Lucia Banci

List of Publications by Year
in descending order

375 papers	21,620 citations	6592 79 h-index	17546 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.	1.8	887
2	Zinc through the Three Domains of Life. Journal of Proteome Research, 2006, 5, 3173-3178.	1.8	544
3	Opposing cardioprotective actions and parallel hypertrophic effects of ÂPKC and ÂPKC. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11114-11119.	3.3	510
4	Faster superoxide dismutase mutants designed by enhancing electrostatic guidance. Nature, 1992, 358, 347-351.	13.7	414
5	Affinity gradients drive copper to cellular destinations. Nature, 2010, 465, 645-648.	13.7	395
6	Solution Structure of Oxidized Horse Heart Cytochrome câ€‚âŠ¥. Biochemistry, 1997, 36, 9867-9877.	1.2	290
7	Metallochaperones and Metal-Transporting ATPases: A Comparative Analysis of Sequences and Structures. Genome Research, 2002, 12, 255-271.	2.4	232
8	MIA40 is an oxidoreductase that catalyzes oxidative protein folding in mitochondria. Nature Structural and Molecular Biology, 2009, 16, 198-206.	3.6	230
9	High-resolution NMR studies of the zinc-binding site of the Alzheimer's amyloid Î²-peptide. FEBS Journal, 2007, 274, 46-59.	2.2	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.	1.6	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.	3.3	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.	3.9	204
14	Atomic-resolution monitoring of protein maturation in live human cells by NMR. Nature Chemical Biology, 2013, 9, 297-299.	3.9	204
15	Occurrence of Copper Proteins through the Three Domains of Life: A Bioinformatic Approach. Journal of Proteome Research, 2008, 7, 209-216.	1.8	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.	3.3	173
17	Solution Structure of the Cu(I) and Apo Forms of the Yeast Metallochaperone, Atx1â€‚â€¡. Biochemistry, 2001, 40, 1528-1539.	1.2	172
18	MetalPDB in 2018: a database of metal sites in biological macromolecular structures. Nucleic Acids Research, 2018, 46, D459-D464.	6.5	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.	3.3	162
20	Structural properties of peroxidases. Journal of Biotechnology, 1997, 53, 253-263.	1.9	161
21	Identification of localized redox states in plant-type two-iron ferredoxins using the nuclear Overhauser effect. Biochemistry, 1990, 29, 2263-2271.	1.2	160
22	SOD1 and Amyotrophic Lateral Sclerosis: Mutations and Oligomerization. PLoS ONE, 2008, 3, e1677.	1.1	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.	3.3	150
24	Cellular copper distribution: a mechanistic systems biology approach. Cellular and Molecular Life Sciences, 2010, 67, 2563-2589.	2.4	145
25	A novel intermembrane spaceâ€“targeting signal docks cysteines onto Mia40 during mitochondrial oxidative folding. Journal of Cell Biology, 2009, 187, 1007-1022.	2.3	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.	1.1	143
27	Proton NOE studies on dicopper(II) dicobalt(II) superoxide dismutase. Inorganic Chemistry, 1989, 28, 4650-4656.	1.9	140
28	Functional reconstitution of mitochondrial Fe/S cluster synthesis on Isu1 reveals the involvement of ferredoxin. Nature Communications, 2014, 5, 5013.	5.8	136
29	Solution Structure of Reduced Monomeric Q133M2 Copper, Zinc Superoxide Dismutase (SOD). Why Is SOD a Dimeric Enzyme?â€‚â€¡. Biochemistry, 1998, 37, 11780-11791.	1.2	135
30	Rational Design of a Meningococcal Antigen Inducing Broad Protective Immunity. Science Translational Medicine, 2011, 3, 91ra62.	5.8	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.	1.6	132
32	A New Zincâ€“protein Coordination Site in Intracellular Metal Trafficking: Solution Structure of the Apo and Zn(II) forms of ZntA(46â€“118). Journal of Molecular Biology, 2002, 323, 883-897.	2.0	132
33	Solution Structure of Apo Cu,Zn Superoxide Dismutase:Â Role of Metal Ions in Protein Foldingâ€. Biochemistry, 2003, 42, 9543-9553.	1.2	127
34	Solution Structure of OxidizedSaccharomyces cerevisiaeIso-1-cytochromecâ€‚â€¡. Biochemistry, 1997, 36, 8992-9001.	1.2	125
35	Solution Structure of the Apo and Copper(I)-Loaded Human Metallochaperone HAH1â€. Biochemistry, 2004, 43, 13046-13053.	1.2	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.	1.6	122

