List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Crystal structure of the first dissimilatory nitrate reductase at 1.9 Ã solved by MAD methods. Structure, 1999, 7, 65-79.	3.3	288
2	A structure-based catalytic mechanism for the xanthine oxidase family of molybdenum enzymes Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 8846-8851.	7.1	257
3	Cellulosome assembly revealed by the crystal structure of the cohesin-dockerin complex. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13809-13814.	7.1	230
4	Mammalian molybdo-flavoenzymes, an expanding family of proteins: structure, genetics, regulation, function and pathophysiology. Biochemical Journal, 2003, 372, 15-32.	3.7	221
5	CORM-3 Reactivity toward Proteins: The Crystal Structure of a Ru(II) Dicarbonylâ^'Lysozyme Complex. Journal of the American Chemical Society, 2011, 133, 1192-1195.	13.7	178
6	Molybdenum and tungsten enzymes: a crystallographic and mechanistic overview. Dalton Transactions, 2009, , 4053.	3.3	163
7	Gene Sequence and the 1.8 Ã Crystal Structure of the Tungsten-Containing Formate Dehydrogenase from Desulfovibrio gigas. Structure, 2002, 10, 1261-1272.	3.3	161
8	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
9	The crystal structures of two spermadhesins reveal the CUB domain fold. Nature Structural Biology, 1997, 4, 783-788.	9.7	124
10	Mo and W bis-MGD enzymes: nitrate reductases and formate dehydrogenases. Journal of Biological Inorganic Chemistry, 2004, 9, 791-799.	2.6	124
11	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
12	Xyloglucan Is Recognized by Carbohydrate-binding Modules That Interact with β-Glucan Chains. Journal of Biological Chemistry, 2006, 281, 8815-8828.	3.4	102
13	Molybdenum and tungsten enzymes: the xanthine oxidase family. Current Opinion in Chemical Biology, 2006, 10, 109-114.	6.1	99
14	Cytochrome c Nitrite Reductase from Desulfovibrio desulfuricans ATCC 27774. Journal of Biological Chemistry, 2003, 278, 17455-17465.	3.4	98
15	The Family 11 Carbohydrate-binding Module of Clostridium thermocellum Lic26A-Cel5E Accommodates β-1,4- and β-1,3–1,4-Mixed Linked Glucans at a Single Binding Site. Journal of Biological Chemistry, 2004, 279, 34785-34793.	3.4	95
16	Structure and function of mammalian aldehyde oxidases. Archives of Toxicology, 2016, 90, 753-780.	4.2	95
17	Periplasmic nitrate reductase revisited: a sulfur atom completes the sixth coordination of the catalytic molybdenum. Journal of Biological Inorganic Chemistry, 2008, 13, 737-753.	2.6	94
18	Crystal Structure of Desulforedoxin fromDesulfovibrio gigasDetermined at 1.8 Ã Resolution: A Novel Non-heme Iron Protein Structure. Journal of Molecular Biology, 1995, 251, 690-702.	4.2	93

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19	Structural insights into a unique cellulase fold and mechanism of cellulose hydrolysis. Proceedings of the United States of America, 2011, 108, 5237-5242.	7.1	88
20	Structure refinement of the aldehyde oxidoreductase from Desulfovibrio gigas (MOP) at 1.28ÂÃ Journal of Biological Inorganic Chemistry, 2001, 6, 791-800.	2.6	87
21	Structural insights into xenobiotic and inhibitor binding to human aldehyde oxidase. Nature Chemical Biology, 2015, 11, 779-783.	8.0	85
22	Ion jelly: a tailor-made conducting material for smart electrochemical devices. Chemical Communications, 2008, , 5842.	4.1	83
23	The First Mammalian Aldehyde Oxidase Crystal Structure. Journal of Biological Chemistry, 2012, 287, 40690-40702.	3.4	83
24	Crystal Structure of a Prostate Kallikrein Isolated from Stallion Seminal Plasma: A Homologue of Human PSA. Journal of Molecular Biology, 2002, 322, 325-337.	4.2	81
