

Antonio Rosato

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Counting the zinc-proteins encoded in the human genome. <i>Journal of Proteome Research</i> , 2006 , 5, 196-201	29.1	693
137	Zinc through the three domains of life. <i>Journal of Proteome Research</i> , 2006 , 5, 3173-8	5.6	434
136	Solution structure of oxidized horse heart cytochrome c. <i>Biochemistry</i> , 1997 , 36, 9867-77	3.2	282
135	Metalloproteomes: a bioinformatic approach. <i>Accounts of Chemical Research</i> , 2009 , 42, 1471-9	24.3	214
134	Cytochrome c: occurrence and functions. <i>Chemical Reviews</i> , 2006 , 106, 90-115	68.1	208
133	The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. <i>Nature Chemical Biology</i> , 2006 , 2, 367-8	11.7	186
132	Magnetic susceptibility tensor anisotropies for a lanthanide ion series in a fixed protein matrix. <i>Journal of the American Chemical Society</i> , 2001 , 123, 4181-8	16.4	170
131	Occurrence of copper proteins through the three domains of life: a bioinformatic approach. <i>Journal of Proteome Research</i> , 2008 , 7, 209-16	5.6	151
130	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012 , 10, 743-767	4.2	142
129	Solution structure of the apo and copper(I)-loaded human metallochaperone HAH1. <i>Biochemistry</i> , 2004 , 43, 13046-53	3.2	113
128	From correlation to causation: analysis of metabolomics data using systems biology approaches. <i>Metabolomics</i> , 2018 , 14, 37	4.7	110
127	COordination of Standards in MetabOmicS (COSMOS): facilitating integrated metabolomics data access. <i>Metabolomics</i> , 2015 , 11, 1587-1597	4.7	109
126	A hint to search for metalloproteins in gene banks. <i>Bioinformatics</i> , 2004 , 20, 1373-80	7.2	106
125	Partial Orientation of Oxidized and Reduced Cytochrome b5 at High Magnetic Fields: Magnetic Susceptibility Anisotropy Contributions and Consequences for Protein Solution Structure Determination. <i>Journal of the American Chemical Society</i> , 1998 , 120, 12903-12909	16.4	102
124	MetalPDB: a database of metal sites in biological macromolecular structures. <i>Nucleic Acids Research</i> , 2013 , 41, D312-9	20.1	86
123	Mitochondrial cytochromes c: a comparative analysis. <i>Journal of Biological Inorganic Chemistry</i> , 1999 , 4, 824-37	3.7	85
122	MetalPDB in 2018: a database of metal sites in biological macromolecular structures. <i>Nucleic Acids Research</i> , 2018 , 46, D459-D464	20.1	81

121	An NMR study of the interaction of the N-terminal cytoplasmic tail of the Wilson disease protein with copper(I)-HAH1. <i>Journal of Biological Chemistry</i> , 2009 , 284, 9354-60	5.4	81
120	Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces. <i>Biochemical Journal</i> , 2009 , 422, 37-42	3.8	78
119	Paramagnetically induced residual dipolar couplings for solution structure determination of lanthanide binding proteins. <i>Journal of the American Chemical Society</i> , 2002 , 124, 5581-7	16.4	77
118	Menkes disease. <i>Cellular and Molecular Life Sciences</i> , 2008 , 65, 89-91	10.3	75
117	The solution structure of oxidized Escherichia coli cytochrome b562. <i>Biochemistry</i> , 1999 , 38, 8657-70	3.2	74
116	Predicting zinc binding at the proteome level. <i>BMC Bioinformatics</i> , 2007 , 8, 39	3.6	70
115	Molecular recognition in copper trafficking. <i>Natural Product Reports</i> , 2010 , 27, 695-710	15.1	65
114	Blind testing of routine, fully automated determination of protein structures from NMR data. <i>Structure</i> , 2012 , 20, 227-36	5.2	64
113	A systematic investigation of multiheme c-type cytochromes in prokaryotes. <i>Journal of Biological Inorganic Chemistry</i> , 2010 , 15, 559-71	3.7	64
112	The solution structure refinement of the paramagnetic reduced high-potential iron-sulfur protein I from <i>Ectothiorhodospira halophila</i> by using stable isotope labeling and nuclear relaxation. <i>FEBS Journal</i> , 1996 , 241, 440-52		64
111	Non-heme iron through the three domains of life. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 317-24	4.2	62
110	The solution structure of paramagnetic metalloproteins. <i>Progress in Biophysics and Molecular Biology</i> , 1996 , 66, 43-80	4.7	60
109	Backbone dynamics of human Cu,Zn superoxide dismutase and of its monomeric F50E/G51E/E133Q mutant: the influence of dimerization on mobility and function. <i>Biochemistry</i> , 2000 , 39, 9108-18	3.2	59
108	Solution structure and backbone dynamics of the Cu(I) and apo forms of the second metal-binding domain of the Menkes protein ATP7A. <i>Biochemistry</i> , 2004 , 43, 3396-403	3.2	58
107	Paramagnetic relaxation as a tool for solution structure determination: Clostridium pasteurianum ferredoxin as an example 1997 , 29, 348-358		55
106	A NMR study of the interaction of a three-domain construct of ATP7A with copper(I) and copper(I)-HAH1: the interplay of domains. <i>Journal of Biological Chemistry</i> , 2005 , 280, 38259-63	5.4	54
105	Structural genomics of proteins involved in copper homeostasis. <i>Accounts of Chemical Research</i> , 2003 , 36, 215-21	24.3	53
104	A Grid-enabled web portal for NMR structure refinement with AMBER. <i>Bioinformatics</i> , 2011 , 27, 2384-90	7.2	51

