

# Emil F Pai

## List of Publications by Year in descending order

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179  
papers

12,686  
citations

31976

53  
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24982

109  
g-index

187  
all docs

187  
docs citations

187  
times ranked

11873  
citing authors

#	ARTICLE	IF	CITATIONS
1	Atomic structure of the actin: DNase I complex. <i>Nature</i> , 1990, 347, 37-44.	27.8	1,871
2	Structure of the guanine-nucleotide-binding domain of the Ha-ras oncogene product p21 in the triphosphate conformation. <i>Nature</i> , 1989, 341, 209-214.	27.8	918
3	Crystal structure of metarhodopsin II. <i>Nature</i> , 2011, 471, 651-655.	27.8	620
4	Time-resolved X-ray crystallographic study of the conformational change in Ha-Ras p21 protein on GTP hydrolysis. <i>Nature</i> , 1990, 345, 309-315.	27.8	520
5	Three-dimensional structures of H-ras p21 mutants: Molecular basis for their inability to function as signal switch molecules. <i>Cell</i> , 1990, 62, 539-548.	28.9	394
6	An Extremely Potent Inhibitor of Xanthine Oxidoreductase. <i>Journal of Biological Chemistry</i> , 2003, 278, 1848-1855.	3.4	353
7	Substrate positions and induced-fit in crystalline adenylate kinase. <i>Journal of Molecular Biology</i> , 1977, 114, 37-45.	4.2	317
8	Mammalian xanthine oxidoreductase â€™ mechanism of transition from xanthine dehydrogenase to xanthine oxidase. <i>FEBS Journal</i> , 2008, 275, 3278-3289.	4.7	305
9	Structural proteomics of an archaeon. <i>Nature Structural Biology</i> , 2000, 7, 903-909.	9.7	272
10	Three-dimensional structure of glutathione reductase at 2 Å... resolution. <i>Journal of Molecular Biology</i> , 1981, 152, 763-782.	4.2	266
11	The crystal structure of xanthine oxidoreductase during catalysis: Implications for reaction mechanism and enzyme inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7931-7936.	7.1	263
12	Structure of the detoxification catalyst mercuric ion reductase from <i>Bacillus</i> sp. strain RC607. <i>Nature</i> , 1991, 352, 168-172.	27.8	211
13	Electrostatic stress in catalysis: Structure and mechanism of the enzyme orotidine monophosphate decarboxylase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 2017-2022.	7.1	210
14	Mitochondrial ClpP-Mediated Proteolysis Induces Selective Cancer Cell Lethality. <i>Cancer Cell</i> , 2019, 35, 721-737.e9.	16.8	206
15	The structure of OmpF porin in a tetragonal crystal form. <i>Structure</i> , 1995, 3, 1041-1050.	3.3	183
16	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
17	The role of dimer asymmetry and protomer dynamics in enzyme catalysis. <i>Science</i> , 2017, 355, .	12.6	155
18	FAD-binding site of glutathione reductase. <i>Journal of Molecular Biology</i> , 1982, 160, 287-308.	4.2	147

