

Maria João Romão

List of Publications by Year in descending order

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151
papers

6,235
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61984

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168
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Advances in Membrane-Bound Catechol-O-Methyltransferase Stability Achieved Using a New Ionic Liquid-Based Storage Formulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7264.	4.1	6
2	Spectroscopic and Structural Characterization of Reduced <i>Desulfovibrio vulgaris</i> Hildenborough W-FdhAB Reveals Stable Metal Coordination during Catalysis. <i>ACS Chemical Biology</i> , 2022, 17, 1901-1909.	3.4	9
3	Magnetic particles used in a new approach for designed protein crystallization. <i>CrystEngComm</i> , 2021, 23, 1083-1090.	2.6	5
4	Interrogating the Inhibition Mechanisms of Human Aldehyde Oxidase by X-ray Crystallography and NMR Spectroscopy: The Raloxifene Case. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13025-13037.	6.4	5
5	SLMP53-1 interacts with wild-type and mutant p53 DNA-binding domain and reactivates multiple hotspot mutations. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129440.	2.4	13
6	Improving the Anti-inflammatory Response via Gold Nanoparticle Vectorization of CO-Releasing Molecules. <i>ACS Biomaterials Science and Engineering</i> , 2020, 6, 1090-1101.	5.2	17
7	Catalytic Mechanism of Human Aldehyde Oxidase. <i>ACS Catalysis</i> , 2020, 10, 9276-9286.	11.2	20
8	Evolution, expression, and substrate specificities of aldehyde oxidase enzymes in eukaryotes. <i>Journal of Biological Chemistry</i> , 2020, 295, 5377-5389.	3.4	39
9	Toward the Mechanistic Understanding of Enzymatic CO ₂ Reduction. <i>ACS Catalysis</i> , 2020, 10, 3844-3856.	11.2	76
10	Human aldehyde oxidase (hAOX 1): structure determination of the Moco-free form of the natural variant G1269R and biophysical studies of single nucleotide polymorphisms. <i>FEBS Open Bio</i> , 2019, 9, 925-934.	2.3	9
11	Systematic exploration of predicted destabilizing nonsynonymous single nucleotide polymorphisms (nsSNPs) of human aldehyde oxidase: A Bioinformatics study. <i>Pharmacology Research and Perspectives</i> , 2019, 7, e00538.	2.4	9
12	The crystal structure of human Aldehyde oxidase. <i>Drug Metabolism and Pharmacokinetics</i> , 2018, 33, S10-S11.	2.2	0
13	Critical overview on the structure and metabolism of human aldehyde oxidase and its role in pharmacokinetics. <i>Coordination Chemistry Reviews</i> , 2018, 368, 35-59.	18.8	21
14	First insights of peptidoglycan amidation in Gram-positive bacteria - the high-resolution crystal structure of <i>Staphylococcus aureus</i> glutamine amidotransferase GatD. <i>Scientific Reports</i> , 2018, 8, 5313.	3.3	12
15	The Crystal Structure of the R280K Mutant of Human p53 Explains the Loss of DNA Binding. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1184.	4.1	23
16	Irreversible Magnetic Behaviour Caused by the Thermosensitive Phenomenon in an Iron(III) Spin Crossover Complex. <i>European Journal of Inorganic Chemistry</i> , 2018, 2018, 2976-2983.	2.0	17
17	Infrared light-induced protein crystallization. Structuring of protein interfacial water and periodic self-assembly. <i>Journal of Crystal Growth</i> , 2017, 457, 362-368.	1.5	5
18	Structural basis for the role of mammalian aldehyde oxidases in the metabolism of drugs and xenobiotics. <i>Current Opinion in Chemical Biology</i> , 2017, 37, 39-47.	6.1	33

