Antonio Rosato

List of Publications by Year
in descending order

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Version: 2024-02-01

		50276	53230
141	8,218	46	85
papers	citations	h-index	g-index

223	223	223	9042
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
2	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. Journal of Chemical Information and Modeling, 2022, 62, 2951-2960.	5.4	6
3	The zinc proteome of SARS-CoV-2. Metallomics, 2022, 14, .	2.4	6
4	Structural Bioinformatics and Deep Learning of Metalloproteins: Recent Advances and Applications. International Journal of Molecular Sciences, 2022, 23, 7684.	4.1	6
5	Insights into the Dynamics of the Human Zinc Transporter ZnT8 by MD Simulations. Journal of Chemical Information and Modeling, 2021, 61, 901-912.	5.4	10
6	Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. Frontiers in Molecular Biosciences, 2021, 8, 729513.	3.5	308
7	Automated Determination of Nuclear Magnetic Resonance Chemical Shift Perturbations in Ligand Screening Experiments: The PICASSO Web Server. Journal of Chemical Information and Modeling, 2021, , .	5.4	4
8	Decreased amount of vimentin N-terminal truncated proteolytic products in parkin-mutant skin fibroblasts. Biochemical and Biophysical Research Communications, 2020, 521, 693-698.	2.1	5
9	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.	4.1	3
10	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.	3.5	27
11	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.	5.4	42
12	Mechanistic and Structural Basis for Inhibition of Copper Trafficking by Platinum Anticancer Drugs. Journal of the American Chemical Society, 2019, 141, 12109-12120.	13.7	24
13	Protein structure prediction assisted with sparse NMR data in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1315-1332.	2.6	21
14	Oxidation of Human Copper Chaperone Atox1 and Disulfide Bond Cleavage by Cisplatin and Glutathione. International Journal of Molecular Sciences, 2019, 20, 4390.	4.1	3
15	Insights into telomeric G-quadruplex DNA recognition by HMGB1 protein. Nucleic Acids Research, 2019, 47, 9950-9966.	14.5	38
16	An atomistic view of the YiiP structural changes upon zinc(II) binding. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1560-1567.	2.4	13
17	Metabolomics in systems medicine: an overview of methods and applications. Current Opinion in Systems Biology, 2019, 15, 91-99.	2.6	9
18	West-Life: A Virtual Research Environment for structural biology. Journal of Structural Biology: X, 2019, 1, 100006.	1.3	2

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19	PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, .	6.4	60
20	From correlation to causation: analysis of metabolomics data using systems biology approaches. Metabolomics, 2018, 14, 37.	3.0	151
21	MetalPDB in 2018: a database of metal sites in biological macromolecular structures. Nucleic Acids Research, 2018, 46, D459-D464.	14.5	165
22	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. Analytical Chemistry, 2018, 90, 649-656.	6.5	50
23	To what extent do structural changes in catalytic metal sites affect enzyme function?. Journal of Inorganic Biochemistry, 2018, 179, 40-53.	3.5	55
24	Application of Molecular Dynamics to the Investigation of Metalloproteins Involved in Metal Homeostasis. European Journal of Inorganic Chemistry, 2018, 2018, 4661-4677.	2.0	12
25	Monitoring Interactions Inside Cells by Advanced Spectroscopies: Overview of Copper Transporters and Cisplatin. Current Medicinal Chemistry, 2018, 25, 462-477.	2.4	15
26	The human iron-proteomeâ€. Metallomics, 2018, 10, 1223-1231.	2.4	106
27	Molecular dynamics simulations of metalloproteins: A folding study of rubredoxin from Pyrococcus furiosus. AIMS Biophysics, 2018, 5, 77-96.	0.6	5
28	The DisVis and PowerFit Web Servers: Explorative and Integrative Modeling of Biomolecular Complexes. Journal of Molecular Biology, 2017, 429, 399-407.	4.2	43
29	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.	5.4	22
30	Copper Homeostasis in Humans and Bacteria. , 2017, , .		0
31	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	1.6	19
32	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	1.6	11
33	The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. PLoS ONE, 2017, 12, e0171279.	2.5	49
34	EGI federated platforms supporting accelerated computing. , 2017, , .		3
35	Minimal Functional Sites in Metalloproteins and Their Usage in Structural Bioinformatics. International Journal of Molecular Sciences, 2016, 17, 671.	4.1	12
36	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.	2.8	10