103	CASD-NMR: critical assessment of automated structure determination by NMR. <i>Nature Methods</i> , 2009 , 6, 625-6	21.6	51
102	The functions of Sco proteins from genome-based analysis. <i>Journal of Proteome Research</i> , 2007 , 6, 1568-73	3.8	51
101	An NMR study of the interaction between the human copper(I) chaperone and the second and fifth metal-binding domains of the Menkes protein. <i>FEBS Journal</i> , 2005 , 272, 865-71	5.7	51
100	The different intermolecular interactions of the soluble copper-binding domains of the menkes protein, ATP7A. <i>Journal of Biological Chemistry</i> , 2007 , 282, 23140-6	5.4	49
99	The human iron-proteome. <i>Metallomics</i> , 2018 , 10, 1223-1231	4.5	48
98	Browsing gene banks for Fe2S2 ferredoxins and structural modeling of 88 plant-type sequences: an analysis of fold and function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 46, 110-27	4.2	48
97	Solution structure and characterization of the heme chaperone CcmE. <i>Biochemistry</i> , 2002 , 41, 13587-94	3.2	46
96	Solution structure of the oxidized Fe7S8 ferredoxin from the thermophilic bacterium <i>Bacillus schlegelii</i> by 1H NMR spectroscopy. <i>Biochemistry</i> , 1998 , 37, 9812-26	3.2	45
95	RPF: a quality assessment tool for protein NMR structures. <i>Nucleic Acids Research</i> , 2012 , 40, W542-6	20.1	43
94	Genome-based analysis of heme biosynthesis and uptake in prokaryotic systems. <i>Journal of Proteome Research</i> , 2008 , 7, 4946-54	5.6	43
93	Solution structure calculations through self-orientation in a magnetic field of a cerium(III) substituted calcium-binding protein. <i>Journal of Magnetic Resonance</i> , 2001 , 148, 23-30	3	43
92	Solution structure of oxidized microsomal rabbit cytochrome b5. Factors determining the heterogeneous binding of the heme. <i>FEBS Journal</i> , 2000 , 267, 755-66		42
91	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019 , 8,	7.6	41
90	Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 729513	5.6	39
89	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. <i>Analytical Chemistry</i> , 2018 , 90, 649-656	7.8	37
88	Structural and dynamical properties of a partially unfolded Fe4S4 protein: role of the cofactor in protein folding. <i>Biochemistry</i> , 1999 , 38, 4669-80	3.2	37
87	Solution structure and intermolecular interactions of the third metal-binding domain of ATP7A, the Menkes disease protein. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29141-7	5.4	36
86	Bioinorganic chemistry in the postgenomic era. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 3601-4	11.5	36