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19	Stability and Ligand Promiscuity of Type A Carbohydrate-binding Modules Are Illustrated by the Structure of Spirochaeta thermophila StCBM64C. Journal of Biological Chemistry, 2017, 292, 4847-4860.	3.4	19
20	Electron transfer through arsenite oxidase: Insights into Rieske interaction with cytochrome c. Biochimica Et Biophysica Acta - Bioenergetics, 2017, 1858, 865-872.	1.0	13
21	A synthetic route to novel 3-substituted-2,1-benzisoxazoles from 5-(2-nitrobenzylidene)(thio)barbiturates. Comptes Rendus Chimie, 2017, 20, 990-995.	0.5	10
22	Ion-Exchange Membranes for Stable Derivatization of Protein Crystals. Crystal Growth and Design, 2017, 17, 4563-4572.	3.0	9
23	Optimization of the Expression of Human Aldehyde Oxidase for Investigations of Single-Nucleotide Polymorphisms. Drug Metabolism and Disposition, 2016, 44, 1277-1285.	3.3	34
24	Diverse specificity of cellulosome attachment to the bacterial cell surface. Scientific Reports, 2016, 6, 38292.	3.3	20
25	The <i>Escherichia coli</i> Periplasmic Aldehyde Oxidoreductase Is an Exceptional Member of the Xanthine Oxidase Family of Molybdoenzymes. ACS Chemical Biology, 2016, 11, 2923-2935.	3.4	26
26	Structure and function of mammalian aldehyde oxidases. Archives of Toxicology, 2016, 90, 753-780.	4.2	95
27	Structural and mechanistic insights on nitrate reductases. Protein Science, 2015, 24, 1901-1911.	7.6	49
28	Insights into the structural determinants of substrate specificity and activity in mouse aldehyde oxidases. Journal of Biological Inorganic Chemistry, 2015, 20, 209-217.	2.6	19
29	Aromatic aldehydes at the active site of aldehyde oxidoreductase from <i>Desulfovibrio gigas</i> : reactivity and molecular details of the enzyme-substrate and enzyme-product interaction. Journal of Biological Inorganic Chemistry, 2015, 20, 219-229.	2.6	4
30	Ionic-Liquid-Functionalized Mineral Particles for Protein Crystallization. Crystal Growth and Design, 2015, 15, 2994-3003.	3.0	8
31	Structural insights into xenobiotic and inhibitor binding to human aldehyde oxidase. Nature Chemical Biology, 2015, 11, 779-783.	8.0	85
32	A contribution to the rational design of Ru(CO) ₃ Cl ₂ L complexes for in vivo delivery of CO. Dalton Transactions, 2015, 44, 5058-5075.	3.3	67
33	Structural Data on the Periplasmic Aldehyde Oxidoreductase PaoABC from <i>Escherichia coli</i> : SAXS and Preliminary X-ray Crystallography Analysis. International Journal of Molecular Sciences, 2014, 15, 2223-2236.	4.1	13
34	Correction to Use of Gold Nanoparticles as Additives in Protein Crystallization. Crystal Growth and Design, 2014, 14, 888-888.	3.0	0
35	Use of Gold Nanoparticles as Additives in Protein Crystallization. Crystal Growth and Design, 2014, 14, 222-227.	3.0	22
36	Biochemical, Stabilization and Crystallization Studies on a Molecular Chaperone (PaoD) Involved in the Maturation of Molybdoenzymes. PLoS ONE, 2014, 9, e87295.	2.5	10

