# Antonio Rosato

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 138 papers | 6,390 citations | 43 h-index | 76 g-index |
| 223 ext. papers | 7,393 ext. citations | 6.5 avg, IF | 5.69 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 138 | PDBe-KB: collaboratively defining the biological context of structural data. *Nucleic Acids Research*, **2021**, | 20.1 | 7 |
| 137 | Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. *Frontiers in Molecular Biosciences*, **2021**, 8, 729513 | 5.6 | 39 |
| 136 | Insights into the Dynamics of the Human Zinc Transporter ZnT8 by MD Simulations. *Journal of Chemical Information and Modeling*, **2021**, 61, 901-912 | 6.1 | 3 |
| 135 | Upgraded AMBER Force Field for Zinc-Binding Residues and Ligands for Predicting Structural Properties and Binding Affinities in Zinc-Proteins. *ACS Omega*, **2020**, 5, 15301-15310 | 3.9 | 8 |
| 134 | Decreased amount of vimentin N-terminal truncated proteolytic products in parkin-mutant skin fibroblasts. *Biochemical and Biophysical Research Communications*, **2020**, 521, 693-698 | 3.4 | 2 |
| 133 | A protocol to automatically calculate homo-oligomeric protein structures through the integration of evolutionary constraints and NMR ambiguous contacts. *Computational and Structural Biotechnology Journal*, **2020**, 18, 114-124 | 6.8 | 0 |
| 132 | Oxidation of Human Copper Chaperone Atox1 and Disulfide Bond Cleavage by Cisplatin and Glutathione. *International Journal of Molecular Sciences*, **2019**, 20, | 6.3 | 2 |
| 131 | Insights into telomeric G-quadruplex DNA recognition by HMGB1 protein. *Nucleic Acids Research*, **2019**, 47, 9950-9966 | 20.1 | 18 |
| 130 | An atomistic view of the YiiP structural changes upon zinc(II) binding. *Biochimica Et Biophysica Acta - General Subjects*, **2019**, 1863, 1560-1567 | 4 | 6 |
| 129 | Metabolomics in systems medicine: an overview of methods and applications. *Current Opinion in Systems Biology*, **2019**, 15, 91-99 | 3.2 | 7 |
| 128 | Upgrading and Validation of the AMBER Force Field for Histidine and Cysteine Zinc(II)-Binding Residues in Sites with Four Protein Ligands. *Journal of Chemical Information and Modeling*, **2019**, 59, 3803-3816 | 6.1 | 18 |
| 127 | Mechanistic and Structural Basis for Inhibition of Copper Trafficking by Platinum Anticancer Drugs. *Journal of the American Chemical Society*, **2019**, 141, 12109-12120 | 16.4 | 14 |
| 126 | Protein structure prediction assisted with sparse NMR data in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1315-1332 | 4.2 | 9 |
| 125 | West-Life: A Virtual Research Environment for structural biology. *Journal of Structural Biology: X*, **2019**, 1, 100006 | 2.9 | 1 |
| 124 | PhenoMeNal: processing and analysis of metabolomics data in the cloud. *GigaScience*, **2019**, 8, | 7.6 | 41 |
| 123 | From correlation to causation: analysis of metabolomics data using systems biology approaches. *Metabolomics*, **2018**, 14, 37 | 4.7 | 110 |
| 122 | MetalPDB in 2018: a database of metal sites in biological macromolecular structures. *Nucleic Acids Research*, **2018**, 46, D459-D464 | 20.1 | 81 |

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| 121 | nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. *Analytical Chemistry*, **2018**, 90, 649-656 | 7.8 | 37 |
| 120 | Monitoring Interactions Inside Cells by Advanced Spectroscopies: Overview of Copper Transporters and Cisplatin. *Current Medicinal Chemistry*, **2018**, 25, 462-477 | 4.3 | 9 |
| 119 | The human iron-proteome. *Metallomics*, **2018**, 10, 1223-1231 | 4.5 | 48 |