25	The 2.4 Ã 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. Journal of Molecular Biology, 1997, 274, 635-649.	4.2	80
26	The Crystal Structure of Cupriavidus necator Nitrate Reductase in Oxidized and Partially Reduced States. Journal of Molecular Biology, 2011, 408, 932-948.	4.2	78
27	Toward the Mechanistic Understanding of Enzymatic CO ₂ Reduction. ACS Catalysis, 2020, 10, 3844-3856.	11.2	76
28	Interaction of vanadium(IV) with human serum apo-transferrin. Journal of Inorganic Biochemistry, 2013, 121, 187-195.	3.5	72
29	Structure and function of molybdopterin containing enzymes. Progress in Biophysics and Molecular Biology, 1997, 68, 121-144.	2.9	69
30	Towards Improved Therapeutic CORMs: Understanding the Reactivity of CORM-3 with Proteins. Current Medicinal Chemistry, 2011, 18, 3361-3366.	2.4	67
31	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
32	Gene sequence and crystal structure of the aldehyde oxidoreductase from Desulfovibrio desulfuricans ATCC 27774. Journal of Molecular Biology, 2000, 297, 135-146.	4.2	64
33	Characterization of a versatile organometallic pro-drug (CORM) for experimental CO based therapeutics. Dalton Transactions, 2013, 42, 5985-5998.	3.3	61
34	The isolation and characterization of cytochrome <i>c</i> nitrite reductase subunits (NrfA and NrfH) from <i>Desulfovibrio desulfuricans</i> ATCC 27774. FEBS Journal, 2003, 270, 3904-3915.	0.2	57
35	New insights into the chemistry of fac-[Ru(CO)3]2+ fragments in biologically relevant conditions: The CO releasing activity of [Ru(CO)3Cl2(1,3-thiazole)], and the X-ray crystal structure of its adduct with lysozyme. Journal of Inorganic Biochemistry, 2012, 117, 285-291.	3.5	57
36	Molecular cloning and sequence analysis of the gene of the molybdenum-containing aldehyde oxido-reductase of Desulfovibrio gigas. The deduced amino acid sequence shows similarity to xanthine dehydrogenase. FEBS Journal, 1994, 220, 901-910.	0.2	55

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37	Structural Basis for the Mechanism of Ca2+ Activation of the Di-Heme Cytochrome c Peroxidase from Pseudomonas nautica 617. Structure, 2004, 12, 961-973.	3.3	53
38	Putting an N-terminal end to the Clostridium thermocellum xylanase Xyn10B story: Crystal structure of the CBM22-1–CH10 modules complexed with xylohexaose. Journal of Structural Biology, 2010, 172, 353-362.	2.8	52
39	Substrate Oxidation in the Active Site of Xanthine Oxidase and Related Enzymes. A Model Density Functional Study. Inorganic Chemistry, 1998, 37, 176-180.	4.0	50
40	Structural and mechanistic insights on nitrate reductases. Protein Science, 2015, 24, 1901-1911.	7.6	49
41	The effect of the sixth sulfur ligand in the catalytic mechanism of periplasmic nitrate reductase. Journal of Computational Chemistry, 2009, 30, 2466-2484.	3.3	48
42	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
43	Crystal structure analysis, refinement and enzymatic reaction mechanism of N-carbamoylsarcosine amidohydrolase from Arthrobacter sp. at 2·OÃresolution. Journal of Molecular Biology, 1992, 226, 1111-1130.	4.2	45
44	Tungsten-containing formate dehydrogenase from Desulfovibrio gigas: metal identification and preliminary structural data by multi-wavelength crystallography. Journal of Biological Inorganic Chemistry, 2001, 6, 398-404.	2.6	44
45	Prediction of Alternative Structures of the Molybdenum Site in the Xanthine Oxidase-Related Aldehyde Oxido Reductase. Journal of the American Chemical Society, 1997, 119, 3159-3160.	13.7	43
46	Crystal structure of acidic seminal fluid protein (aSFP) at 1.9 Ã resolution: a bovine polypeptide of the spermadhesin family. Journal of Molecular Biology, 1997, 274, 650-660.	4.2	42
