

# Lucia Banci

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7450191/publications.pdf>

Version: 2024-02-01

375  
papers

21,620  
citations

6613

79  
h-index

17592

121  
g-index

392  
all docs

392  
docs citations

392  
times ranked

15584  
citing authors

#	ARTICLE	IF	CITATIONS
1	Counting the Zinc-Proteins Encoded in the Human Genome. Journal of Proteome Research, 2006, 5, 196-201.	3.7	887
2	Zinc through the Three Domains of Life. Journal of Proteome Research, 2006, 5, 3173-3178.	3.7	544
3	Opposing cardioprotective actions and parallel hypertrophic effects of $\hat{A}PKC$ and $\hat{A}PKC$ . Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11114-11119.	7.1	510
4	Faster superoxide dismutase mutants designed by enhancing electrostatic guidance. Nature, 1992, 358, 347-351.	27.8	414
5	Affinity gradients drive copper to cellular destinations. Nature, 2010, 465, 645-648.	27.8	395
6	Solution Structure of Oxidized Horse Heart Cytochrome $\hat{c}$ . Biochemistry, 1997, 36, 9867-9877.	2.5	290
7	Metallochaperones and Metal-Transporting ATPases: A Comparative Analysis of Sequences and Structures. Genome Research, 2002, 12, 255-271.	5.5	232
8	MIA40 is an oxidoreductase that catalyzes oxidative protein folding in mitochondria. Nature Structural and Molecular Biology, 2009, 16, 198-206.	8.2	230
9	High-resolution NMR studies of the zinc-binding site of the Alzheimer's amyloid $\hat{A}^{25}$ -peptide. FEBS Journal, 2007, 274, 46-59.	4.7	226
10	The Unusually Stable Quaternary Structure of Human Cu,Zn-Superoxide Dismutase 1 Is Controlled by Both Metal Occupancy and Disulfide Status. Journal of Biological Chemistry, 2004, 279, 47998-48003.	3.4	223
11	Metal-free superoxide dismutase forms soluble oligomers under physiological conditions: A possible general mechanism for familial ALS. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11263-11267.	7.1	219
12	Spectral-structural correlations in high-spin cobalt(II) complexes. , 1982, , 37-86.		209
13	The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. Nature Chemical Biology, 2006, 2, 367-368.	8.0	204
14	Atomic-resolution monitoring of protein maturation in live human cells by NMR. Nature Chemical Biology, 2013, 9, 297-299.	8.0	204
15	Occurrence of Copper Proteins through the Three Domains of Life: A Bioinformatic Approach. Journal of Proteome Research, 2008, 7, 209-216.	3.7	184
16	A redox switch in CopC: An intriguing copper trafficking protein that binds copper(I) and copper(II) at different sites. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3814-3819.	7.1	173
17	Solution Structure of the Cu(I) and Apo Forms of the Yeast Metallochaperone, Atx1. Biochemistry, 2001, 40, 1528-1539.	2.5	172
18	MetalPDB in 2018: a database of metal sites in biological macromolecular structures. Nucleic Acids Research, 2018, 46, D459-D464.	14.5	165

#	ARTICLE	IF	CITATIONS
19	Mitochondrial copper(I) transfer from Cox17 to Sco1 is coupled to electron transfer. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6803-6808.	7.1	162
20	Structural properties of peroxidases. Journal of Biotechnology, 1997, 53, 253-263.	3.8	161
21	Identification of localized redox states in plant-type two-iron ferredoxins using the nuclear Overhauser effect. Biochemistry, 1990, 29, 2263-2271.	2.5	160
22	SOD1 and Amyotrophic Lateral Sclerosis: Mutations and Oligomerization. PLoS ONE, 2008, 3, e1677.	2.5	160
23	Structure of human Wilson protein domains 5 and 6 and their interplay with domain 4 and the copper chaperone HAH1 in copper uptake. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5729-5734.	7.1	150
24	Cellular copper distribution: a mechanistic systems biology approach. Cellular and Molecular Life Sciences, 2010, 67, 2563-2589.	5.4	145
25	A novel intermembrane space targeting signal docks cysteines onto Mia40 during mitochondrial oxidative folding. Journal of Cell Biology, 2009, 187, 1007-1022.	5.2	144
26	The use of pseudocontact shifts to refine solution structures of paramagnetic metalloproteins: Met80Ala cyano-cytochrome c as an example. Journal of Biological Inorganic Chemistry, 1996, 1, 117-126.	2.6	143
27	Proton NOE studies on dicopper(II) dicobalt(II) superoxide dismutase. Inorganic Chemistry, 1989, 28, 4650-4656.	4.0	140
28	Functional reconstitution of mitochondrial Fe/S cluster synthesis on Isu1 reveals the involvement of ferredoxin. Nature Communications, 2014, 5, 5013.	12.8	136
29	Solution Structure of Reduced Monomeric Q133M2 Copper, Zinc Superoxide Dismutase (SOD). Why Is SOD a Dimeric Enzyme? Biochemistry, 1998, 37, 11780-11791.	2.5	135
30	Rational Design of a Meningococcal Antigen Inducing Broad Protective Immunity. Science Translational Medicine, 2011, 3, 91ra62.	12.4	135
31	Characterization of the Binding Interface between the Copper Chaperone Atx1 and the First Cytosolic Domain of Ccc2 ATPase. Journal of Biological Chemistry, 2001, 276, 41365-41376.	3.4	132
32	A New Zinc protein Coordination Site in Intracellular Metal Trafficking: Solution Structure of the Apo and Zn(II) forms of ZntA(46-118). Journal of Molecular Biology, 2002, 323, 883-897.	4.2	132
33	Solution Structure of Apo Cu,Zn Superoxide Dismutase: Role of Metal Ions in Protein Folding. Biochemistry, 2003, 42, 9543-9553.	2.5	127
34	Solution Structure of Oxidized Saccharomyces cerevisiae iso-1-cytochrome c. Biochemistry, 1997, 36, 8992-9001.	2.5	125
35	Solution Structure of the Apo and Copper(I)-Loaded Human Metallochaperone HAH1. Biochemistry, 2004, 43, 13046-13053.	2.5	123
36	Solution Structure of the Yeast Copper Transporter Domain Ccc2a in the Apo and Cu(I)-loaded States. Journal of Biological Chemistry, 2001, 276, 8415-8426.	3.4	122

#	ARTICLE	IF	CITATIONS
37	Folding Studies of Cox17 Reveal an Important Interplay of Cysteine Oxidation and Copper Binding. Structure, 2005, 13, 713-722.	3.3	121
38	Spectroscopic studies on Cu2Zn2SOD: a continuous advancement of investigation tools. Coordination Chemistry Reviews, 1990, 100, 67-103.	18.8	120
39	Solution Structure of Sco1. Structure, 2003, 11, 1431-1443.	3.3	120
40	Human Sco1 functional studies and pathological implications of the P174L mutant. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15-20.	7.1	120
41	Human superoxide dismutase 1 (hSOD1) maturation through interaction with human copper chaperone for SOD1 (hCCS). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13555-13560.	7.1	120
42	Paramagnetism-Based Restraints for Xplor-NIH. Journal of Biomolecular NMR, 2004, 28, 249-261.	2.8	119
43	Solution structure of reduced horse heart cytochrome c. Journal of Biological Inorganic Chemistry, 1999, 4, 21-31.	2.6	116
44	Molecular chaperone function of Mia40 triggers consecutive induced folding steps of the substrate in mitochondrial protein import. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20190-20195.	7.1	116
45	[2Fe-2S] cluster transfer in iron-sulfur protein biogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6203-6208.	7.1	116
46	Probing the Interaction of Cisplatin with the Human Copper Chaperone Atox1 by Solution and In-Cell NMR Spectroscopy. Journal of the American Chemical Society, 2011, 133, 18361-18369.	13.7	114
47	Formation of [4Fe-4S] Clusters in the Mitochondrial Iron-Sulfur Cluster Assembly Machinery. Journal of the American Chemical Society, 2014, 136, 16240-16250.	13.7	114
48	Mechanism of CuA assembly. Nature Chemical Biology, 2008, 4, 599-601.	8.0	113
49	Partial Orientation of Oxidized and Reduced Cytochrome b5 at High Magnetic Fields: A Magnetic Susceptibility Anisotropy Contributions and Consequences for Protein Solution Structure Determination. Journal of the American Chemical Society, 1998, 120, 12903-12909.	13.7	110
50	Structural and dynamic aspects related to oligomerization of apo SOD1 and its mutants. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6980-6985.	7.1	109
51	Copper Trafficking: the Solution Structure of Bacillus subtilis CopZ. Biochemistry, 2001, 40, 15660-15668.	2.5	106
52	The human iron-proteome. Metallomics, 2018, 10, 1223-1231.	2.4	106
53	Solution Structure of CopC. Structure, 2002, 10, 1337-1347.	3.3	104
54	In-cell NMR: a topical review. IUCr, 2017, 4, 108-118.	2.2	104

