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List of Publications by Year in descending order

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45
papers

3,184
citations

257357

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41
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48
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docs citations

48
times ranked

3758
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | RuvBL1 and RuvBL2 and Their Complex Proteins Implicated in Many Cellular Pathways. NATO Science for Peace and Security Series A: Chemistry and Biology, 2012, , 55-63. | 0.5 | 0 |
| 2 | Structural and functional insights into a dodecameric molecular machine – The RuvBL1/RuvBL2 complex. Journal of Structural Biology, 2011, 176, 279-291. | 1.3 | 98 |
| 3 | Crystal structure of a junction between two Z-DNA helices. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9088-9092. | 3.3 | 40 |
| 4 | 1,3-Propanediol Dehydrogenase from <i>Klebsiella pneumoniae</i> : Decameric Quaternary Structure and Possible Subunit Cooperativity. Journal of Bacteriology, 2009, 191, 1143-1151. | 1.0 | 64 |
| 5 | Crystal Structure of the Full-Length Sorbitol Operon Regulator SorC from <i>Klebsiella pneumoniae</i> : Structural Evidence for a Novel Transcriptional Regulation Mechanism. Journal of Molecular Biology, 2009, 387, 759-770. | 2.0 | 13 |
| 6 | 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. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 665-674. | 2.5 | 30 |
| 7 | Overproduction, crystallization and preliminary X-ray characterization of Abn2, an endo-1,5- α -arabinanase from <i>Bacillus subtilis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 636-638. | 0.7 | 3 |
| 8 | Cloning, expression, purification, crystallization and preliminary X-ray analysis of the human RuvBL1-RuvBL2 complex. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 840-846. | 0.7 | 8 |
| 9 | Crystallographic analysis of the intact metal centres $[3Fe^{4+}4S]^{1+}$ and $[4Fe^{4+}4S]^{2+}$ in a Zn ²⁺ -containing ferredoxin. FEBS Letters, 2008, 582, 763-767. | 1.3 | 10 |
| 10 | Quaternary Structure of Flavorubredoxin as Revealed by Synchrotron Radiation Small-Angle X-Ray Scattering. Structure, 2008, 16, 1428-1436. | 1.6 | 14 |
| 11 | Structural Studies on Flavodiiron Proteins. Methods in Enzymology, 2008, 437, 3-19. | 0.4 | 34 |
| 12 | Auto-induction and purification of a <i>Bacillus subtilis</i> transglutaminase (Tgl) and its preliminary crystallographic characterization. Protein Expression and Purification, 2008, 59, 1-8. | 0.6 | 18 |
| 13 | Expression, purification, crystallization and preliminary X-ray analysis of the human RuvB-like protein RuvBL1. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 61-66. | 0.7 | 4 |
| 14 | Crystal structures of the free and sterol-bound forms of β^2 -cinnamomin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 110-121. | 1.1 | 24 |
| 15 | Structural evidence for a proton transfer pathway coupled with haem reduction of cytochrome c_{553} from <i>Methylophilus methylotrophus</i> . Journal of Biological Inorganic Chemistry, 2006, 11, 189-196. | 1.1 | 12 |
| 16 | Crystal Structure of the Human AAA+ Protein RuvBL1. Journal of Biological Chemistry, 2006, 281, 38918-38929. | 1.6 | 141 |
| 17 | Sulphate respiration from hydrogen in <i>Desulfovibrio</i> bacteria: a structural biology overview. Progress in Biophysics and Molecular Biology, 2005, 89, 292-329. | 1.4 | 141 |
| 18 | Crystallization and preliminary X-ray characterization of a ferritin from the hyperthermophilic archaeon and anaerobe <i>Pyrococcus furiosus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 503-506. | 0.7 | 15 |

