Crystallization of the alanine dehydrogenase from Phormidium lapideum. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 407-408.	2.5	3
81	Analysis of the Quaternary Structure, Substrate Specificity, and Catalytic Mechanism of Valine Dehydrogenase. Journal of Biological Chemistry, 1997, 272, 25105-25111.	3.4	23
82	Determinants of Substrate Specificity in the Superfamily of Amino Acid Dehydrogenases,. Biochemistry, 1997, 36, 16109-16115.	2.5	45
83	Crystallization and preliminary X-ray studies of nitrogenase component 1 (the MoFe protein) from Klebsiella pneumoniae. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 227-228.	2.5	5
84	Isocitrate lyase from Aspergillus nidulans: crystallization and X-ray analysis of a glyoxylate cycle enzyme. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 488-490.	2.5	2
85	Crystal Structure of DNA Recombination Protein RuvA and a Model for Its Binding to the Holliday Junction. Science, 1996, 274, 415-421.	12.6	172
86	Improving the engineered activity of mutants of clostridial glutamate dehydrogenase towards monocarboxylic substrates: Substitution of Ala 163 with glycine. Biochemical Society Transactions, 1996, 24, 126S-126S.	3.4	0
87	A Mechanism of Drug Action Revealed by Structural Studies of Enoyl Reductase. Science, 1996, 274, 2107-2110.	12.6	239
88	Crystallization of the NAD(P)-dependent glutamate dehydrogenase from the hyperthermophile Pyrococcus furiosus. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 240-242.	2.5	3
89	Crystallization of glycerol dehydrogenase from Bacillus stearothermophilus. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 830-832.	2.5	2
90	Crystallization and analysis of the subunit assembly and quaternary structure of imidazoleglycerol phosphate dehydratase from Saccharomyces cerevisiae. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 845-847.	2.5	7

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91	A role for quaternary structure in the substrate specificity of leucine dehydrogenase. <i>Structure</i> , 1995, 3, 693-705.	3.3	97
92	Common themes in redox chemistry emerge from the X-ray structure of oilseed rape (<i>Brassica napus</i>) enoyl acyl carrier protein reductase. <i>Structure</i> , 1995, 3, 927-938.	3.3	110
93	The structure of <i>Pyrococcus furiosus</i> glutamate dehydrogenase reveals a key role for ion-pair networks in maintaining enzyme stability at extreme temperatures. <i>Structure</i> , 1995, 3, 1147-1158.	3.3	445
94	Correlation of intron-exon organisation with the three-dimensional structure in glutamate dehydrogenase. <i>BBA - Proteins and Proteomics</i> , 1995, 1247, 231-238.	2.1	9
95	Alteration of the amino acid substrate specificity of clostridial glutamate dehydrogenase by site-directed mutagenesis of an active-site lysine residue. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 147-152.	2.1	13
96	Alteration in relative activities of phenylalanine dehydrogenase towards different substrates by site-directed mutagenesis. <i>FEBS Letters</i> , 1995, 370, 93-96.	2.8	31
97	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from <i>Pyrococcus furiosus</i> and <i>Thermococcus litoralis</i> . <i>FEBS Journal</i> , 1995, 229, 688-695.	0.2	28
98	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from <i>Pyrococcus furiosus</i> and <i>Thermococcus litoralis</i> . <i>FEBS Journal</i> , 1995, 229, 688-695.	0.2	89
99	Crystallization and Quaternary Structure Analysis of the NAD ⁺ -dependent Leucine Dehydrogenase from <i>Bacillus sphaericus</i> . <i>Journal of Molecular Biology</i> , 1994, 236, 663-665.	4.2	12
100	The changed pattern of substrate specificity in the K89L mutant of glutamate dehydrogenase of <i>Clostridium symbiosum</i> . <i>Biochemical Society Transactions</i> , 1994, 22, 320S-320S.	3.4	1
101	Evolution of Substrate Diversity in the Superfamily of Amino Acid Dehydrogenases. <i>Journal of Molecular Biology</i> , 1993, 234, 938-945.	4.2	73
102	Conformational Flexibility in Glutamate Dehydrogenase. <i>Journal of Molecular Biology</i> , 1993, 234, 1131-1139.	4.2	224
103	Crystallization of the NADP ⁺ -dependent Glutamate Dehydrogenase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1993, 234, 1270-1273.	4.2	11
104	Purification and crystallization of the light harvesting LH1 complex from <i>Rhodobacter sphaeroides</i> . <i>Journal of Molecular Biology</i> , 1992, 228, 1259-1262.	4.2	25
105	Effect of additives on the crystallization of glutamate dehydrogenase from <i>Clostridium symbiosum</i> . <i>Journal of Molecular Biology</i> , 1992, 224, 1181-1184.	4.2	24
106	Structural consequences of sequence patterns in the fingerprint region of the nucleotide binding fold. <i>Journal of Molecular Biology</i> , 1992, 228, 662-671.	4.2	163
107	Subunit assembly and active site location in the structure of glutamate dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 75-86.	2.6	221
108	Structural relationship between the hexameric and tetrameric family of glutamate dehydrogenases. <i>FEBS Journal</i> , 1992, 209, 851-859.	0.2	74

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109	Use of chemical modification in the crystallization of isocitrate lyase from Escherichia coli. Journal of Molecular Biology, 1991, 220, 13-16.	4.2	13
110	The partial amino acid sequence of the NAD -dependent glutamate dehydrogenase of Clostridium symbiosum: implications for the evolution and structural basis of coenzyme specificity. BBA - Proteins and Proteomics, 1991, 1080, 191-197.	2.1	36
111	Recent progress on the structure and function of glutamate dehydrogenase. Biochemical Society Transactions, 1987, 15, 748-751.	3.4	25
112	Crystallization of an NADP+-dependent malic enzyme from rat liver. Journal of Molecular Biology, 1987, 193, 233-235.	4.2	13