| 118 | Molecular dynamics simulations of metalloproteins: A folding study of rubredoxin from Pyrococcus furiosus. *AIMS Biophysics*, **2018**, 5, 77-96 | 0.8 | 3 |
| 117 | To what extent do structural changes in catalytic metal sites affect enzyme function?. *Journal of Inorganic Biochemistry*, **2018**, 179, 40-53 | 4.2 | 33 |
| 116 | Application of Molecular Dynamics to the Investigation of Metalloproteins Involved in Metal Homeostasis. *European Journal of Inorganic Chemistry*, **2018**, 2018, 4661-4677 | 2.3 | 7 |
| 115 | The DisVis and PowerFit Web Servers: Explorative and Integrative Modeling of Biomolecular Complexes. *Journal of Molecular Biology*, **2017**, 429, 399-407 | 6.5 | 25 |
| 114 | Copper Homeostasis in Humans and Bacteria **2017**, | | |
| 113 | Investigation of the Iron(II) Release Mechanism of Human H-Ferritin as a Function of pH. *Journal of Chemical Information and Modeling*, **2017**, 57, 2112-2118 | 6.1 | 16 |
| 112 | The future of metabolomics in ELIXIR. *F1000Research*, **2017**, 6, | 3.6 | 18 |
| 111 | The future of metabolomics in ELIXIR. *F1000Research*, **2017**, 6, 1649 | 3.6 | 10 |
| 110 | The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. *PLoS ONE*, **2017**, 12, e0171279 | 3.7 | 30 |
| 109 | EGI federated platforms supporting accelerated computing **2017**, | | 2 |
| 108 | A protocol for the refinement of NMR structures using simultaneously pseudocontact shift restraints from multiple lanthanide ions. *Journal of Biomolecular NMR*, **2016**, 66, 175-185 | 3 | 9 |
| 107 | MetalPredator: a web server to predict iron-sulfur cluster binding proteomes. *Bioinformatics*, **2016**, 32, 2850-2 | 7.2 | 31 |
| 106 | Exploiting Bacterial Operons To Illuminate Human Iron-Sulfur Proteins. *Journal of Proteome Research*, **2016**, 15, 1308-22 | 5.6 | 30 |
| 105 | Minimal Functional Sites in Metalloproteins and Their Usage in Structural Bioinformatics. *International Journal of Molecular Sciences*, **2016**, 17, | 6.3 | 7 |
| 104 | Hidden relationships between metalloproteins unveiled by structural comparison of their metal sites. *Scientific Reports*, **2015**, 5, 9486 | 4.9 | 8 |

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| 103 | The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. *Journal of Biomolecular NMR*, **2015**, 62, 413-24 | 3 | 21 |
| 102 | Analysis of the structural quality of the CASD-NMR 2013 entries. *Journal of Biomolecular NMR*, **2015**, 62, 527-40 | 3 | 4 |
| 101 | The Da Vinci European BioBank: A Metabolomics-Driven Infrastructure. *Journal of Personalized Medicine*, **2015**, 5, 107-19 | 3.6 | 8 |
| 100 | COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. *Metabolomics*, **2015**, 11, 1587-1597 | 4.7 | 109 |
| 99 | MetalS(3), a database-mining tool for the identification of structurally similar metal sites. *Journal of Biological Inorganic Chemistry*, **2014**, 19, 937-45 | 3.7 | 20 |
| 98 | Zinc proteome interaction network as a model to identify nutrient-affected pathways in human pathologies. *Genes and Nutrition*, **2014**, 9, 436 | 4.3 | 18 |
| 97 | SedNMR: a web tool for optimizing sedimentation of macromolecular solutes for SSNMR. *Journal of Biomolecular NMR*, **2013**, 57, 319-26 | 3 | 12 |
| 96 | Quality assessment of protein NMR structures. *Current Opinion in Structural Biology*, **2013**, 23, 715-24 | 8.1 | 20 |
| 95 | MetalS2: a tool for the structural alignment of minimal functional sites in metal-binding proteins and nucleic acids. *Journal of Chemical Information and Modeling*, **2013**, 53, 3064-75 | 6.1 | 10 |
| 94 | MetalPDB: a database of metal sites in biological macromolecular structures. *Nucleic Acids Research*, **2013**, 41, D312-9 | 20.1 | 86 |
