

Emil F Pai

List of Publications by Year in descending order

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31976

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24982

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times ranked

11873
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#	ARTICLE	IF	CITATIONS
1	Defluorination Capability of α -Haloacid Dehalogenases in the HAD-Like Hydrolase Superfamily Correlates with Active Site Compactness. <i>ChemBioChem</i> , 2022, 23, .	2.6	12
2	Signal transfer in human protein tyrosine phosphatase PTP1B from allosteric inhibitor P00058. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 13823-13832.	3.5	4
3	Serial femtosecond and serial synchrotron crystallography can yield data of equivalent quality: A systematic comparison. <i>Science Advances</i> , 2021, 7, .	10.3	25
4	Development of Antibiotics That Dysregulate the <i>Neisseria</i> ClpP Protease. <i>ACS Infectious Diseases</i> , 2020, 6, 3224-3236.	3.8	15
5	Preclinical evaluation of the selective small-molecule UBA1 inhibitor, TAK-243, in acute myeloid leukemia. <i>Leukemia</i> , 2019, 33, 37-51.	7.2	56
6	Targeting a Large Active Site: Structure-Based Design of Nanomolar Inhibitors of <i>Trypanosoma brucei</i> Trypanothione Reductase. <i>Chemistry - A European Journal</i> , 2019, 25, 11416-11421.	3.3	16
7	Time-resolved crystallography reveals allosteric communication aligned with molecular breathing. <i>Science</i> , 2019, 365, 1167-1170.	12.6	78
8	Substrate-Based Allosteric Regulation of a Homodimeric Enzyme. <i>Journal of the American Chemical Society</i> , 2019, 141, 11540-11556.	13.7	26
9	Mitochondrial ClpP-Mediated Proteolysis Induces Selective Cancer Cell Lethality. <i>Cancer Cell</i> , 2019, 35, 721-737.e9.	16.8	206
10	ClpP protease activation results from the reorganization of the electrostatic interaction networks at the entrance pores. <i>Communications Biology</i> , 2019, 2, 410.	4.4	20
11	Biological Evaluation and X-ray Crystal Structures of Cyclohexylpyrrolidine Ligands for Trypanothione Reductase, an Enzyme from the Redox Metabolism of <i>Trypanosoma</i> . <i>ChemMedChem</i> , 2018, 13, 957-967.	3.2	13
12	Crystal structure of <i>Staphylococcus aureus</i> Zn-glyoxalase I: new subfamily of glyoxalase I family. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 376-386.	3.5	5
13	The hit-and-return system enables efficient time-resolved serial synchrotron crystallography. <i>Nature Methods</i> , 2018, 15, 901-904.	19.0	67
14	The mechanism of GM-CSF inhibition by human GM-CSF auto-antibodies suggests novel therapeutic opportunities. <i>MAbs</i> , 2018, 10, 1-12.	5.2	5
15	The prion protein is embedded in a molecular environment that modulates transforming growth factor β^2 and integrin signaling. <i>Scientific Reports</i> , 2018, 8, 8654.	3.3	14
16	First experimental visualization of the gaseous product CO ₂ in the active site of ODCase supports substrate strain as an integral part of the catalytic mechanism. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a453-a453.	0.1	0
17	Time-resolved serial synchrotron crystallography: an efficient interlacing system enables milliseconds to seconds time delays. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a53-a53.	0.1	0
18	Time-resolved crystallography via an interlacing approach allows elucidation of milliseconds to seconds time delays. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e138-e138.	0.1	0