#	ARTICLE	IF	CITATIONS
55	In-cell NMR reveals potential precursor of toxic species from SOD1 fALS mutants. <i>Nature Communications</i> , 2014, 5, 5502.	12.8	103
56	[4Fe-4S] Cluster Assembly in Mitochondria and Its Impairment by Copper. <i>Journal of the American Chemical Society</i> , 2017, 139, 719-730.	13.7	103
57	Emergence of a Homo sapiens-specific gene family and chromosome 16p11.2 CNV susceptibility. <i>Nature</i> , 2016, 536, 205-209.	27.8	102
58	The three-dimensional structure in solution of the paramagnetic high-potential iron-sulfur protein I from <i>Ectothiorhodospira halophila</i> through nuclear magnetic resonance. <i>FEBS Journal</i> , 1994, 225, 715-725.	0.2	99
59	Pseudocontact shifts as constraints for energy minimization and molecular dynamics calculations on solution structures of paramagnetic metalloproteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 68-76.	2.6	99
60	A hint for the function of human Sco1 from different structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8595-8600.	7.1	99
61	A Strategy for the NMR Characterization of Type II Copper(II) Proteins: The Case of the Copper Trafficking Protein CopC from <i>Pseudomonas Syringae</i> . <i>Journal of the American Chemical Society</i> , 2003, 125, 7200-7208.	13.7	98
62	Mitochondrial Bol1 and Bol3 function as assembly factors for specific iron-sulfur proteins. <i>ELife</i> , 2016, 5, .	6.0	96
63	Solution Structure of Cox11, a Novel Type of $\beta^2$ -Immunoglobulin-like Fold Involved in CuB Site Formation of Cytochrome c Oxidase. <i>Journal of Biological Chemistry</i> , 2004, 279, 34833-34839.	3.4	93
64	Metal Binding Domains 3 and 4 of the Wilson Disease Protein: Solution Structure and Interaction with the Copper(I) Chaperone HAH1. <i>Biochemistry</i> , 2008, 47, 7423-7429.	2.5	93
65	Proton NMR investigation into the basis for the relatively high redox potential of lignin peroxidase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 6956-6960.	7.1	92
66	Molecular recognition and substrate mimicry drive the electron-transfer process between MIA40 and ALR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4811-4816.	7.1	92
67	Mitochondrial cytochromes c: a comparative analysis. <i>Journal of Biological Inorganic Chemistry</i> , 1999, 4, 824-837.	2.6	91
68	A Structural-Dynamical Characterization of Human Cox17. <i>Journal of Biological Chemistry</i> , 2008, 283, 7912-7920.	3.4	91
69	Cyanobacterial metallochaperone inhibits deleterious side reactions of copper. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 95-100.	7.1	91
70	Three-Dimensional Solution Structure of <i>Saccharomyces cerevisiae</i> Reduced Iso-1-cytochrome c. <i>Biochemistry</i> , 1996, 35, 13788-13796.	2.5	89
71	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, 9354-9360.	3.4	88
72	The $^1\text{H}$ NMR parameters of magnetically coupled dimers of the Fe <sub>2</sub> S <sub>2</sub> proteins as an example. , 1990, , 113-136.		87

#	ARTICLE	IF	CITATIONS
73	Lignin and Mn Peroxidase-Catalyzed Oxidation of Phenolic Lignin Oligomers. <i>Biochemistry</i> , 1999, 38, 3205-3210.	2.5	87
74	A copper(I) protein possibly involved in the assembly of Cu <sub>A</sub> center of bacterial cytochrome <i>c</i> <sub>1</sub> oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3994-3999.	7.1	87
75	The electronic structure of iron-sulfur [Fe <sub>4</sub> S <sub>4</sub> ] <sup>3+</sup> clusters in proteins. An investigation of the oxidized high-potential iron-sulfur protein II from <i>Ectothiorhodospira vacuolata</i> . <i>Biochemistry</i> , 1993, 32, 9387-9397.	2.5	86
76	The Solution Structure of Oxidized Rat Microsomal Cytochrome b <sub>5</sub> . <i>Biochemistry</i> , 1998, 37, 173-184.	2.5	86
77	Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces. <i>Biochemical Journal</i> , 2009, 422, 37-42.	3.7	85
78	The solution structure of reduced dimeric copper zinc superoxide dismutase. <i>FEBS Journal</i> , 2002, 269, 1905-1915.	0.2	84
79	Understanding Copper Trafficking in Bacteria: A Interaction between the Copper Transport Protein CopZ and the N-Terminal Domain of the Copper ATPase CopA from <i>Bacillus subtilis</i> . <i>Biochemistry</i> , 2003, 42, 1939-1949.	2.5	84
80	NMR structures of paramagnetic metalloproteins. <i>Quarterly Reviews of Biophysics</i> , 2005, 38, 167-219.	5.7	84
81	The Solution Structure of Oxidized <i>Escherichia coli</i> Cytochrome b <sub>562</sub> . <i>Biochemistry</i> , 1999, 38, 8657-8670.	2.5	82
82	Preparation, physico-chemical and pharmacokinetic characterization of monomethoxypoly(ethylene) Tj ETQq0 0 0 rgBT /Overlock 10 Tf .	9.9	80
83	The three-dimensional solution structure of the reduced high-potential iron-sulfur protein from <i>Chromatium vinosum</i> through NMR. <i>Biochemistry</i> , 1995, 34, 206-219.	2.5	80
84	Characterization of proteins by in-cell NMR spectroscopy in cultured mammalian cells. <i>Nature Protocols</i> , 2016, 11, 1101-1111.	12.0	80
85	A Unique Tool for Cellular Structural Biology: In-cell NMR. <i>Journal of Biological Chemistry</i> , 2016, 291, 3776-3784.	3.4	80
86	Protein networks in the maturation of human iron-sulfur proteins. <i>Metallomics</i> , 2018, 10, 49-72.	2.4	79
87	Molecular recognition in copper trafficking. <i>Natural Product Reports</i> , 2010, 27, 695.	10.3	78
88	Binding of Bicarbonate to Human Carbonic Anhydrase II: A Continuum of Binding States. <i>Journal of the American Chemical Society</i> , 1997, 119, 863-871.	13.7	77
89	Perspectives in Inorganic Structural Genomics: A Trafficking Route for Copper. <i>European Journal of Inorganic Chemistry</i> , 2004, 2004, 1583-1593.	2.0	77
90	Protein interaction patterns in different cellular environments are revealed by in-cell NMR. <i>Scientific Reports</i> , 2015, 5, 14456.	3.3	77

#	ARTICLE	IF	CITATIONS
91	The crystal structure of the monomeric human SOD mutant F50E/G51E/E133Q at atomic resolution. the enzyme mechanism revisited. Journal of Molecular Biology, 1999, 288, 413-426.	4.2	75
92	Human SOD1 before Harboring the Catalytic Metal. Journal of Biological Chemistry, 2006, 281, 2333-2337.	3.4	73
93	In-Cell NMR in Human Cells: Direct Protein Expression Allows Structural Studies of Protein Folding and Maturation. Accounts of Chemical Research, 2018, 51, 1550-1557.	15.6	73
94	Molecular dynamics simulations of metalloproteins. Current Opinion in Chemical Biology, 2003, 7, 143-149.	6.1	71
95	N-terminal domains mediate [2Fe-2S] cluster transfer from glutaredoxin-3 to anamorsin. Nature Chemical Biology, 2015, 11, 772-778.	8.0	71
96	The cysteine-reactive small molecule ebselen facilitates effective SOD1 maturation. Nature Communications, 2018, 9, 1693.	12.8	71
97	Proton NMR spectra of oxidized high-potential iron-sulfur protein (HiPIP) from Rhodocyclus gelatinosus. A model for oxidized HiPIPs. Inorganic Chemistry, 1991, 30, 4517-4524.	4.0	70
98	Non-heme iron through the three domains of life. Proteins: Structure, Function and Bioinformatics, 2007, 67, 317-324.	2.6	70
99	Structure and dynamics of copper-free SOD: The protein before binding copper. Protein Science, 2002, 11, 2479-2492.	7.6	70
100	The iron-sulfur cluster in the oxidized high-potential iron protein from Ectothiorhodospira halophila. Journal of the American Chemical Society, 1993, 115, 3431-3440.	13.7	69
101	Proton NMR investigation of manganese peroxidase from Phanerochaete chrysosporium. A comparison with other peroxidases. Biochemistry, 1992, 31, 10009-10017.	2.5	68
102	Structural basis for the mutual antagonism of cAMP and TRIP8b in regulating HCN channel function. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14577-14582.	7.1	68
103	Solution structure of the N-terminal domain of a potential copper-translocating P-type ATPase from Bacillus subtilis in the apo and Cu(I) loaded states. Journal of Molecular Biology, 2002, 317, 415-429.	4.2	67
104	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 16873-16879.	13.7	67
105	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. Metallomics, 2018, 10, 1755-1776.	2.4	66
106	Three-Dimensional Solution Structure of the Cyanide Adduct of a Variant of Saccharomyces cerevisiae Iso-1-cytochrome c Containing the Met80Ala Mutation. Identification of Ligand-Residue Interactions in the Distal Heme Cavity. Biochemistry, 1995, 34, 11385-11398.	2.5	65
107	PSEUDYANA for NMR structure calculation of paramagnetic metalloproteins using torsion angle molecular dynamics. Journal of Biomolecular NMR, 1998, 12, 553-557.	2.8	65
108	Oxidation of a Tetrameric Nonphenolic Lignin Model Compound by Lignin Peroxidase. Journal of Biological Chemistry, 2001, 276, 22985-22990.	3.4	65



