Patrick J Baker

List of Publications by Year
in descending order

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112 papers	5,311 citations	109137 35 h-index	85405 71 g-index
113 all docs	113 docs citations	113 times ranked	5054 citing authors

#	Article	IF	Citations
1	Molecular basis of triclosan activity. Nature, 1999, 398, 383-384.	13.7	473
2	The structure of Pyrococcus furiosus glutamate dehydrogenase reveals a key role for ion-pair networks in maintaining enzyme stability at extreme temperatures. Structure, 1995, 3, 1147-1158.	1.6	445
3	An Inhibitor of FtsZ with Potent and Selective Anti-Staphylococcal Activity. Science, 2008, 321, 1673-1675.	6.0	389
4	A Mechanism of Drug Action Revealed by Structural Studies of Enoyl Reductase. Science, 1996, 274, 2107-2110.	6.0	239
5	Conformational Flexibility in Glutamate Dehydrogenase. Journal of Molecular Biology, 1993, 234, 1131-1139.	2.0	224
6	Antibiotic Activity and Characterization of BB-3497, a Novel Peptide Deformylase Inhibitor. Antimicrobial Agents and Chemotherapy, 2001, 45, 563-570.	1.4	224
7	Subunit assembly and active site location in the structure of glutamate dehydrogenase. Proteins: Structure, Function and Bioinformatics, 1992, 12, 75-86.	1.5	221
8	Crystal Structure of DNA Recombination Protein RuvA and a Model for Its Binding to the Holliday Junction. Science, 1996, 274, 415-421.	6.0	172
9	Structural consequences of sequence patterns in the fingerprint region of the nucleotide binding fold. Journal of Molecular Biology, 1992, 228, 662-671.	2.0	163
10	Analysis of protein solvent interactions in glucose dehydrogenase from the extreme halophile Haloferax mediterranei. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4846-4851.	3.3	134
11	X-Ray Crystallographic Studies on Butyryl-ACP Reveal Flexibility of the Structure around a Putative Acyl Chain Binding Site. Structure, 2002, 10, 825-835.	1.6	114
12	Common themes in redox chemistry emerge from the X-ray structure of oilseed rape (Brassica napus) enoyl acyl carrier protein reductase. Structure, 1995, 3, 927-938.	1.6	110
13	A <i>Burkholderia pseudomallei</i> Toxin Inhibits Helicase Activity of Translation Factor eIF4A. Science, 2011, 334, 821-824.	6.0	107
14	Glycerol Dehydrogenase. Structure, 2001, 9, 789-802.	1.6	101
15	A role for quaternary structure in the substrate specificity of leucine dehydrogenase. Structure, 1995, 3, 693-705.	1.6	97
16	Crystallographic analysis of triclosan bound to enoyl reductase. Journal of Molecular Biology, 1999, 294, 527-535.	2.0	90
17	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from Pyrococcus furiosus and Thermococcus litoralis. FEBS Journal, 1995, 229, 688-695.	0.2	89
18	The 1.2 Ã… structure of a novel quorum-sensing protein, Bacillus subtilis LuxS 1 1Edited by J. Thornton. Journal of Molecular Biology, 2001, 313, 111-122.	2.0	79