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19	The role of dimer asymmetry and protomer dynamics in enzyme catalysis. <i>Science</i> , 2017, 355, .	12.6	155
20	Mild orotic aciduria in <i>UMPS</i> heterozygotes: a metabolic finding without clinical consequences. <i>Journal of Inherited Metabolic Disease</i> , 2017, 40, 423-431.	3.6	14
21	Protein crystals IR laser ablated from aqueous solution at high speed retain their diffractive properties: applications in high-speed serial crystallography. <i>Journal of Applied Crystallography</i> , 2017, 50, 1773-1781.	4.5	10
22	Dimer asymmetry and protomer dynamics in enzyme catalysis. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a291-a291.	0.1	0
23	EspP, an Extracellular Serine Protease from Enterohemorrhagic <i>E. coli</i> , Reduces Coagulation Factor Activities, Reduces Clot Strength, and Promotes Clot Lysis. <i>PLoS ONE</i> , 2016, 11, e0149830.	2.5	2
24	Structures of Preferred Human IgV Genes-Based Protective Antibodies Identify How Conserved Residues Contact Diverse Antigens and Assign Source of Specificity to CDR3 Loop Variation. <i>Journal of Immunology</i> , 2016, 196, 4723-4730.	0.8	18
25	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882.	12.8	113
26	Development and Characterization of Potent Cyclic Acyldepsipeptide Analogues with Increased Antimicrobial Activity. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 624-646.	6.4	44
27	Hydrophobic Gating of Ion Permeation in Magnesium Channel CorA. <i>PLoS Computational Biology</i> , 2015, 11, e1004303.	3.2	48
28	The C-terminal peptide plays a role in the formation of an intermediate form during the transition between xanthine dehydrogenase and xanthine oxidase. <i>FEBS Journal</i> , 2015, 282, 3075-3090.	4.7	38
29	Nicotinamide mononucleotide adenylyltransferase displays alternate binding modes for nicotinamide nucleotides. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2032-2039.	2.5	3
30	The structure of SAV1646 from <i>Staphylococcus aureus</i> belonging to a new 'ribosome-associated' subfamily of bacterial proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 332-337.	2.5	5
31	Orotidine Monophosphate Decarboxylase - A Fascinating Workhorse Enzyme with Therapeutic Potential. <i>Journal of Genetics and Genomics</i> , 2015, 42, 221-234.	3.9	6
32	Characterization of Vis Toxin, a Novel ADP-Ribosyltransferase from <i>Vibrio splendidus</i> . <i>Biochemistry</i> , 2015, 54, 5920-5936.	2.5	15
33	X-ray Structure of a Hg ²⁺ Complex of Mercuric Reductase (MerA) and Quantum Mechanical/Molecular Mechanical Study of Hg ²⁺ Transfer between the C-Terminal and Buried Catalytic Site Cysteine Pairs. <i>Biochemistry</i> , 2014, 53, 7211-7222.	2.5	46
34	Structural insights into Noonan/LEOPARD syndrome-related mutants of protein-tyrosine phosphatase SHP2 (PTPN11). <i>BMC Structural Biology</i> , 2014, 14, 10.	2.3	55
35	Insights into the binding of PARP inhibitors to the catalytic domain of human tankyrase-2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2740-2753.	2.5	24
36	Structure and Immunogenicity of a Peptide Vaccine, Including the Complete HIV-1 gp41 2F5 Epitope. <i>Journal of Biological Chemistry</i> , 2014, 289, 6565-6580.	3.4	26

