

Maria Armnia Afde Ct Carrondo

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L-index

#	Paper	IF	Citations
46	Structural evidence for ligand specificity in the binding domain of the human androgen receptor. Implications for pathogenic gene mutations. <i>Journal of Biological Chemistry</i> , 2000 , 275, 26164-71	5.4	438
45	Crystal structure of a bacterial endospore coat component. A laccase with enhanced thermostability properties. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19416-25	5.4	267
44	Ferritins, iron uptake and storage from the bacterioferritin viewpoint. <i>EMBO Journal</i> , 2003 , 22, 1959-68	13	209
43	[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 c3. <i>Journal of Biological Inorganic Chemistry</i> , 2001 , 6, 63-81	3.7	179
42	Substrate and dioxygen binding to the endospore coat laccase from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2004 , 279, 23472-6	5.4	141
41	Dioxygen reduction by multi-copper oxidases; a structural perspective. <i>Dalton Transactions</i> , 2005 , 3507-13	13	131
40	Crystal structure of the human AAA+ protein RuvBL1. <i>Journal of Biological Chemistry</i> , 2006 , 281, 38918-29	9.4	121
39	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	4.7	110
38	Structural and functional insights into a dodecameric molecular machine - the RuvBL1/RuvBL2 complex. <i>Journal of Structural Biology</i> , 2011 , 176, 279-91	3.4	80
37	The architecture of the binding site in redox protein complexes: implications for fast dissociation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 603-12	4.2	76
36	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, 1439-46	8.3	74
35	Cytochrome c3 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, 1342-54	6.3	74
34	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	4.3	71
33	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, 119-30	5.2	71
32	Improved modeling of side-chains in proteins with rotamer-based methods: a flexible rotamer model. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 530-43	4.2	62
31	1,3-Propanediol dehydrogenase from <i>Klebsiella pneumoniae</i> : decameric quaternary structure and possible subunit cooperativity. <i>Journal of Bacteriology</i> , 2009 , 191, 1143-51	3.5	51
30	Sulfate respiration in <i>Desulfovibrio vulgaris</i> Hildenborough. Structure of the 16-heme cytochrome c HmcA AT 2.5-Å resolution and a view of its role in transmembrane electron transfer. <i>Journal of Biological Chemistry</i> , 2002 , 277, 47907-16	5.4	49

29	Crystal structure of low-potential cytochrome c549 from <i>Synechocystis</i> sp. PCC 6803 at 1.21 Å resolution. <i>Journal of Biological Inorganic Chemistry</i> , 2001 , 6, 324-32	3-7	39
28	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 c3. <i>Journal of Biological Inorganic Chemistry</i> , 1999 , 4, 478-94	3-7	37
27	Conformational component in the coupled transfer of multiple electrons and protons in a monomeric tetraheme cytochrome. <i>Journal of Biological Chemistry</i> , 2001 , 276, 44044-51	5-4	36
26	Improvement of side-chain modeling in proteins with the self-consistent mean field theory method based on an analysis of the factors influencing prediction. <i>Biopolymers</i> , 1999 , 50, 111-31	2.2	35
25	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, 9088-92	11.5	30
24	An iterative structure-assisted approach to sequence alignment and comparative modeling 1999 , 37, 55-60		29
23	Structural studies on flavodiiron proteins. <i>Methods in Enzymology</i> , 2008 , 437, 3-19	1.7	28
22	A preliminary analysis of the three-dimensional structure of dimeric di-haem split-Soret cytochrome c from <i>Desulfovibrio desulfuricans</i> ATCC 27774 at 2.5-Å 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	3-7	26
21	Proton-assisted two-electron transfer in natural variants of tetraheme cytochromes from <i>Desulfomicrobium</i> Sp. <i>Journal of Biological Chemistry</i> , 2004 , 279, 52227-37	5-4	22
20	Structure of dimeric cytochrome c3 from <i>Desulfovibrio gigas</i> at 1.2 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 644-53		21
19	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	2.2	21
18	Crystal structures of the free and sterol-bound forms of beta-cinnamomin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006 , 1764, 110-21	4	20
17	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	2	16
16	Structural and functional relationships in the hybrid cluster protein family: structure of the anaerobically purified hybrid cluster protein from <i>Desulfovibrio vulgaris</i> at 1.35 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 665-74		15
15	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, 360-70	3-7	15
14	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, 721-40	4.2	15
13	Quaternary structure of flavorubredoxin as revealed by synchrotron radiation small-angle X-ray scattering. <i>Structure</i> , 2008 , 16, 1428-36	5.2	13
12	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, 1490-3		13

11	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, 503-6		13
10	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, 759-70	6.5	11
9	Structural evidence for a proton transfer pathway coupled with haem reduction of cytochrome c" from <i>Methylophilus methylotrophus</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2006 , 11, 189-96	3.7	10
8	Crystallographic analysis of the intact metal centres [3Fe-4S](1+/0) and [4Fe-4S](2+/1+) in a Zn(2+) -containing ferredoxin. <i>FEBS Letters</i> , 2008 , 582, 763-7	3.8	9
7	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, 840-6		7
6	Structure determination of bacterioferritin from <i>Desulfovibrio desulfuricans</i> by the MAD method at the Fe K-edge. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 326-9		7
5	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, 61-6		4
4	Overproduction, crystallization and preliminary X-ray characterization of Abn2, an endo-1,5-alpha-arabinanase from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 636-8		3
3	Crystallization and preliminary X-ray characterization of cytochrome c" from the obligate methylotroph <i>Methylophilus methylotrophus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 580-3		2
2	Flavodiiron Proteins: Nitric Oxide and/or Oxygen Reductases 2011 ,		1
1	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	0.1	