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19	Analysis of the structure and substrate binding of Phormidium lapideum alanine dehydrogenase. Nature Structural Biology, 1998, 5, 561-567.	9.7	78
20	Structural relationship between the hexameric and tetrameric family of glutamate dehydrogenases. FEBS Journal, 1992, 209, 851-859.	0.2	74
21	Evolution of Substrate Diversity in the Superfamily of Amino Acid Dehydrogenases. Journal of Molecular Biology, 1993, 234, 938-945.	2.0	73
22	The crystal structure and active site location of isocitrate lyase from the fungus Aspergillus nidulans. Structure, 2000, 8, 349-362.	1.6	64
23	Active site dynamics in the zinc-dependent medium chain alcohol dehydrogenase superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 779-784.	3.3	61
24	The Crystal Structure of Diadenosine Tetraphosphate Hydrolase from Caenorhabditis elegans in Free and Binary Complex Forms. Structure, 2002, 10, 589-600.	1.6	57
25	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 1 0.784314 rg BT /Overl page.. Structure, 2000, 8, 809-815.	1.6	55
26	Substrate Specificity and Mechanism from the Structure of Pyrococcus furiosus Galactokinase. Journal of Molecular Biology, 2004, 337, 387-398.	2.0	53
27	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.	2.0	52
28	Columnar Liquid Crystals in Cylindrical Nanoconfinement. ACS Nano, 2015, 9, 1759-1766.	7.3	51
29	The molecular basis of phosphite and hypophosphite recognition by ABC-transporters. Nature Communications, 2017, 8, 1746.	5.8	50
30	Substrate-Induced Conformational Changes in Bacillus subtilis Glutamate Racemase and Their Implications for Drug Discovery. Structure, 2005, 13, 1707-1713.	1.6	49
31	The mechanism of a formaldehyde-sensing transcriptional regulator. Scientific Reports, 2016, 6, 38879.	1.6	46
32	Determinants of Substrate Specificity in the Superfamily of Amino Acid Dehydrogenases,. Biochemistry, 1997, 36, 16109-16115.	1.2	45
33	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.	2.0	41
34	Structural insights into the function of type VI secretion system TssA subunits. Nature Communications, 2018, 9, 4765.	5.8	41
35	Insights into Enzyme Evolution Revealed by the Structure of Methylaspartate Ammonia Lyase. Structure, 2002, 10, 105-113.	1.6	37
36	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.	1.6	37

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37	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
38	The structure and domain organization ofEscherichia coliisocitrate lyase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1209-1218.	2.5	35
39	Crystal Structure of Pyrococcus furiosus Phosphoglucose Isomerase. Journal of Biological Chemistry, 2003, 278, 33290-33297.	1.6	32
40	Analysis of the Open and Closed Conformations of the GTP-binding Protein YsxC from Bacillus subtilis. Journal of Molecular Biology, 2004, 339, 265-278.	2.0	32
41	Alteration in relative activities of phenylalanine dehydrogenase towards different substrates by site-directed mutagenesis. FEBS Letters, 1995, 370, 93-96.	1.3	31
42	Structure and Mechanism of Imidazoleglycerol-Phosphate Dehydratase. Structure, 2005, 13, 1809-1817.	1.6	31
43	Crystal Structures Reveal that the Reaction Mechanism of Imidazoleglycerol-Phosphate Dehydratase Is Controlled by Switching Mn(II) Coordination. Structure, 2015, 23, 1236-1245.	1.6	31
44	Evidence Supporting a cis-enediol-based Mechanism for Pyrococcus furiosus Phosphoglucose Isomerase. Journal of Molecular Biology, 2006, 358, 1353-1366.	2.0	29
45	Structural origins of pHâ€dependent chemical shifts in the B1 domain of protein G. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3000-3016.	1.5	29
46	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from <i>Pyrococcus furiosus</i> and <i>Thermococcus litoralis</i>. FEBS Journal, 1995, 229, 688-695.	0.2	28
47	Recent progress on the structure and function of glutamate dehydrogenase. Biochemical Society Transactions, 1987, 15, 748-751.	1.6	25
48	Purification and crystallization of the light harvesting LH1 complex from Rhodobacter sphaeroides. Journal of Molecular Biology, 1992, 228, 1259-1262.	2.0	25
49	Structure and Function of Amino Acid Ammonia-lyases. Biocatalysis and Biotransformation, 2004, 22, 133-140.	1.1	25
50	Effect of additives on the crystallization of glutamate dehydrogenase from Clostridium symbiosum. Journal of Molecular Biology, 1992, 224, 1181-1184.	2.0	24
51	The Structure of Escherichia coli RusA Endonuclease Reveals a New Holliday Junction DNA Binding Fold. Structure, 2003, 11, 1557-1567.	1.6	24
52	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.	3.3	24
53	Analysis of the Quaternary Structure, Substrate Specificity, and Catalytic Mechanism of Valine Dehydrogenase. Journal of Biological Chemistry, 1997, 272, 25105-25111.	1.6	23
54	Identification and structural analysis of the tripartite Î±-pore forming toxin of Aeromonas hydrophila. Nature Communications, 2019, 10, 2900.	5.8	20