| 93 | Blind testing of routine, fully automated determination of protein structures from NMR data. *Structure*, **2012**, 20, 227-36 | 5.2 | 64 |
| 92 | What Can be Learned about the Structure and Dynamics of Biomolecules from NMR **2012**, 33-50 | | 1 |
| 91 | Grid Computing **2012**, 509-518 | | |
| 90 | WeNMR: Structural Biology on the Grid. *Journal of Grid Computing*, **2012**, 10, 743-767 | 4.2 | 142 |
| 89 | MaxOcc: a web portal for maximum occurrence analysis. *Journal of Biomolecular NMR*, **2012**, 53, 271-80 | 3 | 31 |
| 88 | RPF: a quality assessment tool for protein NMR structures. *Nucleic Acids Research*, **2012**, 40, W542-6 | 20.1 | 43 |
| 87 | A Grid-enabled web portal for NMR structure refinement with AMBER. *Bioinformatics*, **2011**, 27, 2384-90 | 7.2 | 51 |
| 86 | Principles and patterns in the interaction between mono-heme cytochrome c and its partners in electron transfer processes. *Metallomics*, **2011**, 3, 354-62 | 4.5 | 8 |

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| 85 | A simple protocol for the comparative analysis of the structure and occurrence of biochemical pathways across superkingdoms. *Journal of Chemical Information and Modeling*, **2011**, 51, 730-8 | 6.1 | 21 |
| 84 | The binding mode of ATP revealed by the solution structure of the N-domain of human ATP7A. *Journal of Biological Chemistry*, **2010**, 285, 2537-44 | 5.4 | 20 |
| 83 | Molecular recognition in copper trafficking. *Natural Product Reports*, **2010**, 27, 695-710 | 15.1 | 65 |
| 82 | A systematic investigation of multiheme c-type cytochromes in prokaryotes. *Journal of Biological Inorganic Chemistry*, **2010**, 15, 559-71 | 3.7 | 64 |
| 81 | The annotation of full zinc proteomes. *Journal of Biological Inorganic Chemistry*, **2010**, 15, 1071-8 | 3.7 | 25 |
| 80 | The eNMR platform for structural biology. *Journal of Structural and Functional Genomics*, **2010**, 11, 1-8 | | 17 |
| 79 | An NMR study of the interaction of the N-terminal cytoplasmic tail of the Wilson disease protein with copper(I)-HAH1. *Journal of Biological Chemistry*, **2009**, 284, 9354-60 | 5.4 | 81 |
| 78 | CASD-NMR: critical assessment of automated structure determination by NMR. *Nature Methods*, **2009**, 6, 625-6 | 21.6 | 51 |
| 77 | Solution structures of the actuator domain of ATP7A and ATP7B, the Menkes and Wilson disease proteins. *Biochemistry*, **2009**, 48, 7849-55 | 3.2 | 31 |
| 76 | Role of the N-terminal tail of metal-transporting P(1B)-type ATPases from genome-wide analysis and molecular dynamics simulations. *Journal of Chemical Information and Modeling*, **2009**, 49, 76-83 | 6.1 | 10 |
| 75 | Metalloproteomes: a bioinformatic approach. *Accounts of Chemical Research*, **2009**, 42, 1471-9 | 24.3 | 214 |
| 74 | Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces. *Biochemical Journal*, **2009**, 422, 37-42 | 3.8 | 78 |
| 73 | Occurrence of copper proteins through the three domains of life: a bioinformatic approach. *Journal of Proteome Research*, **2008**, 7, 209-16 | 5.6 | 151 |
| 72 | Genome-based analysis of heme biosynthesis and uptake in prokaryotic systems. *Journal of Proteome Research*, **2008**, 7, 4946-54 | 5.6 | 43 |
| 71 | The war of tools: how can NMR spectroscopists detect errors in their structures?. *Journal of Biomolecular NMR*, **2008**, 40, 251-61 | 3 | 19 |
| 70 | Menkes disease. *Cellular and Molecular Life Sciences*, **2008**, 65, 89-91 | 10.3 | 75 |
| 69 | The functions of Sco proteins from genome-based analysis. *Journal of Proteome Research*, **2007**, 6, 1568-78 | 3.8 | 51 |
