

Ignacio Fita

List of Publications by Year in descending order

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119
papers

5,594
citations

57631

44
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88477

70
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126
all docs

126
docs citations

126
times ranked

5383
citing authors

#	ARTICLE	IF	CITATIONS
1	Tumor mesenquimático fosfatásico de pelvis: abordaje multidisciplinario. Revista De La Asociación Argentina De Ortopedia Y Traumatología, 2022, 87, 360-370.	0.0	1
2	Immunodominant proteins P1 and P40/P90 from human pathogen <i>Mycoplasma pneumoniae</i> . Nature Communications, 2020, 11, 5188.	5.8	22
3	Alternative conformation of the C-domain of the P140 protein from <i>Mycoplasma genitalium</i> . Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 508-516.	0.4	2
4	Structure and mechanism of the Nap adhesion complex from the human pathogen <i>Mycoplasma genitalium</i> . Nature Communications, 2020, 11, 2877.	5.8	19
5	L amino acid transporter structure and molecular bases for the asymmetry of substrate interaction. Nature Communications, 2019, 10, 1807.	5.8	57
6	<i>Cis</i> - <i>trans</i> proline isomers in the catalytic domain of calcineurin. FEBS Journal, 2019, 286, 1230-1239.	2.2	6
7	Theory Uncovers the Role of the Methionine-Tyrosine-Tryptophan Radical Adduct in the Catalase Reaction of KatGs: O ₂ Release Mediated by Proton-Coupled Electron Transfer. Chemistry - A European Journal, 2018, 24, 5388-5395.	1.7	4
8	KatG-Mediated Oxidation Leading to Reduced Susceptibility of Bacteria to Kanamycin. ACS Omega, 2018, 3, 4213-4219.	1.6	10
9	Prediction of Protein Configurational Entropy (Popcoen). Journal of Chemical Theory and Computation, 2018, 14, 1811-1819.	2.3	11
10	The nucleotide-bound/substrate-bound conformation of the <i>Mycoplasma genitalium</i> DnaK chaperone. Protein Science, 2018, 27, 1000-1007.	3.1	8
11	Entropic Stabilization of Cas4 Protein SSO0001 Predicted with Popcoen. Entropy, 2018, 20, 580.	1.1	1
12	<i>Mycoplasma genitalium</i> adhesin P110 binds sialic-acid human receptors. Nature Communications, 2018, 9, 4471.	5.8	29
13	Structural Insights into Subunits Assembly and the Oxyester Splicing Mechanism of Neq pol Split Intein. Cell Chemical Biology, 2018, 25, 871-879.e2.	2.5	5
14	The Catalase Activity of Catalase-Peroxidases Is Modulated by Changes in the p <i>K_a</i> of the Distal Histidine. Biochemistry, 2017, 56, 2271-2281.	1.2	11
15	Structural characterization of the NAP; the major adhesion complex of the human pathogen <i>Mycoplasma genitalium</i> . Molecular Microbiology, 2017, 105, 869-879.	1.2	24
16	Testing the mutual information expansion of entropy with multivariate Gaussian distributions. Journal of Chemical Physics, 2017, 147, 224102.	1.2	6
17	Structure-Guided Mutations in the Terminal Organelle Protein MG491 Cause Major Motility and Morphologic Alterations on <i>Mycoplasma genitalium</i> . PLoS Pathogens, 2016, 12, e1005533.	2.1	5
18	Thermal motion in proteins: Large effects on the time-averaged interaction energies. AIP Advances, 2016, 6, 035020.	0.6	2