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37	Binding to Large Enzyme Pockets: Small-Molecule Inhibitors of Trypanothione Reductase. <i>ChemMedChem</i> , 2014, 9, 1880-1891.	3.2	40
38	A Porphodimethene Chemical Inhibitor of Uroporphyrinogen Decarboxylase. <i>PLoS ONE</i> , 2014, 9, e89889.	2.5	4
39	Opsin, a Structural Model for Olfactory Receptors?. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 11021-11024.	13.8	66
40	The structure and regulation of magnesium selective ion channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2778-2792.	2.6	57
41	Substrate Distortion Contributes to the Catalysis of Orotidine 5-Monophosphate Decarboxylase. <i>Journal of the American Chemical Society</i> , 2013, 135, 17432-17443.	13.7	27
42	Antimalarial Activities of 6-Iodouridine and Its Prodrugs and Potential for Combination Therapy. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 2348-2358.	6.4	9
43	Resolution of structural heterogeneity in dynamic crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 946-959.	2.5	32
44	Crystal structure of the CN-hydrolase SA0302 from the pathogenic bacterium <i>Staphylococcus aureus</i> belonging to the Nit and NitFhit Branch of the nitrilase superfamily. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1057-1065.	3.5	3
45	Atomic Resolution Structure of the Orotidine 5-Monophosphate Decarboxylase Product Complex Combined with Surface Plasmon Resonance Analysis. <i>Journal of Biological Chemistry</i> , 2013, 288, 9011-9016.	3.4	13
46	3P035 Opsin, Structural Model for Olfactory Receptors(01A. Protein: Structure,Poster). <i>Seibutsu Butsuri</i> , 2013, 53, S217.	0.1	0
47	N-Terminal Helix-Cap in α -Helix 2 Modulates β -State Misfolding in Rabbit and Hamster Prion Proteins. <i>PLoS ONE</i> , 2013, 8, e63047.	2.5	17
48	5 The xanthine oxidoreductase enzyme family: xanthine dehydrogenase , xanthine oxidase , and aldehyde oxidase. , 2013, , 103-124.		1
49	Structural asymmetry in the magnesium channel CorA points to sequential allosteric regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18809-18814.	7.1	62
50	Neutralizing Epitopes in the Membrane-Proximal External Region of HIV-1 gp41 Are Influenced by the Transmembrane Domain and the Plasma Membrane. <i>Journal of Virology</i> , 2012, 86, 2930-2941.	3.4	55
51	Protein Conformational Gating of Enzymatic Activity in Xanthine Oxidoreductase. <i>Journal of the American Chemical Society</i> , 2012, 134, 999-1009.	13.7	49
52	Novel Cytidine-Based Orotidine-5-Monophosphate Decarboxylase Inhibitors with an Unusual Twist. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9988-9997.	6.4	9
53	Computational Design of High-Affinity Epitope Scaffolds by Backbone Grafting of a Linear Epitope. <i>Journal of Molecular Biology</i> , 2012, 415, 175-192.	4.2	99
54	Mapping the Reaction Coordinates of Enzymatic Defluorination. <i>Journal of the American Chemical Society</i> , 2011, 133, 7461-7468.	13.7	73

