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List of Publications by Year in descending order

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45
papers

3,184
citations

257357

24
h-index

276775

41
g-index

48
all docs

48
docs citations

48
times ranked

3758
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Evidence for Ligand Specificity in the Binding Domain of the Human Androgen Receptor. <i>Journal of Biological Chemistry</i> , 2000, 275, 26164-26171.	1.6	530
2	Crystal Structure of a Bacterial Endospore Coat Component. <i>Journal of Biological Chemistry</i> , 2003, 278, 19416-19425.	1.6	322
3	NEW EMBO MEMBER'S REVIEW: Ferritins, iron uptake and storage from the bacterioferritin viewpoint. <i>EMBO Journal</i> , 2003, 22, 1959-1968.	3.5	255
4	[NiFe] hydrogenase from <i>Desulfovibrio desulfuricans</i> ATCC 27774: gene sequencing, three-dimensional structure determination and refinement at 1.8 Å... and modelling studies of its interaction with the tetrahaem cytochrome c 3. <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 63-81.	1.1	198
5	Substrate and Dioxygen Binding to the Endospore Coat Laccase from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 23472-23476.	1.6	161
6	Dioxygen reduction by multi-copper oxidases; a structural perspective. <i>Dalton Transactions</i> , 2005, , 3507.	1.6	145
7	Sulphate respiration from hydrogen in <i>Desulfovibrio</i> bacteria: a structural biology overview. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 292-329.	1.4	141
8	Crystal Structure of the Human AAA+ Protein RuvBL1. <i>Journal of Biological Chemistry</i> , 2006, 281, 38918-38929.	1.6	141
9	Structural and functional insights into a dodecameric molecular machine – The RuvBL1/RuvBL2 complex. <i>Journal of Structural Biology</i> , 2011, 176, 279-291.	1.3	98
10	The architecture of the binding site in redox protein complexes: Implications for fast dissociation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 603-612.	1.5	85
11	Kinetics and Crystal Structure of Catechol-O-Methyltransferase Complex with Co-Substrate and a Novel Inhibitor with Potential Therapeutic Application. <i>Molecular Pharmacology</i> , 2002, 62, 795-805.	1.0	81
12	Cytochrome c ₃ from <i>Desulfovibrio gigas</i> : Crystal structure at 1.8 Å... resolution and evidence for a specific calcium-binding site. <i>Protein Science</i> , 1996, 5, 1342-1354.	3.1	80
13	Structural Basis for the Glucocorticoid Response in a Mutant Human Androgen Receptor (AR _{CCR}) Derived from an Androgen-Independent Prostate Cancer. <i>Journal of Medicinal Chemistry</i> , 2002, 45, 1439-1446.	2.9	80
14	The primary and three-dimensional structures of a nine-haem cytochrome c from <i>Desulfovibrio desulfuricans</i> ATCC 27774 reveal a new member of the Hmc family. <i>Structure</i> , 1999, 7, 119-130.	1.6	79
15	Improved modeling of side-chains in proteins with rotamer-based methods: A flexible rotamer model. , 1999, 37, 530-543.		68
16	1,3-Propanediol Dehydrogenase from <i>Klebsiella pneumoniae</i> : Decameric Quaternary Structure and Possible Subunit Cooperativity. <i>Journal of Bacteriology</i> , 2009, 191, 1143-1151.	1.0	64
17	Sulfate Respiration in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Biological Chemistry</i> , 2002, 277, 47907-47916.	1.6	55
18	Nine-haem cytochrome c from <i>Desulfovibrio desulfuricans</i> ATCC 27774 – Primary sequence determination, crystallographic refinement at 1.8 Å and modelling studies of its interaction with the tetrahaem cytochrome c 3. <i>Journal of Biological Inorganic Chemistry</i> , 1999, 4, 478-494.	1.1	46