85	To what extent do structural changes in catalytic metal sites affect enzyme function?. <i>Journal of Inorganic Biochemistry</i> , 2018 , 179, 40-53	4.2	33
84	An atomic-level investigation of the disease-causing A629P mutant of the Menkes protein, ATP7A. <i>Journal of Molecular Biology</i> , 2005 , 352, 409-17	6.5	32
83	MetalPredator: a web server to predict iron-sulfur cluster binding proteomes. <i>Bioinformatics</i> , 2016 , 32, 2850-2	7.2	31
82	MaxOcc: a web portal for maximum occurrence analysis. <i>Journal of Biomolecular NMR</i> , 2012 , 53, 271-80	3	31
81	Solution structures of the actuator domain of ATP7A and ATP7B, the Menkes and Wilson disease proteins. <i>Biochemistry</i> , 2009 , 48, 7849-55	3.2	31
80	Evolution of mitochondrial-type cytochrome c domains and of the protein machinery for their assembly. <i>Journal of Inorganic Biochemistry</i> , 2007 , 101, 1798-811	4.2	31
79	Bioinformatic comparison of structures and homology-models of matrix metalloproteinases. <i>Journal of Proteome Research</i> , 2004 , 3, 21-31	5.6	31
78	Exploiting Bacterial Operons To Illuminate Human Iron-Sulfur Proteins. <i>Journal of Proteome Research</i> , 2016 , 15, 1308-22	5.6	30
77	The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. <i>PLoS ONE</i> , 2017 , 12, e0171279	3.7	30
76	Comparative analysis of the ADAM and ADAMTS families. <i>Journal of Proteome Research</i> , 2005 , 4, 881-8	5.6	26
75	Solution structure of reduced <i>Clostridium pasteurianum</i> rubredoxin. <i>Journal of Biological Inorganic Chemistry</i> , 1998 , 3, 401	3.7	26
74	The DisVis and PowerFit Web Servers: Explorative and Integrative Modeling of Biomolecular Complexes. <i>Journal of Molecular Biology</i> , 2017 , 429, 399-407	6.5	25
73	The annotation of full zinc proteomes. <i>Journal of Biological Inorganic Chemistry</i> , 2010 , 15, 1071-8	3.7	25
72	Solution structure of reduced microsomal rat cytochrome b5. <i>FEBS Journal</i> , 1997 , 249, 270-9		25
71	From Genes to Metalloproteins: A Bioinformatic Approach. <i>European Journal of Inorganic Chemistry</i> , 2007 , 2007, 2546-2555	2.3	25
70	A structural model for the adduct between cytochrome c and cytochrome c oxidase. <i>Journal of Biological Inorganic Chemistry</i> , 2005 , 10, 613-24	3.7	24
69	¹ H and (¹³ C) NMR Studies of an Oxidized HiPIP. <i>Inorganic Chemistry</i> , 1997 , 36, 4798-4803	5.1	22
68	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. <i>Journal of Biomolecular NMR</i> , 2015 , 62, 413-24	3	21

67	A simple protocol for the comparative analysis of the structure and occurrence of biochemical pathways across superkingdoms. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 730-8	6.1	21
66	Interaction of the two soluble metal-binding domains of yeast Ccc2 with copper(I)-Atx1. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 364, 645-9	3.4	21
65	NMR solution structure, backbone mobility, and homology modeling of c-type cytochromes from gram-positive bacteria. <i>ChemBioChem</i> , 2002 , 3, 299-310	3.8	21
64	Solution structure of a monoheme ferrocycytochrome c from <i>Shewanella putrefaciens</i> and structural analysis of sequence-similar proteins: functional implications. <i>Biochemistry</i> , 2002 , 41, 5112-9	3.2	21
63	The unfolding of oxidized c-type cytochromes: the instructive case of <i>Bacillus pasteurii</i> . <i>Journal of Molecular Biology</i> , 2002 , 321, 693-701	6.5	21
62	Can the axial ligand strength be monitored through spectroscopic measurements?. <i>Journal of Biological Inorganic Chemistry</i> , 1996 , 1, 364-367	3.7	21
61	¹ H NMR studies of the Fe7S8 ferredoxin from <i>Bacillus schlegelii</i> : a further attempt to understand Fe3S4 clusters. <i>Journal of Biological Inorganic Chemistry</i> , 1996 , 1, 523-528	3.7	21
60	MetalS(3), a database-mining tool for the identification of structurally similar metal sites. <i>Journal of Biological Inorganic Chemistry</i> , 2014 , 19, 937-45	3.7	20
59	Quality assessment of protein NMR structures. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 715-24	8.1	20
58	The binding mode of ATP revealed by the solution structure of the N-domain of human ATP7A. <i>Journal of Biological Chemistry</i> , 2010 , 285, 2537-44	5.4	20
57	The war of tools: how can NMR spectroscopists detect errors in their structures?. <i>Journal of Biomolecular NMR</i> , 2008 , 40, 251-61	3	19
56	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: reduced HiPIP I from <i>Ectothiorhodospira halophila</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 24, 158-64	4.2	19
55	Insights into telomeric G-quadruplex DNA recognition by HMGB1 protein. <i>Nucleic Acids Research</i> , 2019 , 47, 9950-9966	20.1	18
54	Upgrading and Validation of the AMBER Force Field for Histidine and Cysteine Zinc(II)-Binding Residues in Sites with Four Protein Ligands. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 3803-3816 ¹⁸	6.1	18
53	Zinc proteome interaction network as a model to identify nutrient-affected pathways in human pathologies. <i>Genes and Nutrition</i> , 2014 , 9, 436	4.3	18
52	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017 , 6,	3.6	18
51	The eNMR platform for structural biology. <i>Journal of Structural and Functional Genomics</i> , 2010 , 11, 1-8		17
50	Structure and dynamics of reduced <i>Bacillus pasteurii</i> cytochrome c: oxidation state dependent properties and implications for electron transfer processes. <i>Biochemistry</i> , 2003 , 42, 739-45	3.2	17

