

# Antonio Rosato

## List of Publications by Year in descending order

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141  
papers

8,218  
citations

50276

46  
h-index

53230

85  
g-index

223  
all docs

223  
docs citations

223  
times ranked

9042  
citing authors

#	ARTICLE	IF	CITATIONS
1	Counting the Zinc-Proteins Encoded in the Human Genome. <i>Journal of Proteome Research</i> , 2006, 5, 196-201.	3.7	887
2	Zinc through the Three Domains of Life. <i>Journal of Proteome Research</i> , 2006, 5, 3173-3178.	3.7	544
3	Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 729513.	3.5	308
4	Solution Structure of Oxidized Horse Heart Cytochrome c. <i>Biochemistry</i> , 1997, 36, 9867-9877.	2.5	290
5	Metalloproteomes: A Bioinformatic Approach. <i>Accounts of Chemical Research</i> , 2009, 42, 1471-1479.	15.6	281
6	Cytochrome c Occurrence and Functions. <i>Chemical Reviews</i> , 2006, 106, 90-115.	47.7	255
7	The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. <i>Nature Chemical Biology</i> , 2006, 2, 367-368.	8.0	204
8	Occurrence of Copper Proteins through the Three Domains of Life: A Bioinformatic Approach. <i>Journal of Proteome Research</i> , 2008, 7, 209-216.	3.7	184
9	Magnetic Susceptibility Tensor Anisotropies for a Lanthanide Ion Series in a Fixed Protein Matrix. <i>Journal of the American Chemical Society</i> , 2001, 123, 4181-4188.	13.7	183
10	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	3.9	170
11	MetalPDB in 2018: a database of metal sites in biological macromolecular structures. <i>Nucleic Acids Research</i> , 2018, 46, D459-D464.	14.5	165
12	MetalPDB: a database of metal sites in biological macromolecular structures. <i>Nucleic Acids Research</i> , 2012, 41, D312-D319.	14.5	157
13	From correlation to causation: analysis of metabolomics data using systems biology approaches. <i>Metabolomics</i> , 2018, 14, 37.	3.0	151
14	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. <i>Metabolomics</i> , 2015, 11, 1587-1597.	3.0	140
15	Solution Structure of the Apo and Copper(I)-Loaded Human Metallochaperone HAH1. <i>Biochemistry</i> , 2004, 43, 13046-13053.	2.5	123
16	A hint to search for metalloproteins in gene banks. <i>Bioinformatics</i> , 2004, 20, 1373-1380.	4.1	120
17	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.	13.7	110
18	The human iron-proteome. <i>Metallomics</i> , 2018, 10, 1223-1231.	2.4	106

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19	Menkes disease. Cellular and Molecular Life Sciences, 2008, 65, 89-91.	5.4	94
20	Mitochondrial cytochromes c: a comparative analysis. Journal of Biological Inorganic Chemistry, 1999, 4, 824-837.	2.6	91
21	Predicting zinc binding at the proteome level. BMC Bioinformatics, 2007, 8, 39.	2.6	89
22	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, 9354-9360.	3.4	88
23	Paramagnetically Induced Residual Dipolar Couplings for Solution Structure Determination of Lanthanide Binding Proteins. Journal of the American Chemical Society, 2002, 124, 5581-5587.	13.7	86
24	Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces. Biochemical Journal, 2009, 422, 37-42.	3.7	85
25	The Solution Structure of Oxidized Escherichia coli Cytochrome b562,. Biochemistry, 1999, 38, 8657-8670.	2.5	82
26	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
27	Molecular recognition in copper trafficking. Natural Product Reports, 2010, 27, 695.	10.3	78
28	A systematic investigation of multiheme c-type cytochromes in prokaryotes. Journal of Biological Inorganic Chemistry, 2010, 15, 559-571.	2.6	76
29	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
30	Paramagnetic relaxation as a tool for solution structure determination: Clostridium pasteurianum ferredoxin as an example. , 1997, 29, 348-358.		71
31	Non-heme iron through the three domains of life. Proteins: Structure, Function and Bioinformatics, 2007, 67, 317-324.	2.6	70
32	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, 440-452.	0.2	69
33	The solution structure of paramagnetic metalloproteins. Progress in Biophysics and Molecular Biology, 1996, 66, 43-80.	2.9	66
34	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, 3396-3403.	2.5	63
35	A NMR Study of the Interaction of a Three-domain Construct of ATP7A with Copper(I) and Copper(I)-HAH1. Journal of Biological Chemistry, 2005, 280, 38259-38263.	3.4	62
36	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, 9108-9118.	2.5	61

