
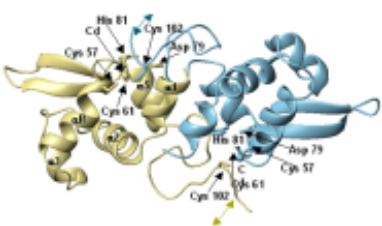


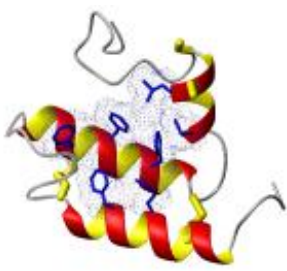


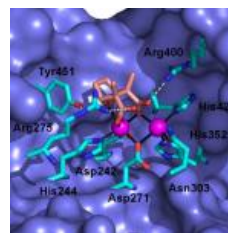
MISCELLANEOUS OF OTHER PROTEINS

<p>Cantini, F., Savino, S., Scarselli, M., Massignani, V., Pizza, M. G., Romagnoli, G., Swennen, E., Veggi, D., Banci, L., Rappuoli, R</p> <p>Solution structure of the immunodominant domain of protective antigen GNA1870 of <i>Neisseria meningitidis</i></p> <p>J.Biol.Chem., 281: 7220-7227, 2006</p>	 <p>PDB code: 1YS5</p>
<p>Banci, L., Bertini, I., Cantini, F., Ciofi-Baffoni, S., Cavet, J. S., Dennison C., Graham, A. I., Harvie, D. R., Robinson, N. J.</p> <p>NMR structural analysis of cadmium sensing by winged helix repressor CmtR</p> <p>J.Biol.Chem., 282: 30181-30188, 2007</p>	 <p>PDB code: 2JSC</p>
<p>Caillet-Saguy, C., Turano, P., Piccioli, M., Lukat-Rodgers, G., Czjzek, M., Guigliarelli, B., Izadi-Pruneyre, N., Delepierre, M., Rodgers, K., Lecroisey, A.</p> <p>Deciphering the structural role of histidine 83 for heme binding in hemophore HasA</p> <p>J.Biol.Chem., 283: 5960-5970, 2008</p>	 <p>PDB code: 2UYD</p>
<p>Cantini, F., Veggi, D., Dragonetti, S., Savino, S., Scarselli, M., Romagnoli, G., Pizza, M., Banci, L., Rappuoli, R.</p> <p>Solution structure of the factor H binding protein, a survival factor and protective antigen of <i>Neisseria meningitidis</i></p> <p>J.Biol.Chem. 284: 9022-9026, 2009</p>	 <p>PDB code: 2KC0</p>
<p>Banci, L., Bertini, I., Cefaro, C., Ciofi Baffoni, S., Gallo A., Martinelli, M., Sideris. D.P., Katrakili, N, Toklatidis, K.</p> <p>MIA40 is an oxidoreductase that catalyzes oxidative protein folding in mitochondria</p> <p>Nat. Struct. Mol. Biol. 16: 198-206, 2009</p>	 <p>PDB code: 2K3J</p>

Bertini, I., Calderone, V., Fragai, M., Luchinat, C., and Talluri, E.

Structural basis of serine/threonine phosphatase inhibition by the archetypal small molecules cantharidin and norcantharidin.

J.Med.Chem., 15: 4838-4843, 2009

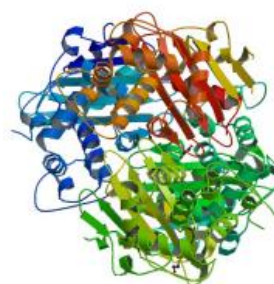


PDB code: 3H60, 3H61, 3H62, 3H63, 3H64, 3H66, 3H67, 3H68, 3H69

Docquier, J. D., Calderone, V., De Luca, F., Benvenuti, M., Giuliani, F., Bellucci, L., Tafi, A., Nordmann, P., Botta, M., Rossolini, G. M., and Mangani, S.

Crystal structure of the OXA-48 beta-lactamase reveals mechanistic diversity among class D carbapenemases

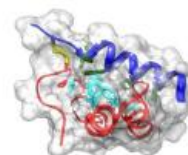
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PDB code: 3HBR

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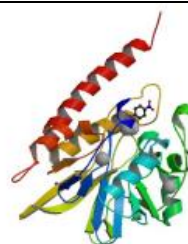


PDB code: 2LOY

Docquier, J.D., Benvenuti, M., Calderone, V., Stoczko, M., Menciassi, N., Rossolini, G.M., Mangani, S.,

High-resolution crystal structure of the subclass B3 metallo-beta-lactamase BJP-1: rational basis for substrate specificity and interaction with sulfonamides

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PDB code: 3M8T, 3LVZ

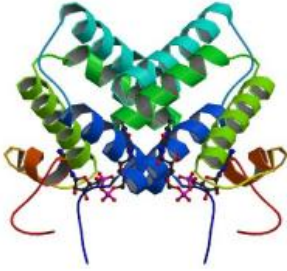




Gentile, M. A., Melchiorre, S., Emolo, C., Moschioni, M., Gianfaldoni, C., Pancotto, L., Ferlenghi, I., Scarselli, M., Pansegrau, W., Veggi, D., Merola, M., Cantini, F., Ruggiero, P., Banci, L., and Massignani, V.