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19	Inhibitory properties of 1,4-dideoxy-1,4-imino-d-arabinitol (DAB) derivatives acting on glycogen metabolising enzymes. <i>Organic and Biomolecular Chemistry</i> , 2016, 14, 9105-9113.	1.5	8
20	Structure of human carbamoyl phosphate synthetase: deciphering the on/off switch of human ureagenesis. <i>Scientific Reports</i> , 2015, 5, 16950.	1.6	64
21	Calcineurin Undergoes a Conformational Switch Evoked via Peptidyl-Prolyl Isomerization. <i>PLoS ONE</i> , 2015, 10, e0134569.	1.1	10
22	Selective photoregulation of the activity of glycogen synthase and glycogen phosphorylase, two key enzymes in glycogen metabolism. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 7282-7288.	1.5	19
23	Eukaryotic Catalase-Peroxidase: The Role of the Trp-Tyr-Met Adduct in Protein Stability, Substrate Accessibility, and Catalysis of Hydrogen Peroxide Dismutation. <i>Biochemistry</i> , 2015, 54, 5425-5438.	1.2	3
24	Vibrational Entropy of a Protein: Large Differences between Distinct Conformations. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 351-359.	2.3	27
25	A Major Determinant for Gliding Motility in <i>Mycoplasma genitalium</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 1699-1711.	1.6	8
26	Binding of the Antitubercular Pro-Drug Isoniazid in the Heme Access Channel of Catalase-Peroxidase (KatG). A Combined Structural and Metadynamics Investigation. <i>Journal of Physical Chemistry B</i> , 2014, 118, 2924-2931.	1.2	27
27	An Ionizable Active-Site Tryptophan Imparts Catalase Activity to a Peroxidase Core. <i>Journal of the American Chemical Society</i> , 2014, 136, 7249-7252.	6.6	28
28	Structure and interaction with phospholipids of a prokaryotic lipoxygenase from <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , 2013, 27, 4811-4821.	0.2	78
29	Spectroscopic and Kinetic Investigation of the Reactions of Peroxyacetic Acid with <i>Burkholderia pseudomallei</i> Catalase-Peroxidase, KatG. <i>Biochemistry</i> , 2013, 52, 7271-7282.	1.2	18
30	Structure of <i>Pisum sativum</i> Rubisco with bound ribulose 1,5-bisphosphate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 10-14.	0.7	5
31	Structural Asymmetry and Disulfide Bridges among Subunits Modulate the Activity of Human Malonyl-CoA Decarboxylase*. <i>Journal of Biological Chemistry</i> , 2013, 288, 11907-11919.	1.6	10
32	New features of vault architecture and dynamics revealed by novel refinement using the deformable elastic network approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1054-1061.	2.5	12
33	High Conformational Stability of Secreted Eukaryotic Catalase-peroxidases. <i>Journal of Biological Chemistry</i> , 2012, 287, 32254-32262.	1.6	21
34	The EAGR box structure: a motif involved in mycoplasma motility. <i>Molecular Microbiology</i> , 2012, 86, 382-393.	1.2	14
35	Crystal Structure of <i>Brucella abortus</i> Deoxyxylulose-5-phosphate Reductoisomerase-like (DRL) Enzyme Involved in Isoprenoid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2012, 287, 15803-15809.	1.6	9
36	Thirty years of heme catalases structural biology. <i>Archives of Biochemistry and Biophysics</i> , 2012, 525, 102-110.	1.4	90

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37	Influence of main channel structure on H ₂ O ₂ access to the heme cavity of catalase KatE of <i>Escherichia coli</i> . <i>Archives of Biochemistry and Biophysics</i> , 2012, 526, 54-59.	1.4	12
38	Structure of glycerol-3-phosphate dehydrogenase (GPD1) from <i>Saccharomyces cerevisiae</i> at 2.45 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1279-1283.	0.7	8
39	Vault particles: a new generation of delivery nanodevices. <i>Current Opinion in Biotechnology</i> , 2012, 23, 972-977.	3.3	19
40	Insight on an Arginine Synthesis Metabolon from the Tetrameric Structure of Yeast Acetylglutamate Kinase. <i>PLoS ONE</i> , 2012, 7, e34734.	1.1	18
41	Lyase activity of glycogen synthase: Is an elimination/addition mechanism a possible reaction pathway for retaining glycosyltransferases?. <i>IUBMB Life</i> , 2012, 64, 649-658.	1.5	14
42	Modulation of Heme Orientation and Binding by a Single Residue in Catalase HPII of <i>Escherichia coli</i> . <i>Biochemistry</i> , 2011, 50, 2101-2110.	1.2	14
43	Oxygen Binding to Catalase-Peroxidase. <i>Journal of Physical Chemistry Letters</i> , 2011, 2, 196-200.	2.1	18
44	Re-engineering specificity in 1,3-β-D-glucanase to accept branched xyloglucan substrates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 365-375.	1.5	12
45	Processivity and Subcellular Localization of Glycogen Synthase Depend on a Non-catalytic High Affinity Glycogen-binding Site. <i>Journal of Biological Chemistry</i> , 2011, 286, 18505-18514.	1.6	25
46	Molecular basis of substrate-induced permeation by an amino acid antiporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3935-3940.	3.3	139
47	Isonicotinic Acid Hydrazide Conversion to Isonicotinyl-NAD by Catalase-peroxidases. <i>Journal of Biological Chemistry</i> , 2010, 285, 26662-26673.	1.6	55
48	Substrate Binding and Catalysis in Carbamate Kinase Ascertained by Crystallographic and Site-Directed Mutagenesis Studies: Movements and Significance of a Unique Globular Subdomain of This Key Enzyme for Fermentative ATP Production in Bacteria. <i>Journal of Molecular Biology</i> , 2010, 397, 1261-1275.	2.0	19
49	Two Crystal Structures of <i>Escherichia coli</i> N-Acetyl-L-Glutamate Kinase Demonstrate the Cycling between Open and Closed Conformations. <i>Journal of Molecular Biology</i> , 2010, 399, 476-490.	2.0	15
50	The dynamic role of distal side residues in heme hydroperoxidase catalysis. Interplay between X-ray crystallography and ab initio MD simulations. <i>Archives of Biochemistry and Biophysics</i> , 2010, 500, 37-44.	1.4	16
51	Three-dimensional Structure and Enzymatic Function of Proapoptotic Human p53-inducible Quinone Oxidoreductase PIG3. <i>Journal of Biological Chemistry</i> , 2009, 284, 17194-17205.	1.6	48
52	Essential Role of Proximal Histidine-Asparagine Interaction in Mammalian Peroxidases. <i>Journal of Biological Chemistry</i> , 2009, 284, 25929-25937.	1.6	68
53	Structural and mechanistic insights into the association of PKC ζ -C2 domain to PtdIns(4,5)P ₂ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6603-6607.	3.3	99
54	Minor group human rhinovirus receptor interactions: Geometry of multimodular attachment and basis of recognition. <i>FEBS Letters</i> , 2009, 583, 235-240.	1.3	26