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19	Improvement of side-chain modeling in proteins with the self-consistent mean field theory method based on an analysis of the factors influencing prediction. , 1999, 50, 111-131.		44
20	Crystal structure of low-potential cytochrome c 549 from <i>Synechocystis</i> sp. PCC 6803 at 1.21Å... resolution. <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 324-332.	1.1	40
21	Crystal structure of a junction between two Z-DNA helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9088-9092.	3.3	40
22	Conformational Component in the Coupled Transfer of Multiple Electrons and Protons in a Monomeric Tetraheme Cytochrome. <i>Journal of Biological Chemistry</i> , 2001, 276, 44044-44051.	1.6	39
23	A preliminary analysis of the three-dimensional structure of dimeric di-haem split-Soret cytochrome c from <i>Desulfovibrio desulfuricans</i> ATCC 27774 at 2.5Å... resolution using the MAD phasing method: a novel cytochrome fold with a stacked-haem arrangement. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 507-514.	1.1	36
24	Structural Studies on Flavodiiron Proteins. <i>Methods in Enzymology</i> , 2008, 437, 3-19.	0.4	34
25	An iterative structure-assisted approach to sequence alignment and comparative modeling. , 1999, 37, 55-60.		32
26	Structural and functional relationships in the hybrid cluster protein family: structure of the anaerobically purified hybrid cluster protein from <i>Desulfovibrio vulgaris</i> at 1.35Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 665-674.	2.5	30
27	Incorporating knowledge-based biases into an energy-based side-chain modeling method: Application to comparative modeling of protein structure. <i>Biopolymers</i> , 2001, 59, 72-86.	1.2	26
28	Structure of dimeric cytochromec ₃ from <i>Desulfovibrio gigas</i> at 1.2Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 644-653.	2.5	24
29	Proton-assisted Two-electron Transfer in Natural Variants of Tetraheme Cytochromes from <i>Desulfomicrobium</i> Sp.. <i>Journal of Biological Chemistry</i> , 2004, 279, 52227-52237.	1.6	24
30	Crystal structures of the free and sterol-bound forms of $\hat{1}^2$ -cinnamomin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 110-121.	1.1	24
31	A novel iron centre in the split-Soret cytochrome c from <i>Desulfovibrio desulfuricans</i> ATCC 27774. <i>Journal of Biological Inorganic Chemistry</i> , 2003, 8, 360-370.	1.1	20
32	Spore-coat laccase CotA from <i>Bacillus subtilis</i> : crystallization and preliminary X-ray characterization by the MAD method. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1490-1493.	2.5	18
33	Auto-induction and purification of a <i>Bacillus subtilis</i> transglutaminase (Tgl) and its preliminary crystallographic characterization. <i>Protein Expression and Purification</i> , 2008, 59, 1-8.	0.6	18
34	Implicit solvation in the self-consistent mean field theory method: sidechain modelling and prediction of folding free energies of protein mutants. <i>Journal of Computer-Aided Molecular Design</i> , 2001, 15, 721-740.	1.3	16
35	Crystallization and preliminary X-ray characterization of a ferritin from the hyperthermophilic archaeon and anaerobe <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 503-506.	0.7	15
36	Quaternary Structure of Flavorubredoxin as Revealed by Synchrotron Radiation Small-Angle X-Ray Scattering. <i>Structure</i> , 2008, 16, 1428-1436.	1.6	14

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37	Crystal Structure of the Full-Length Sorbitol Operon Regulator SorC from <i>Klebsiella pneumoniae</i> : Structural Evidence for a Novel Transcriptional Regulation Mechanism. <i>Journal of Molecular Biology</i> , 2009, 387, 759-770.	2.0	13
38	Structural evidence for a proton transfer pathway coupled with haem reduction of cytochrome c ₃ from <i>Methylophilus methylotrophus</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2006, 11, 189-196.	1.1	12
39	Crystallographic analysis of the intact metal centres [3Fe ⁴⁺ S] ¹⁺ and [4Fe ⁴⁺ S] ²⁺ in a Zn ²⁺ -containing ferredoxin. <i>FEBS Letters</i> , 2008, 582, 763-767.	1.3	10
40	Cloning, expression, purification, crystallization and preliminary X-ray analysis of the human RuvBL1-RuvBL2 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 840-846.	0.7	8
41	Structure determination of bacterioferritin from <i>Desulfovibrio desulfuricans</i> by the MAD method at the FeK-edge. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 326-329.	2.5	7
42	Expression, purification, crystallization and preliminary X-ray analysis of the human RuvB-like protein RuvBL1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 61-66.	0.7	4
43	Overproduction, crystallization and preliminary X-ray characterization of Abn2, an endo-1,5- α -arabinanase from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 636-638.	0.7	3
44	Crystallization and preliminary X-ray characterization of cytochrome c ₂ from the obligate methylotroph <i>Methylophilus methylotrophus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 580-583.	2.5	2
45	RuvBL1 and RuvBL2 and Their Complex Proteins Implicated in Many Cellular Pathways. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 55-63.	0.5	0