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37	Interaction of vanadium(IV) with human serum apo-transferrin. <i>Journal of Inorganic Biochemistry</i> , 2013, 121, 187-195.	3.5	72
38	Induced peroxidase activity of haem containing nitrate reductases revealed by protein film electrochemistry. <i>Journal of Electroanalytical Chemistry</i> , 2013, 693, 105-113.	3.8	7
39	Solution structure, dynamics and binding studies of a family 11 carbohydrate-binding module from <i>Clostridium thermocellum</i> (CtCBM11). <i>Biochemical Journal</i> , 2013, 451, 289-300.	3.7	18
40	Characterization of a versatile organometallic pro-drug (CORM) for experimental CO based therapeutics. <i>Dalton Transactions</i> , 2013, 42, 5985-5998.	3.3	61
41	Overexpression, crystallization and preliminary X-ray crystallographic analysis of glucuronoxylan xylanohydrolase (Xyn30A) from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1440-1442.	0.7	4
42	Identification of Crucial Amino Acids in Mouse Aldehyde Oxidase 3 That Determine Substrate Specificity. <i>PLoS ONE</i> , 2013, 8, e82285.	2.5	20
43	Kinetic and Structural Studies of Aldehyde Oxidoreductase from <i>Desulfovibrio gigas</i> Reveal a Dithiolene-Based Chemistry for Enzyme Activation and Inhibition by H ₂ O ₂ . <i>PLoS ONE</i> , 2013, 8, e83234.	2.5	9
44	Novel <i>Clostridium thermocellum</i> Type I Cohesin-Dockerin Complexes Reveal a Single Binding Mode. <i>Journal of Biological Chemistry</i> , 2012, 287, 44394-44405.	3.4	27
45	The First Mammalian Aldehyde Oxidase Crystal Structure. <i>Journal of Biological Chemistry</i> , 2012, 287, 40690-40702.	3.4	83
46	<i>Escherichia coli</i> Expression, Purification, Crystallization, and Structure Determination of Bacterial Cohesin-Dockerin Complexes. <i>Methods in Enzymology</i> , 2012, 510, 395-415.	1.0	6
47	New insights into the chemistry of fac-[Ru(CO) ₃] ²⁺ fragments in biologically relevant conditions: The CO releasing activity of [Ru(CO) ₃ Cl ₂ (1,3-thiazole)], and the X-ray crystal structure of its adduct with lysozyme. <i>Journal of Inorganic Biochemistry</i> , 2012, 117, 285-291.	3.5	57
48	Hofmeister effects of ionic liquids in protein crystallization: Direct and water-mediated interactions. <i>CrystEngComm</i> , 2012, 14, 4912.	2.6	41
49	Structural insights into a unique cellulase fold and mechanism of cellulose hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5237-5242.	7.1	88
50	Overproduction, purification, crystallization and preliminary X-ray characterization of a novel carbohydrate-binding module of endoglucanase Cel5A from <i>Eubacterium cellulosolvens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 491-493.	0.7	2
51	CORM-3 Reactivity toward Proteins: The Crystal Structure of a Ru(II) Dicarboxylate-Lysozyme Complex. <i>Journal of the American Chemical Society</i> , 2011, 133, 1192-1195.	13.7	178
52	Molecular Architecture and Structural Transitions of a <i>Clostridium thermocellum</i> Mini-Cellulosome. <i>Journal of Molecular Biology</i> , 2011, 407, 571-580.	4.2	28
53	The Crystal Structure of <i>Cupriavidus necator</i> Nitrate Reductase in Oxidized and Partially Reduced States. <i>Journal of Molecular Biology</i> , 2011, 408, 932-948.	4.2	78
54	Crystal structure of the zinc-, cobalt-, and iron-containing adenylate kinase from <i>Desulfovibrio gigas</i> : a novel metal-containing adenylate kinase from Gram-negative bacteria. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 51-61.	2.6	8

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55	Purification, crystallization and preliminary X-ray characterization of the pentamodular arabinoxylanase <i>Xyl5A</i> from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 833-836.	0.7	4
56	Characterization and Crystallization of Mouse Aldehyde Oxidase 3: From Mouse Liver to <i>Escherichia coli</i> Heterologous Protein Expression. <i>Drug Metabolism and Disposition</i> , 2011, 39, 1939-1945.	3.3	29
57	Towards Improved Therapeutic CORMs: Understanding the Reactivity of CORM-3 with Proteins. <i>Current Medicinal Chemistry</i> , 2011, 18, 3361-3366.	2.4	67
58	The use of ionic liquids as crystallization additives allowed to overcome nanodrop scaling up problems: A success case for producing diffraction-quality crystals of a nitrate reductase. <i>Journal of Crystal Growth</i> , 2010, 312, 714-719.	1.5	11
59	Family 42 carbohydrate-binding modules display multiple arabinoxylan-binding interfaces presenting different ligand affinities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 2054-2062.	2.3	9
60	The 1.4 Å resolution structure of <i>Paracoccus pantotrophus</i> pseudoazurin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 627-635.	0.7	15
61	X-Ray Crystallography in Drug Discovery. <i>Methods in Molecular Biology</i> , 2010, 572, 31-56.	0.9	32
62	Putting an N-terminal end to the <i>Clostridium thermocellum</i> xylanase Xyn10B story: Crystal structure of the CBM22-GH10 modules complexed with xylohexaose. <i>Journal of Structural Biology</i> , 2010, 172, 353-362.	2.8	52
63	The effect of the sixth sulfur ligand in the catalytic mechanism of periplasmic nitrate reductase. <i>Journal of Computational Chemistry</i> , 2009, 30, 2466-2484.	3.3	48
64	Preliminary structural characterization of human SOUL, a haem-binding protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 723-726.	0.7	3
65	Crystallization and crystallographic analysis of the apo form of the orange protein (ORP) from <i>Desulfovibrio gigas</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 730-732.	0.7	9
66	Cobalt-, zinc- and iron-bound forms of adenylate kinase (AK) from the sulfate-reducing bacterium <i>Desulfovibrio gigas</i> : purification, crystallization and preliminary X-ray diffraction analysis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 926-929.	0.7	4
67	Ring-Functionalized Molybdenocene Complexes. <i>Organometallics</i> , 2009, 28, 2871-2879.	2.3	23
68	Molybdenum and tungsten enzymes: a crystallographic and mechanistic overview. <i>Dalton Transactions</i> , 2009, , 4053.	3.3	163
69	Real-Time Monitoring of Molecular Dynamics of Ethylene Glycol Dimethacrylate Glass Former. <i>Journal of Physical Chemistry B</i> , 2009, 113, 14209-14217.	2.6	22
70	Kinetic, Structural, and EPR Studies Reveal That Aldehyde Oxidoreductase from <i>Desulfovibrio gigas</i> Does Not Need a Sulfido Ligand for Catalysis and Give Evidence for a Direct Mo-C Interaction in a Biological System. <i>Journal of the American Chemical Society</i> , 2009, 131, 7990-7998.	13.7	33
71	Periplasmic nitrate reductase revisited: a sulfur atom completes the sixth coordination of the catalytic molybdenum. <i>Journal of Biological Inorganic Chemistry</i> , 2008, 13, 737-753.	2.6	94
72	Purification, crystallization and preliminary X-ray diffraction analysis of adenosine triphosphate sulfurylase (ATPS) from the sulfate-reducing bacterium <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 593-595.	0.7	2