#	ARTICLE	IF	CITATIONS
109	Anamorsin Is a [2Fe-2S] Cluster-Containing Substrate of the Mia40-Dependent Mitochondrial Protein Trapping Machinery. <i>Chemistry and Biology</i> , 2011, 18, 794-804.	6.0	65
110	Interaction of Cisplatin with Human Superoxide Dismutase. <i>Journal of the American Chemical Society</i> , 2012, 134, 7009-7014.	13.7	65
111	Correlation between anisotropic exchange and structure of di- $\mu$ -hydroxy bridged copper(II) complexes. <i>Journal of the American Chemical Society</i> , 1983, 105, 761-764.	13.7	64
112	Binding of horseradish, lignin, and manganese peroxidases to their respective substrates. <i>Biochemistry</i> , 1993, 32, 5825-5831.	2.5	64
113	Analysis of the Temperature Dependence of the $^1\text{H}$ and $^{13}\text{C}$ Isotropic Shifts of Horse Heart Ferricytochrome c: A Explanation of Curie and Anti-Curie Temperature Dependence and Nonlinear Pseudocontact Shifts in a Common Two-Level Framework. <i>Journal of the American Chemical Society</i> , 1998, 120, 8472-8479.	13.7	64
114	Elucidating the Molecular Function of Human BOLA2 in GRX3-Dependent Anamorsin Maturation Pathway. <i>Journal of the American Chemical Society</i> , 2015, 137, 16133-16143.	13.7	64
115	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, 3396-3403.	2.5	63
116	Molecular view of an electron transfer process essential for iron-sulfur protein biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7136-7141.	7.1	63
117	Structural Basis for the Function of the N-terminal Domain of the ATPase CopA from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 50506-50513.	3.4	62
118	A NMR Study of the Interaction of a Three-domain Construct of ATP7A with Copper(I) and Copper(I)-HAH1. <i>Journal of Biological Chemistry</i> , 2005, 280, 38259-38263.	3.4	62
119	In-cell NMR in <i>E. coli</i> to Monitor Maturation Steps of hSOD1. <i>PLoS ONE</i> , 2011, 6, e23561.	2.5	62
120	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, 9108-9118.	2.5	61
121	Dynamic Properties of the G93A Mutant of Copper-Zinc Superoxide Dismutase As Detected by NMR Spectroscopy: Implications for the Pathology of Familial Amyotrophic Lateral Sclerosis. <i>Biochemistry</i> , 2003, 42, 1890-1899.	2.5	60
122	An investigation of superoxide dismutase Lys-143, Ile-143, and Glu-143 mutants: Cu <sub>2</sub> Co <sub>2</sub> SOD derivatives. <i>Journal of the American Chemical Society</i> , 1988, 110, 3629-3633.	13.7	59
123	Structural Basis for Metal Binding Specificity: the N-terminal Cadmium Binding Domain of the P1-type ATPase CadA. <i>Journal of Molecular Biology</i> , 2006, 356, 638-650.	4.2	59
124	Structural Genomics of Proteins Involved in Copper Homeostasis. <i>Accounts of Chemical Research</i> , 2003, 36, 215-221.	15.6	58
125	Loop recognition and copper-mediated disulfide reduction underpin metal site assembly of Cu <sub>A</sub> in human cytochrome oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11771-11776.	7.1	58
126	MetalPredator: a web server to predict iron-sulfur cluster binding proteomes. <i>Bioinformatics</i> , 2016, 32, 2850-2852.	4.1	58



#	ARTICLE	IF	CITATIONS
127	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
128	EPR spectra of trinuclear complexes. Octachlorodiadeniniumtricopper(II) tetrahydrate. <i>Inorganic Chemistry</i> , 1983, 22, 2681-2683.	4.0	56
129	Superoxide Dismutase Folding/Unfolding Pathway: Role of the Metal Ions in Modulating Structural and Dynamical Features. <i>Journal of Molecular Biology</i> , 2003, 330, 145-158.	4.2	56
130	A Docking Approach to the Study of Copper Trafficking Proteins. <i>Structure</i> , 2004, 12, 669-676.	3.3	56
131	Fully Metallated S134N Cu,Zn-Superoxide Dismutase Displays Abnormal Mobility and Intermolecular Contacts in Solution. <i>Journal of Biological Chemistry</i> , 2005, 280, 35815-35821.	3.4	56
132	The Functions of Sco Proteins from Genome-Based Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 1568-1579.	3.7	56
133	HIV-1 Tat Promotes Integrin-Mediated HIV Transmission to Dendritic Cells by Binding Env Spikes and Competes Neutralization by Anti-HIV Antibodies. <i>PLoS ONE</i> , 2012, 7, e48781.	2.5	56
134	Active Site Coordination Chemistry of the Cytochrome c Peroxidase Asp235Ala Variant: Spectroscopic and Functional Characterization. <i>Biochemistry</i> , 1994, 33, 7819-7829.	2.5	55
135	The delivery of copper for thylakoid import observed by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8320-8325.	7.1	55
136	Solution Structure of the Factor H-binding Protein, a Survival Factor and Protective Antigen of <i>Neisseria meningitidis</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 9022-9026.	3.4	55
137	Paramagnetic <sup>1</sup> H NMR Spectroscopy of the Cyanide Derivative of Met80Ala-iso-1-cytochrome c. <i>Journal of the American Chemical Society</i> , 1995, 117, 8067-8073.	13.7	54
138	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
139	A Structural Characterization of Human SCO2. <i>Structure</i> , 2007, 15, 1132-1140.	3.3	54
140	Structure of Nucleophosmin DNA-binding Domain and Analysis of Its Complex with a G-quadruplex Sequence from the c-MYC Promoter. <i>Journal of Biological Chemistry</i> , 2012, 287, 26539-26548.	3.4	54
141	Visualization of Redox-Controlled Protein Fold in Living Cells. <i>Chemistry and Biology</i> , 2013, 20, 747-752.	6.0	54
142	Enzyme-catalyzed Mechanism of Isoniazid Activation in Class I and Class III Peroxidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 39000-39009.	3.4	53
143	The Evolutionarily Conserved Trimeric Structure of CutA1 Proteins Suggests a Role in Signal Transduction. <i>Journal of Biological Chemistry</i> , 2003, 278, 45999-46006.	3.4	52
144	New Type 2 Copper <sup>2+</sup> -Cysteinate Proteins. Copper Site Histidine-to-Cysteine Mutants of Yeast Copper <sup>2+</sup> -Zinc Superoxide Dismutase. <i>Inorganic Chemistry</i> , 1996, 35, 1692-1700.	4.0	51