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55	Aldo-keto reductases from the AKR1B subfamily: Retinoid specificity and control of cellular retinoic acid levels. <i>Chemico-Biological Interactions</i> , 2009, 178, 171-177.	1.7	70
56	The mechanism of vault opening from the high resolution structure of the N-terminal repeats of MVP. <i>EMBO Journal</i> , 2009, 28, 3450-3457.	3.5	30
57	Arginine and nitrogen storage. <i>Current Opinion in Structural Biology</i> , 2008, 18, 673-681.	2.6	92
58	Electronic State of the Molecular Oxygen Released by Catalase. <i>Journal of Physical Chemistry A</i> , 2008, 112, 12842-12848.	1.1	14
59	Structural and biochemical studies of TREX1 inhibition by metals. Identification of a new active histidine conserved in DEDDh exonucleases. <i>Protein Science</i> , 2008, 17, 2059-2069.	3.1	27
60	The crystal structure of the complex of PII and acetylglutamate kinase reveals how PII controls the storage of nitrogen as arginine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17644-17649.	3.3	113
61	The Structure of Human 4F2hc Ectodomain Provides a Model for Homodimerization and Electrostatic Interaction with Plasma Membrane. <i>Journal of Biological Chemistry</i> , 2007, 282, 31444-31452.	1.6	101
62	Structure of the Dimeric Exonuclease TREX1 in Complex with DNA Displays a Proline-rich Binding Site for WW Domains. <i>Journal of Biological Chemistry</i> , 2007, 282, 14547-14557.	1.6	45
63	A Novel Two-domain Architecture Within the Amino Acid Kinase Enzyme Family Revealed by the Crystal Structure of <i>Escherichia coli</i> Glutamate 5-kinase. <i>Journal of Molecular Biology</i> , 2007, 367, 1431-1446.	2.0	62
64	Structural basis for the high <i>all-trans</i> -retinaldehyde reductase activity of the tumor marker AKR1B10. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20764-20769.	3.3	172
65	Versatility of the Electronic Structure of Compound I in Catalase-Peroxidases. <i>Journal of the American Chemical Society</i> , 2007, 129, 13436-13446.	6.6	47
66	The Structures and Electronic Configuration of Compound I Intermediates of <i>Helicobacter pylori</i> and <i>Penicillium vitale</i> Catalases Determined by X-ray Crystallography and QM/MM Density Functional Theory Calculations. <i>Journal of the American Chemical Society</i> , 2007, 129, 4193-4205.	6.6	58
67	Biosynthesis of isoprenoids in plants: Structure of the 2C-methyl-erythritol 2,4-cyclodiphosphate synthase from <i>Arabidopsis thaliana</i> . Comparison with the bacterial enzymes. <i>Protein Science</i> , 2007, 16, 2082-2088.	3.1	21
68	Roles for Arg426 and Trp111 in the Modulation of NADH Oxidase Activity of the Catalase-peroxidase KatG from <i>Burkholderia pseudomallei</i> Inferred from pH-Induced Structural Changes. <i>Biochemistry</i> , 2006, 45, 5171-5179.	1.2	39
69	Structural Bases of Feed-back Control of Arginine Biosynthesis, Revealed by the Structures of Two Hexameric N-Acetylglutamate Kinases, from <i>Thermotoga maritima</i> and <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2006, 356, 695-713.	2.0	63
70	Combining experimental data for structure determination of flexible multimeric macromolecules by molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 467-475.	2.5	9
71	Two alternative substrate paths for compound I formation and reduction in catalase-peroxidase KatG from <i>Burkholderia pseudomallei</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 219-228.	1.5	22
72	A first principles study of the binding of formic acid in catalase complementing high resolution X-ray structures. <i>Chemical Physics</i> , 2006, 323, 129-137.	0.9	11