47	Hofmeister effects of ionic liquids in protein crystallization: Direct and water-mediated interactions. CrystEngComm, 2012, 14, 4912.	2.6	41
48	Evolution, expression, and substrate specificities of aldehyde oxidase enzymes in eukaryotes. Journal of Biological Chemistry, 2020, 295, 5377-5389.	3.4	39
49	The first crystal structure of class III superoxide reductase from Treponema pallidum. Journal of Biological Inorganic Chemistry, 2006, 11, 548-558.	2.6	37
50	Crystal Structure of Flavodoxin from Desulfovibrio desulfuricans ATCC 27774 in Two Oxidation States. FEBS Journal, 1996, 239, 190-196.	0.2	36
51	X-ray Crystal Structure and EPR Spectra of "Arsenite-Inhibitedâ€DesulfovibriogigasAldehyde Dehydrogenase:Â A Member of the Xanthine Oxidase Family. Journal of the American Chemical Society, 2004, 126, 8614-8615.	13.7	35
52	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
53	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
54	Kinetic, Structural, and EPR Studies Reveal That Aldehyde Oxidoreductase from Desulfovibrio gigas Does Not Need a Sulfido Ligand for Catalysis and Give Evidence for a Direct Moâ^'C Interaction in a Biological System. Journal of the American Chemical Society, 2009, 131, 7990-7998.	13.7	33

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55	Structural basis for the role of mammalian aldehyde oxidases in the metabolism of drugs and xenobiotics. Current Opinion in Chemical Biology, 2017, 37, 39-47.	6.1	33
56	.eta.3-Allyl complexes of molybdenum: the preparation and structure of [Mo(.eta.3-C3H5)2(.eta.5-C5H5)]. Organometallics, 1984, 3, 936-937.	2.3	32
57	X-Ray Crystallography in Drug Discovery. Methods in Molecular Biology, 2010, 572, 31-56.	0.9	32
58	Preparation and reactivity of 2â€Azaâ€1,3â€butadienes: A Dielsâ€Alder route to 5,6â€dihydroâ€2 <i>H</i> â€1,3â derivatives. Chemische Berichte, 1985, 118, 3652-3663.	i€oxazine 0.2	30
59	Altered specificity mutations define residues essential for substrate positioning in xanthine dehydrogenase 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 278, 431-438.	4.2	30
60	Molecular determinants of ligand specificity in family 11 carbohydrate binding modules – an NMR, Xâ€ray crystallography and computational chemistry approach. FEBS Journal, 2008, 275, 2524-2535.	4.7	29
61	Characterization and Crystallization of Mouse Aldehyde Oxidase 3: From Mouse Liver to <i>Escherichia coli</i> Heterologous Protein Expression. Drug Metabolism and Disposition, 2011, 39, 1939-1945.	3.3	29
62	Subunit composition, crystallization and preliminary crystallographic studies of the Desulfovibrio gigas aldehyde oxidoreductase containing molybdenum and [2Fe-2S] centers. FEBS Journal, 1993, 215, 729-732.	0.2	28
63	Structure and function of the xanthine-oxidase family of molybdenum enzymes. Structure and Bonding, 1998, , 69-95.	1.0	28
64	Molecular Architecture and Structural Transitions of a Clostridium thermocellum Mini-Cellulosome. Journal of Molecular Biology, 2011, 407, 571-580.	4.2	28
65	Novel Clostridium thermocellum Type I Cohesin-Dockerin Complexes Reveal a Single Binding Mode. Journal of Biological Chemistry, 2012, 287, 44394-44405.	3.4	27
66	Crystallographic and Fluorescence Studies of Ligand Binding toN-Carbamoylsarcosine Amidohydrolase fromArthrobactersp Journal of Molecular Biology, 1996, 263, 269-283.	4.2	26
67	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
68	Structural studies by Xâ€ray diffraction on metal substituted desulforedoxin, a rubredoxinâ€ŧype protein. Protein Science, 1999, 8, 1536-1545.	7.6	23
69	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
70	Ring-Functionalized Molybdenocene Complexes. Organometallics, 2009, 28, 2871-2879.	2.3	23