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37	MetalPredator: a web server to predict ironâ€“sulfur cluster binding proteomes. Bioinformatics, 2016, 32, 2850-2852.	4.1	58
38	Exploiting Bacterial Operons To Illuminate Human Ironâ€“Sulfur Proteins. Journal of Proteome Research, 2016, 15, 1308-1322.	3.7	42
39	The Da Vinci European BioBank: A Metabolomics-Driven Infrastructure. Journal of Personalized Medicine, 2015, 5, 107-119.	2.5	9
40	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. Metabolomics, 2015, 11, 1587-1597.	3.0	140
41	Automated protein structure determination by NMR. Journal of Biomolecular NMR, 2015, 62, 411-412.	2.8	4
42	Hidden relationships between metalloproteins unveiled by structural comparison of their metal sites. Scientific Reports, 2015, 5, 9486.	3.3	13
43	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. Journal of Biomolecular NMR, 2015, 62, 413-424.	2.8	27
44	Analysis of the structural quality of the CASD-NMR 2013 entries. Journal of Biomolecular NMR, 2015, 62, 527-540.	2.8	4
45	Zinc proteome interaction network as a model to identify nutrient-affected pathways in human pathologies. Genes and Nutrition, 2014, 9, 436.	2.5	28
46	MetalS3, a database-mining tool for the identification of structurally similar metal sites. Journal of Biological Inorganic Chemistry, 2014, 19, 937-945.	2.6	28
47	SedNMR: a web tool for optimizing sedimentation of macromolecular solutes for SSNMR. Journal of Biomolecular NMR, 2013, 57, 319-326.	2.8	13
48	Quality assessment of protein NMR structures. Current Opinion in Structural Biology, 2013, 23, 715-724.	5.7	31
49	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, 3064-3075.	5.4	16
50	RPF: a quality assessment tool for protein NMR structures. Nucleic Acids Research, 2012, 40, W542-W546.	14.5	55
51	MetalPDB: a database of metal sites in biological macromolecular structures. Nucleic Acids Research, 2012, 41, D312-D319.	14.5	157
52	What Can be Learned about the Structure and Dynamics of Biomolecules from NMR. , 2012, , 33-50.		1
53	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	3.9	170
54	MaxOcc: a web portal for maximum occurrence analysis. Journal of Biomolecular NMR, 2012, 53, 271-280.	2.8	36

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55	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
56	Principles and patterns in the interaction between mono-heme cytochrome c and its partners in electron transfer processes. Metallomics, 2011, 3, 354.	2.4	8
57	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, 730-738.	5.4	28
58	A Grid-enabled web portal for NMR structure refinement with AMBER. Bioinformatics, 2011, 27, 2384-2390.	4.1	55
59	A systematic investigation of multiheme c-type cytochromes in prokaryotes. Journal of Biological Inorganic Chemistry, 2010, 15, 559-571.	2.6	76
60	The annotation of full zinc proteomes. Journal of Biological Inorganic Chemistry, 2010, 15, 1071-1078.	2.6	27
61	The eNMR platform for structural biology. Journal of Structural and Functional Genomics, 2010, 11, 1-8.	1.2	18
62	The Binding Mode of ATP Revealed by the Solution Structure of the N-domain of Human ATP7A. Journal of Biological Chemistry, 2010, 285, 2537-2544.	3.4	23
63	Molecular recognition in copper trafficking. Natural Product Reports, 2010, 27, 695.	10.3	78
64	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
65	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
66	Solution Structures of the Actuator Domain of ATP7A and ATP7B, the Menkes and Wilson Disease Proteins. Biochemistry, 2009, 48, 7849-7855.	2.5	36
67	Role of the N-Terminal Tail of Metal-Transporting P1B-type ATPases from Genome-Wide Analysis and Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2009, 49, 76-83.	5.4	11
68	Metalloproteomes: A Bioinformatic Approach. Accounts of Chemical Research, 2009, 42, 1471-1479.	15.6	281
69	Copper(I)-mediated proteinâ€“protein interactions result from suboptimal interaction surfaces. Biochemical Journal, 2009, 422, 37-42.	3.7	85
70	The war of tools: how can NMR spectroscopists detect errors in their structures?. Journal of Biomolecular NMR, 2008, 40, 251-261.	2.8	21
71	Menkes disease. Cellular and Molecular Life Sciences, 2008, 65, 89-91.	5.4	94
72	Occurrence of Copper Proteins through the Three Domains of Life: A Bioinformatic Approach. Journal of Proteome Research, 2008, 7, 209-216.	3.7	184