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55	Relative and Regional Stabilities of the Hamster, Mouse, Rabbit, and Bovine Prion Proteins toward Urea Unfolding Assessed by Nuclear Magnetic Resonance and Circular Dichroism Spectroscopies. <i>Biochemistry</i> , 2011, 50, 7536-7545.	2.5	22
56	Novel Interactions of Fluorinated Nucleotide Derivatives Targeting Orotidine 5'-Monophosphate Decarboxylase. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 2891-2901.	6.4	12
57	Crystal Structure of the Passenger Domain of the Escherichia coli Autotransporter EspP. <i>Journal of Molecular Biology</i> , 2011, 413, 985-1000.	4.2	49
58	Linkage between the bacterial acid stress and stringent responses: the structure of the inducible lysine decarboxylase. <i>EMBO Journal</i> , 2011, 30, 931-944.	7.8	166
59	Crystal structure of metarhodopsin II. <i>Nature</i> , 2011, 471, 651-655.	27.8	620
60	Activators of Cylindrical Proteases as Antimicrobials: Identification and Development of Small Molecule Activators of ClpP Protease. <i>Chemistry and Biology</i> , 2011, 18, 1167-1178.	6.0	86
61	Crystal structure of alkyl hydroperoxidase D like protein PA0269 from <i>Pseudomonas aeruginosa</i> : Homology of the AhpD-like structural family. <i>BMC Structural Biology</i> , 2011, 11, 27.	2.3	19
62	X-CHIP: an integrated platform for high-throughput protein crystallization and on-the-chip X-ray diffraction data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 533-539.	2.5	42
63	Interaction of Anti-HIV Type 1 Antibody 2F5 with Phospholipid Bilayers and Its Relevance for the Mechanism of Virus Neutralization. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 863-876.	1.1	11
64	Crystal Structures of Urate Bound Form of Xanthine Oxidoreductase: Substrate Orientation and Structure of the Key Reaction Intermediate. <i>Journal of the American Chemical Society</i> , 2010, 132, 17080-17083.	13.7	42
65	Structural determinants for the inhibitory ligands of orotidine-5'-monophosphate decarboxylase. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 4032-4041.	3.0	14
66	Sequence- and activity- based screening of microbial genomes for novel dehalogenases. <i>Microbial Biotechnology</i> , 2010, 3, 107-120.	4.2	53
67	Crystal structure of a truncated urease accessory protein UreF from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2839-2848.	2.6	37
68	Prion disease susceptibility is affected by β^2 -structure folding propensity and local side-chain interactions in PrP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19808-19813.	7.1	119
69	Ablation of the Complementarity-Determining Region H3 Apex of the Anti-HIV-1 Broadly Neutralizing Antibody 2F5 Abrogates Neutralizing Capacity without Affecting Core Epitope Binding. <i>Journal of Virology</i> , 2010, 84, 4136-4147.	3.4	64
70	Iris-Like Mechanism of Pore Dilatation in the CorA Magnesium Transport System. <i>Biophysical Journal</i> , 2010, 98, 646a.	0.5	0
71	An Iris-Like Mechanism of Pore Dilatation in the CorA Magnesium Transport System. <i>Biophysical Journal</i> , 2010, 98, 784-792.	0.5	83
72	Structural factors underlying the species barrier and susceptibility to infection in prion disease This paper is one of a selection of papers published in this special issue entitled "Canadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting - Protein Folding: Principles and Diseases" and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 195-202.	2.0	23

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73	Conformational Determinants of Phosphotyrosine Peptides Complexed with the Src SH2 Domain. PLoS ONE, 2010, 5, e11215.	2.5	11
74	Crystallographic Definition of the Epitope Promiscuity of the Broadly Neutralizing Anti-Human Immunodeficiency Virus Type 1 Antibody 2F5: Vaccine Design Implications. Journal of Virology, 2009, 83, 11862-11875.	3.4	52
75	Structure-Activity Relationships of Orotidine-5-Monophosphate Decarboxylase Inhibitors as Anticancer Agents. Journal of Medicinal Chemistry, 2009, 52, 1648-1658.	6.4	33
76	Structural Constraints Imposed by the Conserved Fusion Peptide on the HIV-1 gp41 Epitope Recognized by the Broadly Neutralizing Antibody 2F5. Journal of Physical Chemistry B, 2009, 113, 13626-13637.	2.6	21
77	Structural Characterization of the Molecular Events during a Slow Substrate-Product Transition in Orotidine 5-Monophosphate Decarboxylase. Journal of Molecular Biology, 2009, 387, 1199-1210.	4.2	16
78	P04-39. Recognizing a dynamic HIV-1 target: a structural look at the interaction between bnAb 2F5 and varying gp41 MPER sequences. Retrovirology, 2009, 6, .	2.0	0
79	Crystallization and preliminary X-ray analysis of the inducible lysine decarboxylase from <i>Escherichia coli</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 700-706.	0.7	8
80	Mechanism of Inhibition of Xanthine Oxidoreductase by Allopurinol: Crystal Structure of Reduced Bovine Milk Xanthine Oxidoreductase Bound with Oxipurinol. Nucleosides, Nucleotides and Nucleic Acids, 2008, 27, 888-893.	1.1	90
81	Mammalian xanthine oxidoreductase - mechanism of transition from xanthine dehydrogenase to xanthine oxidase. FEBS Journal, 2008, 275, 3278-3289.	4.7	305
82	Germline V-genes sculpt the binding site of a family of antibodies neutralizing human cytomegalovirus. EMBO Journal, 2008, 27, 2592-2602.	7.8	65
83	Crystal Structure of the Complex between the Fab Fragment of the Cross-Neutralizing Anti-HIV-1 Antibody 2F5 and the Fab Fragment of Its Anti-idiotypic Antibody 3H6. Journal of Molecular Biology, 2008, 382, 910-919.	4.2	20
84	Structural Details of HIV-1 Recognition by the Broadly Neutralizing Monoclonal Antibody 2F5: Epitope Conformation, Antigen-Recognition Loop Mobility, and Anion-Binding Site. Journal of Molecular Biology, 2008, 384, 377-392.	4.2	81
85	Structure-Activity Relationships of C6-Uridine Derivatives Targeting <i>Plasmodia</i> Orotidine Monophosphate Decarboxylase. Journal of Medicinal Chemistry, 2008, 51, 439-448.	6.4	45
86	Structural Diversity and Plasticity Associated with Nucleotides Targeting Orotidine Monophosphate Decarboxylase. Journal of Medicinal Chemistry, 2008, 51, 432-438.	6.4	12
87	Two Mutations Convert Mammalian Xanthine Oxidoreductase to Highly Superoxide-productive Xanthine Oxidase. Journal of Biochemistry, 2008, 144, 691-691.	1.7	1
88	Probing Structure-Function Relationships and Gating Mechanisms in the CorA Mg ²⁺ Transport System. Journal of Biological Chemistry, 2008, 283, 11721-11733.	3.4	60
89	Catalytic promiscuity and mechanistic determinants of ODCase - a high-resolution investigation. Acta Crystallographica Section A: Foundations and Advances, 2008, 64, C259-C260.	0.3	0
90	1P-025 Structural investigation of orotidine monophosphate decarboxylase : the role of the catalytic lysine(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S24.	0.1	0

