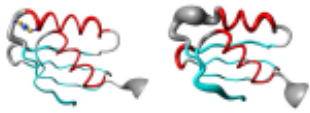
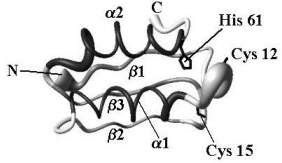



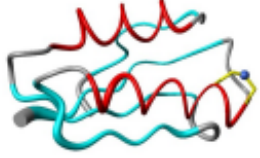
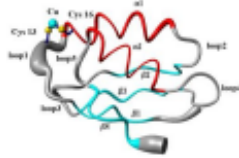


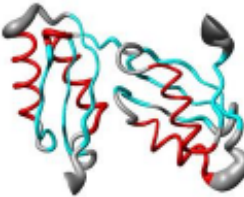





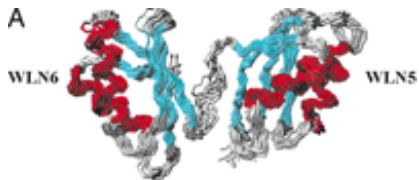
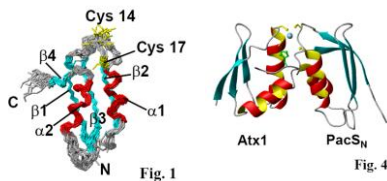
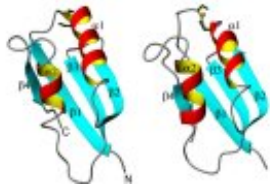
COPPER BINDING PROTEINS

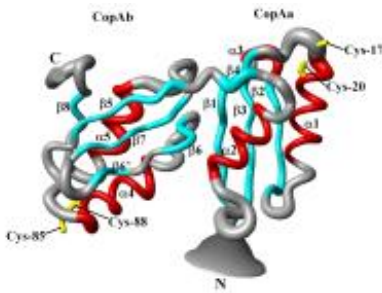
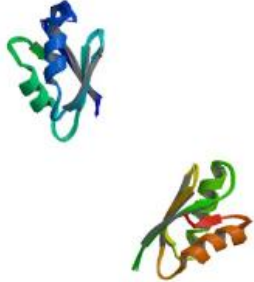
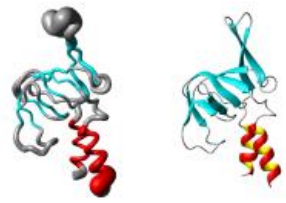

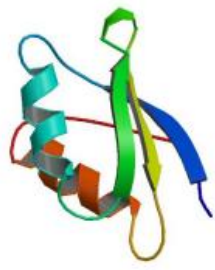
Copper chaperons

<p>Arnesano, F., Banci, L., Bertini, I., Huffman D.L., O'Halloran, T.V. Solution structure of the Cu(I) and apo forms of the yeast metallochaperone, Atx1 Biochemistry, 40: 1528-1539, 2001</p>	 <p>PDB code: 1FD8, 1FES</p>
<p>Banci, L., Bertini, I., Borrelly, G. P. M., Ciofi-Baffoni, S., Robinson, N. J., Su, X. C. Solution structures of a cyanobacterial metallochaperone: insight into an atypical copper binding motif J.Biol.Chem., 279: 27502-27510, 2004</p>	 <p>PDB code: 1SB6</p>
<p>Anastassopoulou, J., Banci, L., Bertini, I., Cantini, F., Katsari, E., Rosato, A. Solution structure of the apo-and copper(I) loaded human metallochaperone Hah1 Biochemistry, 43: 13046-13053, 2004</p>	 <p>PDB code: 1TL4, 1TL5</p>
<p>Totter, S., Patterson, A. M., Banci, L., Bertini, I., Felli, I. C., Pavelkova, A., Dainty, S. J., Pernil, R., Waldron, K. J., Foster, A. W., Robinson, N. J. Cyanobacterial metallochaperone inhibits deleterious side reactions of copper Proc.Natl.Acad.Sci.USA: 109: 95-100, 2012</p>	 <p>PDB code: 2LDI</p>
<p>Banci, L., Cantini, F., Kozyreva, T., Rubino, J. T. Mechanistic aspects of hSOD1 maturation from the solution structure of Cu1-loaded hCCS domain 1 and analysis of disulfide-free hSOD1 mutants ChemBioChem, 2013, Epub ahead of print</p>	 <p>PDB code: 2RSQ</p>