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73	Genome-Based Analysis of Heme Biosynthesis and Uptake in Prokaryotic Systems. Journal of Proteome Research, 2008, 7, 4946-4954.	3.7	49
74	The Different Intermolecular Interactions of the Soluble Copper-binding Domains of the Menkes Protein, ATP7A*. Journal of Biological Chemistry, 2007, 282, 23140-23146.	3.4	54
75	Interaction of the two soluble metal-binding domains of yeast Ccc2 with copper(I)â€“Atx1. Biochemical and Biophysical Research Communications, 2007, 364, 645-649.	2.1	24
76	The Functions of Sco Proteins from Genome-Based Analysis. Journal of Proteome Research, 2007, 6, 1568-1579.	3.7	56
77	From Genes to Metalloproteins: A Bioinformatic Approach. European Journal of Inorganic Chemistry, 2007, 2007, 2546-2555.	2.0	29
78	Evolution of mitochondrial-type cytochrome c domains and of the protein machinery for their assembly. Journal of Inorganic Biochemistry, 2007, 101, 1798-1811.	3.5	39
79	Non-heme iron through the three domains of life. Proteins: Structure, Function and Bioinformatics, 2007, 67, 317-324.	2.6	70
80	Predicting zinc binding at the proteome level. BMC Bioinformatics, 2007, 8, 39.	2.6	89
81	Cytochrome c:â€‰ Occurrence and Functions. Chemical Reviews, 2006, 106, 90-115.	47.7	255
82	Counting the Zinc-Proteins Encoded in the Human Genome. Journal of Proteome Research, 2006, 5, 196-201.	3.7	887
83	Zinc through the Three Domains of Life. Journal of Proteome Research, 2006, 5, 3173-3178.	3.7	544
84	SPINE bioinformatics and data-management aspects of high-throughput structural biology. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1184-1195.	2.5	19
85	The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. Nature Chemical Biology, 2006, 2, 367-368.	8.0	204
86	An Italian contribution to structural genomics: Understanding metalloproteins. Coordination Chemistry Reviews, 2006, 250, 1419-1450.	18.8	14
87	Solution Structure and Intermolecular Interactions of the Third Metal-binding Domain of ATP7A, the Menkes Disease Protein. Journal of Biological Chemistry, 2006, 281, 29141-29147.	3.4	38
88	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, 865-871.	4.7	57
89	A structural model for the adduct between cytochrome c and cytochrome c oxidase. Journal of Biological Inorganic Chemistry, 2005, 10, 613-624.	2.6	24
90	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

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91	An Atomic-level Investigation of the Disease-causing A629P Mutant of the Menkes Protein, ATP7A. Journal of Molecular Biology, 2005, 352, 409-417.	4.2	37
92	Comparative Analysis of the ADAM and ADAMTS Families. Journal of Proteome Research, 2005, 4, 881-888.	3.7	32
93	A hint to search for metalloproteins in gene banks. Bioinformatics, 2004, 20, 1373-1380.	4.1	120
94	Cytochrome c folding / unfolding: a unifying picture. Journal of Porphyrins and Phthalocyanines, 2004, 08, 238-245.	0.8	4
95	Protein stability and mutations in the axial methionine loop of a minimal cytochrome c. Journal of Biological Inorganic Chemistry, 2004, 9, 600-608.	2.6	12
96	Solution Structure and Backbone Dynamics of the Cu(I) and Apo Forms of the Second Metal-Binding Domain of the Menkes Protein ATP7Aâ€. Biochemistry, 2004, 43, 3396-3403.	2.5	63
97	Solution Structure of the Apo and Copper(I)-Loaded Human Metallochaperone HAH1â€. Biochemistry, 2004, 43, 13046-13053.	2.5	123
98	Bioinformatic Comparison of Structures and Homology-Models of Matrix Metalloproteinases. Journal of Proteome Research, 2004, 3, 21-31.	3.7	35
99	A Genomic Frontier in Bioinorganic Chemistry. Chemistry Letters, 2004, 33, 946-951.	1.3	0
100	A further investigation of the cytochrome b 5â€“cytochrome c complex. Journal of Biological Inorganic Chemistry, 2003, 8, 777-786.	2.6	14
101	Structural Genomics of Proteins Involved in Copper Homeostasis. ChemInform, 2003, 34, no.	0.0	0
102	Structural Genomics of Proteins Involved in Copper Homeostasis. Accounts of Chemical Research, 2003, 36, 215-221.	15.6	58
103	A High-Resolution NMR Study of Long-Lived Water Molecules in Both Oxidation States of a Minimal Cytochrome c. Biochemistry, 2003, 42, 3457-3463.	2.5	11
104	Structure and Dynamics of ReducedBacillus pasteuriiCytochromec:Â Oxidation State Dependent Properties and Implications for Electron Transfer Processesâ€. Biochemistry, 2003, 42, 739-745.	2.5	18
105	Hydrogen Exchange in a Bacterial Cytochrome c:â€‰ A Fingerprint of the Cytochrome c Fold. Biochemistry, 2003, 42, 10923-10930.	2.5	10
106	Bioinorganic chemistry in the postgenomic era. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3601-3604.	7.1	39
107	Solution Structure of a Monoheme FerrocytochromecfromShewanella putrefaciensand Structural Analysis of Sequence-Similar Proteins:Â Functional Implicationsâ€. Biochemistry, 2002, 41, 5112-5119.	2.5	22
108	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