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91	Two Mutations Convert Mammalian Xanthine Oxidoreductase to Highly Superoxide-productive Xanthine Oxidase. <i>Journal of Biochemistry</i> , 2007, 141, 525-534.	1.7	31
92	A Potent, Covalent Inhibitor of Orotidine 5â€-Monophosphate Decarboxylase with Antimalarial Activity. <i>Journal of Medicinal Chemistry</i> , 2007, 50, 915-921.	6.4	53
93	Transition State Infrared Spectra for the Transâ†Cis Isomerization of a Simple Peptide Model. <i>Journal of Physical Chemistry A</i> , 2007, 111, 8384-8389.	2.5	6
94	Quantifying the Intrinsic Effects of Two Point Mutation Models of Pro-Pro-Pro Triamino Acid Diamide. A First-Principle Computational Study. <i>Journal of Physical Chemistry B</i> , 2007, 111, 13135-13142.	2.6	14
95	Quantifying the Intrinsic Effects of Two Point Mutation Models of Prolineâ~Proline Diamino Acid Diamide: A First-Principle Computational Study. <i>Journal of Physical Chemistry B</i> , 2007, 111, 11592-11602.	2.6	15
96	Atomic model of human Rcd-1 reveals anarmadillo-like-repeat protein with in vitro nucleic acid binding properties. <i>Protein Science</i> , 2007, 16, 176-188.	7.6	54
97	Enzyme-Driven Speciation: Crystallizing Archaea via Lipid Capture. <i>Journal of Molecular Evolution</i> , 2007, 64, 364-374.	1.8	17
98	Design of Inhibitors of Orotidine Monophosphate Decarboxylase Using Bioisosteric Replacement and Determination of Inhibition Kinetics. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 4937-4945.	6.4	46
99	First-Principle Computational Study on the Full Conformational Space of l-Threonine Diamide, the Energetic Stability of Cis and Trans Isomers. <i>Journal of Physical Chemistry A</i> , 2006, 110, 11527-11536.	2.5	14
100	Crystallization and preliminary X-ray diffraction analysis of the magnesium transporter CorA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 148-152.	0.7	6
101	A structural basis for Mg ²⁺ homeostasis and the CorA translocation cycle. <i>EMBO Journal</i> , 2006, 25, 3762-3773.	7.8	121
102	The Crystal Structure of (S)-3-O-Geranylgeranylgeranyl Phosphate Synthase Reveals an Ancient Fold for an Ancient Enzyme. <i>Journal of Biological Chemistry</i> , 2006, 281, 6070-6078.	3.4	47
103	Distinct Conformation-mediated Functions of an Active Site Loop in the Catalytic Reactions of NAD-dependent D-Lactate Dehydrogenase and Formate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2005, 280, 17068-17075.	3.4	23
104	Mechanism of the Conversion of Xanthine Dehydrogenase to Xanthine Oxidase. <i>Journal of Biological Chemistry</i> , 2005, 280, 24888-24894.	3.4	136
105	First Principle Computational Study on the Full Conformational Space of l-Proline Diamides. <i>Journal of Physical Chemistry A</i> , 2005, 109, 2660-2679.	2.5	29
106	A point mutation in the Ch3 domain of human IgG3 inhibits antibody secretion without affecting antigen specificity. <i>Molecular Immunology</i> , 2005, 42, 1111-1119.	2.2	4
107	An Unprecedented Twist to ODCase Catalytic Activity. <i>Journal of the American Chemical Society</i> , 2005, 127, 15048-15050.	13.7	38
108	NmerA, the Metal Binding Domain of Mercuric Ion Reductase, Removes Hg ²⁺ from Proteins, Delivers It to the Catalytic Core, and Protects Cells under Glutathione-Depleted Conditions. <i>Biochemistry</i> , 2005, 44, 11402-11416.	2.5	66