| 68 | From Genes to Metalloproteins: A Bioinformatic Approach. *European Journal of Inorganic Chemistry*, **2007**, 2007, 2546-2555 | 2.3 | 25 |

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|---|---|---|---|
| 67 | Evolution of mitochondrial-type cytochrome c domains and of the protein machinery for their assembly. *Journal of Inorganic Biochemistry*, **2007**, 101, 1798-811 | 4.2 | 31 |
| 66 | Non-heme iron through the three domains of life. *Proteins: Structure, Function and Bioinformatics*, **2007**, 67, 317-24 | 4.2 | 62 |
| 65 | Predicting zinc binding at the proteome level. *BMC Bioinformatics*, **2007**, 8, 39 | 3.6 | 70 |
| 64 | The different intermolecular interactions of the soluble copper-binding domains of the menkes protein, ATP7A. *Journal of Biological Chemistry*, **2007**, 282, 23140-6 | 5.4 | 49 |
| 63 | Interaction of the two soluble metal-binding domains of yeast Ccc2 with copper(I)-Atx1. *Biochemical and Biophysical Research Communications*, **2007**, 364, 645-9 | 3.4 | 21 |
| 62 | Solution structure and intermolecular interactions of the third metal-binding domain of ATP7A, the Menkes disease protein. *Journal of Biological Chemistry*, **2006**, 281, 29141-7 | 5.4 | 36 |
| 61 | Cytochrome c: occurrence and functions. *Chemical Reviews*, **2006**, 106, 90-115 | 68.1 | 208 |
| 60 | Counting the zinc-proteins encoded in the human genome. *Journal of Proteome Research*, **2006**, 5, 196-201 | 5.6 | 693 |
| 59 | Zinc through the three domains of life. *Journal of Proteome Research*, **2006**, 5, 3173-8 | 5.6 | 434 |
| 58 | SPINE bioinformatics and data-management aspects of high-throughput structural biology. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 1184-95 | | 15 |
| 57 | The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. *Nature Chemical Biology*, **2006**, 2, 367-8 | 11.7 | 186 |
| 56 | An Italian contribution to structural genomics: Understanding metalloproteins. *Coordination Chemistry Reviews*, **2006**, 250, 1419-1450 | 23.2 | 12 |
| 55 | Improving Prediction of Zinc Binding Sites by Modeling the Linkage Between Residues Close in Sequence. *Lecture Notes in Computer Science*, **2006**, 309-320 | 0.9 | 5 |
| 54 | An atomic-level investigation of the disease-causing A629P mutant of the Menkes protein, ATP7A. *Journal of Molecular Biology*, **2005**, 352, 409-17 | 6.5 | 32 |
| 53 | Comparative analysis of the ADAM and ADAMTS families. *Journal of Proteome Research*, **2005**, 4, 881-8 | 5.6 | 26 |
| 52 | An NMR study of the interaction between the human copper(I) chaperone and the second and fifth metal-binding domains of the Menkes protein. *FEBS Journal*, **2005**, 272, 865-71 | 5.7 | 51 |
| 51 | A structural model for the adduct between cytochrome c and cytochrome c oxidase. *Journal of Biological Inorganic Chemistry*, **2005**, 10, 613-24 | 3.7 | 24 |
| 50 | A NMR study of the interaction of a three-domain construct of ATP7A with copper(I) and copper(I)-HAH1: the interplay of domains. *Journal of Biological Chemistry*, **2005**, 280, 38259-63 | 5.4 | 54 |

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|---|---|---|---|
| 49 | A hint to search for metalloproteins in gene banks. *Bioinformatics*, **2004**, 20, 1373-80 | 7.2 | 106 |
| 48 | Cytochrome c folding / unfolding: a unifying picture. *Journal of Porphyrins and Phthalocyanines*, **2004**, 08, 238-245 | 1.8 | 4 |
| 47 | Protein stability and mutations in the axial methionine loop of a minimal cytochrome c. *Journal of Biological Inorganic Chemistry*, **2004**, 9, 600-8 | 3.7 | 11 |
| 46 | Solution structure and backbone dynamics of the Cu(I) and apo forms of the second metal-binding domain of the Menkes protein ATP7A. *Biochemistry*, **2004**, 43, 3396-403 | 3.2 | 58 |