#	ARTICLE	IF	CITATIONS
145	A characterization of copper/zinc superoxide dismutase mutants at position 124 Zinc-deficient proteins. FEBS Journal, 1991, 196, 123-128.	0.2	50
146	Solution Structures of a Cyanobacterial Metallochaperone. Journal of Biological Chemistry, 2004, 279, 27502-27510.	3.4	50
147	Human anamorsin binds [2Fe-2S] clusters with unique electronic properties. Journal of Biological Inorganic Chemistry, 2013, 18, 883-893.	2.6	50
148	Comparative proton NMR study of ferric low-spin cytochrome c peroxidase and horseradish peroxidase. Inorganic Chemistry, 1991, 30, 4510-4516.	4.0	49
149	Seeking the determinants of the elusive functions of Sco proteins. FEBS Journal, 2011, 278, 2244-2262.	4.7	49
150	The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. PLoS ONE, 2017, 12, e0171279.	2.5	49
151	Characterization and Peroxidase Activity of a Myoglobin Mutant Containing a Distal Arginine. ChemBioChem, 2002, 3, 226-233.	2.6	48
152	Solution Structure and Characterization of the Heme Chaperone CcmE. Biochemistry, 2002, 41, 13587-13594.	2.5	47
153	X-Ray Absorption and NMR Spectroscopic Studies of CopZ, a Copper Chaperone in Bacillus subtilis: The Coordination Properties of the Copper Ion. Biochemistry, 2003, 42, 2467-2474.	2.5	47
154	Individual Reduction Potentials of the Iron Ions in Fe <sub>2</sub> S <sub>2</sub> and High-Potential Fe <sub>4</sub> S <sub>4</sub> Ferredoxins. Inorganic Chemistry, 1996, 35, 4248-4253.	4.0	46
155	Structural Consequences of heme b <sub>L</sub> -type Heme Conversion in Oxidized Escherichia coli Cytochrome b <sub>562</sub> . Biochemistry, 2000, 39, 1499-1514.	2.5	46
156	Structural insights into the molecular function of human [2Fe-2S] BOLA1-GRX5 and [2Fe-2S] BOLA3-GRX5 complexes. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2119-2131.	2.4	46
157	Molecular Dynamics Studies on Peroxidases: A Structural Model for Horse Radish Peroxidase and a Substrate Adduct. Biochemistry, 1994, 33, 12356-12366.	2.5	45
158	Epitope Mapping of a Bactericidal Monoclonal Antibody against the Factor H Binding Protein of Neisseria meningitidis. Journal of Molecular Biology, 2009, 386, 97-108.	4.2	44
159	IBA57 Recruits ISCA2 to Form a [2Fe-2S] Cluster-Mediated Complex. Journal of the American Chemical Society, 2018, 140, 14401-14412.	13.7	44
160	Protein in-cell NMR spectroscopy at 1.2 ÅHz. Journal of Biomolecular NMR, 2021, 75, 97-107.	2.8	44
161	Drug Screening in Human Cells by NMR Spectroscopy Allows the Early Assessment of Drug Potency. Angewandte Chemie - International Edition, 2020, 59, 6535-6539.	13.8	44
162	Molecular dynamics studies on superoxide dismutase and its mutants: the structural and functional role of Arg 143. Journal of the American Chemical Society, 1992, 114, 6994-7001.	13.7	43

#	ARTICLE	IF	CITATIONS
163	Factoring of the Hyperfine Shifts in the Cyanide Adduct of Lignin Peroxidase from <i>P. chrysosporium</i> . <i>Journal of the American Chemical Society</i> , 1995, 117, 8659-8667.	13.7	43
164	Solution structure of oxidized microsomal rabbit cytochrome b5. <i>FEBS Journal</i> , 2000, 267, 755-766.	0.2	43
165	Molecular Dynamics Characterization of the C2 Domain of Protein Kinase C $\beta$ . <i>Journal of Biological Chemistry</i> , 2002, 277, 12988-12997.	3.4	43
166	A synthetic peptide that prevents cAMP regulation in mammalian hyperpolarization-activated cyclic nucleotide-gated (HCN) channels. <i>ELife</i> , 2018, 7, .	6.0	43
167	Exploiting Bacterial Operons To Illuminate Human Iron-Sulfur Proteins. <i>Journal of Proteome Research</i> , 2016, 15, 1308-1322.	3.7	42
168	Direct structural evidence of protein redox regulation obtained by in-cell NMR. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 198-204.	4.1	42
169	Radio Signals from Live Cells: The Coming of Age of In-Cell Solution NMR. <i>Chemical Reviews</i> , 2022, 122, 9267-9306.	47.7	42
170	An investigation of a human erythrocyte SOD modified at position 137. <i>Journal of the American Chemical Society</i> , 1989, 111, 714-719.	13.7	41
171	NMR Structural Analysis of Cadmium Sensing by Winged Helix Repressor CmtR. <i>Journal of Biological Chemistry</i> , 2007, 282, 30181-30188.	3.4	41
172	A molecular chaperone activity of CCS restores the maturation of SOD1 fALS mutants. <i>Scientific Reports</i> , 2017, 7, 17433.	3.3	41
173	Solution Structure of Oxidized Cytochrome c6 from the Green Alga <i>Monoraphidium braunii</i> . <i>Biochemistry</i> , 1998, 37, 4831-4843.	2.5	40
174	Ortholog Search of Proteins Involved in Copper Delivery to Cytochrome cOxidase and Functional Analysis of Paralogs and Gene Neighbors by Genomic Context. <i>Journal of Proteome Research</i> , 2005, 4, 63-70.	3.7	40
175	An Electron-Transfer Path through an Extended Disulfide Relay System: The Case of the Redox Protein ALR. <i>Journal of the American Chemical Society</i> , 2012, 134, 1442-1445.	13.7	40
176	Molecular dynamics characterization of the active cavity of carboxypeptidase A and some of its inhibitor adducts. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 13, 288-305.	2.6	39
177	pH-dependent equilibria of yeast Met80Ala-iso-1-cytochrome c probed by NMR spectroscopy: a comparison with the wild-type protein. <i>Chemistry and Biology</i> , 1995, 2, 377-383.	6.0	39
178	Probing the Backbone Dynamics of Oxidized and Reduced Rat Microsomal Cytochrome b5 via $^{15}\text{N}$ Rotating Frame NMR Relaxation Measurements: A Biological Implications. <i>Biochemistry</i> , 1998, 37, 12320-12330.	2.5	39
179	Cadmium effects on superoxide dismutase 1 in human cells revealed by NMR. <i>Redox Biology</i> , 2019, 21, 101102.	9.0	39
180	Real-Time Quantitative In-Cell NMR: Ligand Binding and Protein Oxidation Monitored in Human Cells Using Multivariate Curve Resolution. <i>Analytical Chemistry</i> , 2020, 92, 9997-10006.	6.5	39

#	ARTICLE	IF	CITATIONS
181	Structural Interplay between Calcium(II) and Copper(II) Binding to S100A13 Protein. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 6341-6344.	13.8	38
182	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
183	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
184	Solution Structure of the Immunodominant Domain of Protective Antigen GNA1870 of <i>Neisseria meningitidis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 7220-7227.	3.4	37
185	NOE and two-dimensional correlated <sup>1</sup> H-NMR spectroscopy of cytochrome c' from <i>Chromatium vinosum</i> . <i>FEBS Journal</i> , 1992, 204, 107-112.	0.2	36
186	800 MHz <sup>1</sup> H NMR solution structure refinement of oxidized cytochrome c7 from <i>Desulfuromonas acetoxidans</i> . <i>FEBS Journal</i> , 1998, 256, 261-270.	0.2	36
187	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
188	Metallomics and the Cell: Some Definitions and General Comments. <i>Metal Ions in Life Sciences</i> , 2013, 12, 1-13.	2.8	36
189	A pathway for assembling [4Fe-4S] <sup>2+</sup> clusters in mitochondrial iron-sulfur protein biogenesis. <i>FEBS Journal</i> , 2020, 287, 2312-2327.	4.7	36
190	Cytochrome P450 and Aromatic Bases: A <sup>1</sup> H NMR Study. <i>Journal of the American Chemical Society</i> , 1994, 116, 4866-4873.	13.7	35
191	Bioinformatic Comparison of Structures and Homology-Models of Matrix Metalloproteinases. <i>Journal of Proteome Research</i> , 2004, 3, 21-31.	3.7	35
192	The Characterization and Role of Zinc Binding in Yeast Cox4. <i>Journal of Biological Chemistry</i> , 2007, 282, 8926-8934.	3.4	35
193	NMR in structural proteomics and beyond. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2010, 56, 247-266.	7.5	35
194	Real-Time Insights into Biological Events: In-Cell Processes and Protein-Ligand Interactions. <i>Biophysical Journal</i> , 2019, 116, 239-247.	0.5	35
195	Hydrogen-1 NOE and ligand field studies of copper-cobalt superoxide dismutase with anions. <i>Inorganic Chemistry</i> , 1990, 29, 4867-4873.	4.0	34
196	Indirect determination of magnetic susceptibility tensors in peroxidases: a novel approach to structure elucidation by NMR. <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 320-329.	2.6	34
197	Structure and Cu(I)-binding properties of the N-terminal soluble domains of <i>Bacillus subtilis</i> CopA. <i>Biochemical Journal</i> , 2008, 411, 571-579.	3.7	34
198	X-ray crystal structure of bis(N,N'-ethylene-bis- (salicylideneiminato)-oxovanadium(V)) di-1/4-chlorodicopper(I) chloride, a compound with a three- coordinate copper(I) chloride. <i>Inorganica Chimica Acta</i> , 1984, 84, L11-L12.	2.4	33

