Simone Ciofi-Baffoni

List of Publications by Year
in descending order

88 papers	5,403 citations	57631 44 h-index	82410 72 g-index
91 all docs	91 docs citations	91 times ranked	4628 citing authors

#	Article	IF	Citations
1	Interconversion between [2Feâ€“2S] and [4Feâ€“4S] cluster glutathione complexes. Chemical Communications, 2022, 58, 3533-3536.	2.2	7
2	Ironâ€“sulfur clusters as inhibitors and catalysts of viral replication. Nature Chemistry, 2022, 14, 253-266.	6.6	23
3	Protein-Interaction Affinity Gradient Drives [4Feâ€“4S] Cluster Insertion in Human Lipoyl Synthase. Journal of the American Chemical Society, 2022, 144, 5713-5717.	6.6	6
4	The Intriguing Role of Iron-Sulfur Clusters in the CIAPIN1 Protein Family. Inorganics, 2022, 10, 52.	1.2	1
5	The human YAE1-ORAOV1 complex of the cytosolic iron-sulfur protein assembly machinery binds a [4Fe-4S] cluster. Inorganica Chimica Acta, 2021, 518, 120252.	1.2	3
6	Inâ€...Cellulo MÃ¶ssbauer and EPR Studies Bring New Evidence to the Longâ€Standing Debate on Ironâ€“Sulfur Cluster Binding in Human Anamorsin. Angewandte Chemie, 2021, 133, 14967-14971.	1.6	0
7	ISCA1 Orchestrates ISCA2 and NFU1 in the Maturation of Human Mitochondrial [4Fe-4S] Proteins. Journal of Molecular Biology, 2021, 433, 166924.	2.0	11
8	Molecular Basis of Multiple Mitochondrial Dysfunctions Syndrome 2 Caused by CYS59TYR BOLA3 Mutation. International Journal of Molecular Sciences, 2021, 22, 4848.	1.8	6
9	Inâ€...Cellulo MÃ¶ssbauer and EPR Studies Bring New Evidence to the Longâ€Standing Debate on Ironâ€“Sulfur Cluster Binding in Human Anamorsin. Angewandte Chemie - International Edition, 2021, 60, 14841-14845.	7.2	8
10	A pathway for assembling [4Feâ€4S]²⁺ clusters in mitochondrial ironâ€“sulfur protein biogenesis. FEBS Journal, 2020, 287, 2312-2327.	2.2	36
11	GLRX3 Acts as a [2Feâ€“2S] Cluster Chaperone in the Cytosolic Ironâ€“Sulfur Assembly Machinery Transferring [2Feâ€“2S] Clusters to NUBP1. Journal of the American Chemical Society, 2020, 142, 10794-10805.	6.6	17
12	7. Basic Iron-Sulfur Centers. , 2020, 20, 199-256.		2
13	Paramagnetic 1H NMR Spectroscopy to Investigate the Catalytic Mechanism of Radical S-Adenosylmethionine Enzymes. Journal of Molecular Biology, 2019, 431, 4514-4522.	2.0	16
14	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. Acta Crystallographica Section D: Structural Biology, 2019, 75, 317-324.	1.1	4
15	Structural properties of [2Fe-2S] ISCA2-IBA57: a complex of the mitochondrial iron-sulfur cluster assembly machinery. Scientific Reports, 2019, 9, 18986.	1.6	22
16	Protein networks in the maturation of human ironâ€“sulfur proteins. Metallomics, 2018, 10, 49-72.	1.0	79
17	The NMR contribution to proteinâ€“protein networking in Feâ€“S protein maturation. Journal of Biological Inorganic Chemistry, 2018, 23, 665-685.	1.1	25
18	IBA57 Recruits ISCA2 to Form a [2Fe-2S] Cluster-Mediated Complex. Journal of the American Chemical Society, 2018, 140, 14401-14412.	6.6	44