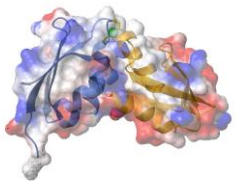

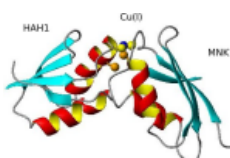
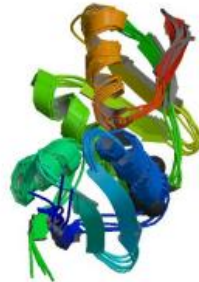
P1-type ATPases's

<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Huffman, D.L., O'Halloran, T.V. Solution structure of the yeast copper transporter domain Ccc2a in the apo and Cu(I)-loaded states <i>J.Biol.Chem.</i>, 276: 8415-8426, 2001</p>	 <p>PDB code: 1FVS, 1FVQ</p>
<p>Banci, L., Bertini, I., Del Conte, R., Markey, J., Ruiz-Duenas, F.J. Copper trafficking: the solution structures of <i>Bacillus subtilis</i> CopZ <i>Biochemistry</i>, 40: 15660-15668, 2001</p>	 <p>PDB code: 1K0V</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., D'Onofrio, M., Gonnelli, L., Marhuenda-Egea, F. C., Ruiz-Dueñas, F. J. Solution structure of the N-terminal domain of a potential copper-translocating P-Type ATPase from <i>Bacillus subtilis</i> in the Apo and Cu(I) loaded states <i>J.Mol.Biol.</i>, 317: 415-422, 2002</p>	 <p>PDB code: 1JWW, 1KQK</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Gonnelli, L., Su, X.C. A core mutation affecting the folding properties of a soluble domain of the ATPase protein CopA from <i>Bacillus subtilis</i> <i>J.Mol.Biol.</i>, 331: 473-484, 2003</p>	 <p>PDB code: 1OQ3, 1OQ6, 1OPZ</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Gonnelli, L., Su, X.C. Structural basis for the function of the N terminal domain of the APTase CopA from <i>Bacillus subtilis</i> <i>J.Biol.Chem.</i>, 278: 50506-50513, 2003</p>	 <p>PDB code: 1P6T</p>

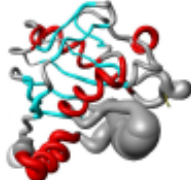
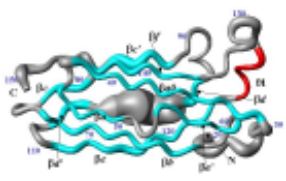


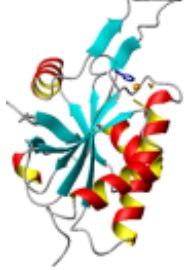
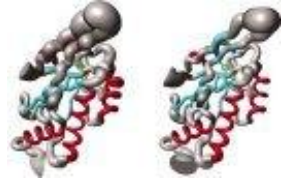
<p>Banci, L., Bertini, I., Del Conte, R., D'Onofrio, M., Rosato, A. Solution structure and backbone dynamics of the Cu(I) and Apo forms of the second metal-binding domain of the Menkes protein ATP7A <i>Biochemistry</i>, 43: 3396-3403, 2004</p>	 <p>PDB code: 1S6O, 1S6U</p>
<p>Banci, L., Bertini, I., Chasapis, C. T., Ciofi-Baffoni, S., Hadjiliadis, N., Rosato, A. 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 J.</i>, 272: 865-871, 2005</p>	 <p>PDB code: 1Y3J, 1Y3K</p>
<p>Banci, L., Bertini, I., Cantini, F., Migliardi, M., Rosato, A., Wang, S. An atomic-level investigation of the disease-causing A629P mutant of the Menkes protein, ATP7A <i>J.Mol.Biol.</i>, 352: 409-417, 2005</p>	 <p>PDB code: 1YJU, 1YJV, 1YJR, 1YJT</p>
<p>Achila, D., Banci, L., Bertini, I., Bunce, J., Ciofi Baffoni, S., Huffman, D.L. Structure of human Wilson protein domains 5 and 6 and their interplay with domain 4 and the copper chaperone HAH1 in copper uptake <i>Proc.Natl.Acad.Sci.USA</i>, 103: 5729-5734, 2006</p>	 <p>PDB code: 2EW9</p>
<p>Banci, L., Bertini, I., Ciofi Baffoni, S., Kandias, N.G., Robinson, N.J., Spyroulias, G.A., Su, X.C., Tottey, S., Vanarotti, M. The delivery of copper for thylakoid import observed by NMR <i>Proc.Natl.Acad.Sci.USA.</i>, 103: 8320-8325, 2006</p>	 <p>PDB code: 2GCF</p>
<p>Banci, L., Bertini, I., Cantini, F., Della Malva, N., Herrmann, T., Rosato, A., Wütrich, K. Solution structure and intermolecular interactions of the third metal-binding domain of ATP7A, the Menkes disease protein <i>J.Biol.Chem.</i>, 281: 29141-29147, 2006</p>	 <p>PDB code: 2G9O, 2GA7</p>