71	The Crystal Structure of the R280K Mutant of Human p53 Explains the Loss of DNA Binding. International Journal of Molecular Sciences, 2018, 19, 1184.	4.1	23
72	Real-Time Monitoring of Molecular Dynamics of Ethylene Glycol Dimethacrylate Glass Former. Journal of Physical Chemistry B, 2009, 113, 14209-14217.	2.6	22

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73	Use of Gold Nanoparticles as Additives in Protein Crystallization. Crystal Growth and Design, 2014, 14, 222-227.	3.0	22
74	(.eta.2-trans-Cyclooctene)2Fe(CO)3 and related complexes: structure and dynamic behavior. Organometallics, 1988, 7, 1994-2004.	2.3	21
75	Effects of protein-protein interactions on electron transfer: docking and electron transfer calculations for complexes between flavodoxin and c-type cytochromes. Journal of Biological Inorganic Chemistry, 1999, 4, 360-374.	2.6	21
76	Critical overview on the structure and metabolism of human aldehyde oxidase and its role in pharmacokinetics. Coordination Chemistry Reviews, 2018, 368, 35-59.	18.8	21
77	Identification of Crucial Amino Acids in Mouse Aldehyde Oxidase 3 That Determine Substrate Specificity. PLoS ONE, 2013, 8, e82285.	2.5	20
78	Diverse specificity of cellulosome attachment to the bacterial cell surface. Scientific Reports, 2016, 6, 38292.	3.3	20
79	Catalytic Mechanism of Human Aldehyde Oxidase. ACS Catalysis, 2020, 10, 9276-9286.	11.2	20
80	Crystal structure of cytochrome c' from Rhodocyclus gelatinosus and comparison with other cytochromes c'. Journal of Biological Inorganic Chemistry, 1997, 2, 611-622.	2.6	19
81	Mutagenesis study on the role of a lysine residue highly conserved in formate dehydrogenases and periplasmic nitrate reductases. Biochemical and Biophysical Research Communications, 2003, 310, 40-47.	2.1	19
82	Heterodimeric nitrate reductase (NapAB) fromCupriavidus necatorH16: purification, crystallization and preliminary X-ray analysis. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 516-519.	0.7	19
83	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
84	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
85	1,5-Dihydropyrrol-2-ones from (1,4-diaza-1,3-diene)tricarbonyliron and alkyne. 2. Structure of a [2.2.2] bicyclic intermediate with iron at the bridgehead position. Organometallics, 1985, 4, 948-949.	2.3	18
86	Direct electrochemistry of the Desulfovibrio gigas aldehyde oxidoreductase. FEBS Journal, 2004, 271, 1329-1338.	0.2	18
87	Solution structure, dynamics and binding studies of a family 11 carbohydrate-binding module from <i>Clostridium thermocellum</i> (<i>Ct</i> CBM11). Biochemical Journal, 2013, 451, 289-300.	3.7	18
88	Biologically relevant O,S-donor compounds. Synthesis, molybdenum complexation and xanthine oxidase inhibition. Dalton Transactions, 2008, , 1773.	3.3	17
89	Irreversible Magnetic Behaviour Caused by the Thermosalient Phenomenon in an Iron(III) Spin Crossover Complex. European Journal of Inorganic Chemistry, 2018, 2018, 2976-2983.	2.0	17
90	Improving the Anti-inflammatory Response via Gold Nanoparticle Vectorization of CO-Releasing Molecules. ACS Biomaterials Science and Engineering, 2020, 6, 1090-1101.	5.2	17

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91	The molybdenum site in the xanthine oxidase-related aldehyde oxidoreductase from Desulfovibrio gigas and a catalytic mechanism for this class of enzymes. Journal of Biological Inorganic Chemistry, 1997, 2, 782-785.	2.6	16
92	Mutagenesis study on amino acids around the molybdenum centre of the periplasmic nitrate reductase from Ralstonia eutropha. Biochemical and Biophysical Research Communications, 2004, 320, 1211-1219.	2.1	16
93	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