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37	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, .	6.4	60
38	Structural Genomics of Proteins Involved in Copper Homeostasis. <i>Accounts of Chemical Research</i> , 2003, 36, 215-221.	15.6	58
39	MetalPredator: a web server to predict iron-sulfur cluster binding proteomes. <i>Bioinformatics</i> , 2016, 32, 2850-2852.	4.1	58
40	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, 865-871.	4.7	57
41	The Functions of Sco Proteins from Genome-Based Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 1568-1579.	3.7	56
42	Browsing gene banks for Fe <sub>2</sub> S <sub>2</sub> ferredoxins and structural modeling of 88 plant-type sequences: An analysis of fold and function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 110-127.	2.6	55
43	A Grid-enabled web portal for NMR structure refinement with AMBER. <i>Bioinformatics</i> , 2011, 27, 2384-2390.	4.1	55
44	RPF: a quality assessment tool for protein NMR structures. <i>Nucleic Acids Research</i> , 2012, 40, W542-W546.	14.5	55
45	To what extent do structural changes in catalytic metal sites affect enzyme function?. <i>Journal of Inorganic Biochemistry</i> , 2018, 179, 40-53.	3.5	55
46	The Different Intermolecular Interactions of the Soluble Copper-binding Domains of the Menkes Protein, ATP7A*. <i>Journal of Biological Chemistry</i> , 2007, 282, 23140-23146.	3.4	54
47	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. <i>Analytical Chemistry</i> , 2018, 90, 649-656.	6.5	50
48	Genome-Based Analysis of Heme Biosynthesis and Uptake in Prokaryotic Systems. <i>Journal of Proteome Research</i> , 2008, 7, 4946-4954.	3.7	49
49	The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. <i>PLoS ONE</i> , 2017, 12, e0171279.	2.5	49
50	Solution Structure of the Oxidized Fe <sub>7</sub> S <sub>8</sub> Ferredoxin from the Thermophilic Bacterium <i>Bacillus schlegelii</i> by 1H NMR Spectroscopy. <i>Biochemistry</i> , 1998, 37, 9812-9826.	2.5	48
51	Solution Structure and Characterization of the Heme Chaperone CcmE. <i>Biochemistry</i> , 2002, 41, 13587-13594.	2.5	47
52	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	14.5	46
53	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.	2.1	44
54	Solution structure of oxidized microsomal rabbit cytochrome b5. <i>FEBS Journal</i> , 2000, 267, 755-766.	0.2	43

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55	The DisVis and PowerFit Web Servers: Explorative and Integrative Modeling of Biomolecular Complexes. <i>Journal of Molecular Biology</i> , 2017, 429, 399-407.	4.2	43
56	Exploiting Bacterial Operons To Illuminate Human Iron-Sulfur Proteins. <i>Journal of Proteome Research</i> , 2016, 15, 1308-1322.	3.7	42
57	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.	5.4	42
58	Bioinorganic chemistry in the postgenomic era. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3601-3604.	7.1	39
59	Evolution of mitochondrial-type cytochrome c domains and of the protein machinery for their assembly. <i>Journal of Inorganic Biochemistry</i> , 2007, 101, 1798-1811.	3.5	39
60	Structural and Dynamical Properties of a Partially Unfolded Fe <sub>4</sub> S <sub>4</sub> Protein: A Role of the Cofactor in Protein Folding. <i>Biochemistry</i> , 1999, 38, 4669-4680.	2.5	38
61	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, 29141-29147.	3.4	38
62	Insights into telomeric G-quadruplex DNA recognition by HMGB1 protein. <i>Nucleic Acids Research</i> , 2019, 47, 9950-9966.	14.5	38
63	An Atomic-level Investigation of the Disease-causing A629P Mutant of the Menkes Protein, ATP7A. <i>Journal of Molecular Biology</i> , 2005, 352, 409-417.	4.2	37
64	Solution Structures of the Actuator Domain of ATP7A and ATP7B, the Menkes and Wilson Disease Proteins. <i>Biochemistry</i> , 2009, 48, 7849-7855.	2.5	36
65	MaxOcc: a web portal for maximum occurrence analysis. <i>Journal of Biomolecular NMR</i> , 2012, 53, 271-280.	2.8	36
66	Bioinformatic Comparison of Structures and Homology-Models of Matrix Metalloproteinases. <i>Journal of Proteome Research</i> , 2004, 3, 21-31.	3.7	35
67	Comparative Analysis of the ADAM and ADAMTS Families. <i>Journal of Proteome Research</i> , 2005, 4, 881-888.	3.7	32
68	Quality assessment of protein NMR structures. <i>Current Opinion in Structural Biology</i> , 2013, 23, 715-724.	5.7	31
69	Solution structure of reduced <i>Clostridium pasteurianum</i> rubredoxin. <i>Journal of Biological Inorganic Chemistry</i> , 1998, 3, 401.	2.6	30
70	From Genes to Metalloproteins: A Bioinformatic Approach. <i>European Journal of Inorganic Chemistry</i> , 2007, 2007, 2546-2555.	2.0	29
71	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, 730-738.	5.4	28
72	Zinc proteome interaction network as a model to identify nutrient-affected pathways in human pathologies. <i>Genes and Nutrition</i> , 2014, 9, 436.	2.5	28