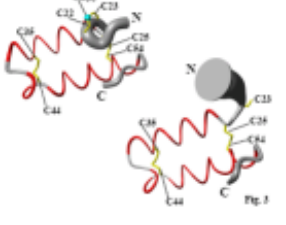
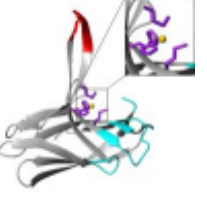

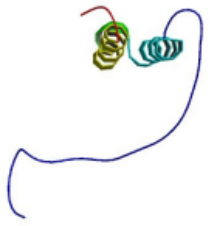
<p>Singleton, C., Banci, L., Ciofi-Baffoni, S., Tenori, L., Kihlken, M. A., Boetzel, R., and Le Brun, N. E. Structure and Cu(I)-binding properties of the N-terminal soluble domains of <i>Bacillus subtilis</i> CopA <i>Biochem J.</i>, 411: 571-579, 2008</p>	 <p>PDB code: 2RML</p>
<p>Banci L, Bertini I, Cantini F, Rosenzweig AC, Yatsunyk LA. Metal binding domains 3 and 4 of the Wilson disease protein: solution structure and interaction with the copper(I) chaperone HAH1 <i>Biochemistry</i>, 47: 7423-7429, 2008</p>	 <p>PDB code: 2ROP</p>
<p>Banci, L., Bertini, I., Cantini, F., Migliardi, M., Natile, G., Nushi, F., and Rosato, A. Solution structures of the actuator domain of ATP7A and ATP7B, the menkes and wilson disease proteins <i>Biochemistry</i>, 48: 7849-7855, 2009</p>	 <p>PDB code: 2KIJ</p>
<p>Banci, L., Bertini, I., Cantini, F., Inagaki, S., Migliardi, M., and Rosato, A. The binding mode of ATP revealed by the solution structure of the N-domain of human ATP7A <i>J.Biol.Chem.</i>, 285: 2537-2544, 2010</p>	 <p>PDB code: 2KMX, 2KMV</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Poggi, L., Vanarotti, M., Tottey, S., Waldron, K.J., Robinson, N.J. NMR structural analysis of the soluble domain of ZiaA-ATPase and the basis of selective interactions with copper metallochaperone Atx1 <i>J.Biol.Inorg. Chem.</i>, 15: 87-98, 2010</p>	 <p>PDB code: 2OFG, 2OFH</p>

Protein-protein complexes

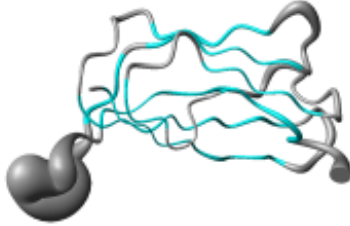
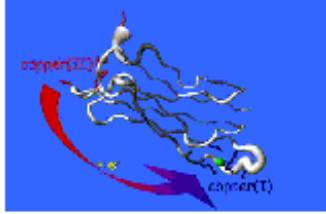
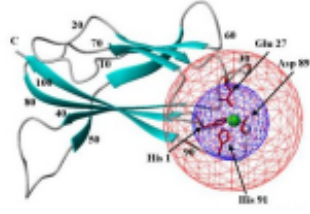
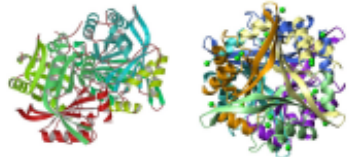

<p>Arnesano, F., Banci, L., Bertini, I., Bonvin, A. M. J. J. A docking approach to the study of copper trafficking proteins: interaction between metallochaperones and soluble domains of copper ATPases Structure, 12: 669-676, 2004</p>	 <p>Cover</p> <p>PDB code: 1UV1, 1UV2</p>
<p>Banci, L., Bertini, I., Cantini, F., Felli, I. C., Gonnelli, L., Hadjiliadis, N., Pierattelli, R., Rosato, A., Voulgaris, P. The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction Nat.Chem.Biol. 2: 367-8, 2006</p>	 <p>PDB code: 2GGP</p>
<p>Banci, L., Bertini, I., Calderone, V., Della Malva, N., Felli, I. C., Pavelkova, A., and Rosato, A. Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces Biochem.J., 422: 37-42, 2009</p>	 <p>PDB code: 3CJK</p>
<p>Bertini, I., Banci, L., Felli, I. C., Pavelkova, A., Rosato, A. The solution structure of the copper(I)-mediated complex between the first soluble domain of the Menkes protein and the metallochaperone HAH1 To be published</p>	 <p>PDB code: 2K1R</p>