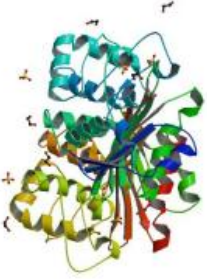
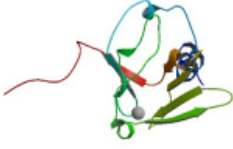
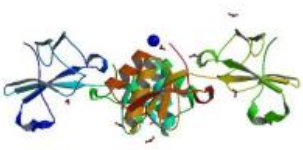
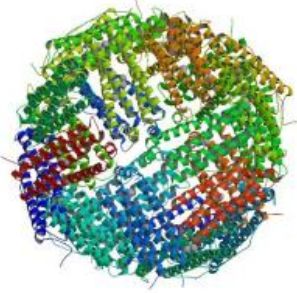

Structural and functional characterization of the *Streptococcus pneumoniae* RrgB pilus backbone D1 domain

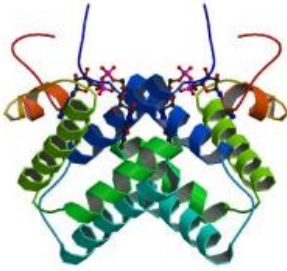
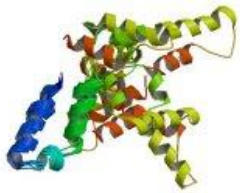
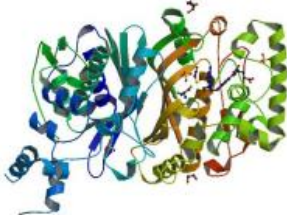

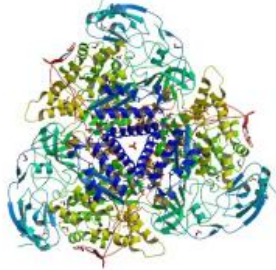
J.Biol.Chem., 286: 14588-14597, 2011



PDB code: 2L4O

<p>Banci, L., Bertini, I., Calderone, V., Cefaro, C., Ciofi-Baffoni, S., Gallo, A., Kallergi, E., Lionaki, E., Pozidis, C., Tokatlidis, K. Molecular recognition and substrate mimicry drive the electron-transfer process between MIA40 and ALR Proc.Natl.Acad.Sci. USA., 108: 4811-4816, 2011</p>	 <p>PDB code: 3O55</p>
<p>Benini, S., Cianci, M., Ciurli, S. Holo-Ni(2+)Helicobacter pylori NikR contains four square-planar nickel-binding sites at physiological pH Dalton Trans., 40: 7831-7833, 2011</p>	 <p>PDB code: 2Y3Y</p>
<p>Banci, L., Bertini, I, Ciofi-Baffoni, S., Boscaro, F., Chatzi, A., Mikolajczyk, M., Tokatlidis, K., Winkelmann, J. Anamorsin is a [2Fe-2S] cluster-containing substrate of the Mia40-dependent mitochondrial protein trapping machinery Chem. Biol., 18: 794-804, 2011</p>	 <p>PDB code: 2LD4</p>
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<p>De Luca, F., Benvenuti, M., Carboni, F., Pozzi, C., Rossolini, G. M., Mangani, S., and Docquier, J. D. Evolution to carbapenem-hydrolyzing in noncarbapenemase class D β-lactamase OXA-10 by rational protein design Proc.Natl.Acad.Sci.USA, 108: 18424-18429, 2011</p>	 <p>PDB code: 3QNC</p>
<p>Aachmann, F. L., Del Conte, R., Kim, H-Y., Gladyshev, V. N., Dikiy, A. Structural and biochemical analysis of mammalian methionine sulfoxide reductase B2 Proteins, 79: 3123-3131, 2011</p>	 <p>PDB code: 2L1U</p>
<p>Banaszak, K., Martin-Diaconescu, V., Bellucci, M., Zambelli, B., Rypniewski, W., Maroney, M. J., Ciurli, S., Crystallographic and X-ray absorption spectroscopic characterization of <i>Helicobacter pylori</i> UreE bound to Ni²⁺ and Zn²⁺ reveal a role for the disordered C-terminal arm in metal trafficking Biochem. J., 441: 1017-1026, 2012</p>	 <p>PDB code: 3TJ8, 3TJ9, 3TJA</p>
<p>Bertini, I., Lalli, D., Mangani, S., Pozzi, C., Rosa, C., Theil, E. C., Turano, P., Structural insight into the iron pathway in ferritin J.Am.Chem.Soc.: 134, 6196-6176, 2012</p>	 <p>PDB code: 3RBC, 3RE7, 3RGD</p>
<p>Gallo, A., Lo Sterzo, C., Mori, M., Di Matteo, A., Bertini, I., Banci, L., Brunori, M., and Federici, L., Structure of nucleophosmin DNA-binding domain and analysis of its complex with a G-quadruplex sequence from the c-MYC promoter J.Biol.Chem.: 287, 26539-26548, 2012</p>	 <p>PDB code: 2LLH</p>

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<p>Pozzi, C., Ferrari, S., Cortesi, D., Luciani, R., Stroud, R. M., Catalano, A., Costi, M. P. Mangani, S. The structure of <i>Enterococcus faecalis</i> thymidylate synthase provides clues about folate bacterial metabolism Acta Crystallogr. D Biol.Crystallogr.: 68, 1232-1241, 2012</p>	 <p>PDB code: 3UWL</p>
<p>Bertini, I., Lalli, D., Mangani, S., Pozzi, C., Rosa, C., Turano, P. Structural insight into the iron at the ferroxidase site of high eukaryotic ferritins J. Amer. Chem. Soc.: 134: 6169-6176, 2012</p>	 <p>PDB code: 4DAS</p>
<p>Benini, S., Kosikowska, P., Cianci, M., Mazzei, L., Berlicki, L., Ciurli, S. The crystal structure of sporacina pasteurii urease in a complex with citrate provides new hints for inhibitor design J.Biol.Inorg.Chem.: 18, 391-399, 2013</p>	 <p>PDB code: 4AC7</p>