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73	Crystal Structure of an Archaeal Glycogen Synthase. <i>Journal of Biological Chemistry</i> , 2006, 281, 2923-2931.	1.6	74
74	A molecular switch and electronic circuit modulate catalase activity in catalase- ϵ -peroxidases. <i>EMBO Reports</i> , 2005, 6, 1156-1162.	2.0	45
75	Characterization of a Large Subunit Catalase Truncated by Proteolytic Cleavage. <i>Biochemistry</i> , 2005, 44, 5597-5605.	1.2	17
76	Structural Characterization of the Ser324Thr Variant of the Catalase-peroxidase (KatG) from <i>Burkholderia pseudomallei</i> . <i>Journal of Molecular Biology</i> , 2005, 345, 21-28.	2.0	34
77	Preliminary analysis of two and three dimensional crystals of vault ribonucleoprotein particles. <i>Journal of Structural Biology</i> , 2005, 151, 111-115.	1.3	4
78	Catalase-peroxidases (KatG) Exhibit NADH Oxidase Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 43098-43106.	1.6	68
79	X-ray structure of a minor group human rhinovirus bound to a fragment of its cellular receptor protein. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 429-434.	3.6	143
80	Structure of the C-terminal domain of the catalase- ϵ -peroxidase KatG from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1824-1832.	2.5	15
81	Structure of <i>Helicobacter pylori</i> Catalase, with and without Formic Acid Bound, at 1.6 Å... Resolution. <i>Biochemistry</i> , 2004, 43, 3089-3103.	1.2	65
82	Apo and Holo Structures of an NADP(H)-dependent Cinnamyl Alcohol Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2004, 341, 1049-1062.	2.0	49
83	Structure of the Clade 1 catalase, CatF of <i>Pseudomonas syringae</i> , at 1.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 423-436.	1.5	45
84	Retinoic Acid Binds to the C2-Domain of Protein Kinase C β . <i>Biochemistry</i> , 2003, 42, 8774-8779.	1.2	76
85	The Proximal Hydrogen-Bonded Residue Controls the Stability of the Compound III Intermediate of Peroxidases and Catalases. <i>Journal of Physical Chemistry B</i> , 2003, 107, 5300-5305.	1.2	29
86	Catalase-peroxidase KatG of <i>Burkholderia pseudomallei</i> at 1.7 Å... resolution. <i>Journal of Molecular Biology</i> , 2003, 327, 475-489.	2.0	126
87	Crystal Structure of the Vertebrate NADP(H)-dependent Alcohol Dehydrogenase (ADH8). <i>Journal of Molecular Biology</i> , 2003, 330, 75-85.	2.0	20
88	The Course of Phosphorus in the Reaction of N-Acetyl-l-glutamate Kinase, Determined from the Structures of Crystalline Complexes, Including a Complex with an AlF $_4$ Transition State Mimic. <i>Journal of Molecular Biology</i> , 2003, 331, 231-244.	2.0	40
89	An Electrical Potential in the Access Channel of Catalases Enhances Catalysis. <i>Journal of Biological Chemistry</i> , 2003, 278, 31290-31296.	1.6	56
90	Characterization of the Catalase-Peroxidase KatG from <i>Burkholderia pseudomallei</i> by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2003, 278, 35687-35692.	1.6	43