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109	Crystallographic Studies of Native and Mutant Orotidine 5- α -phosphate Decarboxylases. Topics in Current Chemistry, 2004, , 23-42.	4.0	10
110	Anabaena circadian clock proteins KaiA and KaiB reveal a potential common binding site to their partner KaiC. EMBO Journal, 2004, 23, 1688-1698.	7.8	85
111	Y-700 [1-[3-Cyano-4-(2,2-dimethylpropoxy)phenyl]-1H-pyrazole-4-carboxylic Acid]: A Potent Xanthine Oxidoreductase Inhibitor with Hepatic Excretion. Journal of Pharmacology and Experimental Therapeutics, 2004, 311, 519-528.	2.5	106
112	The crystal structure of xanthine oxidoreductase during catalysis: Implications for reaction mechanism and enzyme inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7931-7936.	7.1	263
113	An ab initio exploratory study of the full conformational space of MeCO-l-threonine-NH-Me. Computational and Theoretical Chemistry, 2003, 666-667, 251-267.	1.5	7
114	A model study of the IgA hinge region: an exploratory study of selected backbone conformations of MeCO-l-Pro-l-Thr-NH-Me. Computational and Theoretical Chemistry, 2003, 666-667, 311-319.	1.5	5
115	Unique amino acids cluster for switching from the dehydrogenase to oxidase form of xanthine oxidoreductase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8170-8175.	7.1	89
116	Mutational, Structural, and Kinetic Studies of the ATP-binding Site of Methanobacterium thermoautotrophicum Nicotinamide Mononucleotide Adenylyltransferase. Journal of Biological Chemistry, 2003, 278, 34356-34363.	3.4	13
117	An Extremely Potent Inhibitor of Xanthine Oxidoreductase. Journal of Biological Chemistry, 2003, 278, 1848-1855.	3.4	353
118	Structural and functional analysis of a truncated form of Saccharomyces cerevisiae ATP sulfurylase: C-terminal domain essential for oligomer formation but not for activity. Protein Engineering, Design and Selection, 2003, 16, 1071-1079.	2.1	17
119	Crystal Structures of Inhibitor Complexes Reveal an Alternate Binding Mode in Orotidine-5- α -monophosphate Decarboxylase. Journal of Biological Chemistry, 2002, 277, 28080-28087.	3.4	35
120	Mapping the Active Site \sim Ligand Interactions of Orotidine 5- α -Monophosphate Decarboxylase by Crystallography. Biochemistry, 2002, 41, 4002-4011.	2.5	42
121	Improvements in Single Particle Cryo-Em: 11Å... Structure of 290 kDa Xdh Refined From Multiple 3D Reconstructions. Microscopy and Microanalysis, 2002, 8, 848-849.	0.4	0
122	Crystal structure ofMethanobacterium thermoautotrophicum conserved protein MTH1020 reveals an NTN-hydrolase fold. Proteins: Structure, Function and Bioinformatics, 2002, 48, 141-143.	2.6	9
123	The Molybdenum-Containing Xanthine Oxidoreductases and Picolinate Dehydrogenases. Metal Ions in Biological Systems, 2002, , .	0.4	2
124	The molybdenum-containing xanthine oxidoreductases and picolinate dehydrogenases. Metal Ions in Biological Systems, 2002, 39, 431-54.	0.4	3
125	Insights into Ligand Binding and Catalysis of a Central Step in NAD ⁺ Synthesis. Journal of Biological Chemistry, 2001, 276, 7225-7232.	3.4	50
126	Cross-Neutralizing Human Monoclonal Anti-HIV-1 Antibody 2F5: Preparation and Crystallographic Analysis of the Free and Epitope-Complexed Forms of its F ab Fragment. Protein and Peptide Letters, 2001, 8, 413-418.	0.9	11

