

Domain motions in the mercuric ion reductase - MerA

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Bacterial resistance to inorganic and organic mercury compounds is mediated by the *mer* operon, a suite of genes typically located on transposons or plasmids. The *mer* operon consists of several structural genes encoding proteins involved in Hg(II) transport, Hg(II) reduction and protonolysis of organomercurials^{1,2}.

We have chosen to focus on the structure and function of the mercuric ion reductase, MerA, an enzyme responsible for catalyzing the NADPH-dependent reduction of Hg(II) to uncharged, and much less harmful, Hg(0). This enzyme consists of a large homodimeric catalytic core unit (core-MerA) which is connected to two small metallochaperone-like N-terminal domains (NmerA) by flexible linkers², Figure 1. Studies of intact full-length MerA have been hampered by proteolysis in the flexible linkers, however studies of the separately expressed core-MerA and NmerA domains have shown that NmerA can bind Hg(II) with its pair of cysteines and deliver it to core-MerA for reduction³. For this reason it is important to understand the internal dynamics of the intact full length protein, in particular the relative motions of the NmerA domains relative to the core of the enzyme. We have recently expressed pure, full-length MerA⁴ and here address this question using neutron spin echo spectroscopy, a technique that has previously been used to gain valuable insight into the internal dynamics in proteins.⁵

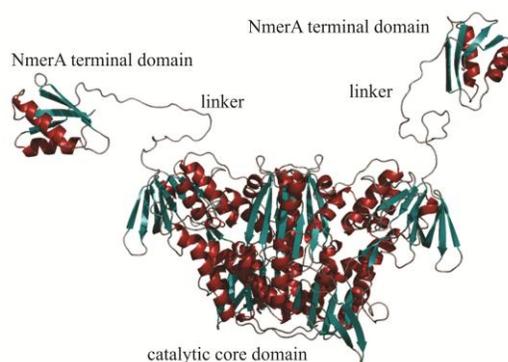


Figure 1: ribbon diagram of full-length MerA

References

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