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91	Additional Binding Sites for Anionic Phospholipids and Calcium Ions in the Crystal Structures of Complexes of the C2 Domain of Protein Kinase C β . <i>Journal of Molecular Biology</i> , 2002, 320, 277-291.	2.0	74
92	Structure of Acetylglutamate Kinase, a Key Enzyme for Arginine Biosynthesis and a Prototype for the Amino Acid Kinase Enzyme Family, during Catalysis. <i>Structure</i> , 2002, 10, 329-342.	1.6	126
93	Crystallization and preliminary X-ray analysis of the hydroperoxidase I C-terminal domain from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 853-855.	2.5	5
94	Crystallization and preliminary X-ray analysis of the catalase β -peroxidase KatG from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2184-2186.	2.5	7
95	Theoretical Study of the Mechanisms of Substrate Recognition by Catalase. <i>Journal of the American Chemical Society</i> , 2001, 123, 9665-9672.	6.6	50
96	Structure of the C2 domain from novel protein kinase C μ . A membrane binding model for Ca ²⁺ -independent C2 domains. <i>Journal of Molecular Biology</i> , 2001, 311, 837-849.	2.0	97
97	Crystallization and preliminary X-ray analysis of clade I catalases from <i>Pseudomonas syringae</i> and <i>Listeria seeligeri</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1184-1186.	2.5	6
98	Substrate flow in catalases deduced from the crystal structures of active site variants of HP11 from <i>Escherichia coli</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 270-281.	1.5	50
99	The 1.5 Å... resolution crystal structure of the carbamate kinase-like carbamoyl phosphate synthetase from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> , bound to ADP, confirms that this thermostable enzyme is a carbamate kinase, and provides insight into substrate binding and stability in carbamate kinases. 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 463-476.	2.0	49
100	Enzymology and structure of catalases. <i>Advances in Inorganic Chemistry</i> , 2000, 51, 51-106.	0.4	236
101	The Carbamoyl-phosphate Synthetase of <i>Pyrococcus furiosus</i> Is Enzymologically and Structurally a Carbamate Kinase. <i>Journal of Biological Chemistry</i> , 1999, 274, 16295-16303.	1.6	29
102	Mutants That Alter the Covalent Structure of Catalase Hydroperoxidase II from <i>Escherichia coli</i> xs. <i>Journal of Biological Chemistry</i> , 1999, 274, 27717-27725.	1.6	30
103	Crystallization and preliminary structural results of catalase from human erythrocytes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1066-1068.	2.5	2
104	N-Acetyl-L-glutamate kinase from <i>Escherichia coli</i> : cloning of the gene, purification and crystallization of the recombinant enzyme and preliminary X-ray analysis of the free and ligand-bound forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1350-1352.	2.5	10
105	Structure of catalase HP11 from <i>Escherichia coli</i> at 1.9 Å resolution. , 1999, 34, 155-166.		60
106	Ca ²⁺ bridges the C2 membrane-binding domain of protein kinase C β directly to phosphatidylserine. <i>EMBO Journal</i> , 1999, 18, 6329-6338.	3.5	323
107	Structure of catalase-A from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1999, 286, 135-149.	2.0	106
108	Role of the lateral channel in catalase HP11 of <i>Escherichia coli</i> . <i>Protein Science</i> , 1999, 8, 490-498.	3.1	31

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109	Carbamate kinase: New structural machinery for making carbamoyl phosphate, the common precursor of pyrimidines and arginine. <i>Protein Science</i> , 1999, 8, 934-940.	3.1	46
110	Crystallization and preliminary structural analysis of catalase A from <i>Saccharomyces cerevisiae</i> . <i>Protein Science</i> , 1997, 6, 481-483.	3.1	17
111	Identification of a novel bond between a histidine and the essential tyrosine in catalase HPII of <i>Escherichia coli</i> . <i>Protein Science</i> , 1997, 6, 1016-1023.	3.1	65
112	Structure of the Heme d of <i>Penicillium vitale</i> and <i>Escherichia coli</i> Catalases. <i>Journal of Biological Chemistry</i> , 1996, 271, 8863-8868.	1.6	64
113	Crystal structure of catalase HPII from <i>Escherichia coli</i> . <i>Structure</i> , 1995, 3, 491-502.	1.6	99
114	Representation of noncovalent interactions in protein structures. <i>Journal of Molecular Graphics</i> , 1992, 10, 96-100.	1.7	8
115	Crystallization and preliminary X-ray diffraction analysis of catalase HPII from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1990, 213, 219-220.	2.0	7
116	Three-dimensional structure of catalase from <i>Penicillium vitale</i> at 2.0 Å... resolution. <i>Journal of Molecular Biology</i> , 1986, 188, 49-61.	2.0	160
117	Comparison of beef liver and <i>Penicillium vitale</i> catalases. <i>Journal of Molecular Biology</i> , 1986, 188, 63-72.	2.0	87
118	The refined structure of beef liver catalase at 2.5 Å... resolution. <i>Acta Crystallographica Section B: Structural Science</i> , 1986, 42, 497-515.	1.8	99
119	The active center of catalase. <i>Journal of Molecular Biology</i> , 1985, 185, 21-37.	2.0	404