94	The 1.4â€Ã resolution structure of <i>Paracoccus pantotrophus</i> pseudoazurin. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 627-635.	0.7	15
95	Protein-Crystal Density by Volume Measurement and Amino-Acid Analysis. Journal of Applied Crystallography, 1996, 29, 311-317.	4.5	14
96	The solution structure of desulforedoxin, a simple iron-sulfur protein. Journal of Biological Inorganic Chemistry, 1996, 1, 341-354.	2.6	13
97	Structural Data on the Periplasmic Aldehyde Oxidoreductase PaoABC from Escherichia coli: SAXS and Preliminary X-ray Crystallography Analysis. International Journal of Molecular Sciences, 2014, 15, 2223-2236.	4.1	13
98	Electron transfer through arsenite oxidase: Insights into Rieske interaction with cytochrome c. Biochimica Et Biophysica Acta - Bioenergetics, 2017, 1858, 865-872.	1.0	13
99	SLMP53-1 interacts with wild-type and mutant p53 DNA-binding domain and reactivates multiple hotspot mutations. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129440.	2.4	13
100	First insights of peptidoglycan amidation in Gram-positive bacteria - the high-resolution crystal structure of Staphylococcus aureus glutamine amidotransferase GatD. Scientific Reports, 2018, 8, 5313.	3.3	12
101	Activity of Coordinated 1,4-Diaza-1,3-dienes (dad) in CC Bond Forming Reactions: 1,5-Dihydropyrrol-2-ones from (dad)Fe(CO)3and Dimethyl Acetylenedicarboxylate. Angewandte Chemie International Edition in English, 1983, 22, 992-993.	4.4	11
102	Biochemical/Spectroscopic Characterization and Preliminary X-Ray Analysis of a New Aldehyde Oxidoreductase Isolated from Desulfovibrio desulfuricans ATCC 27774. Biochemical and Biophysical Research Communications, 2000, 268, 745-749.	2.1	11
103	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. Journal of Crystal Growth, 2010, 312, 714-719.	1.5	11
104	η3-allyl complexes of molybdenum: reactions of [MoCl(η3-C3H5)3]2 and the crystal structure of [MoOAc(η3-C3H5)3]. Polyhedron, 1986, 5, 461-471.	2.2	10
105	Overexpression, purification and crystallization of the two C-terminal domains of the bifunctional cellulasectCel9D-Cel44A fromClostridium thermocellum. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1043-1045.	0.7	10
106	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
107	Biochemical, Stabilization and Crystallization Studies on a Molecular Chaperone (PaoD) Involved in the Maturation of Molybdoenzymes. PLoS ONE, 2014, 9, e87295.	2.5	10
108	Analysis, Design and Engineering of Simple Iron-Sulfur Proteins: Tales from Rubredoxin and Desulforedoxin. Comments on Inorganic Chemistry, 1996, 19, 47-66.	5.2	9

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109	Ionic strength dependence of the non-physiological electron transfer between flavodoxin and cytochrome c 553 from D. vulgaris. Journal of Biological Inorganic Chemistry, 2000, 5, 730-737.	2.6	9
110	Crystallization and crystallographic analysis of the apo form of the orange protein (ORP) from <i>Desulfovibrio gigas</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 730-732.	0.7	9
111	Family 42 carbohydrate-binding modules display multiple arabinoxylan-binding interfaces presenting different ligand affinities. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 2054-2062.	2.3	9
112	Human aldehyde oxidase (hAOX 1): structure determination of the Mocoâ€free form of the natural variant G1269R and biophysical studies of single nucleotide polymorphisms. FEBS Open Bio, 2019, 9, 925-934.	2.3	9
113	Systematic exploration of predicted destabilizing nonsynonymous single nucleotide polymorphisms (nsSNPs) of human aldehyde oxidase: A Bioâ€informatics study. Pharmacology Research and Perspectives, 2019, 7, e00538.	2.4	9