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19	Crystallographic analysis of the binding of NADPH, NADPH fragments, and NADPH analogues to glutathione reductase. <i>Biochemistry</i> , 1988, 27, 4465-4474.	2.5	143
20	A crystallographic study of the glutathione binding site of glutathione reductase at 0.3-nm resolution. <i>FEBS Journal</i> , 1989, 178, 693-703.	0.2	143
21	Mechanism of the Conversion of Xanthine Dehydrogenase to Xanthine Oxidase. <i>Journal of Biological Chemistry</i> , 2005, 280, 24888-24894.	3.4	136
22	A structural basis for Mg <sup>2+</sup> homeostasis and the CorA translocation cycle. <i>EMBO Journal</i> , 2006, 25, 3762-3773.	7.8	121
23	Prion disease susceptibility is affected by $\beta^2$ -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
24	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882.	12.8	113
25	Y-700 [1-[3-Cyano-4-(2,2-dimethylpropoxy)phenyl]-1H-pyrazole-4-carboxylic Acid]: A Potent Xanthine Oxidoreductase Inhibitor with Hepatic Excretion. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2004, 311, 519-528.	2.5	106
26	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
27	Absolute stereochemistry of flavins in enzyme-catalyzed reactions. <i>Biochemistry</i> , 1986, 25, 6807-6816.	2.5	98
28	Mechanism of Inhibition of Xanthine Oxidoreductase by Allopurinol: Crystal Structure of Reduced Bovine Milk Xanthine Oxidoreductase Bound with Oxipurinol. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2008, 27, 888-893.	1.1	90
29	Unique amino acids cluster for switching from the dehydrogenase to oxidase form of xanthine oxidoreductase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8170-8175.	7.1	89
30	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
31	Anabaena circadian clock proteins KaiA and KaiB reveal a potential common binding site to their partner KaiC. <i>EMBO Journal</i> , 2004, 23, 1688-1698.	7.8	85
32	An Iris-Like Mechanism of Pore Dilatation in the CorA Magnesium Transport System. <i>Biophysical Journal</i> , 2010, 98, 784-792.	0.5	83
33	Structural Details of HIV-1 Recognition by the Broadly Neutralizing Monoclonal Antibody 2F5: Epitope Conformation, Antigen-Recognition Loop Mobility, and Anion-Binding Site. <i>Journal of Molecular Biology</i> , 2008, 384, 377-392.	4.2	81
34	The Structure of Trypanosoma cruzi trypanothione Reductase in the Oxidized and NADPH Reduced State. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 18, 161-173.	2.6	78
35	Time-resolved crystallography reveals allosteric communication aligned with molecular breathing. <i>Science</i> , 2019, 365, 1167-1170.	12.6	78
36	GTPase domains of ras p21 oncogene protein and elongation factor Tu: analysis of three-dimensional structures, sequence families, and functional sites.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 5443-5447.	7.1	76

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37	Study of (tetraphenylporphinato)manganese(III)-catalyzed epoxidation and demethylation using p-cyano-N,N-dimethylaniline N-oxide as oxygen donor in a homogeneous system. Kinetics, radiochemical ligation studies, and reaction mechanism for a model of cytochrome P-450. <i>Journal of the American Chemical Society</i> , 1984, 106, 3277-3285.	13.7	74
38	Mapping the Reaction Coordinates of Enzymatic Defluorination. <i>Journal of the American Chemical Society</i> , 2011, 133, 7461-7468.	13.7	73
39	X-ray Crystal Structure Analysis of the Catalytic Domain of the Oncogene Product p21H-rasComplexed with Caged GTP and Mant dCpNHp. <i>Journal of Molecular Biology</i> , 1995, 253, 132-150.	4.2	70
40	The hit-and-return system enables efficient time-resolved serial synchrotron crystallography. <i>Nature Methods</i> , 2018, 15, 901-904.	19.0	67
41	The Grb2-mSos1 Complex Binds Phosphopeptides with Higher Affinity than Grb2. <i>Journal of Biological Chemistry</i> , 1996, 271, 30472-30478.	3.4	66
42	NmerA, the Metal Binding Domain of Mercuric Ion Reductase, Removes Hg <sup>2+</sup> 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
43	Opsin, a Structural Model for Olfactory Receptors?. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 11021-11024.	13.8	66
44	Germline V-genes sculpt the binding site of a family of antibodies neutralizing human cytomegalovirus. <i>EMBO Journal</i> , 2008, 27, 2592-2602.	7.8	65
45	Primary and Tertiary Structure of the Principal Human Adenylate Kinase. <i>FEBS Journal</i> , 1976, 68, 281-290.	0.2	64
46	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
47	Differences in Binding Modes of Enantiomers of 1-Acetamido Boronic Acid Based Protease Inhibitors:Â Crystal Structures of I <sup>3</sup> -Chymotrypsin and Subtilisin Carlsberg Complexesâ€¢. <i>Biochemistry</i> , 1998, 37, 451-462.	2.5	63
48	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
49	Probing Structure-Function Relationships and Gating Mechanisms in the CorA Mg <sup>2+</sup> Transport System. <i>Journal of Biological Chemistry</i> , 2008, 283, 11721-11733.	3.4	60
50	Glutathione Reductase Turned into Trypanothione Reductase:Â Structural Analysis of an Engineered Change in Substrate Specificityâ€¢. <i>Biochemistry</i> , 1997, 36, 6437-6447.	2.5	57
51	Crystal Structure of dTDP-4-keto-6-deoxy-d-hexulose 3,5-Epimerase from <i>Methanobacterium thermoautotrophicum</i> Complexed with dTDP. <i>Journal of Biological Chemistry</i> , 2000, 275, 24608-24612.	3.4	57
52	The structure and regulation of magnesium selective ion channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2778-2792.	2.6	57
53	Insights into substrate binding by D-2-ketoacid dehydrogenases from the structure of <i>Lactobacillus pentosus</i> D-lactate dehydrogenase. <i>Structure</i> , 1996, 4, 437-447.	3.3	56
54	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