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73	Purification, crystallization and crystallographic analysis of Clostridium thermocellumendo-1,4-β-D-xylanase 10B in complex with xylohexanase. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 715-718.	0.7	3
74	Molecular determinants of ligand specificity in family 11 carbohydrate binding modules – an NMR, X-ray crystallography and computational chemistry approach. FEBS Journal, 2008, 275, 2524-2535.	4.7	29
75	Ion jelly: a tailor-made conducting material for smart electrochemical devices. Chemical Communications, 2008, , 5842.	4.1	83
76	Biologically relevant O,S-donor compounds. Synthesis, molybdenum complexation and xanthine oxidase inhibition. Dalton Transactions, 2008, , 1773.	3.3	17
77	Evidence for a dual binding mode of dockerin modules to cohesins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3089-3094.	7.1	124
78	Crystal Structure of the 16 Heme Cytochrome from Desulfovibrio gigas: A Glycosylated Protein in a Sulphate-reducing Bacterium. Journal of Molecular Biology, 2007, 370, 659-673.	4.2	23
79	Heterodimeric nitrate reductase (NapAB) from Cupriavidus necator H16: purification, crystallization and preliminary X-ray analysis. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 516-519.	0.7	19
80	Correlating EPR and X-ray structural analysis of arsenite-inhibited forms of aldehyde oxidoreductase. Journal of Biological Inorganic Chemistry, 2007, 12, 353-366.	2.6	15
81	Xyloglucan Is Recognized by Carbohydrate-binding Modules That Interact with β-Glucan Chains. Journal of Biological Chemistry, 2006, 281, 8815-8828.	3.4	102
82	Structural and Electron Paramagnetic Resonance (EPR) Studies of Mononuclear Molybdenum Enzymes from Sulfate-Reducing Bacteria. Accounts of Chemical Research, 2006, 39, 788-796.	15.6	47
83	Purification, crystallization and preliminary X-ray diffraction analysis of the glyoxalase II from Leishmania infantum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 805-807.	0.7	3
84	Molybdenum and tungsten enzymes: the xanthine oxidase family. Current Opinion in Chemical Biology, 2006, 10, 109-114.	6.1	99
85	The first crystal structure of class III superoxide reductase from Treponema pallidum. Journal of Biological Inorganic Chemistry, 2006, 11, 548-558.	2.6	37
86	Formate-reduced E. coli formate dehydrogenase H: the reinterpretation of the crystal structure suggests a new reaction mechanism. Journal of Biological Inorganic Chemistry, 2006, 11, 849-854.	2.6	140
87	On the purification and preliminary crystallographic analysis of isoquinoline 1-oxidoreductase from Brevundimonas diminuta 7. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 137-140.	0.7	6
88	Superoxide reductase from the syphilis spirochete Treponema pallidum: crystallization and structure determination using soft X-rays. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 967-970.	0.7	5
89	Overexpression, purification and crystallization of the two C-terminal domains of the bifunctional cellulase Cel9D-Cel44A from Clostridium thermocellum. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1043-1045.	0.7	10
90	Insights into the Structural Determinants of Cohesin – Dockerin Specificity Revealed by the Crystal Structure of the Type II Cohesin from Clostridium thermocellum SdbA. Journal of Molecular Biology, 2005, 349, 909-915.	4.2	34