#	ARTICLE	IF	CITATIONS
199	Electronic relaxation of a copper(II) dimer in a macromolecular complex as evaluated from solvent proton relaxation. <i>Inorganic Chemistry</i> , 1988, 27, 951-953.	4.0	33
200	Molecular dynamics simulations on HiPIP from <i>Chromatium vinosum</i> and comparison with NMR data. <i>Journal of the American Chemical Society</i> , 1992, 114, 10683-10689.	13.7	33
201	<sup>1</sup> H- <sup>13</sup> C HETCOR Investigations on Heme-Containing Systems. <i>Inorganic Chemistry</i> , 1994, 33, 4338-4343.	4.0	33
202	Synthesis and Characterization of a Monomeric Mutant Cu/Zn Superoxide Dismutase with Partially Reconstituted Enzymic Activity. <i>FEBS Journal</i> , 1995, 234, 855-860.	0.2	33
203	Effects of Heme on the Structure of the Denatured State and Folding Kinetics of Cytochrome b562. <i>Journal of Molecular Biology</i> , 2005, 346, 331-344.	4.2	33
204	Methylglyoxal interaction with superoxide dismutase 1. <i>Redox Biology</i> , 2020, 30, 101421.	9.0	33
205	Effects of extrinsic imidazole ligation on the molecular and electronic structure of cytochrome c. <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 628-637.	2.6	32
206	A Core Mutation Affecting the Folding Properties of a Soluble Domain of the ATPase Protein CopA from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2003, 331, 473-484.	4.2	32
207	Comparative Analysis of the ADAM and ADAMTS Families. <i>Journal of Proteome Research</i> , 2005, 4, 881-888.	3.7	32
208	NMR proton relaxation in bimetallic complexes of zinc(II), nickel(II), and copper(II). <i>Journal of the American Chemical Society</i> , 1986, 108, 3298-3303.	13.7	30
209	Investigation of copper-zinc superoxide dismutase Ser-137 and Ala-137 mutants. <i>Inorganic Chemistry</i> , 1990, 29, 2398-2403.	4.0	30
210	A comment on the proton NMR spectra of cobalt(II)-substituted superoxide dismutases with histidines deuteriated in the .epsilon.1-position. <i>Inorganic Chemistry</i> , 1990, 29, 1438-1440.	4.0	30
211	pH, Electrolyte, and Substrate-Linked Variation in Active Site Structure of the Trp51Ala Variant of Cytochrome c Peroxidase. <i>Biochemistry</i> , 1995, 34, 13895-13905.	2.5	30
212	Anamorsin/Ndor1 Complex Reduces [2Fe-2S]-MitoNEET via a Transient Protein-Protein Interaction. <i>Journal of the American Chemical Society</i> , 2017, 139, 9479-9482.	13.7	30
213	Water in the active cavity of copper/zinc superoxide dismutase. A water <sup>1</sup> H-nuclear-magnetic-relaxation-dispersion study. <i>FEBS Journal</i> , 1989, 184, 125-129.	0.2	29
214	<sup>1</sup> H NOE studies of oxidized high potential iron sulfur protein II from <i>Ectothiorhodospira halophila</i> . <i>Inorganica Chimica Acta</i> , 1991, 180, 171-175.	2.4	29
215	A proton-NMR investigation of the fully reduced cytochrome c7 from <i>Desulfuromonas acetoxidans</i> . Comparison between the reduced and the oxidized forms. <i>FEBS Journal</i> , 1999, 266, 634-643.	0.2	29
216	Matrix metalloproteinase-inhibitor interaction: the solution structure of the catalytic domain of human matrix metalloproteinase-3 with different inhibitors. <i>Journal of Biological Inorganic Chemistry</i> , 2007, 12, 1197-1206.	2.6	29

#	ARTICLE	IF	CITATIONS
217	Molecular dynamics studies on mutants of Cu, Zn superoxide dismutase: The functional role of charged residues in the electrostatic loop VII. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 18, 216-230.	2.6	28
218	[17] Two-dimensional nuclear magnetic resonance spectra of paramagnetic systems. <i>Methods in Enzymology</i> , 1994, 239, 485-514.	1.0	28
219	Binding of Azide to Human Carbonic Anhydrase II: The Role Electrostatic Complementarity Plays in Selecting the Preferred Resonance Structure of Azide. <i>The Journal of Physical Chemistry</i> , 1996, 100, 17414-17420.	2.9	28
220	Solution structure of the B form of oxidized rat microsomal cytochrome b <sub>5</sub> and backbone dynamics via <sup>15</sup> N rotating-frame NMR-relaxation measurements. <i>FEBS Journal</i> , 1999, 260, 347-354.	0.2	28
221	A prokaryotic superoxide dismutase paralog lacking two Cu ligands: From largely unstructured in solution to ordered in the crystal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7541-7546.	7.1	28
222	NMR investigation of isotopically labeled cyanide derivatives of lignin peroxidase and manganese peroxidase. <i>Biochemistry</i> , 1993, 32, 13483-13489.	2.5	27
223	Chemical shift-based constraints for solution structure determination of paramagnetic low-spin heme proteins with bis-His and His-CN axial ligands: the cases of oxidized cytochrome b <sub>5</sub> and Met80Ala cyano-cytochrome c. <i>Journal of Biological Inorganic Chemistry</i> , 2002, 7, 416-426.	2.6	27
224	Integration of XAS and NMR techniques for the structure determination of metalloproteins. Examples from the study of copper transport proteins. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 94-97.	2.4	27
225	Modeling Protein-Protein Complexes Involved in the Cytochrome c Oxidase Copper-Delivery Pathway. <i>Journal of Proteome Research</i> , 2007, 6, 1530-1539.	3.7	27
226	NMR study of cobalt(II)-substituted yeast and human copper-zinc superoxide dismutase. <i>Inorganic Chemistry</i> , 1988, 27, 728-733.	4.0	26
227	The solution structure of cytochrome c <sub>6</sub> from the green alga <i>Monoraphidium braunii</i> . <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 330-340.	2.6	26
228	Structural characterization of CHCHD5 and CHCHD7: Two atypical human twin CX9C proteins. <i>Journal of Structural Biology</i> , 2012, 180, 190-200.	2.8	26
229	Intracellular metal binding and redox behavior of human DJ-1. <i>Journal of Biological Inorganic Chemistry</i> , 2018, 23, 61-69.	2.6	26
230	Solution Structure of Reduced Microsomal Rat Cytochrome b <sub>5</sub> . <i>FEBS Journal</i> , 1997, 249, 270-279.	0.2	25
231	The Conformational Flexibility of Oxidized Cytochrome c Studied through Its Interaction with NH <sub>3</sub> and at High Temperatures. <i>European Journal of Inorganic Chemistry</i> , 1998, 1998, 583-591.	2.0	25
232	The auto-orientation in high magnetic fields of oxidized cytochrome b <sub>562</sub> as source of constraints for solution structure determination. <i>Journal of Biomolecular NMR</i> , 2000, 17, 295-304.	2.8	25
233	Metalation of the Amyotrophic Lateral Sclerosis Mutant Glycine 37 to Arginine Superoxide Dismutase (SOD1) Apoprotein Restores Its Structural and Dynamical Properties in Solution to Those of Metalated Wild-Type SOD1. <i>Biochemistry</i> , 2007, 46, 9953-9962.	2.5	25
234	The coiled coil-helix-coiled coil-helix proteins may be redox proteins. <i>FEBS Letters</i> , 2009, 583, 1699-1702.	2.8	25