49	Investigation of the Iron(II) Release Mechanism of Human H-Ferritin as a Function of pH. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 2112-2118	6.1	16
48	From NOESY Cross Peaks to Structural Constraints in a Paramagnetic Metalloprotein. <i>Magnetic Resonance in Chemistry</i> , 1996 , 34, 948-950	2.1	16
47	SPINE bioinformatics and data-management aspects of high-throughput structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1184-95		15
46	Mechanistic and Structural Basis for Inhibition of Copper Trafficking by Platinum Anticancer Drugs. <i>Journal of the American Chemical Society</i> , 2019 , 141, 12109-12120	16.4	14
45	A further investigation of the cytochrome b5-cytochrome c complex. <i>Journal of Biological Inorganic Chemistry</i> , 2003 , 8, 777-86	3.7	14
44	SedNMR: a web tool for optimizing sedimentation of macromolecular solutes for SSNMR. <i>Journal of Biomolecular NMR</i> , 2013 , 57, 319-26	3	12
43	An Italian contribution to structural genomics: Understanding metalloproteins. <i>Coordination Chemistry Reviews</i> , 2006 , 250, 1419-1450	23.2	12
42	Protein stability and mutations in the axial methionine loop of a minimal cytochrome c. <i>Journal of Biological Inorganic Chemistry</i> , 2004 , 9, 600-8	3.7	11
41	Metals2: a tool for the structural alignment of minimal functional sites in metal-binding proteins and nucleic acids. <i>Journal of Chemical Information and Modeling</i> , 2013 , 53, 3064-75	6.1	10
40	Role of the N-terminal tail of metal-transporting P(1B)-type ATPases from genome-wide analysis and molecular dynamics simulations. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 76-83	6.1	10
39	A high-resolution NMR study of long-lived water molecules in both oxidation states of a minimal cytochrome c. <i>Biochemistry</i> , 2003 , 42, 3457-63	3.2	10
38	Hydrogen exchange in a bacterial cytochrome c: a fingerprint of the cytochrome c fold. <i>Biochemistry</i> , 2003 , 42, 10923-30	3.2	10
37	NMR Spectra of Iron-Sulfur Proteins. <i>Advances in Inorganic Chemistry</i> , 1999 , 47, 251-282	2.1	10
36	Solution structure of paramagnetic metalloproteins. <i>Pure and Applied Chemistry</i> , 1999 , 71, 1717-1725	2.1	10
35	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017 , 6, 1649	3.6	10
34	A protocol for the refinement of NMR structures using simultaneously pseudocontact shift restraints from multiple lanthanide ions. <i>Journal of Biomolecular NMR</i> , 2016 , 66, 175-185	3	9
33	Monitoring Interactions Inside Cells by Advanced Spectroscopies: Overview of Copper Transporters and Cisplatin. <i>Current Medicinal Chemistry</i> , 2018 , 25, 462-477	4.3	9
32	Protein structure prediction assisted with sparse NMR data in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1315-1332	4.2	9