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37	Folding Studies of Cox17 Reveal an Important Interplay of Cysteine Oxidation and Copper Binding. Structure, 2005, 13, 713-722.	1.6	121
38	Spectroscopic studies on Cu2Zn2SOD: a continuous advancement of investigation tools. Coordination Chemistry Reviews, 1990, 100, 67-103.	9.5	120
39	Solution Structure of Sco1. Structure, 2003, 11, 1431-1443.	1.6	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.	3.3	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.	3.3	120
42	Paramagnetism-Based Restraints for Xplor-NIH. Journal of Biomolecular NMR, 2004, 28, 249-261.	1.6	119
43	Solution structure of reduced horse heart cytochrome c. Journal of Biological Inorganic Chemistry, 1999, 4, 21-31.	1.1	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.	3.3	116
45	[2Fe-2S] cluster transfer in ironâ€“sulfur protein biogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6203-6208.	3.3	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.	6.6	114
47	Formation of [4Fe-4S] Clusters in the Mitochondrial Ironâ€“Sulfur Cluster Assembly Machinery. Journal of the American Chemical Society, 2014, 136, 16240-16250.	6.6	114
48	Mechanism of CuA assembly. Nature Chemical Biology, 2008, 4, 599-601.	3.9	113
49	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.	6.6	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.	3.3	109
51	Copper Trafficking:â€‰ the Solution Structure of Bacillus subtilis CopZ. Biochemistry, 2001, 40, 15660-15668.	1.2	106
52	The human iron-proteomeâ€. Metallomics, 2018, 10, 1223-1231.	1.0	106
53	Solution Structure of CopC. Structure, 2002, 10, 1337-1347.	1.6	104
54	In-cell NMR: a topical review. IUCrJ, 2017, 4, 108-118.	1.0	104

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55	In-cell NMR reveals potential precursor of toxic species from SOD1 fALS mutants. Nature Communications, 2014, 5, 5502.	5.8	103
56	[4Fe-4S] Cluster Assembly in Mitochondria and Its Impairment by Copper. Journal of the American Chemical Society, 2017, 139, 719-730.	6.6	103
57	Emergence of a Homo sapiens-specific gene family and chromosome 16p11.2 CNV susceptibility. Nature, 2016, 536, 205-209.	13.7	102
58	The three-dimensional structure in solution of the paramagnetic high-potential iron-sulfur protein I from Ectothiorhodospira halophila through nuclear magnetic resonance. FEBS Journal, 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. , 1997, 29, 68-76.		99
60	A hint for the function of human Sco1 from different structures. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8595-8600.	3.3	99
61	A Strategy for the NMR Characterization of Type II Copper(II) Proteins:Â the Case of the Copper Trafficking Protein CopC fromPseudomonasSyringae. Journal of the American Chemical Society, 2003, 125, 7200-7208.	6.6	98
62	Mitochondrial Bol1 and Bol3 function as assembly factors for specific iron-sulfur proteins. ELife, 2016, 5, .	2.8	96
63	Solution Structure of Cox11, a Novel Type of Î²-Immunoglobulin-like Fold Involved in CuB Site Formation of Cytochrome c Oxidase. Journal of Biological Chemistry, 2004, 279, 34833-34839.	1.6	93
64	Metal Binding Domains 3 and 4 of the Wilson Disease Protein: Solution Structure and Interaction with the Copper(I) Chaperone HAH1. Biochemistry, 2008, 47, 7423-7429.	1.2	93
65	Proton NMR investigation into the basis for the relatively high redox potential of lignin peroxidase.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 6956-6960.	3.3	92
66	Molecular recognition and substrate mimicry drive the electron-transfer process between MIA40 and ALR. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4811-4816.	3.3	92
67	Mitochondrial cytochromes c: a comparative analysis. Journal of Biological Inorganic Chemistry, 1999, 4, 824-837.	1.1	91
68	A Structural-Dynamical Characterization of Human Cox17. Journal of Biological Chemistry, 2008, 283, 7912-7920.	1.6	91
69	Cyanobacterial metallochaperone inhibits deleterious side reactions of copper. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 95-100.	3.3	91
70	Three-Dimensional Solution Structure of Saccharomyces cerevisiae Reduced Iso-1-cytochrome c. Biochemistry, 1996, 35, 13788-13796.	1.2	89
71	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.	1.6	88
72	The 1H NMR parameters of magnetically coupled dimersâ€"The Fe2S2 proteins as an example. , 1990, , 113-136.		87