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109	Solution Structure and Characterization of the Heme Chaperone CcmE. Biochemistry, 2002, 41, 13587-13594.	2.5	47
110	The Unfolding of Oxidized c-Type Cytochromes: The Instructive Case of Bacillus pasteurii. Journal of Molecular Biology, 2002, 321, 693-701.	4.2	23
111	NMR Solution Structure, Backbone Mobility, and Homology Modeling ofc-Type Cytochromes from Gram-Positive Bacteria. ChemBioChem, 2002, 3, 299-310.	2.6	23
112	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, 110-127.	2.6	55
113	Magnetic Susceptibility Tensor Anisotropies for a Lanthanide Ion Series in a Fixed Protein Matrix. Journal of the American Chemical Society, 2001, 123, 4181-4188.	13.7	183
114	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.	2.1	44
115	The use of propionate Î±-proton contact shifts as structural constraints. Inorganica Chimica Acta, 2000, 297, 199-205.	2.4	4
116	Solution structure of oxidized microsomal rabbit cytochrome b5. FEBS Journal, 2000, 267, 755-766.	0.2	43
117	Backbone Dynamics of Human Cu,Zn Superoxide Dismutase and of Its Monomeric F50E/G51E/E133Q Mutant:â€‰ The Influence of Dimerization on Mobility and Function. Biochemistry, 2000, 39, 9108-9118.	2.5	61
118	The use of the Electron-Nucleus Hyperfine Interaction for Solution Structure Determination. , 2000, , 1-17.		0
119	Mitochondrial cytochromes c: a comparative analysis. Journal of Biological Inorganic Chemistry, 1999, 4, 824-837.	2.6	91
120	Three-dimensional solution structures of two DNA dodecamers through full relaxation matrix analysis. , 1999, 37, 564-572.		1
121	The Solution Structure of Oxidized Escherichia coli Cytochrome b562,. Biochemistry, 1999, 38, 8657-8670.	2.5	82
122	Structural and Dynamical Properties of a Partially Unfolded Fe4S4Protein:Â Role of the Cofactor in Protein Foldingâ€. Biochemistry, 1999, 38, 4669-4680.	2.5	38
123	NMR Spectra of Iron-Sulfur Proteins. Advances in Inorganic Chemistry, 1999, 47, 251-282.	1.0	14
124	Solution structure of paramagnetic metalloproteins. Pure and Applied Chemistry, 1999, 71, 1717-1725.	1.9	11
125	Solution Structure of the Oxidized Fe7S8Ferredoxin from the Thermophilic BacteriumBacillusschlegeliiby1H NMR Spectroscopyâ€,â€¡. Biochemistry, 1998, 37, 9812-9826.	2.5	48
126	Partial Orientation of Oxidized and Reduced Cytochromeb5at High Magnetic Fields:Â Magnetic Susceptibility Anisotropy Contributions and Consequences for Protein Solution Structure Determination. Journal of the American Chemical Society, 1998, 120, 12903-12909.	13.7	110

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127	Solution structure of reduced Clostridium pasteurianum rubredoxin. Journal of Biological Inorganic Chemistry, 1998, 3, 401.	2.6	30
128	1H and 13C NMR Studies of an Oxidized HiPIP. Inorganic Chemistry, 1997, 36, 4798-4803.	4.0	27
129	Solution Structure of Oxidized Horse Heart Cytochrome câ€‚âŠ¥. Biochemistry, 1997, 36, 9867-9877.	2.5	290
130	Solution Structure of Reduced Microsomal Rat Cytochrome b5. FEBS Journal, 1997, 249, 270-279.	0.2	25
131	Paramagnetic relaxation as a tool for solution structure determination:Clostridium pasteurianum ferredoxin as an example. , 1997, 29, 348-358.		71
132	Solution Structures Of Proteins Containing Paramagnetic Metal Ions. , 1997, , 1-19.		3
133	Can the axial ligand strength be monitored through spectroscopic measurements?. Journal of Biological Inorganic Chemistry, 1996, 1, 364-367.	2.6	21
134	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.	2.6	24
135	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
136	The solution structure of paramagnetic metalloproteins. Progress in Biophysics and Molecular Biology, 1996, 66, 43-80.	2.9	66
137	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I fromEctothiorhodospira halophila. , 1996, 24, 158-164.		22
138	From NOESY Cross Peaks to Structural Constraints in a Paramagnetic Metalloprotein. Magnetic Resonance in Chemistry, 1996, 34, 948-950.	1.9	16
139	Evaluation of paramagnetic relaxation rates in a J-coupled two-spin system. Chemical Physics Letters, 1996, 250, 495-504.	2.6	4
140	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, 158-164.	2.6	2
141	Systematic classification of metalloproteins based on three-dimensional structural similarity of their metal sites. Protocol Exchange, 0, , .	0.3	1