Cytochrome c oxidase copper incorporation proteins




<p>Balatri, E., Banci, L., Bertini, I., Cantini, F., Ciofi-Baffoni, S. Solution structure of Sco1: a thioredoxin-like protein involved in cytochrome c oxidase assembly Structure 11: 1431-1443, 2003</p>	 <p>PDB code: 1ON4</p>
<p>Banci, L., Bertini, I., Cantini, F., Ciofi-Baffoni, S., Gonnelli, L., and Mangani, S. Solution structure of Cox11: a novel type of β-immunoglobulin-like fold involved in CuB site formation of cytochrome c oxidase J.Biol.Chem., 279: 34833-34839, 2004</p>	 <p>PDB code: 1SP0, 1SO9</p>
<p>Arnesano, F., Balatri, E., Banci, L., Bertini, I., Winge, D.R. Folding studies of Cox17 reveal an important interplay of cysteine oxidation and copper binding Structure 13: 713-722, 2005</p>	 <p>PDB code: 1Z2G</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Katsari, E., Katsaros, N., Kubicek, K., Mangani, S. A copper(I) protein possibly involved in the assembly of CuA center of bacterial cytochrome c oxidase Proc.Natl.Acad.Sci.USA, 102: 3994-3999, 2005</p>	 <p>PDB code: 1X7L, 1X9L, 2JQA</p>
<p>Banci, L., Bertini, I., Calderone, V., Ciofi-Baffoni, S., Mangani, S., Martinelli, M., Palumaa P., Wang, S. A hint for the function of human Sco1 from different structures Proc.Natl.Acad.Sci.USA, 103: 8595-8600, 2006</p>	 <p>PDB code: 2GGT, 2GQK, 2GQL, 2GQM, 2GT5, 2GT6, 2GVP</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Leontari, I., Martinelli, M., Palumaa, P., Sillard, R., Wang, S. Human Sco1 functional studies and pathological implications of the P174L mutant Proc.Natl.Acad.Sci.USA, 104: 15-20, 2007</p>	 <p>PDB code: 2HRF, 2HRN</p>

<p>Coyne, H. J., Ciofi-Baffoni, S., Banci, L., Bertini, I., Zhang, L., Graham, N. G., Winge D.E. The characterization and the role of zinc binding in yeast cox4. <i>J.Biol.Chem.</i>, 282: 8926-34, 2007</p>	 <p>PDB code: 2ODX</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Gerotherannasis, I. P., Leontari, I., Martinelli, M., Wang, S. A structural characterization of human Sco2 <i>Structure</i>, 15: 1132-1140, 2007</p>	 <p>PDB code: 2RLI</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Janicka, A., Martinelli, M., Kozlowski, H., Palumaa, P. A structural–dynamical characterization of human cox 17 <i>J.Biol.Chem.</i>, 283: 7912-7920, 2008</p>	 <p>PDB code: 2RN9, 2RNB</p>
<p>Abriata, L.A., Banci, L., Bertini, I., Ciofi-Baffoni, Gkazonis, P., Spyroulias, G.A., Vila, A.J., Wang, S. A Mechanism of Cu(A) assembly <i>Nat.Chem.Biol.</i>, 4: 599-601, 2008</p>	 <p>PDB code: 2K6V, 2K6W, 2K6Y, 2K6Z, 2K70</p>
<p>Banci, L., Bertini, I., Ciofi-Baffoni, S., Kozyreva, T., Mori, M., and Wang, S. SCO proteins are involved in electron transfer processes <i>J.Biol.Inorg.Chem.</i>, 13: 391-403, 2011</p>	 <p>PDB code: 2L4D</p>
<p>Banci, L., Bertini, I., Cefaro, C., Ciofi-Baffoni, S., Gallo, A. The functional role of two interhelical disulfide bonds in human Cox17 from a structural perspective <i>J.Biol.Chem.</i>, 286: 34382-34390, 2011</p>	 <p>PDB code: 2LGQ</p>