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73	Lignin and Mn Peroxidase-Catalyzed Oxidation of Phenolic Lignin Oligomers. Biochemistry, 1999, 38, 3205-3210.	1.2	87
74	A copper(I) protein possibly involved in the assembly of CuA center of bacterial cytochrome c oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3994-3999.	3.3	87
75	The electronic structure of iron-sulfur [Fe4S4]3+ clusters in proteins. An investigation of the oxidized high-potential iron-sulfur protein II from Ectothiorhodospira vacuolata. Biochemistry, 1993, 32, 9387-9397.	1.2	86
76	The Solution Structure of Oxidized Rat Microsomal Cytochromeb5â€‚â€¡. Biochemistry, 1998, 37, 173-184.	1.2	86
77	Copper(I)-mediated proteinâ€“protein interactions result from suboptimal interaction surfaces. Biochemical Journal, 2009, 422, 37-42.	1.7	85
78	The solution structure of reduced dimeric copper zinc superoxide dismutase. FEBS Journal, 2002, 269, 1905-1915.	0.2	84
79	Understanding Copper Trafficking in Bacteria:Â Interaction between the Copper Transport Protein CopZ and the N-Terminal Domain of the Copper ATPase CopA fromBacillus subtilisâ€. Biochemistry, 2003, 42, 1939-1949.	1.2	84
80	NMR structures of paramagnetic metalloproteins. Quarterly Reviews of Biophysics, 2005, 38, 167-219.	2.4	84
81	The Solution Structure of Oxidized Escherichia coli Cytochrome b562,. Biochemistry, 1999, 38, 8657-8670.	1.2	82
82	Preparation, physico-chemical and pharmacokinetic characterization of monomethoxypoly(ethylene) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	4.8	80
83	The three-dimensional solution structure of the reduced high-potential iron-sulfur protein from Chromatium vinosum through NMR. Biochemistry, 1995, 34, 206-219.	1.2	80
84	Characterization of proteins by in-cell NMR spectroscopy in cultured mammalian cells. Nature Protocols, 2016, 11, 1101-1111.	5.5	80
85	A Unique Tool for Cellular Structural Biology: In-cell NMR. Journal of Biological Chemistry, 2016, 291, 3776-3784.	1.6	80
86	Protein networks in the maturation of human ironâ€“sulfur proteins. Metallomics, 2018, 10, 49-72.	1.0	79
87	Molecular recognition in copper trafficking. Natural Product Reports, 2010, 27, 695.	5.2	78
88	Binding of Bicarbonate to Human Carbonic Anhydrase II:Â A Continuum of Binding States. Journal of the American Chemical Society, 1997, 119, 863-871.	6.6	77
89	Perspectives in Inorganic Structural Genomics: A Trafficking Route for Copper. European Journal of Inorganic Chemistry, 2004, 2004, 1583-1593.	1.0	77
90	Protein interaction patterns in different cellular environments are revealed by in-cell NMR. Scientific Reports, 2015, 5, 14456.	1.6	77

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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.	2.0	75
92	Human SOD1 before Harboring the Catalytic Metal. Journal of Biological Chemistry, 2006, 281, 2333-2337.	1.6	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.	7.6	73
94	Molecular dynamics simulations of metalloproteins. Current Opinion in Chemical Biology, 2003, 7, 143-149.	2.8	71
95	N-terminal domains mediate [2Fe-2S] cluster transfer from glutaredoxin-3 to anamorsin. Nature Chemical Biology, 2015, 11, 772-778.	3.9	71
96	The cysteine-reactive small molecule ebselen facilitates effective SOD1 maturation. Nature Communications, 2018, 9, 1693.	5.8	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.	1.9	70
98	Non-heme iron through the three domains of life. Proteins: Structure, Function and Bioinformatics, 2007, 67, 317-324.	1.5	70
99	Structure and dynamics of copper-free SOD: The protein before binding copper. Protein Science, 2009, 11, 2479-2492.	3.1	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.	6.6	69
101	Proton NMR investigation of manganese peroxidase from Phanerochaete chrysosporium. A comparison with other peroxidases. Biochemistry, 1992, 31, 10009-10017.	1.2	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.	3.3	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.	2.0	67
104	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 16873-16879.	6.6	67
105	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. Metallomics, 2018, 10, 1755-1776.	1.0	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.	1.2	65
107	PSEUDYANA for NMR structure calculation of paramagnetic metalloproteins using torsion angle molecular dynamics. Journal of Biomolecular NMR, 1998, 12, 553-557.	1.6	65
108	Oxidation of a Tetrameric Nonphenolic Lignin Model Compound by Lignin Peroxidase. Journal of Biological Chemistry, 2001, 276, 22985-22990.	1.6	65