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91	The Family 11 Carbohydrate-binding Module of <i>Clostridium thermocellum</i> Lic26A-Cel5E Accommodates β -1,4- and β -1,3-linked 1,4-Mixed Linked Glucans at a Single Binding Site. <i>Journal of Biological Chemistry</i> , 2004, 279, 34785-34793.	3.4	95
92	Direct electrochemistry of the <i>Desulfovibrio gigas</i> aldehyde oxidoreductase. <i>FEBS Journal</i> , 2004, 271, 1329-1338.	0.2	18
93	Structural Basis for the Mechanism of Ca ²⁺ Activation of the Di-Heme Cytochrome c Peroxidase from <i>Pseudomonas nautica</i> 617. <i>Structure</i> , 2004, 12, 961-973.	3.3	53
94	Mo and W bis-MGD enzymes: nitrate reductases and formate dehydrogenases. <i>Journal of Biological Inorganic Chemistry</i> , 2004, 9, 791-799.	2.6	124
95	Crystallization and preliminary X-ray diffraction analysis of the 16-haem cytochrome of <i>Desulfovibrio gigas</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 968-970.	2.5	3
96	Mutagenesis study on amino acids around the molybdenum centre of the periplasmic nitrate reductase from <i>Ralstonia eutropha</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 1211-1219.	2.1	16
97	X-ray Crystal Structure and EPR Spectra of α -Arsenite-Inhibited <i>Desulfovibrio gigas</i> Aldehyde Dehydrogenase: A Member of the Xanthine Oxidase Family. <i>Journal of the American Chemical Society</i> , 2004, 126, 8614-8615.	13.7	35
98	The isolation and characterization of cytochrome <i>c</i> nitrite reductase subunits (NrfA and NrfH) from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>FEBS Journal</i> , 2003, 270, 3904-3915.	0.2	57
99	Crystallization and preliminary X-ray diffraction analysis of the di-haem cytochrome c peroxidase from <i>Pseudomonas stutzeri</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 345-347.	2.5	0
100	Mammalian molybdo-flavoenzymes, an expanding family of proteins: structure, genetics, regulation, function and pathophysiology. <i>Biochemical Journal</i> , 2003, 372, 15-32.	3.7	221
101	Mutagenesis study on the role of a lysine residue highly conserved in formate dehydrogenases and periplasmic nitrate reductases. <i>Biochemical and Biophysical Research Communications</i> , 2003, 310, 40-47.	2.1	19
102	Cytochrome c Nitrite Reductase from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Journal of Biological Chemistry</i> , 2003, 278, 17455-17465.	3.4	98
103	Cellulosome assembly revealed by the crystal structure of the cohesin-dockerin complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13809-13814.	7.1	230
104	Crystal Structure of a Prostate Kallikrein Isolated from Stallion Seminal Plasma: A Homologue of Human PSA. <i>Journal of Molecular Biology</i> , 2002, 322, 325-337.	4.2	81
105	Gene Sequence and the 1.8 Å... Crystal Structure of the Tungsten-Containing Formate Dehydrogenase from <i>Desulfovibrio gigas</i> . <i>Structure</i> , 2002, 10, 1261-1272.	3.3	161
106	Crystallization and preliminary X-ray diffraction analysis of two pH-dependent forms of a di-haem cytochrome c peroxidase from <i>Pseudomonas nautica</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 697-699.	2.5	6
107	Molybdenum enzymes in reactions involving aldehydes and acids. <i>Metal Ions in Biological Systems</i> , 2002, 39, 539-70.	0.4	3
108	Structure refinement of the aldehyde oxidoreductase from <i>Desulfovibrio gigas</i> (MOP) at 1.28 Å... <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 791-800.	2.6	87