Copper resistance proteins

<p>Arnesano, F., Banci, L., Bertini, I., Thompsett, A.R. Solution structure of CopC: a cupredoxin-like protein involved in copper homeostasis <i>Structure</i>, 10: 1337-1347, 2002</p>	 <p>PDB code: 1M42</p>
<p>Arnesano F., Banci L., Bertini I., Mangani S., Thompsett A.R. A redox switch in CopC: an intriguing copper trafficking protein that binds copper(I) and copper(II) at different sites <i>Proc.Natl.Acad.Sci.USA</i>, 100: 3814-3819, 2003</p>	 <p>PDB code: 1NM4</p>
<p>Arnesano, F., Banci, L., Bertini, I., Felli, I. C., Luchinat, C., Thompsett, A. R.: 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>J.Am.Chem.Soc.</i>, 125: 7200-7208, 2003</p>	 <p>PDB code: 1OT4</p>
<p>Arnesano, F., Banci, L., Benvenuti, M., Bertini, I. Calderone, V., Mangani, S., Viezzoli., M.S. The evolutionarily conserved trimeric structure of Cutal proteins suggests a role in signal transduction <i>J.Biol.Chem.</i>, 278: 45999-46006, 2003</p>	 <p>PDB code: 1OSC, 1NAQ</p>
<p>Cantini, F., Banci, L., Solioz, M. The copper-responsive repressor CopR of <i>Lactococcus lactis</i> is a 'winged helix' protein <i>Biochem.J.</i>, 417: 493-499, 2009</p>	 <p>PDB code: 2K4B</p>

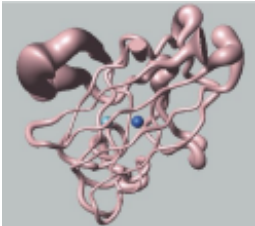

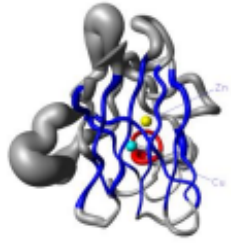
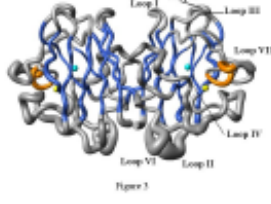
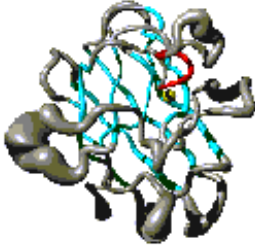
Blue copper proteins

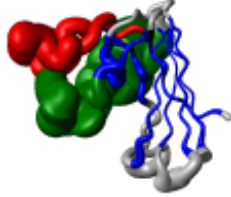
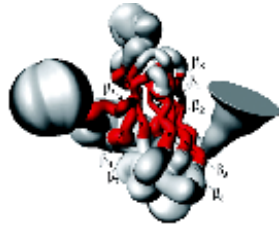
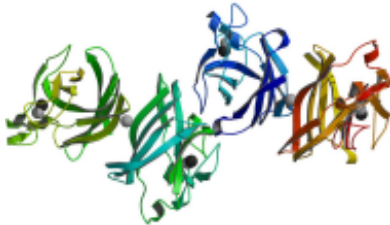
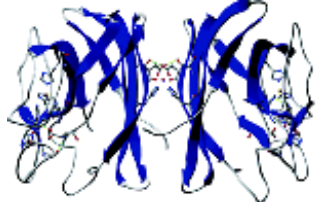
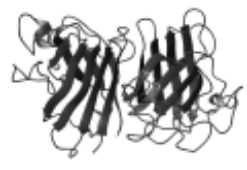
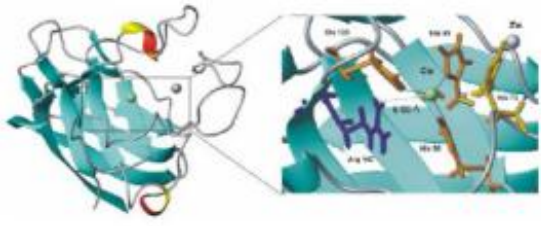
<p>Bertini, I., Ciurli, S., Dikiy, A., Fernandez, C.O., Luchinat, C., Safarov, N., Shumilin, S., Vila, A.J. The first solution structure of a paramagnetic copper (II) protein: the case of oxidized plastocyanin from the cyanobacterium <i>Synechocystis PCC6803</i> J.Am.Chem.Soc., 123: 2405-2413, 2001</p>	 <p>PDB code: 1J5C, 1J5D</p>
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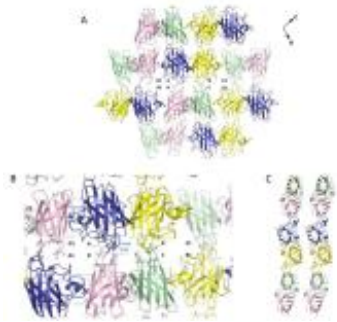


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