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55	The Structures of Inhibitor Complexes of Pyrococcus furiosus Phosphoglucose Isomerase Provide Insights into Substrate Binding and Catalysis. Journal of Molecular Biology, 2004, 343, 649-657.	2.0	19
56	RusA Holliday junction resolvase: DNA complex structureâ€"insights into selectivity and specificity. Nucleic Acids Research, 2006, 34, 5577-5584.	6.5	19
57	Alanine dehydrogenase from the psychrophilic bacterium strain PA-43: overexpression, molecular characterization, and sequence analysis. Extremophiles, 2003, 7, 135-143.	0.9	16
58	Pnc1 piggy-back import into peroxisomes relies on Gpd1 homodimerisation. Scientific Reports, 2017, 7, 42579.	1.6	16
59	The crystal structure of Thermotoga maritima maltosyltransferase and its implications for the molecular basis of the novel transfer specificity 1 1Edited by R. Huber. Journal of Molecular Biology, 2001, 312, 119-131.	2.0	14
60	Expression, purification and preliminary X-ray analysis of crystals ofBacillus subtilisglutamate racemase. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2031-2034.	2.5	14
61	Crystallization of an NADP+-dependent malic enzyme from rat liver. Journal of Molecular Biology, 1987, 193, 233-235.	2.0	13
62	Use of chemical modification in the crystallization of isocitrate lyase from Escherichia coli. Journal of Molecular Biology, 1991, 220, 13-16.	2.0	13
63	Alteration of the amino acid substrate specificity of clostridial glutamate dehydrogenase by site-directed mutagenesis of an active-site lysine residue. Protein Engineering, Design and Selection, 1995, 8, 147-152.	1.0	13
64	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.	7.2	13
65	Crystallization and Quaternary Structure Analysis of the NAD+-dependent Leucine Dehydrogenase from Bacillus sphaericus. Journal of Molecular Biology, 1994, 236, 663-665.	2.0	12
66	Conserved residues in Ycf54 are required for protochlorophyllide formation in Synechocystis sp. PCC 6803. Biochemical Journal, 2017, 474, 667-681.	1.7	12
67	Structural and functional studies of histidine biosynthesis in Acanthamoeba spp. demonstrates a novel molecular arrangement and target for antimicrobials. PLoS ONE, 2018, 13, e0198827.	1.1	12
68	Crystallization of the NADP+-dependent Glutamate Dehydrogenase from Escherichia coli. Journal of Molecular Biology, 1993, 234, 1270-1273.	2.0	11
69	Crystallization and preliminary X-ray analysis of glucose dehydrogenase fromHaloferax mediterranei. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1887-1889.	2.5	11
70	Crystallization and preliminary X-ray crystallographic studies on acyl-(acyl carrier protein) fromEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 330-332.	2.5	11
71	Distant Non-Obvious Mutations Influence the Activity of a Hyperthermophilic Pyrococcus furiosus Phosphoglucose Isomerase. Biomolecules, 2019, 9, 212.	1.8	11
72	Correlation of intron-exon organisation with the three-dimensional structure in glutamate dehydrogenase. BBA - Proteins and Proteomics, 1995, 1247, 231-238.	2.1	9

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73	From hyperthermophiles to psychrophiles: the structural basis of temperature stability of the amino acid dehydrogenases. Biochemical Society Transactions, 2004, 32, 264-268.	1.6	9
74	Crystal structure of S. aureus YlaN, an essential leucine rich protein involved in the control of cell shape. Proteins: Structure, Function and Bioinformatics, 2007, 68, 438-445.	1.5	9
75	The structure of a major surface antigen SAG19 from Eimeria tenella unifies the Eimeria SAG family. Communications Biology, 2021, 4, 376.	2.0	9
76	Purification, crystallization and preliminary crystallographic analysis of phosphoglucose isomerase from the hyperthermophilic archaeonPyrococcus furiosus. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1822-1823.	2.5	8
77	Optimization of selenium substructures as obtained fromSHELXD. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1987-1994.	2.5	8
78	Crystallization and preliminary X-ray analysis of binary and ternary complexes ofHaloferax mediterraneiglucose dehydrogenase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 743-746.	0.7	8
79	Crystallization and analysis of the subunit assembly and quaternary structure of imidazoleglycerol phosphate dehydratase fromSaccharomyces cerevisiae. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 845-847.	2.5	7
80	Characterisation of a tripartite Î±-pore forming toxin from Serratia marcescens. Scientific Reports, 2021, 11, 6447.	1.6	7
81	Crystallization of NAD+-dependent phenylalanine dehydrogenase fromNocardia sp239. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 269-272.	2.5	6
82	The human granulocyte/macrophage colony-stimulating factor receptor Î±2 isoform influences haemopoietic lineage commitment and divergence. British Journal of Haematology, 2003, 122, 150-158.	1.2	6
83	Crystallization and preliminary crystallographic analysis of a surface antigen glycoprotein, SAG19, fromEimeria tenella. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1380-1383.	0.7	6
84	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
85	Expression, purification, crystallization and preliminary crystallographic analysis of a putative GTP-binding protein, YsxC, fromBacillus subtilis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 166-168.	2.5	5
86	Cloning, purification, crystallization and preliminary crystallographic analysis of galactokinase fromPyrococcus furiosus. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1819-1821.	2.5	4
87	Crystallization of the NAD(P)-dependent glutamate dehydrogenase from the hyperthermophilePyrococcus furiosus. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 240-242.	2.5	3
88	Crystallization of the alanine dehydrogenase from Phormidium lapideum. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 407-408.	2.5	3
89	Purification, crystallization and quaternary structure analysis of a glycerol dehydrogenase S305C mutant fromBacillus stearothermophilus. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 165-167.	2.5	3
90	Crystallization and preliminary X-ray analysis of substrate complexes of leucine dehydrogenase fromThermoactinomyces intermedius. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1059-1062.	2.5	3

