Paramagnetic Relaxation-Based Structural Characterization of Hha-H-NS Interaction

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Nucleoid associated proteins (NAP) are key elements in structuring the bacterial genome and are also essential for the differential gene expression of a large number of genes in response to changes in environmental conditions. While some of the NAPs, like H-NS, are indeed DNA binding proteins, other important NAPs do not interact directly with DNA but interact with other DNA binding NAPs. This seems to be the case of Hha.

Hha is specific to bacteria of the enteric group and is an essential component, that is conserved even in endosymbiotic species that have lost a large portion of the genome. A significant proportion of virulence-related genes are co-regulated by Hha. The ability to interact with HNS is emerging as an important theme in the mechanism of modulating the expression of these genes.

From the structural point of view, Hha is a “plastic” protein that shows a dynamic behaviour that complicates the mapping of residues involved in the interactions. On the other hand, H-NS oligomerization, essential for its gene regulation activity, complicates the characterization of the complexes.

We are using paramagnetic relaxation enhancement (PRE) arising from site-directed spin labelling in either Hha or H-NS to probe the structure and dynamics of these proteins and to obtain structural information on the Hha-H-NS interface that could be used to dock the two structures.

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