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The Interaction Between PurR and its Substrates. J. Zhu, A. Bera, S.C. Sinha, H. Zalkin, J.L. Smith. Dept. of Biological Sciences, Purdue Univ., West Lafayette, IN 47906 USA.

Bacillus subtilis PurR represses transcription of several genes involved in purine synthesis. PurR, a 62-kDa homodimer, has high affinity for large segments of DNA within the control regions of the *pur*, *purA*, *purR*, and *pyr* operons. The *pur* operon site to which PurR binds was mapped to a position corresponding to -136 to -26 relative to the start of transcription. Binding is reduced by phosphoribosylpyrophosphate (PRPP), the starting material for *de novo* purine synthesis. The PurR monomer consists of two domains. A large domain has the phosphoribosyltransferase (PRTase) fold and sequence fingerprint, characteristic of the PRT family of PRPP-binding proteins. A small domain has the winged helix-turn-helix fold, typical of DNA-binding proteins. PurR and cPRPP, a stable carbocyclic PRPP analog, were co-crystallized. The complex structure was solved by molecular replacement using the free PurR structure as a search model. Based on the cPRPP complex structure and biochemical data, we propose that PRPP and DNA bind PurR competitively. A PurR-DNA binding model is proposed.