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109	Anamorsin Is a [2Fe-2S] Cluster-Containing Substrate of the Mia40-Dependent Mitochondrial Protein Trapping Machinery. Chemistry and Biology, 2011, 18, 794-804.	6.2	65
110	Interaction of Cisplatin with Human Superoxide Dismutase. Journal of the American Chemical Society, 2012, 134, 7009-7014.	6.6	65
111	Correlation between anisotropic exchange and structure of di-Î¼-hydroxy bridged copper(II) complexes. Journal of the American Chemical Society, 1983, 105, 761-764.	6.6	64
112	Binding of horseradish, lignin, and manganese peroxidases to their respective substrates. Biochemistry, 1993, 32, 5825-5831.	1.2	64
113	Analysis of the Temperature Dependence of the1H and13C Isotropic Shifts of Horse Heart Ferricytochromec:Â Explanation of Curie and Anti-Curie Temperature Dependence and Nonlinear Pseudocontact Shifts in a Common Two-Level Framework. Journal of the American Chemical Society, 1998, 120, 8472-8479.	6.6	64
114	Elucidating the Molecular Function of Human BOLA2 in GRX3-Dependent Anamorsin Maturation Pathway. Journal of the American Chemical Society, 2015, 137, 16133-16143.	6.6	64
115	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.	1.2	63
116	Molecular view of an electron transfer process essential for ironâ€“sulfur protein biogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7136-7141.	3.3	63
117	Structural Basis for the Function of the N-terminal Domain of the ATPase CopA from Bacillus subtilis. Journal of Biological Chemistry, 2003, 278, 50506-50513.	1.6	62
118	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.	1.6	62
119	In-cell NMR in E. coli to Monitor Maturation Steps of hSOD1. PLoS ONE, 2011, 6, e23561.	1.1	62
120	Backbone Dynamics of Human Cu,Zn Superoxide Dismutase and of Its Monomeric F50E/G51E/E133Q Mutant:Â The Influence of Dimerization on Mobility and Functionâ€. Biochemistry, 2000, 39, 9108-9118.	1.2	61
121	Dynamic Properties of the G93A Mutant of Copperâˆ’Zinc Superoxide Dismutase As Detected by NMR Spectroscopy:Â Implications for the Pathology of Familial Amyotrophic Lateral Sclerosisâ€. Biochemistry, 2003, 42, 1890-1899.	1.2	60
122	An investigation of superoxide dismutase Lys-143, Ile-143, and Glu-143 mutants: Cu2Co2SOD derivatives. Journal of the American Chemical Society, 1988, 110, 3629-3633.	6.6	59
123	Structural Basis for Metal Binding Specificity: the N-terminal Cadmium Binding Domain of the P1-type ATPase CadA. Journal of Molecular Biology, 2006, 356, 638-650.	2.0	59
124	Structural Genomics of Proteins Involved in Copper Homeostasis. Accounts of Chemical Research, 2003, 36, 215-221.	7.6	58
125	Loop recognition and copper-mediated disulfide reduction underpin metal site assembly of Cu _A in human cytochrome oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11771-11776.	3.3	58
126	MetalPredator: a web server to predict ironâ€“sulfur cluster binding proteomes. Bioinformatics, 2016, 32, 2850-2852.	1.8	58