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19	Kinetic analysis of copper transfer from a chaperone to its target protein mediated by complex formation. Chemical Communications, 2017, 53, 1397-1400.	2.2	12
20	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
21	[4Fe-4S] Cluster Assembly in Mitochondria and Its Impairment by Copper. Journal of the American Chemical Society, 2017, 139, 719-730.	6.6	103
22	Anamorsin/Ndor1 Complex Reduces [2Feâ€"2S]-MitoNEET via a Transient Proteinâ€"Protein Interaction. Journal of the American Chemical Society, 2017, 139, 9479-9482.	6.6	30
23	Mitochondrial Bol1 and Bol3 function as assembly factors for specific iron-sulfur proteins. ELife, 2016, 5, .	2.8	96
24	Emergence of a Homo sapiens-specific gene family and chromosome 16p11.2 CNV susceptibility. Nature, 2016, 536, 205-209.	13.7	102
25	N-terminal domains mediate [2Fe-2S] cluster transfer from glutaredoxin-3 to anamorsin. Nature Chemical Biology, 2015, 11, 772-778.	3.9	71
26	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
27	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
28	The IR-15N-HSQC-AP experiment: a new tool for NMR spectroscopy of paramagnetic molecules. Journal of Biomolecular NMR, 2014, 58, 123-128.	1.6	34
29	[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
30	An Intrinsically Disordered Domain Has a Dual Function Coupled to Compartment-Dependent Redox Control. Journal of Molecular Biology, 2013, 425, 594-608.	2.0	16
31	Human anamorsin binds [2Feâ€"2S] clusters with unique electronic properties. Journal of Biological Inorganic Chemistry, 2013, 18, 883-893.	1.1	50
32	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
33	Structural characterization of CHCHD5 and CHCHD7: Two atypical human twin CX9C proteins. Journal of Structural Biology, 2012, 180, 190-200.	1.3	26
34	An Electron-Transfer Path through an Extended Disulfide Relay System: The Case of the Redox Protein ALR. Journal of the American Chemical Society, 2012, 134, 1442-1445.	6.6	40
35	Targeting and Maturation of Erv1/ALR in the Mitochondrial Intermembrane Space. ACS Chemical Biology, 2012, 7, 707-714.	1.6	25
36	Copper exposure effects on yeast mitochondrial proteome. Journal of Proteomics, 2011, 74, 2522-2535.	1.2	20

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37	Seeking the determinants of the elusive functions of Sco proteins. FEBS Journal, 2011, 278, 2244-2262.	2.2	49
38	Sco proteins are involved in electron transfer processes. Journal of Biological Inorganic Chemistry, 2011, 16, 391-403.	1.1	19
39	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
40	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
41	Functional Role of Two Interhelical Disulfide Bonds in Human Cox17 Protein from a Structural Perspective. Journal of Biological Chemistry, 2011, 286, 34382-34390.	1.6	22
42	Cellular copper distribution: a mechanistic systems biology approach. Cellular and Molecular Life Sciences, 2010, 67, 2563-2589.	2.4	145
43	NMR structural analysis of the soluble domain of ZiaA-ATPase and the basis of selective interactions with copper metallochaperone Atx1. Journal of Biological Inorganic Chemistry, 2010, 15, 87-98.	1.1	19
44	Affinity gradients drive copper to cellular destinations. Nature, 2010, 465, 645-648.	13.7	395
45	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
46	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
47	The coiled coilâ€helixâ€coiled coilâ€helix proteins may be redox proteins. FEBS Letters, 2009, 583, 1699-1702.	1.3	25
48	MIA40 is an oxidoreductase that catalyzes oxidative protein folding in mitochondria. Nature Structural and Molecular Biology, 2009, 16, 198-206.	3.6	230
49	Copper trafficking in biology: An NMR approach. HFSP Journal, 2009, 3, 165-175.	2.5	14
50	Mechanism of CuA assembly. Nature Chemical Biology, 2008, 4, 599-601.	3.9	113
51	Structure and Cu(I)-binding properties of the N-terminal soluble domains of <i>Bacillus subtilis</i> CopA. Biochemical Journal, 2008, 411, 571-579.	1.7	34
52	A Structural-Dynamical Characterization of Human Cox17. Journal of Biological Chemistry, 2008, 283, 7912-7920.	1.6	91
53	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
54	The Characterization and Role of Zinc Binding in Yeast Cox4. Journal of Biological Chemistry, 2007, 282, 8926-8934.	1.6	35