#	ARTICLE	IF	CITATIONS
235	Targeting and Maturation of Erv1/ALR in the Mitochondrial Intermembrane Space. ACS Chemical Biology, 2012, 7, 707-714.	3.4	25
236	The NMR contribution to proteinâ€“protein networking in Feâ€“S protein maturation. Journal of Biological Inorganic Chemistry, 2018, 23, 665-685.	2.6	25
237	Transient versus steady state NOE in paramagnetic molecules Cu <sub>2</sub> Co <sub>2</sub> SOD as an example. FEBS Letters, 1990, 272, 175-180.	2.8	24
238	The enzymatic mechanism of carboxypeptidase: A molecular dynamics study. Proteins: Structure, Function and Bioinformatics, 1994, 18, 186-197.	2.6	24
239	NMR study of manganese(II) binding by a new versatile peroxidase from the white-rot fungus Pleurotus eryngii. Journal of Biological Inorganic Chemistry, 2003, 8, 751-760.	2.6	24
240	Solution Structure of Apo CopZ from Bacillus subtilis:â€“ Further Analysis of the Changes Associated with the Presence of Copper. Biochemistry, 2003, 42, 13422-13428.	2.5	24
241	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
242	Mechanistic Aspects of hSOD1 Maturation from the Solution Structure of Cu <sup>I</sup> -Loaded hCCS Domain 1 and Analysis of Disulfideâ€“Free hSOD1 Mutants. ChemBioChem, 2013, 14, 1839-1844.	2.6	24
243	ESR spectra of cobalt(II)- and copper(II)-doped bis(N,N-bis(2-(diethylamino)ethyl)(2-hydroxyethyl)amino-O)dinickel(II) diperchlorate. Characterization of nickel(II)-cobalt(II) and nickel(II)-copper(II) exchange-coupled pairs. Inorganic Chemistry, 1981, 20, 393-398.	4.0	23
244	Unusual electronic spectra of the pseudotetrahedral complex [tris(3,5-dimethyl-1-pyrazolyl)ethylamine]cobalt(II) bis(tetraphenylborate). Inorganic Chemistry, 1982, 21, 1133-1136.	4.0	23
245	Phosphorus-31 NMR study of the interaction of inorganic phosphate with bovine copper-zinc superoxide dismutase. Inorganic Chemistry, 1987, 26, 2788-2791.	4.0	23
246	Characterization of copper-nickel and silver-nickel bovine superoxide dismutases by proton NMR spectroscopy. Inorganic Chemistry, 1988, 27, 4458-4463.	4.0	23
247	Rationalization of the reduction potentials within the series of the high potential iron-sulfur proteins. Inorganica Chimica Acta, 1995, 240, 251-256.	2.4	23
248	Synthesis of oligomeric mimics of lignin. Journal of the Chemical Society Perkin Transactions 1, 1998, , 3207-3218.	0.9	23
249	NMR Solution Structure, Backbone Mobility, and Homology Modeling of c-Type Cytochromes from Gram-Positive Bacteria. ChemBioChem, 2002, 3, 299-310.	2.6	23
250	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
251	Intracellular Binding/Unbinding Kinetics of Approved Drugs to Carbonic Anhydrase II Observed by in-Cell NMR. ACS Chemical Biology, 2020, 15, 2792-2800.	3.4	23
252	NMR quality control of fragment libraries for screening. Journal of Biomolecular NMR, 2020, 74, 555-563.	2.8	23



#	ARTICLE	IF	CITATIONS
253	The FDA-Approved Antiviral Raltegravir Inhibits Fascin1-Dependent Invasion of Colorectal Tumor Cells In Vitro and In Vivo. <i>Cancers</i> , 2021, 13, 861.	3.7	23
254	Advances in the NMR investigation of paramagnetic molecules in solution. <i>Coordination Chemistry Reviews</i> , 1992, 120, 1-28.	18.8	22
255	<sup>1</sup> H-NMR study of reduced heme proteins myoglobin and cytochrome P450. <i>FEBS Journal</i> , 1993, 215, 431-437.	0.2	22
256	A Molecular Dynamics Study in Explicit Water of the Reduced and Oxidized forms of Yeast Iso-1-cytochrome c. Solvation and Dynamic Properties of the two Oxidation States. <i>FEBS Journal</i> , 1997, 249, 716-723.	0.2	22
257	Functional Role of Two Interhelical Disulfide Bonds in Human Cox17 Protein from a Structural Perspective. <i>Journal of Biological Chemistry</i> , 2011, 286, 34382-34390.	3.4	22
258	Structural properties of [2Fe-2S] ISCA2-IBA57: a complex of the mitochondrial iron-sulfur cluster assembly machinery. <i>Scientific Reports</i> , 2019, 9, 18986.	3.3	22
259	Charge Reversal of a Critical Active-Site Residue of Cytochrome-c Peroxidase. Characterization of the Arg48Glu Variant. <i>FEBS Journal</i> , 1997, 243, 72-84.	0.2	21
260	Monitoring the conformational flexibility of cytochrome c at low ionic strength by <sup>1</sup> H-NMR spectroscopy. <i>FEBS Journal</i> , 1998, 256, 271-278.	0.2	21
261	Water-protein interaction in native and partially unfolded equine cytochrome c. <i>Molecular Physics</i> , 1998, 95, 797-808.	1.7	21
262	Nuclear magnetic resonance spectroscopy studies on copper proteins. <i>Advances in Protein Chemistry</i> , 2002, 60, 397-449.	4.4	21
263	The copper-responsive repressor CopR of <i>Lactococcus lactis</i> is a "winged helix" protein. <i>Biochemical Journal</i> , 2009, 417, 493-499.	3.7	21
264	Structural and Functional Characterization of the <i>Streptococcus pneumoniae</i> RrgB Pilus Backbone D1 Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 14588-14597.	3.4	21
265	Structural insights of proteins in sub-cellular compartments: In-mitochondria NMR. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 2492-2496.	4.1	21
266	Copper exposure effects on yeast mitochondrial proteome. <i>Journal of Proteomics</i> , 2011, 74, 2522-2535.	2.4	20
267	An essential role for the conserved Glu-133 in the anion interaction with superoxide dismutase. <i>Journal of Inorganic Biochemistry</i> , 1993, 50, 89-100.	3.5	19
268	Crystal structure of cytochrome c' from <i>Rhodocyclus gelatinosus</i> and comparison with other cytochromes c'. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 611-622.	2.6	19
269	Solution Structure of Oxidized Rat Microsomal Cytochrome b5 in the Presence of 2 M Guanidinium Chloride: Monitoring the Early Steps in Protein Unfolding. <i>Biochemistry</i> , 1998, 37, 17082-17092.	2.5	19
270	The solution structure of a monomeric, reduced form of human copper,zinc superoxide dismutase bearing the same charge as the native protein. <i>Journal of Biological Inorganic Chemistry</i> , 1999, 4, 795-803.	2.6	19

#	ARTICLE	IF	CITATIONS
271	Direct Detection of Hydrogen Bonds in Monomeric Superoxide Dismutase: Biological Implications. <i>Biochemistry</i> , 2002, 41, 2913-2920.	2.5	19
272	NMR structural analysis of the soluble domain of ZiaA-ATPase and the basis of selective interactions with copper metallochaperone Atx1. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 87-98.	2.6	19
273	Sco proteins are involved in electron transfer processes. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 391-403.	2.6	19
274	Crystal and molecular structure and ESR spectra of a dimeric dialkoxo-bridged five-coordinate copper(II) complex. <i>Inorganic Chemistry</i> , 1980, 19, 3395-3399.	4.0	18
275	Monitoring Mobility in the Early Steps of Unfolding: The Case of Oxidized Cytochrome b5 in the Presence of 2 M Guanidinium Chloride. <i>Biochemistry</i> , 2000, 39, 7117-7130.	2.5	18
276	Exchange interactions in heterodinuclear complexes with one ion possessing an orbitally degenerate ground state. Nickel(II)-cobalt(II) pairs in diaqua(1,4-dihydrazinophthalazine)nickel(II) chloride hydrate. <i>Inorganic Chemistry</i> , 1982, 21, 3868-3872.	4.0	17
277	[12] Proton magnetic resonance of paramagnetic metalloproteins. <i>Methods in Enzymology</i> , 1989, 177, 246-263.	1.0	17
278	Monitoring the Role of Oxalate in Manganese Peroxidase. <i>Biochemistry</i> , 1998, 37, 9009-9015.	2.5	17
279	Redox equilibria of manganese peroxidase from <i>Phanerochaetes chrysosporium</i> : functional role of residues on the proximal side of the haem pocket. <i>Biochemical Journal</i> , 2000, 349, 85-90.	3.7	17
280	The Factor H Binding Protein of <i>Neisseria meningitidis</i> Interacts with Xenosiderophores in Vitro. <i>Biochemistry</i> , 2012, 51, 9384-9393.	2.5	17
281	GLRX3 Acts as a [2Fe-2S] Cluster Chaperone in the Cytosolic Iron-Sulfur Assembly Machinery Transferring [2Fe-2S] Clusters to NUBP1. <i>Journal of the American Chemical Society</i> , 2020, 142, 10794-10805.	13.7	17
282	The Exploration of the Active-Site Cavity of Copper-Zinc Superoxide Dismutase. <i>Annals of the New York Academy of Sciences</i> , 1988, 542, 37-52.	3.8	16
283	Binding of cyanide, cyanate, and thiocyanate to human carbonic anhydrase II. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 203-216.	2.6	16
284	Assignment of backbone NMR resonances and secondary structural elements of a reduced monomeric mutant of copper/zinc superoxide dismutase. <i>Magnetic Resonance in Chemistry</i> , 1997, 35, 845-853.	1.9	16
285	Structural and functional studies of monomeric mutant of Cu-Zn superoxide dismutase without Arg 143. <i>J. Biol. Chem.</i> , 1999, 274, S33-S41.		16
286	Side chain mobility as monitored by CH-CH cross correlation: the example of cytochrome b5. <i>Journal of Biomolecular NMR</i> , 2001, 20, 1-10.	2.8	16
287	Catalytic domain of MMP20 (Enamelysin) - The NMR structure of a new matrix metalloproteinase. <i>FEBS Letters</i> , 2007, 581, 4723-4726.	2.8	16
288	An Intrinsically Disordered Domain Has a Dual Function Coupled to Compartment-Dependent Redox Control. <i>Journal of Molecular Biology</i> , 2013, 425, 594-608.	4.2	16