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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. FEBS Journal, 2005, 272, 865-871.	2.2	57
128	EPR spectra of trinuclear complexes. Octachlorodiadeniniumtricopper(II) tetrahydrate. Inorganic Chemistry, 1983, 22, 2681-2683.	1.9	56
129	Superoxide Dismutase Folding/Unfolding Pathway: Role of the Metal Ions in Modulating Structural and Dynamical Features. Journal of Molecular Biology, 2003, 330, 145-158.	2.0	56
130	A Docking Approach to the Study of Copper Trafficking Proteins. Structure, 2004, 12, 669-676.	1.6	56
131	Fully Metallated S134N Cu,Zn-Superoxide Dismutase Displays Abnormal Mobility and Intermolecular Contacts in Solution. Journal of Biological Chemistry, 2005, 280, 35815-35821.	1.6	56
132	The Functions of Sco Proteins from Genome-Based Analysis. Journal of Proteome Research, 2007, 6, 1568-1579.	1.8	56
133	HIV-1 Tat Promotes Integrin-Mediated HIV Transmission to Dendritic Cells by Binding Env Spikes and Competes Neutralization by Anti-HIV Antibodies. PLoS ONE, 2012, 7, e48781.	1.1	56
134	Active Site Coordination Chemistry of the Cytochrome c Peroxidase Asp235Ala Variant: Spectroscopic and Functional Characterization. Biochemistry, 1994, 33, 7819-7829.	1.2	55
135	The delivery of copper for thylakoid import observed by NMR. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8320-8325.	3.3	55
136	Solution Structure of the Factor H-binding Protein, a Survival Factor and Protective Antigen of Neisseria meningitidis. Journal of Biological Chemistry, 2009, 284, 9022-9026.	1.6	55
137	Paramagnetic 1H NMR Spectroscopy of the Cyanide Derivative of Met80Ala-iso-1-cytochrome c. Journal of the American Chemical Society, 1995, 117, 8067-8073.	6.6	54
138	The Different Intermolecular Interactions of the Soluble Copper-binding Domains of the Menkes Protein, ATP7A*. Journal of Biological Chemistry, 2007, 282, 23140-23146.	1.6	54
139	A Structural Characterization of Human SCO2. Structure, 2007, 15, 1132-1140.	1.6	54
140	Structure of Nucleophosmin DNA-binding Domain and Analysis of Its Complex with a G-quadruplex Sequence from the c-MYC Promoter. Journal of Biological Chemistry, 2012, 287, 26539-26548.	1.6	54
141	Visualization of Redox-Controlled Protein Fold in Living Cells. Chemistry and Biology, 2013, 20, 747-752.	6.2	54
142	Enzyme-catalyzed Mechanism of Isoniazid Activation in Class I and Class III Peroxidases. Journal of Biological Chemistry, 2004, 279, 39000-39009.	1.6	53
143	The Evolutionarily Conserved Trimeric Structure of CutA1 Proteins Suggests a Role in Signal Transduction. Journal of Biological Chemistry, 2003, 278, 45999-46006.	1.6	52
144	New Type 2 Copperâ˘Cysteinate Proteins. Copper Site Histidine-to-Cysteine Mutants of Yeast Copperâ˘Zinc Superoxide Dismutase. Inorganic Chemistry, 1996, 35, 1692-1700.	1.9	51

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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.	1.6	50
147	Human anamorsin binds [2Feâ€"2S] clusters with unique electronic properties. Journal of Biological Inorganic Chemistry, 2013, 18, 883-893.	1.1	50
148	Comparative proton NMR study of ferric low-spin cytochrome c peroxidase and horseradish peroxidase. Inorganic Chemistry, 1991, 30, 4510-4516.	1.9	49
149	Seeking the determinants of the elusive functions of Sco proteins. FEBS Journal, 2011, 278, 2244-2262.	2.2	49
150	The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. PLoS ONE, 2017, 12, e0171279.	1.1	49
151	Characterization and Peroxidase Activity of a Myoglobin Mutant Containing a Distal Arginine. ChemBioChem, 2002, 3, 226-233.	1.3	48
152	Solution Structure and Characterization of the Heme Chaperone CcmE. Biochemistry, 2002, 41, 13587-13594.	1.2	47
153	X-Ray Absorption and NMR Spectroscopic Studies of CopZ, a Copper Chaperone in Bacillus subtilis:â€‰ The Coordination Properties of the Copper Ion. Biochemistry, 2003, 42, 2467-2474.	1.2	47
154	Individual Reduction Potentials of the Iron Ions in Fe2S2and High-Potential Fe4S4Ferredoxins. Inorganic Chemistry, 1996, 35, 4248-4253.	1.9	46
155	Structural Consequences ofb- toc-type Heme Conversion in OxidizedEscherichia coliCytochromeb562â€‚â€¡. Biochemistry, 2000, 39, 1499-1514.	1.2	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.	1.1	46
157	Molecular Dynamics Studies on Peroxidases: A Structural Model for Horse Radish Peroxidase and a Substrate Adduct. Biochemistry, 1994, 33, 12356-12366.	1.2	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.	2.0	44
159	IBA57 Recruits ISCA2 to Form a [2Fe-2S] Cluster-Mediated Complex. Journal of the American Chemical Society, 2018, 140, 14401-14412.	6.6	44
160	Protein in-cell NMR spectroscopy at 1.2ÂGHz. Journal of Biomolecular NMR, 2021, 75, 97-107.	1.6	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.	7.2	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.	6.6	43

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163	Factoring of the Hyperfine Shifts in the Cyanide Adduct of Lignin Peroxidase from P. chrysosporium. Journal of the American Chemical Society, 1995, 117, 8659-8667.	6.6	43
164	Solution structure of oxidized microsomal rabbit cytochrome b5. FEBS Journal, 2000, 267, 755-766.	0.2	43
165	Molecular Dynamics Characterization of the C2 Domain of Protein Kinase CÎ². Journal of Biological Chemistry, 2002, 277, 12988-12997.	1.6	43
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