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73	MetalS3, a database-mining tool for the identification of structurally similar metal sites. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 937-945.	2.6	28
74	<sup>1</sup> H and <sup>13</sup> C NMR Studies of an Oxidized HiPIP. <i>Inorganic Chemistry</i> , 1997, 36, 4798-4803.	4.0	27
75	The annotation of full zinc proteomes. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 1071-1078.	2.6	27
76	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, 413-424.	2.8	27
77	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.	3.5	27
78	Solution Structure of Reduced Microsomal Rat Cytochrome b5. <i>FEBS Journal</i> , 1997, 249, 270-279.	0.2	25
79	<sup>1</sup> 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.	2.6	24
80	A structural model for the adduct between cytochrome c and cytochrome c oxidase. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 613-624.	2.6	24
81	Interaction of the two soluble metal-binding domains of yeast Ccc2 with copper(I) at Atx1. <i>Biochemical and Biophysical Research Communications</i> , 2007, 364, 645-649.	2.1	24
82	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.	13.7	24
83	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.	4.2	23
84	NMR Solution Structure, Backbone Mobility, and Homology Modeling of c-Type Cytochromes from Gram-Positive Bacteria. <i>ChemBioChem</i> , 2002, 3, 299-310.	2.6	23
85	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, 2537-2544.	3.4	23
86	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I from <i>Ectothiorhodospira halophila</i> . , 1996, 24, 158-164.		22
87	Solution Structure of a Monoheme Ferrocycytochrome from <i>Shewanella putrefaciens</i> and Structural Analysis of Sequence-Similar Proteins: Functional Implications. <i>Biochemistry</i> , 2002, 41, 5112-5119.	2.5	22
88	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.	5.4	22
89	Can the axial ligand strength be monitored through spectroscopic measurements?. <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 364-367.	2.6	21
90	The war of tools: how can NMR spectroscopists detect errors in their structures?. <i>Journal of Biomolecular NMR</i> , 2008, 40, 251-261.	2.8	21

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91	Protein structure prediction assisted with sparse NMR data in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1315-1332.	2.6	21
92	SPINE bioinformatics and data-management aspects of high-throughput structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1184-1195.	2.5	19
93	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	1.6	19
94	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, 739-745.	2.5	18
95	The eNMR platform for structural biology. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 1-8.	1.2	18
96	From NOESY Cross Peaks to Structural Constraints in a Paramagnetic Metalloprotein. <i>Magnetic Resonance in Chemistry</i> , 1996, 34, 948-950.	1.9	16
97	MetalS <sup>2</sup> : 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, 3064-3075.	5.4	16
98	Monitoring Interactions Inside Cells by Advanced Spectroscopies: Overview of Copper Transporters and Cisplatin. <i>Current Medicinal Chemistry</i> , 2018, 25, 462-477.	2.4	15
99	NMR Spectra of Iron-Sulfur Proteins. <i>Advances in Inorganic Chemistry</i> , 1999, 47, 251-282.	1.0	14
100	A further investigation of the cytochrome b 5-cytochrome c complex. <i>Journal of Biological Inorganic Chemistry</i> , 2003, 8, 777-786.	2.6	14
101	An Italian contribution to structural genomics: Understanding metalloproteins. <i>Coordination Chemistry Reviews</i> , 2006, 250, 1419-1450.	18.8	14
102	SedNMR: a web tool for optimizing sedimentation of macromolecular solutes for SSNMR. <i>Journal of Biomolecular NMR</i> , 2013, 57, 319-326.	2.8	13
103	Hidden relationships between metalloproteins unveiled by structural comparison of their metal sites. <i>Scientific Reports</i> , 2015, 5, 9486.	3.3	13
104	An atomistic view of the YiiP structural changes upon zinc(II) binding. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1560-1567.	2.4	13
105	Protein stability and mutations in the axial methionine loop of a minimal cytochrome c. <i>Journal of Biological Inorganic Chemistry</i> , 2004, 9, 600-608.	2.6	12
106	Minimal Functional Sites in Metalloproteins and Their Usage in Structural Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2016, 17, 671.	4.1	12
107	Application of Molecular Dynamics to the Investigation of Metalloproteins Involved in Metal Homeostasis. <i>European Journal of Inorganic Chemistry</i> , 2018, 2018, 4661-4677.	2.0	12
108	Solution structure of paramagnetic metalloproteins. <i>Pure and Applied Chemistry</i> , 1999, 71, 1717-1725.	1.9	11