31	Hidden relationships between metalloproteins unveiled by structural comparison of their metal sites. <i>Scientific Reports</i> , 2015 , 5, 9486	4.9	8
30	Upgraded AMBER Force Field for Zinc-Binding Residues and Ligands for Predicting Structural Properties and Binding Affinities in Zinc-Proteins. <i>ACS Omega</i> , 2020 , 5, 15301-15310	3.9	8
29	The Da Vinci European BioBank: A Metabolomics-Driven Infrastructure. <i>Journal of Personalized Medicine</i> , 2015 , 5, 107-19	3.6	8
28	Principles and patterns in the interaction between mono-heme cytochrome c and its partners in electron transfer processes. <i>Metallomics</i> , 2011 , 3, 354-62	4.5	8
27	Metabolomics in systems medicine: an overview of methods and applications. <i>Current Opinion in Systems Biology</i> , 2019 , 15, 91-99	3.2	7
26	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	7
25	Minimal Functional Sites in Metalloproteins and Their Usage in Structural Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	7
24	Application of Molecular Dynamics to the Investigation of Metalloproteins Involved in Metal Homeostasis. <i>European Journal of Inorganic Chemistry</i> , 2018 , 2018, 4661-4677	2.3	7
23	An atomistic view of the YiiP structural changes upon zinc(II) binding. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019 , 1863, 1560-1567	4	6
22	Improving Prediction of Zinc Binding Sites by Modeling the Linkage Between Residues Close in Sequence. <i>Lecture Notes in Computer Science</i> , 2006 , 309-320	0.9	5
21	Analysis of the structural quality of the CASD-NMR 2013 entries. <i>Journal of Biomolecular NMR</i> , 2015 , 62, 527-40	3	4
20	Cytochrome c folding / unfolding: a unifying picture. <i>Journal of Porphyrins and Phthalocyanines</i> , 2004 , 08, 238-245	1.8	4
19	The use of propionate Eproton contact shifts as structural constraints. <i>Inorganica Chimica Acta</i> , 2000 , 297, 199-205	2.7	4
18	Evaluation of paramagnetic relaxation rates in a J-coupled two-spin system. <i>Chemical Physics Letters</i> , 1996 , 250, 495-504	2.5	4
17	Molecular dynamics simulations of metalloproteins: A folding study of rubredoxin from <i>Pyrococcus furiosus</i> . <i>AIMS Biophysics</i> , 2018 , 5, 77-96	0.8	3
16	Insights into the Dynamics of the Human Zinc Transporter ZnT8 by MD Simulations. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 901-912	6.1	3
15	Oxidation of Human Copper Chaperone Atox1 and Disulfide Bond Cleavage by Cisplatin and Glutathione. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	2
14	EGI federated platforms supporting accelerated computing 2017 ,		2

13	Decreased amount of vimentin N-terminal truncated proteolytic products in parkin-mutant skin fibroblasts. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 521, 693-698	3.4	2
12	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I from <i>Ectothiorhodospira halophila</i> 1996 , 24, 158		2
11	What Can be Learned about the Structure and Dynamics of Biomolecules from NMR 2012 , 33-50		1
10	Three-dimensional solution structures of two DNA dodecamers through full relaxation matrix analysis 1999 , 37, 564-572		1
9	PhenoMeNal: Processing and analysis of Metabolomics data in the Cloud		1
8	Solution Structures Of Proteins Containing Paramagnetic Metal Ions 1997 , 1-19		1
7	Determination of Protein Structure and Dynamics 51-94		1
6	West-Life: A Virtual Research Environment for structural biology. <i>Journal of Structural Biology: X</i> , 2019 , 1, 100006	2.9	1
5	A protocol to automatically calculate homo-oligomeric protein structures through the integration of evolutionary constraints and NMR ambiguous contacts. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 114-124	6.8	0
4	Copper Homeostasis in Humans and Bacteria 2017 ,		
3	Grid Computing 2012 , 509-518		
2	A Genomic Frontier in Bioinorganic Chemistry. <i>Chemistry Letters</i> , 2004 , 33, 946-951	1.7	
1	The use of the Electron-Nucleus Hyperfine Interaction for Solution Structure Determination 2000 , 1-17		