| 45 | Solution structure of the apo and copper(I)-loaded human metallochaperone HAH1. *Biochemistry*, **2004**, 43, 13046-53 | 3.2 | 113 |
| 44 | Bioinformatic comparison of structures and homology-models of matrix metalloproteinases. *Journal of Proteome Research*, **2004**, 3, 21-31 | 5.6 | 31 |
| 43 | A Genomic Frontier in Bioinorganic Chemistry. *Chemistry Letters*, **2004**, 33, 946-951 | 1.7 | |
| 42 | A further investigation of the cytochrome b5-cytochrome c complex. *Journal of Biological Inorganic Chemistry*, **2003**, 8, 777-86 | 3.7 | 14 |
| 41 | Structural genomics of proteins involved in copper homeostasis. *Accounts of Chemical Research*, **2003**, 36, 215-21 | 24.3 | 53 |
| 40 | A high-resolution NMR study of long-lived water molecules in both oxidation states of a minimal cytochrome c. *Biochemistry*, **2003**, 42, 3457-63 | 3.2 | 10 |
| 39 | Structure and dynamics of reduced Bacillus pasteurii cytochrome c: oxidation state dependent properties and implications for electron transfer processes. *Biochemistry*, **2003**, 42, 739-45 | 3.2 | 17 |
| 38 | Hydrogen exchange in a bacterial cytochrome c: a fingerprint of the cytochrome c fold. *Biochemistry*, **2003**, 42, 10923-30 | 3.2 | 10 |
| 37 | Bioinorganic chemistry in the postgenomic era. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 3601-4 | 11.5 | 36 |
| 36 | NMR solution structure, backbone mobility, and homology modeling of c-type cytochromes from gram-positive bacteria. *ChemBioChem*, **2002**, 3, 299-310 | 3.8 | 21 |
| 35 | Browsing gene banks for Fe2S2 ferredoxins and structural modeling of 88 plant-type sequences: an analysis of fold and function. *Proteins: Structure, Function and Bioinformatics*, **2002**, 46, 110-27 | 4.2 | 48 |
| 34 | Solution structure of a monoheme ferrocytochrome c from Shewanella putrefaciens and structural analysis of sequence-similar proteins: functional implications. *Biochemistry*, **2002**, 41, 5112-9 | 3.2 | 21 |
| 33 | Paramagnetically induced residual dipolar couplings for solution structure determination of lanthanide binding proteins. *Journal of the American Chemical Society*, **2002**, 124, 5581-7 | 16.4 | 77 |
| 32 | Solution structure and characterization of the heme chaperone CcmE. *Biochemistry*, **2002**, 41, 13587-94 | 3.2 | 46 |

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|---|---|---|---|
| 31 | The unfolding of oxidized c-type cytochromes: the instructive case of Bacillus pasteurii. *Journal of Molecular Biology*, **2002**, 321, 693-701 | 6.5 | 21 |
| 30 | Solution structure calculations through self-orientation in a magnetic field of a cerium(III) substituted calcium-binding protein. *Journal of Magnetic Resonance*, **2001**, 148, 23-30 | 3 | 43 |
| 29 | Magnetic susceptibility tensor anisotropies for a lanthanide ion series in a fixed protein matrix. *Journal of the American Chemical Society*, **2001**, 123, 4181-8 | 16.4 | 170 |
| 28 | The use of propionate proton contact shifts as structural constraints. *Inorganica Chimica Acta*, **2000**, 297, 199-205 | 2.7 | 4 |
| 27 | Solution structure of oxidized microsomal rabbit cytochrome b5. Factors determining the heterogeneous binding of the heme. *FEBS Journal*, **2000**, 267, 755-66 | | 42 |
| 26 | Backbone dynamics of human Cu,Zn superoxide dismutase and of its monomeric F50E/G51E/E133Q mutant: the influence of dimerization on mobility and function. *Biochemistry*, **2000**, 39, 9108-18 | 3.2 | 59 |
| 25 | The use of the Electron-Nucleus Hyperfine Interaction for Solution Structure Determination **2000**, 1-17 | | |