#	ARTICLE	IF	CITATIONS
289	Identification of a novel nucleophosminâ€interaction motif in the tumor suppressor p14arf. FEBS Journal, 2018, 285, 832-847.	4.7	16
290	Paramagnetic 1H NMR Spectroscopy to Investigate the Catalytic Mechanism of Radical S-Adenosylmethionine Enzymes. Journal of Molecular Biology, 2019, 431, 4514-4522.	4.2	16
291	Homo- and heterodimer formation in metalloporphyrins. Inorganic Chemistry, 1985, 24, 782-786.	4.0	15
292	pH-dependent properties of SOD studied through mutants on Lys-136. Inorganic Chemistry, 1993, 32, 1403-1406.	4.0	15
293	Effect of the redox state on HIV-1 tat protein multimerization and cell internalization and trafficking. Molecular and Cellular Biochemistry, 2010, 345, 105-118.	3.1	15
294	Metal cofactors trafficking and assembly in the cell: a molecular view. Pure and Applied Chemistry, 2019, 91, 231-245.	1.9	15
295	In-cell NMR: From target structure and dynamics to drug screening. Current Opinion in Structural Biology, 2022, 74, 102374.	5.7	15
296	Investigation of a new copper-zinc superoxide dismutase mutant: The Thr .fwdarw. Arg 137 derivative. Biochemistry, 1993, 32, 4384-4388.	2.5	14
297	Spectroscopic Characterization of Active Mutants of Manganese Peroxidase:Â Mutations on the Proximal Side Affect Calcium Binding of the Distal Sideâ€. Biochemistry, 1999, 38, 9617-9625.	2.5	14
298	15N Backbone Dynamics of Ferricytochrome b562:Â Comparison with the Reduced Protein and the R98C Variantâ€. Biochemistry, 2001, 40, 12761-12771.	2.5	14
299	Dimethyl propionate ester heme-containing cytochrome b 5: structure and stability. Journal of Biological Inorganic Chemistry, 2001, 6, 490-503.	2.6	14
300	A further investigation of the cytochrome b 5â€cytochrome c complex. Journal of Biological Inorganic Chemistry, 2003, 8, 777-786.	2.6	14
301	An Italian contribution to structural genomics: Understanding metalloproteins. Coordination Chemistry Reviews, 2006, 250, 1419-1450.	18.8	14
302	Copper trafficking in biology: An NMR approach. HFSP Journal, 2009, 3, 165-175.	2.5	14
303	Determination of intracellular proteinâ€ligand binding affinity by competition binding in-cell NMR. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1270-1281.	2.3	14
304	The electron-nucleus dipolar coupling in slow rotating systems. 4. The effect of zero-field splitting and hyperfine coupling when and. Journal of Magnetic Resonance, 1986, 66, 58-65.	0.5	13
305	Determination of Haem Electronic Structure in Cytochrome b5 and Metcyanomyoglobin. FEBS Journal, 1995, 232, 522-527.	0.2	13
306	Solution structure and interaction with copper in vitro and in living cells of the first BIR domain of XIAP. Scientific Reports, 2017, 7, 16630.	3.3	13

#	ARTICLE	IF	CITATIONS
307	Investigating the role of the human CIA2A-CIAO1 complex in the maturation of aconitase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1980-1987.	2.4	13
308	Copper(II) as a probe of the active centers of alkaline phosphatase. <i>Inorganic Chemistry</i> , 1989, 28, 352-358.	4.0	12
309	Modeling the Backbone Dynamics of Reduced and Oxidized Solvated Rat Microsomal Cytochrome b5. <i>Biophysical Journal</i> , 2004, 87, 498-512.	0.5	12
310	NMR Characterization of a "Fibril-Ready" State of Demetalated Wild-Type Superoxide Dismutase. <i>Journal of the American Chemical Society</i> , 2011, 133, 345-349.	13.7	12
311	SARS-CoV-2 M <sup>pro</sup> inhibition by a zinc ion: structural features and hints for drug design. <i>Chemical Communications</i> , 2021, 57, 7910-7913.	4.1	12
312	HIV-1 Tat Protein Enters Dysfunctional Endothelial Cells via Integrins and Renders Them Permissive to Virus Replication. <i>International Journal of Molecular Sciences</i> , 2021, 22, 317.	4.1	12
313	Redox equilibria of manganese peroxidase from <i>Phanerochaetes chrysosporium</i> : functional role of residues on the proximal side of the haem pocket. <i>Biochemical Journal</i> , 2000, 349, 85.	3.7	11
314	From an Inactive Prokaryotic SOD Homologue to an Active Protein through Site-Directed Mutagenesis. <i>Journal of the American Chemical Society</i> , 2005, 127, 13287-13292.	13.7	11
315	Structural characterization of zinc-bound Zmp1, a zinc-dependent metalloprotease secreted by <i>Clostridium difficile</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2016, 21, 185-196.	2.6	11
316	ISCA1 Orchestrates ISCA2 and NFU1 in the Maturation of Human Mitochondrial [4Fe-4S] Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 166924.	4.2	11
317	Rapid protein delivery to living cells for biomolecular investigation. <i>Biochemical and Biophysical Research Communications</i> , 2021, 570, 82-88.	2.1	11
318	Nuclear Relaxation in Paramagnetic Metalloproteins. <i>Biological Magnetic Resonance</i> , 1993, , 79-111.	0.4	11
319	Synthesis, characterization and properties of dinuclear high-spin five-coordinate 3d metal complexes with NN-bis(2-diethylaminoethyl)-2-hydroxyethylamine. <i>Inorganica Chimica Acta</i> , 1980, 39, 35-41.	2.4	10
320	<sup>1</sup> H one-dimensional and two-dimensional NMR studies of the ferricytochrome c 551 from <i>Rhodocyclus gelatinosus</i> . <i>FEBS Journal</i> , 1994, 219, 663-669.	0.2	10
321	Mutation of the Metal-Bridging Proton-Donor His63 Residue in Human Cu, Zn Superoxide Dismutase. <i>Biochemical and Biophysical Analysis of the His63Cys Mutant</i> . <i>FEBS Journal</i> , 1995, 232, 220-225.	0.2	10
322	Tuning the activity of Cu,Zn superoxide dismutase through site-directed mutagenesis: a relatively active monomeric species. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 295-301.	2.6	10
323	Unfolding and pH studies on manganese peroxidase: Role of heme and calcium on secondary structure stability. <i>Biopolymers</i> , 2003, 72, 38-47.	2.4	10
324	Identification of slow motions in the reduced recombinant high-potential iron sulfur protein I (HiPIP) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Biomolecular NMR, 1998, 12, 307-318.	2.8	9