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109	Purification, crystallization and identification by X-ray analysis of a prostate kallikrein from horse seminal plasma. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1180-1183.	2.5	2
110	Tungsten-containing formate dehydrogenase from <i>Desulfovibrio gigas</i> : metal identification and preliminary structural data by multi-wavelength crystallography. <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 398-404.	2.6	44
111	Crystallization and preliminary X-ray analysis of a membrane-bound nitrite reductase from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 215-217.	2.5	6
112	Ionic strength dependence of the non-physiological electron transfer between flavodoxin and cytochrome c 553 from <i>D. vulgaris</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2000, 5, 730-737.	2.6	9
113	Gene sequence and crystal structure of the aldehyde oxidoreductase from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Journal of Molecular Biology</i> , 2000, 297, 135-146.	4.2	64
114	Biochemical/Spectroscopic Characterization and Preliminary X-Ray Analysis of a New Aldehyde Oxidoreductase Isolated from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Biochemical and Biophysical Research Communications</i> , 2000, 268, 745-749.	2.1	11
115	Crystallization and preliminary X-ray analysis of a nitrate reductase from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 877-879.	2.5	4
116	Structural studies by X-ray diffraction on metal substituted desulforedoxin, a rubredoxin-type protein. <i>Protein Science</i> , 1999, 8, 1536-1545.	7.6	23
117	Effects of protein-protein interactions on electron transfer: docking and electron transfer calculations for complexes between flavodoxin and c-type cytochromes. <i>Journal of Biological Inorganic Chemistry</i> , 1999, 4, 360-374.	2.6	21
118	Crystal structure of the first dissimilatory nitrate reductase at 1.9 Å... solved by MAD methods. <i>Structure</i> , 1999, 7, 65-79.	3.3	288
119	Structure and function of the xanthine-oxidase family of molybdenum enzymes. <i>Structure and Bonding</i> , 1998, , 69-95.	1.0	28
120	Substrate Oxidation in the Active Site of Xanthine Oxidase and Related Enzymes. A Model Density Functional Study. <i>Inorganic Chemistry</i> , 1998, 37, 176-180.	4.0	50
121	Altered specificity mutations define residues essential for substrate positioning in xanthine dehydrogenase 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1998, 278, 431-438.	4.2	30
122	Prediction of Alternative Structures of the Molybdenum Site in the Xanthine Oxidase-Related Aldehyde Oxido Reductase. <i>Journal of the American Chemical Society</i> , 1997, 119, 3159-3160.	13.7	43
123	Crystal structure of acidic seminal fluid protein (aSFP) at 1.9 Å... resolution: a bovine polypeptide of the spermadhesin family. <i>Journal of Molecular Biology</i> , 1997, 274, 650-660.	4.2	42
124	The 2.4 Å... resolution crystal structure of boar seminal plasma PSP-I/PSP-II: a zona pellucida-binding glycoprotein heterodimer of the spermadhesin family built by a CUB domain architecture. <i>Journal of Molecular Biology</i> , 1997, 274, 635-649.	4.2	80
125	The crystal structures of two spermadhesins reveal the CUB domain fold. <i>Nature Structural Biology</i> , 1997, 4, 783-788.	9.7	124
126	Structure and function of molybdopterin containing enzymes. <i>Progress in Biophysics and Molecular Biology</i> , 1997, 68, 121-144.	2.9	69

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127	Crystal structure of cytochrome c' from <i>Rhodocyclus gelatinosus</i> and comparison with other cytochromes c'. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 611-622.	2.6	19
128	The molybdenum site in the xanthine oxidase-related aldehyde oxidoreductase from <i>Desulfovibrio gigas</i> and a catalytic mechanism for this class of enzymes. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 782-785.	2.6	16
129	Crystallization and preliminary X-ray diffraction studies of aSFP, a bovine seminal plasma protein with a single CUB domain architecture. <i>Protein Science</i> , 1997, 6, 725-727.	7.6	8
130	Crystallographic and Fluorescence Studies of Ligand Binding to N-Carbamoylsarcosine Amidohydrolase from <i>Arthrobacter</i> sp.. <i>Journal of Molecular Biology</i> , 1996, 263, 269-283.	4.2	26
131	A structure-based catalytic mechanism for the xanthine oxidase family of molybdenum enzymes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 8846-8851.	7.1	257
132	The solution structure of desulfiredoxin, a simple iron-sulfur protein. <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 341-354.	2.6	13
133	Crystal Structure of Flavodoxin from <i>Desulfovibrio desulfuricans</i> ATCC 27774 in Two Oxidation States. <i>FEBS Journal</i> , 1996, 239, 190-196.	0.2	36
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