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109	A High-Resolution NMR Study of Long-Lived Water Molecules in Both Oxidation States of a Minimal Cytochrome c. <i>Biochemistry</i> , 2003, 42, 3457-3463.	2.5	11
110	Role of the N-Terminal Tail of Metal-Transporting P1B-type ATPases from Genome-Wide Analysis and Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 76-83.	5.4	11
111	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	1.6	11
112	Hydrogen Exchange in a Bacterial Cytochrome c: A Fingerprint of the Cytochrome c Fold. <i>Biochemistry</i> , 2003, 42, 10923-10930.	2.5	10
113	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.	2.8	10
114	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.	5.4	10
115	The Da Vinci European BioBank: A Metabolomics-Driven Infrastructure. <i>Journal of Personalized Medicine</i> , 2015, 5, 107-119.	2.5	9
116	Metabolomics in systems medicine: an overview of methods and applications. <i>Current Opinion in Systems Biology</i> , 2019, 15, 91-99.	2.6	9
117	Principles and patterns in the interaction between mono-heme cytochrome c and its partners in electron transfer processes. <i>Metallomics</i> , 2011, 3, 354.	2.4	8
118	Learning to Identify Physiological and Adventitious Metal-Binding Sites in the Three-Dimensional Structures of Proteins by Following the Hints of a Deep Neural Network. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 2951-2960.	5.4	6
119	The zinc proteome of SARS-CoV-2. <i>Metallomics</i> , 2022, 14, .	2.4	6
120	Structural Bioinformatics and Deep Learning of Metalloproteins: Recent Advances and Applications. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7684.	4.1	6
121	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.	2.1	5
122	Molecular dynamics simulations of metalloproteins: A folding study of rubredoxin from <i>Pyrococcus furiosus</i> . <i>AIMS Biophysics</i> , 2018, 5, 77-96.	0.6	5
123	Evaluation of paramagnetic relaxation rates in a J-coupled two-spin system. <i>Chemical Physics Letters</i> , 1996, 250, 495-504.	2.6	4
124	The use of propionate $\delta$ -proton contact shifts as structural constraints. <i>Inorganica Chimica Acta</i> , 2000, 297, 199-205.	2.4	4
125	Cytochrome c folding / unfolding: a unifying picture. <i>Journal of Porphyrins and Phthalocyanines</i> , 2004, 08, 238-245.	0.8	4
126	Automated protein structure determination by NMR. <i>Journal of Biomolecular NMR</i> , 2015, 62, 411-412.	2.8	4



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127	Analysis of the structural quality of the CASD-NMR 2013 entries. <i>Journal of Biomolecular NMR</i> , 2015, 62, 527-540.	2.8	4
128	Automated Determination of Nuclear Magnetic Resonance Chemical Shift Perturbations in Ligand Screening Experiments: The PICASSO Web Server. <i>Journal of Chemical Information and Modeling</i> , 2021, , .	5.4	4
129	Oxidation of Human Copper Chaperone Atox1 and Disulfide Bond Cleavage by Cisplatin and Glutathione. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4390.	4.1	3
130	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.	4.1	3
131	EGI federated platforms supporting accelerated computing. , 2017, , .		3
132	Solution Structures Of Proteins Containing Paramagnetic Metal Ions. , 1997, , 1-19.		3
133	West-Life: A Virtual Research Environment for structural biology. <i>Journal of Structural Biology: X</i> , 2019, 1, 100006.	1.3	2
134	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, 158-164.	2.6	2
135	Three-dimensional solution structures of two DNA dodecamers through full relaxation matrix analysis. , 1999, 37, 564-572.		1
136	What Can be Learned about the Structure and Dynamics of Biomolecules from NMR. , 2012, , 33-50.		1
137	Systematic classification of metalloproteins based on three-dimensional structural similarity of their metal sites. <i>Protocol Exchange</i> , 0, , .	0.3	1
138	Structural Genomics of Proteins Involved in Copper Homeostasis. <i>ChemInform</i> , 2003, 34, no.	0.0	0
139	A Genomic Frontier in Bioinorganic Chemistry. <i>Chemistry Letters</i> , 2004, 33, 946-951.	1.3	0
140	Copper Homeostasis in Humans and Bacteria. , 2017, , .		0
141	The use of the Electron-Nucleus Hyperfine Interaction for Solution Structure Determination. , 2000, , 1-17.		0