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55	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
56	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
57	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
58	A Potent, Covalent Inhibitor of Orotidine 5'-Monophosphate Decarboxylase with Antimalarial Activity. <i>Journal of Medicinal Chemistry</i> , 2007, 50, 915-921.	6.4	53
59	Sequence- and activity- based screening of microbial genomes for novel dehalogenases. <i>Microbial Biotechnology</i> , 2010, 3, 107-120.	4.2	53
60	Halothane binds in the adenine-specific niche of crystalline adenylate kinase. <i>FEBS Letters</i> , 1977, 79, 310-312.	2.8	52
61	Crystallographic Definition of the Epitope Promiscuity of the Broadly Neutralizing Anti-Human Immunodeficiency Virus Type 1 Antibody 2F5: Vaccine Design Implications. <i>Journal of Virology</i> , 2009, 83, 11862-11875.	3.4	52
62	Insights into Ligand Binding and Catalysis of a Central Step in NAD <sup>+</sup> Synthesis. <i>Journal of Biological Chemistry</i> , 2001, 276, 7225-7232.	3.4	50
63	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
64	Protein Conformational Gating of Enzymatic Activity in Xanthine Oxidoreductase. <i>Journal of the American Chemical Society</i> , 2012, 134, 999-1009.	13.7	49
65	Hydrophobic Gating of Ion Permeation in Magnesium Channel CorA. <i>PLoS Computational Biology</i> , 2015, 11, e1004303.	3.2	48
66	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
67	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
68	X-ray Structure of a Hg <sup>2+</sup> Complex of Mercuric Reductase (MerA) and Quantum Mechanical/Molecular Mechanical Study of Hg <sup>2+</sup> Transfer between the C-Terminal and Buried Catalytic Site Cysteine Pairs. <i>Biochemistry</i> , 2014, 53, 7211-7222.	2.5	46
69	Structure-Activity Relationships of C6-Uridine Derivatives Targeting Plasmodia Orotidine Monophosphate Decarboxylase. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 439-448.	6.4	45
70	The structure of enzyme II <sub>lactose</sub> from <i>Lactococcus lactis</i> reveals a new fold and points to possible interactions of a multicomponent system. <i>Structure</i> , 1997, 5, 775-788.	3.3	44
71	Structural Basis for Specificity Switching of the Src SH2 Domain. <i>Molecular Cell</i> , 2000, 5, 1043-1049.	9.7	44
72	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

