The ‘Active-like’ Structure of the Unphosphorylated Response Regulator StyR

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The crystal structure of unphosphorylated StyR has been solved at 2.2 Å resolution. StyR belongs to the FixJ family of signal transduction response regulators; it controls transcription of the *styABCD* operon coding for styrene catabolism in *Pseudomonas fluorescens* ST [1]. StyR is composed of an N-terminal regulatory domain (StyR-N), and a C-terminal DNA binding domain (StyR-C). The two domains are separated by an elongated linker α-helix (34 residues), a new feature in response regulator known structures. StyR-C is structured similarly to the DNA binding domain of the response regulator NarL [2]. StyR-N shows structural reorganization of the phosphate receiving region involved in activation/homodimerization: specific residues adopt ’active-like‘ conformations, and the α4-helix, involved in dimerization of the homologous FixJ response regulator [3], is trimmed to just one helical turn. Overall, structural considerations suggest that phosphorylation may act as an allosteric switch, shifting a pre-existing StyR equilibrium towards the active, dimeric, DNA-binding form.

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