114	Ion-Exchange Membranes for Stable Derivatization of Protein Crystals. Crystal Growth and Design, 2017, 17, 4563-4572.	3.0	9
115	Kinetic and Structural Studies of Aldehyde Oxidoreductase from Desulfovibrio gigas Reveal a Dithiolene-Based Chemistry for Enzyme Activation and Inhibition by H2O2. PLoS ONE, 2013, 8, e83234.	2.5	9
116	Spectroscopic and Structural Characterization of Reduced <i>Desulfovibrio vulgaris</i> Hildenborough W-FdhAB Reveals Stable Metal Coordination during Catalysis. ACS Chemical Biology, 2022, 17, 1901-1909.	3.4	9
117	Zur Aktivit�t koordinierter 1,4-Diaza-1,3-diene (dad) bei C?C-Verkn�pfungsreaktionen: 3-Pyrrolin-2-one aus (dad)Fe(CO)3 und Dimethyl-acetylendicarboxylat. Angewandte Chemie International Edition in English, 1983, 22, 1435-1450.	4.4	8
118	Crystallization and preliminary X-ray diffraction studies of aSFP, a bovine seminal plasma protein with a single CUB domain architecture. Protein Science, 1997, 6, 725-727.	7.6	8
119	Crystal structure of the zinc-, cobalt-, and iron-containing adenylate kinase from Desulfovibrio gigas: a novel metal-containing adenylate kinase from Gram-negative bacteria. Journal of Biological Inorganic Chemistry, 2011, 16, 51-61.	2.6	8
120	Ionic-Liquid-Functionalized Mineral Particles for Protein Crystallization. Crystal Growth and Design, 2015, 15, 2994-3003.	3.0	8
121	Cationic derivatives of niobocene(IV). Crystal structures of [Cp2NbL2][BF4]2 (L = CNMe, NCMe). Polyhedron, 1993, 12, 765-770.	2.2	7
122	Cytochromec6from the green algaMonoraphidium braunii. Crystallization and preminary diffraction studies. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 232-234.	2.5	7
123	Induced peroxidase activity of haem containing nitrate reductases revealed by protein film electrochemistry. Journal of Electroanalytical Chemistry, 2013, 693, 105-113.	3.8	7
124	Crystallization and preliminary X-ray analysis of a membrane-bound nitrite reductase from <i>Desulfovibrio desulfuricans</i> ATCC 27774. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 215-217.	2.5	6
125	Crystallization and preliminary X-ray diffraction analysis of two pH-dependent forms of a di-haem cytochromecperoxidase fromPseudomonas nautica. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 697-699.	2.5	6
126	On the purification and preliminary crystallographic analysis of isoquinoline 1-oxidoreductase fromBrevundimonas diminuta7. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 137-140.	0.7	6

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127	Escherichia coli Expression, Purification, Crystallization, and Structure Determination of Bacterial Cohesin–Dockerin Complexes. Methods in Enzymology, 2012, 510, 395-415.	1.0	6
128	Advances in Membrane-Bound Catechol-O-Methyltransferase Stability Achieved Using a New Ionic Liquid-Based Storage Formulation. International Journal of Molecular Sciences, 2022, 23, 7264.	4.1	6
129	Superoxide reductase from the syphilis spirocheteTreponema pallidum: crystallization and structure determination using soft X-rays. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 967-970.	0.7	5
130	Infrared light-induced protein crystallization. Structuring of protein interfacial water and periodic self-assembly. Journal of Crystal Growth, 2017, 457, 362-368.	1.5	5
131	Magnetic particles used in a new approach for designed protein crystallization. CrystEngComm, 2021, 23, 1083-1090.	2.6	5
132	Interrogating the Inhibition Mechanisms of Human Aldehyde Oxidase by X-ray Crystallography and NMR Spectroscopy: The Raloxifene Case. Journal of Medicinal Chemistry, 2021, 64, 13025-13037.	6.4	5
133	The use of electron spin resonance and ENDOR and TRIPLE resonance methods for structural elucidation. Journal of the Chemical Society Faraday Transactions I, 1987, 83, 43.	1.0	4