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73	Variations on a theme: the family of FAD-dependent NAD(P)H-(disulphide)-oxidoreductases. <i>Current Opinion in Structural Biology</i> , 1991, 1, 796-803.	5.7	43
74	Mapping the Active Site~Ligand Interactions of Orotidine 5~Monophosphate Decarboxylase by Crystallography~. <i>Biochemistry</i> , 2002, 41, 4002-4011.	2.5	42
75	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
76	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
77	Adenylate kinases from thermosensitive <i>Escherichia coli</i> strains. <i>Journal of Molecular Biology</i> , 1989, 207, 151-162.	4.2	41
78	Binding to Large Enzyme Pockets: Small~Molecule Inhibitors of Trypanothione Reductase. <i>ChemMedChem</i> , 2014, 9, 1880-1891.	3.2	40
79	An Unprecedented Twist to ODCase Catalytic Activity. <i>Journal of the American Chemical Society</i> , 2005, 127, 15048-15050.	13.7	38
80	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
81	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
82	Stereochemistry and accessibility of prosthetic groups in flavoproteins. <i>Biochemistry</i> , 1988, 27, 2300-2305.	2.5	36
83	Crystal Structures of Inhibitor Complexes Reveal an Alternate Binding Mode in Orotidine-5~monophosphate Decarboxylase. <i>Journal of Biological Chemistry</i> , 2002, 277, 28080-28087.	3.4	35
84	Structure~Activity Relationships of Orotidine-5~Monophosphate Decarboxylase Inhibitors as Anticancer Agents. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 1648-1658.	6.4	33
85	Resolution of structural heterogeneity in dynamic crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 946-959.	2.5	32
86	Two Mutations Convert Mammalian Xanthine Oxidoreductase to Highly Superoxide-productive Xanthine Oxidase. <i>Journal of Biochemistry</i> , 2007, 141, 525-534.	1.7	31
87	Purification, crystallization and preliminary X-ray diffraction studies of xanthine dehydrogenase and xanthine oxidase isolated from bovine milk. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1656-1658.	2.5	30
88	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
89	Crystallization and preliminary crystallographic analysis of trypanothione reductase from <i>Trypanosoma cruzi</i> , the causative agent of Chagas' disease. <i>FEBS Letters</i> , 1993, 317, 105-108.	2.8	27
90	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

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91	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
92	Substrate-Based Allosteric Regulation of a Homodimeric Enzyme. <i>Journal of the American Chemical Society</i> , 2019, 141, 11540-11556.	13.7	26
93	Serial femtosecond and serial synchrotron crystallography can yield data of equivalent quality: A systematic comparison. <i>Science Advances</i> , 2021, 7, .	10.3	25
94	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
95	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
96	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
97	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
98	Structural Constraints Imposed by the Conserved Fusion Peptide on the HIV-1 gp41 Epitope Recognized by the Broadly Neutralizing Antibody 2F5. <i>Journal of Physical Chemistry B</i> , 2009, 113, 13626-13637.	2.6	21
99	A thioredoxin fusion protein of VanH, a D-lactate dehydrogenase from <i>Enterococcus faecium</i> : Cloning, expression, purification, kinetic analysis, and crystallization. <i>Protein Science</i> , 1998, 7, 1147-1155.	7.6	20
100	Crystal Structure of the Complex between the Fab <sup>2</sup> Fragment of the Cross-Neutralizing Anti-HIV-1 Antibody 2F5 and the Fab Fragment of Its Anti-idiotypic Antibody 3H6. <i>Journal of Molecular Biology</i> , 2008, 382, 910-919.	4.2	20
101	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
102	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
103	Purification, crystallization and preliminary X-ray study of orotidine 5 <sup>2</sup> -monophosphate decarboxylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 912-914.	2.5	18
104	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
105	Structural and functional analysis of a truncated form of <i>Saccharomyces cerevisiae</i> ATP sulfurylase: C-terminal domain essential for oligomer formation but not for activity. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 1071-1079.	2.1	17
106	Enzyme-Driven Speciation: Crystallizing Archaea via Lipid Capture. <i>Journal of Molecular Evolution</i> , 2007, 64, 364-374.	1.8	17
107	N-Terminal Helix-Cap in $\hat{1}\pm$ -Helix 2 Modulates $\hat{1}^2$ -State Misfolding in Rabbit and Hamster Prion Proteins. <i>PLoS ONE</i> , 2013, 8, e63047.	2.5	17
108	Structural Characterization of the Molecular Events during a Slow Substrate-Product Transition in Orotidine 5 <sup>2</sup> -Monophosphate Decarboxylase. <i>Journal of Molecular Biology</i> , 2009, 387, 1199-1210.	4.2	16