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127	Purification, crystallization and preliminary X-ray study of orotidine 5â€²-monophosphate decarboxylase. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 912-914.	2.5	18
128	Î²-Carbonic anhydrase from <i>Pisum sativum</i> : crystallization and preliminary X-ray analysis. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 927-929.	2.5	5
129	Purification, crystallization and preliminary X-ray diffraction studies of xanthine dehydrogenase and xanthine oxidase isolated from bovine milk. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1656-1658.	2.5	30
130	Structural proteomics of an archaeon. Nature Structural Biology, 2000, 7, 903-909.	9.7	272
131	Penicillopepsinâ€”2, a recombinant enzyme from <i>Penicillium janthinellum</i> and the contribution of a hydrogen bond in subsite S ₃ to k _{cat} . Protein Science, 2000, 9, 991-1001.	7.6	11
132	Crystal Structure of dTDP-4-keto-6-deoxy-d-hexulose 3,5-Epimerase from <i>Methanobacterium thermoautotrophicum</i> Complexed with dTDP. Journal of Biological Chemistry, 2000, 275, 24608-24612.	3.4	57
133	Electrostatic stress in catalysis: Structure and mechanism of the enzyme orotidine monophosphate decarboxylase. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 2017-2022.	7.1	210
134	Structural Basis for Specificity Switching of the Src SH2 Domain. Molecular Cell, 2000, 5, 1043-1049.	9.7	44
135	Catalysis and regulation: There is always another way. Current Opinion in Structural Biology, 1999, 9, 661-662.	5.7	0
136	The alpha and beta of turning on a molecular switch. Nature Structural Biology, 1998, 5, 259-263.	9.7	6
137	A thioredoxin fusion protein of VanH, a lactate dehydrogenase from <i>Enterococcus faecium</i> : Cloning, expression, purification, kinetic analysis, and crystallization. Protein Science, 1998, 7, 1147-1155.	7.6	20
138	Differences in Binding Modes of Enantiomers of 1-Acetamido Boronic Acid Based Protease Inhibitors: Crystal Structures of I ³ -Chymotrypsin and Subtilisin Carlsberg Complexes. Biochemistry, 1998, 37, 451-462.	2.5	63
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