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55	NMR Structural Analysis of Cadmium Sensing by Winged Helix Repressor CmtR. Journal of Biological Chemistry, 2007, 282, 30181-30188.	1.6	41
56	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
57	Modeling Proteinâ˘'Protein Complexes Involved in the CytochromecOxidase Copper-Delivery Pathway. Journal of Proteome Research, 2007, 6, 1530-1539.	1.8	27
58	A Structural Characterization of Human SCO2. Structure, 2007, 15, 1132-1140.	1.6	54
59	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
60	NMR in the SPINE Structural Proteomics project. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1150-1161.	2.5	12
61	An Italian contribution to structural genomics: Understanding metalloproteins. Coordination Chemistry Reviews, 2006, 250, 1419-1450.	9.5	14
62	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
63	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
64	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
65	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
66	The Effects of Ligand Exchange and Mobility on the Peroxidase Activity of a Bacterial Cytochrome c upon Unfolding. ChemBioChem, 2005, 6, 747-758.	1.3	5
67	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
68	Effects of Heme on the Structure of the Denatured State and Folding Kinetics of Cytochrome b562. Journal of Molecular Biology, 2005, 346, 331-344.	2.0	33
69	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
70	Solution Structures of a Cyanobacterial Metallochaperone. Journal of Biological Chemistry, 2004, 279, 27502-27510.	1.6	50
71	Perspectives in Inorganic Structural Genomics: A Trafficking Route for Copper. European Journal of Inorganic Chemistry, 2004, 2004, 1583-1593.	1.0	77
72	Perspectives in Inorganic Structural Genomics: A Trafficking Route for Copper. ChemInform, 2004, 35, no.	0.1	0

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73	Solution Structure of Sco1. Structure, 2003, 11, 1431-1443.	1.6	120
74	Unfolding and pH studies on manganese peroxidase: Role of heme and calcium on secondary structure stability. Biopolymers, 2003, 72, 38-47.	1.2	10
75	A Core Mutation Affecting the Folding Properties of a Soluble Domain of the ATPase Protein CopA from Bacillus subtilis. Journal of Molecular Biology, 2003, 331, 473-484.	2.0	32
76	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
77	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
78	Metallochaperones and Metal-Transporting ATPases: A Comparative Analysis of Sequences and Structures. Genome Research, 2002, 12, 255-271.	2.4	232
79	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
80	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
81	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
82	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
83	15N Backbone Dynamics of Ferricytochromeb562:Â Comparison with the Reduced Protein and the R98C Variantâ€. Biochemistry, 2001, 40, 12761-12771.	1.2	14
84	Oxidation of a Tetrameric Nonphenolic Lignin Model Compound by Lignin Peroxidase. Journal of Biological Chemistry, 2001, 276, 22985-22990.	1.6	65
85	Structural Consequences ofb- toc-type Heme Conversion in OxidizedEscherichia coliCytochromeb562â€,â€¡. Biochemistry, 2000, 39, 1499-1514.	1.2	46
86	Lignin and Mn Peroxidase-Catalyzed Oxidation of Phenolic Lignin Oligomers. Biochemistry, 1999, 38, 3205-3210.	1.2	87
87	A new asymmetric approach toward 5-substituted pyrrolidin-2-one derivatives. Tetrahedron, 1998, 54, 10403-10418.	1.0	24
88	Synthesis of oligomeric mimics of lignin. Journal of the Chemical Society Perkin Transactions 1, 1998, , 3207-3218.	0.9	23