KorB is an archetypal member of the ParB family of proteins that are essential for DNA partitioning for many bacterial chromosomes. It is required for partitioning the IncP plasmid, RK2, in bacterial cells. In addition, it is a global regulator of transcription, acting co-operatively with other plasmid-encoded repressors, such as KorA. To date, only selected domains of four ParB proteins have been crystallised, including two domains of KorB. Using CD and NMR spectroscopy of full length and deletion mutants, we have found that KorB has alternating regions of intrinsic disorder and of ordered tertiary structure. We have modelled a representative ensemble of solution conformations for KorB, based on the known domain structures and small angle scattering data. We have also determined the structure of KorA. While KorA has only a short linker between two domains, it is highly flexible both in the free state and when bound to DNA. We are currently examining the conformation of KorB in complexes with KorA and with its operator. While the secondary structure of KorB appears unaffected by binding to its partners, its radius of gyration changes greatly; indicating a change in conformational range of the disordered regions. The conformational flexibility of the two proteins, KorA and KorB, is likely to be essential for binding to their varied partners and for their co-operative binding to each other over different DNA distances.