134	Crystallization and preliminary X-ray analysis of a nitrate reductase from Desulfovibrio desulfuricans ATCC 27774. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 877-879.	2.5	4
135	Cobalt-, zinc- and iron-bound forms of adenylate kinase (AK) from the sulfate-reducing bacteriumDesulfovibrio gigas: purification, crystallization and preliminary X-ray diffraction analysis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 926-929.	0.7	4
136	Purification, crystallization and preliminary X-ray characterization of the pentamodular arabinoxylanase <i>Ct</i> Xyl5A from <i>Clostridium thermocellum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 833-836.	0.7	4
137	Overexpression, crystallization and preliminary X-ray crystallographic analysis of glucuronoxylan xylanohydrolase (Xyn30A) from <i>Clostridium thermocellum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1440-1442.	0.7	4
138	Aromatic aldehydes at the active site of aldehyde oxidoreductase from Desulfovibrio gigas: reactivity and molecular details of the enzyme–substrate and enzyme–product interaction. Journal of Biological Inorganic Chemistry, 2015, 20, 219-229.	2.6	4
139	Crystallization and preliminary X-ray diffraction analysis of the 16-haem cytochrome ofDesulfovibrio gigas. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 968-970.	2.5	3
140	Purification, crystallization and preliminary X-ray diffraction analysis of the glyoxalase II fromLeishmania infantum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 805-807.	0.7	3
141	Purification, crystallization and crystallographic analysis ofClostridium thermocellumendo-1,4-Î2-D-xylanase 10B in complex with xylohexaose. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 715-718.	0.7	3
142	Preliminary structural characterization of human SOUL, a haem-binding protein. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 723-726.	0.7	3
143	Molybdenum enzymes in reactions involving aldehydes and acids. Metal Ions in Biological Systems, 2002, 39, 539-70.	0.4	3
144	Purification, crystallization and identification by X-ray analysis of a prostate kallikrein from horse seminal plasma. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1180-1183.	2.5	2

#	Article	IF	CITATIONS
145	Purification, crystallization and preliminary X-ray diffraction analysis of adenosine triphosphate sulfurylase (ATPS) from the sulfate-reducing bacteriumDesulfovibrio desulfuricansATCC 27774. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 593-595.	0.7	2
146	Overproduction, purification, crystallization and preliminary X-ray characterization of a novel carbohydrate-binding module of endoglucanase Cel5A fromEubacterium cellulosolvens. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 491-493.	0.7	2
147	Structure of 6-fluoro-10,10'-diphenyl-9-phenanthrone (1), 7-chloro-10,10'-diphenyl-9-phenanthrone (2) and 3-methoxy-10,10'-diphenyl-9-phenanthrone (3). Acta Crystallographica Section C: Crystal Structure Communications, 1986, 42, 1404-1408.	0.4	0
148	13C NMR study of substituted 10,10-diphenyl-9-phenanthrones. Structure determination and signal assignment using 2D NMR techniques. Magnetic Resonance in Chemistry, 1989, 27, 1130-1133.	1.9	0
149	Crystallization and preliminary X-ray diffraction analysis of the di-haem cytochromecperoxidase fromPseudomonas stutzeri. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 345-347.	2.5	0
150	Correction to Use of Gold Nanoparticles as Additives in Protein Crystallization. Crystal Growth and Design, 2014, 14, 888-888.	3.0	0
151	The crystal structure of human Aldehyde oxidase. Drug Metabolism and Pharmacokinetics, 2018, 33, S10-S11.	2.2	0