| 24 | Mitochondrial cytochromes c: a comparative analysis. *Journal of Biological Inorganic Chemistry*, **1999** , 4, 824-37 | 3.7 | 85 |
| 23 | Three-dimensional solution structures of two DNA dodecamers through full relaxation matrix analysis **1999**, 37, 564-572 | | 1 |
| 22 | The solution structure of oxidized Escherichia coli cytochrome b562. *Biochemistry*, **1999**, 38, 8657-70 | 3.2 | 74 |
| 21 | Structural and dynamical properties of a partially unfolded Fe4S4 protein: role of the cofactor in protein folding. *Biochemistry*, **1999**, 38, 4669-80 | 3.2 | 37 |
| 20 | NMR Spectra of Iron-Sulfur Proteins. *Advances in Inorganic Chemistry*, **1999**, 47, 251-282 | 2.1 | 10 |
| 19 | Solution structure of paramagnetic metalloproteins. *Pure and Applied Chemistry*, **1999**, 71, 1717-1725 | 2.1 | 10 |
| 18 | Solution structure of the oxidized Fe7S8 ferredoxin from the thermophilic bacterium Bacillus schlegelii by 1H NMR spectroscopy. *Biochemistry*, **1998**, 37, 9812-26 | 3.2 | 45 |
| 17 | Partial Orientation of Oxidized and Reduced Cytochrome b5 at High Magnetic Fields: Magnetic Susceptibility Anisotropy Contributions and Consequences for Protein Solution Structure Determination. *Journal of the American Chemical Society*, **1998**, 120, 12903-12909 | 16.4 | 102 |
| 16 | Solution structure of reduced Clostridium pasteurianum rubredoxin. *Journal of Biological Inorganic Chemistry*, **1998**, 3, 401 | 3.7 | 26 |
| 15 | 1H and (13)C NMR Studies of an Oxidized HiPIP. *Inorganic Chemistry*, **1997**, 36, 4798-4803 | 5.1 | 22 |
| 14 | Solution structure of oxidized horse heart cytochrome c. *Biochemistry*, **1997**, 36, 9867-77 | 3.2 | 282 |

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|---|---|---|---|
| 13 | Solution structure of reduced microsomal rat cytochrome b5. *FEBS Journal*, **1997**, 249, 270-9 | | 25 |
| 12 | Paramagnetic relaxation as a tool for solution structure determination: Clostridium pasteurianum ferredoxin as an example **1997**, 29, 348-358 | | 55 |
| 11 | Solution Structures Of Proteins Containing Paramagnetic Metal Ions **1997**, 1-19 | | 1 |
| 10 | Can the axial ligand strength be monitored through spectroscopic measurements?. *Journal of Biological Inorganic Chemistry*, **1996**, 1, 364-367 | 3.7 | 21 |
| 9 | 1H NMR studies of the Fe7S8 ferredoxin from Bacillus schlegelii: a further attempt to understand Fe3S4 clusters. *Journal of Biological Inorganic Chemistry*, **1996**, 1, 523-528 | 3.7 | 21 |
| 8 | The solution structure refinement of the paramagnetic reduced high-potential iron-sulfur protein I from Ectothiorhodospira halophila by using stable isotope labeling and nuclear relaxation. *FEBS Journal*, **1996**, 241, 440-52 | | 64 |
| 7 | The solution structure of paramagnetic metalloproteins. *Progress in Biophysics and Molecular Biology*, **1996**, 66, 43-80 | 4.7 | 60 |
| 6 | A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: reduced HiPIP I from Ectothiorhodospira halophila. *Proteins: Structure, Function and Bioinformatics*, **1996**, 24, 158-64 | 4.2 | 19 |
| 5 | From NOESY Cross Peaks to Structural Constraints in a Paramagnetic Metalloprotein. *Magnetic Resonance in Chemistry*, **1996**, 34, 948-950 | 2.1 | 16 |
| 4 | Evaluation of paramagnetic relaxation rates in a J-coupled two-spin system. *Chemical Physics Letters*, **1996**, 250, 495-504 | 2.5 | 4 |
| 3 | A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I from Ectothiorhodospira halophila **1996**, 24, 158 | | 2 |
| 2 | PhenoMeNal: Processing and analysis of Metabolomics data in the Cloud | | 1 |
| 1 | Determination of Protein Structure and Dynamics51-94 | | 1 |