#	ARTICLE	IF	CITATIONS
325	A signalling cascade involving receptor-activated phospholipase A2, glycerophosphoinositol 4-phosphate, Shp1 and Src in the activation of cell motility. <i>Cell Communication and Signaling</i> , 2019, 17, 20.	6.5	9
326	CIAO3 protein forms a stable ternary complex with two key players of the human cytosolic iron-sulfur cluster assembly machinery. <i>Journal of Biological Inorganic Chemistry</i> , 2020, 25, 501-508.	2.6	9
327	The long-standing relationship between paramagnetic NMR and iron-sulfur proteins: the mitoNEET example. An old method for new stories or the other way around?. <i>Magnetic Resonance</i> , 2021, 2, 203-221.	1.9	9
328	Vanadyl binding to bleomycin. <i>Inorganica Chimica Acta</i> , 1982, 67, L53-L55.	2.4	8
329	Solvent 1H NMRD of copper(II) complexes. <i>Chemical Physics Letters</i> , 1985, 118, 345-347.	2.6	8
330	Molecular Engineering of Ghfp, the Gonococcal Orthologue of Neisseria meningitidis Factor H Binding Protein. <i>Vaccine Journal</i> , 2015, 22, 769-777.	3.1	8
331	In...Cellulo Mössbauer and EPR Studies Bring New Evidence to the Long-standing Debate on Iron-Sulfur Cluster Binding in Human Anamorsin. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 14841-14845.	13.8	8
332	Isolation and characterization of a microperoxidase-8 with a modified histidine axial ligand. <i>Journal of Biological Inorganic Chemistry</i> , 2002, 7, 870-878.	2.6	7
333	Ab Initio Molecular Dynamics of Heme in Cytochrome c. <i>Journal of Physical Chemistry B</i> , 2007, 111, 1157-1164.	2.6	7
334	An idea whose time has come. <i>Genome Biology</i> , 2007, 8, 408.	9.6	6
335	Molecular statistics of cytochrome c: structural plasticity and molecular environment. <i>Journal of Biological Inorganic Chemistry</i> , 2007, 12, 180-193.	2.6	6
336	Molecular Basis of Multiple Mitochondrial Dysfunctions Syndrome 2 Caused by CYS59TYR BOLA3 Mutation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4848.	4.1	6
337	Drug Screening in Human Cells by NMR Spectroscopy Allows the Early Assessment of Drug Potency. <i>Angewandte Chemie</i> , 2020, 132, 6597-6601.	2.0	6
338	Protein-Interaction Affinity Gradient Drives [4Fe-4S] Cluster Insertion in Human Lipoyl Synthase. <i>Journal of the American Chemical Society</i> , 2022, 144, 5713-5717.	13.7	6
339	NMR of Paramagnetic Systems. <i>ACS Symposium Series</i> , 1988, , 70-84.	0.5	5
340	1H 3D NOE-NOE spectrum of met-cyanomyoglobin: The first 3D NMR spectrum of a paramagnetic protein. <i>Magnetic Resonance in Chemistry</i> , 1993, 31, S3-S7.	1.9	5
341	Selective versus non-selective T1 experiments to determine metal-nucleus distances in paramagnetic metalloproteins. <i>Inorganica Chimica Acta</i> , 1998, 275-276, 373-379.	2.4	5
342	Solid-state NMR studies of metal-free SOD1 fibrillar structures. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 659-666.	2.6	5

#	ARTICLE	IF	CITATIONS
343	The Casein Kinase 2-Dependent Phosphorylation of NS5A Domain...3 from Hepatitis...C Virus Followed by Time-Resolved NMR Spectroscopy. <i>ChemBioChem</i> , 2016, 17, 328-333.	2.6	5
344	Conformational characterization of full-length X-chromosome-linked inhibitor of apoptosis protein (XIAP) through an integrated approach. <i>IUCr</i> , 2019, 6, 948-957.	2.2	5
345	Conformational characterization of a nickel(II) tetraazamacrocyclic complex through isotropic shift studies of the dinuclear cobalt(II)-nickel(II) derivative. <i>Inorganica Chimica Acta</i> , 1979, 34, L269-L272.	2.4	4
346	A molecular dynamics study of carboxypeptidase A: effect of protonation of Glu 270. <i>Inorganic Chemistry</i> , 1993, 32, 2207-2211.	4.0	4
347	Backbone-only restraints for fast determination of the protein fold: The role of paramagnetism-based restraints. Cytochrome b562 as an example. <i>Journal of Magnetic Resonance</i> , 2005, 172, 191-200.	2.1	4
348	In-house high-energy-remote SAD phasing using the magic triangle: how to tackle the <i>P</i>1 low symmetry using multiple orientations of the same crystal of human IBA57 to increase the multiplicity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 317-324.	2.3	4
349	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments of the SUD domains of SARS-CoV-2 non-structural protein 3c: the N-terminal domain-SUD-N. <i>Biomolecular NMR Assignments</i> , 2021, 15, 85-89.	0.8	4
350	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments of the SUD domains of SARS-CoV-2 non-structural protein 3c: The SUD-M and SUD-C domains. <i>Biomolecular NMR Assignments</i> , 2021, 15, 165-171.	0.8	4
351	Dynamic Jahn-Teller effects in high-spin trigonal-bipyramidal nickel(II) complexes. <i>Inorganic Chemistry</i> , 1984, 23, 3262-3263.	4.0	3
352	Structure and dynamics of heme proteins. <i>Journal of Porphyrins and Phthalocyanines</i> , 2000, 04, 390-391.	0.8	3
353	The human YAE1-ORAOV1 complex of the cytosolic iron-sulfur protein assembly machinery binds a [4Fe-4S] cluster. <i>Inorganica Chimica Acta</i> , 2021, 518, 120252.	2.4	3
354	Iron-Sulfur Proteins: An Insight into their Electronic Structure Through <sup>1</sup> H NMR Spectroscopy. <i>Topics in Molecular Organization and Engineering</i> , 1991, , 73-90.	0.1	3
355	EPR detection of heterodimer species between copper(II), silver (II) and oxovanadium(IV) porphyrins. <i>Inorganica Chimica Acta</i> , 1985, 101, 155-159.	2.4	2
356	<sup>1</sup> H-NMR and relaxometry of copper-containing dimers in proteins. <i>Biology of Metals</i> , 1990, 3, 146-150.	1.1	2
357	Ivano Bertini 1940-2012. <i>Nature Chemical Biology</i> , 2012, 8, 807-807.	8.0	2
358	Interaction of Half Oxa-/Half <i>cis</i>-Platin Complex with Human Superoxide Dismutase and Induced Reduction of Neurotoxicity. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 1094-1098.	2.8	2
359	New structural and functional insights from in-cell NMR. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 29-38.	2.6	2
360	West-Life: A Virtual Research Environment for structural biology. <i>Journal of Structural Biology: X</i> , 2019, 1, 100006.	1.3	2

#	ARTICLE	IF	CITATIONS
361	The solution structure of reduced dimeric copper zinc superoxide dismutase. The structural effects of dimerization. FEBS Journal, 2002, 269, 1905-1915.	0.2	2
362	Determination of Haem Electronic Structure in Cytochrome b 5 and Metcyanomyoglobin. FEBS Journal, 1995, 232, 522-527.	0.2	2
363	Do NMR and ESR provide comparable information in the investigation of metalloporphyrin aggregation?. Inorganica Chimica Acta, 1985, 98, L23-L25.	2.4	1
364	The electron-nucleus coupling: A breakthrough in the investigation of paramagnetic metalloproteins. International Journal of Quantum Chemistry, 1992, 42, 1383-1396.	2.0	1
365	Structure of Biomolecules: Fundamentals. , 2012, , 7-32.		1
366	Structural Knowledge for Molecular Optimization: The Cases of Metal-Mediated Protein-Protein Interactions and Structural Vaccinology. European Journal of Inorganic Chemistry, 2018, 2018, 4108-4116.	2.0	1
367	Pseudocontact shifts as constraints for energy minimization and molecular dynamics calculations on solution structures of paramagnetic metalloproteins. , 1997, 29, 68.		1
368	3D Structure of HiPIPs in Solution through NMR and Molecular Dynamics Studies. , 1995, , 281-296.		1
369	Structural Genomics of Proteins Involved in Copper Homeostasis. ChemInform, 2003, 34, no.	0.0	0
370	Perspectives in Inorganic Structural Genomics: A Trafficking Route for Copper. ChemInform, 2004, 35, no.	0.0	0
371	Biological inorganic chemists pay tribute to Ivano Bertini. Journal of Biological Inorganic Chemistry, 2014, 19, 487-489.	2.6	0
372	Paramagnetic Metalloproteins. , 2021, , 1-8.		0
373	In...Cellulo Mössbauer and EPR Studies Bring New Evidence to the Long-Standing Debate on Iron-Sulfur Cluster Binding in Human Anamorsin. Angewandte Chemie, 2021, 133, 14967-14971.	2.0	0
374	Structural Genomics and Structural Proteomics: A Global Perspective. , 2008, , 505-537.		0
375	Molecular Dynamics Calculations on Metalloproteins. , 1997, , 191-216.		0