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109	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
110	Quantifying the Intrinsic Effects of Two Point Mutation Models of Proline-Proline Diamide: A First-Principle Computational Study. <i>Journal of Physical Chemistry B</i> , 2007, 111, 11592-11602.	2.6	15
111	Characterization of Vis Toxin, a Novel ADP-Ribosyltransferase from <i>Vibrio splendidus</i> . <i>Biochemistry</i> , 2015, 54, 5920-5936.	2.5	15
112	Development of Antibiotics That Dysregulate the <i>Neisseria</i> ClpP Protease. <i>ACS Infectious Diseases</i> , 2020, 6, 3224-3236.	3.8	15
113	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
114	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
115	Structural determinants for the inhibitory ligands of orotidine-5'-monophosphate decarboxylase. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 4032-4041.	3.0	14
116	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
117	The prion protein is embedded in a molecular environment that modulates transforming growth factor $\beta^2$ and integrin signaling. <i>Scientific Reports</i> , 2018, 8, 8654.	3.3	14
118	Mutational, Structural, and Kinetic Studies of the ATP-binding Site of Methanobacterium thermoautotrophicum Nicotinamide Mononucleotide Adenylyltransferase. <i>Journal of Biological Chemistry</i> , 2003, 278, 34356-34363.	3.4	13
119	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
120	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
121	Time-resolved macromolecular crystallography. <i>Current Opinion in Structural Biology</i> , 1992, 2, 821-827.	5.7	12
122	Structural Diversity and Plasticity Associated with Nucleotides Targeting Orotidine Monophosphate Decarboxylase. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 432-438.	6.4	12
123	Novel Interactions of Fluorinated Nucleotide Derivatives Targeting Orotidine 5'-Monophosphate Decarboxylase. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 2891-2901.	6.4	12
124	Defluorination Capability of Haloacid Dehalogenases in the HAD-Like Hydrolase Superfamily Correlates with Active Site Compactness. <i>ChemBioChem</i> , 2022, 23, .	2.6	12
125	Penicillopepsin-T2, a recombinant enzyme from <i>Penicillium janthinellum</i> and the contribution of a hydrogen bond in subsite S <sub>3</sub> to k <sub>cat</sub> . <i>Protein Science</i> , 2000, 9, 991-1001.	7.6	11
126	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



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127	Conformational Determinants of Phosphotyrosine Peptides Complexed with the Src SH2 Domain. PLoS ONE, 2010, 5, e11215.	2.5	11
128	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
129	Crystallographic Studies of Native and Mutant Orotidine 5â€²phosphate Decarboxylases. Topics in Current Chemistry, 2004, , 23-42.	4.0	10
130	Protein crystals IR laser ablated from aqueous solution at high speed retain their diffractive properties: applications in high-speed serial crystallography. Journal of Applied Crystallography, 2017, 50, 1773-1781.	4.5	10
131	Preliminary X-ray studies on the GTP: AMP phosphotransferase from beef heart mitochondria. Journal of Molecular Biology, 1983, 164, 347-350.	4.2	9
132	Crystal structure ofMethanobacterium thermoautotrophicum conserved protein MTH1020 reveals an NTN-hydrolase fold. Proteins: Structure, Function and Bioinformatics, 2002, 48, 141-143.	2.6	9
133	Novel Cytidine-Based Orotidine-5â€²-Monophosphate Decarboxylase Inhibitors with an Unusual Twist. Journal of Medicinal Chemistry, 2012, 55, 9988-9997.	6.4	9
134	Antimalarial Activities of 6-Iodouridine and Its Prodrugs and Potential for Combination Therapy. Journal of Medicinal Chemistry, 2013, 56, 2348-2358.	6.4	9
135	Crystallization and preliminary X-ray analysis of the inducible lysine decarboxylase fromEscherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 700-706.	0.7	8
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