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|----|---|-----|-----------|
| 19 | Dioxygen reduction by multi-copper oxidases; a structural perspective. Dalton Transactions, 2005, , 3507. | 1.6 | 145 |
| 20 | Substrate and Dioxygen Binding to the Endospore Coat Laccase from Bacillus subtilis. Journal of Biological Chemistry, 2004, 279, 23472-23476. | 1.6 | 161 |
| 21 | Proton-assisted Two-electron Transfer in Natural Variants of Tetraheme Cytochromes from Desulfomicrobium Sp.. Journal of Biological Chemistry, 2004, 279, 52227-52237. | 1.6 | 24 |
| 22 | The architecture of the binding site in redox protein complexes: Implications for fast dissociation. Proteins: Structure, Function and Bioinformatics, 2004, 55, 603-612. | 1.5 | 85 |
| 23 | NEW EMBO MEMBER'S REVIEW: Ferritins, iron uptake and storage from the bacterioferritin viewpoint. EMBO Journal, 2003, 22, 1959-1968. | 3.5 | 255 |
| 24 | Crystallization and preliminary X-ray characterization of cytochromecâ€²â€² from the obligate methylotrophMethylophilus methylotrophus. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 580-583. | 2.5 | 2 |
| 25 | Structure of dimeric cytochromec3fromDesulfovibrio gigasat 1.2â€…Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 644-653. | 2.5 | 24 |
| 26 | A novel iron centre in the split-Soret cytochrome c from Desulfovibrio desulfuricans ATCC 27774. Journal of Biological Inorganic Chemistry, 2003, 8, 360-370. | 1.1 | 20 |
| 27 | Crystal Structure of a Bacterial Endospore Coat Component. Journal of Biological Chemistry, 2003, 278, 19416-19425. | 1.6 | 322 |
| 28 | Sulfate Respiration in Desulfovibrio vulgaris Hildenborough. Journal of Biological Chemistry, 2002, 277, 47907-47916. | 1.6 | 55 |
| 29 | Structural Basis for the Glucocorticoid Response in a Mutant Human Androgen Receptor (ARccr) Derived from an Androgen-Independent Prostate Cancer. Journal of Medicinal Chemistry, 2002, 45, 1439-1446. | 2.9 | 80 |
| 30 | Kinetics and Crystal Structure of Catechol-O-Methyltransferase Complex with Co-Substrate and a Novel Inhibitor with Potential Therapeutic Application. Molecular Pharmacology, 2002, 62, 795-805. | 1.0 | 81 |
| 31 | Spore-coat laccase CotA fromBacillus subtilis: crystallization and preliminary X-ray characterization by the MAD method. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1490-1493. | 2.5 | 18 |
| 32 | [NiFe] hydrogenase from Desulfovibrio desulfuricans ATCC 27774: gene sequencing, three-dimensional structure determination and refinement at 1.8Å... and modelling studies of its interaction with the tetrahaem cytochrome c 3. Journal of Biological Inorganic Chemistry, 2001, 6, 63-81. | 1.1 | 198 |
| 33 | Crystal structure of low-potential cytochrome c 549 from Synechocystis sp. PCC 6803 at 1.21Å... resolution. Journal of Biological Inorganic Chemistry, 2001, 6, 324-332. | 1.1 | 40 |
| 34 | Structure determination of bacterioferritin fromDesulfovibrio desulfuricansby the MAD method at the FeK-edge. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 326-329. | 2.5 | 7 |
| 35 | Incorporating knowledge-based biases into an energy-based side-chain modeling method: Application to comparative modeling of protein structure. Biopolymers, 2001, 59, 72-86. | 1.2 | 26 |
| 36 | Implicit solvation in the self-consistent mean field theory method: sidechain modelling and prediction of folding free energies of protein mutants. Journal of Computer-Aided Molecular Design, 2001, 15, 721-740. | 1.3 | 16 |

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|----|--|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | An iterative structure-assisted approach to sequence alignment and comparative modeling. , 1999, 37, 55-60. | | 32 |
| 43 | Improved modeling of side-chains in proteins with rotamer-based methods: A flexible rotamer model. , 1999, 37, 530-543. | | 68 |
| 44 | 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. | 1.1 | 36 |
| 45 | 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 |