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91	Crystallization of glycerol dehydrogenase fromBacillus stearothermophilus. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 830-832.	2.5	2
92	Isocitrate lyase fromAspergillus nidulans: crystallization and X-ray analysis of a glyoxylate cycle enzyme. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 488-490.	2.5	2
93	Crystallization and preliminary X-ray crystallographic studies on maltosyltransferase fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1049-1050.	2.5	2
94	Crystallization and preliminary X-ray analysis ofCitrobacter amalonaticusmethylaspartate ammonia lyase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1922-1924.	2.5	2
95	Crystallization and preliminary X-ray crystallographic studies on the class II cholesterol oxidase fromBurkholderia cepaciacontaining bound flavin. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2182-2183.	2.5	2
96	Purification, crystallization and preliminary crystallographic analysis ofArabidopsis thalianaimidazoleglycerol-phosphate dehydratase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 776-778.	0.7	2
97	Cloning, purification and preliminary crystallographic analysis of a conserved hypothetical protein, SA0961 (YlaN), fromStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 778-780.	0.7	2
98	Cloning, purification and crystallographic analysis of a hypothetical protein, BPSL1549, from <i>Burkholderia pseudomallei</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1623-1626.	0.7	2
99	Molecular basis of specificity and deamidation of eIF4A by Burkholderia Lethal Factor 1. Communications Biology, 2022, 5, 272.	2.0	2
100	The changed pattern of substrate specificity in the K89L mutant of glutamate dehydrogenase of <i>Clostridium symbiosum</i>. Biochemical Society Transactions, 1994, 22, 320S-320S.	1.6	1
101	Crystallization of the dI component of transhydrogenase, a proton-translocating membrane protein. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1170-1172.	2.5	1
102	Mirrorâ€•Image Packing Provides a Molecular Basis for the Nanomolar Equipotency of Enantiomers of an Experimental Herbicide. Angewandte Chemie, 2016, 128, 13683-13687.	1.6	1
103	TssA from Aeromonas hydrophila: expression, purification and crystallographic studies. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 578-582.	0.4	1
104	TssA from Burkholderia cenocepacia: expression, purification, crystallization and crystallographic analysis. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 536-542.	0.4	1
105	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.	0.4	1
106	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.	1.6	0
107	The mechanism of the oxidation of glycerol to dihydroxyacetone in Bacillus stearothermophilus. Biochemical Society Transactions, 2000, 28, A331-A331.	1.6	0
108	Crystallization and preliminary X-ray analysis of theytxMgene product fromBacillus subtilis. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2138-2140.	2.5	0

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109	Cloning, purification and preliminary crystallographic analysis of a putative DNA-binding membrane protein, YmfM, fromStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 656-658.	0.7	0
110	Crystallization and preliminary X-ray analysis of the receiver domain of a putative response regulator, BPSL0128, fromBurkholderia pseudomallei. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 917-922.	0.7	0
111	Cloning, purification, crystallization and preliminary X-ray analysis of theBurkholderia pseudomalleiL1 ribosomal protein. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 347-350.	0.7	0
112	Crystallization and preliminary crystallographic analysis of the putative sugar-binding protein Msmeg_0515 (AgaE) fromMycobacterium smegmatis. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 189-193.	0.4	0