Figure S1

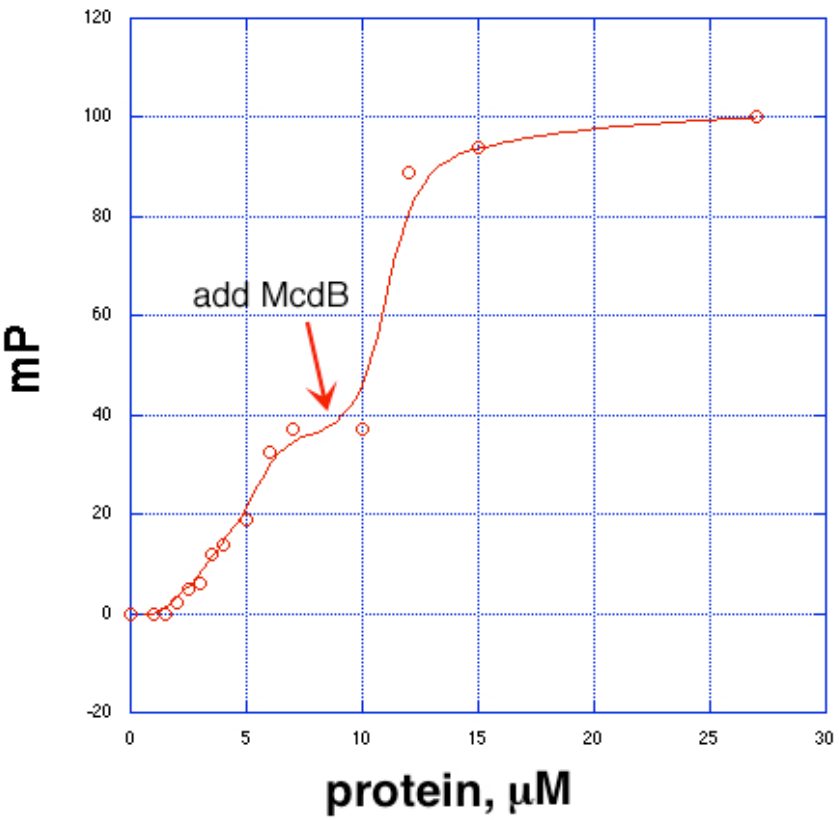

Figure S1: Fluorescence polarization (FP) binding experiment analyzing ability of McdB to interact with McdA(D38A)-ATP-DNA complex. The y-axis is millipolarization units (mP) and the x-axis is the concentration of protein in μM. The McdA(D38A) protein was added first to a concentration of 10 μM. Then McdB protein was added (as indicated by the red arrow). A second binding event was observed.

Figure S2

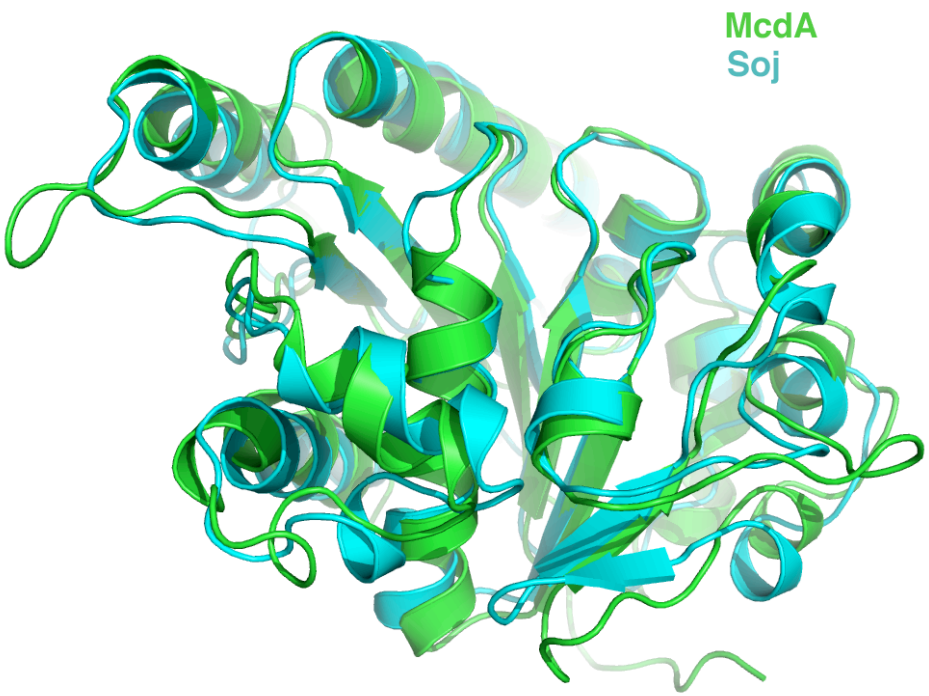

Figure S2: Superimposition of the apo McdA structure (green) onto *T. thermophilus* Soj protein (cyan) (pdb code: 2WCV). The overlay of McdA and Soj results in a root mean squared deviation (rmsd) of 1.9 Å for 224 Cα atoms.

Figure S3

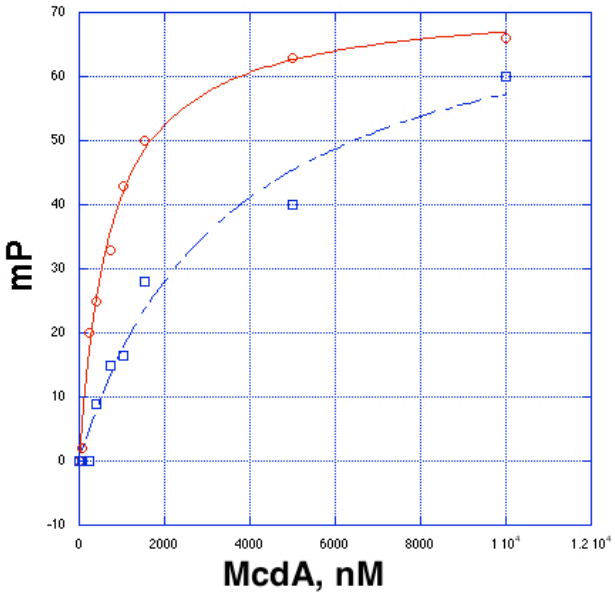

Figure S3: F-ATP binding by McdA(D38A) (red) and McdA(D38A-K151A) (blue). The y-axis is millipolarization units (mP) and the x-axis is the concentration of McdA protein in nM.

Figure S4

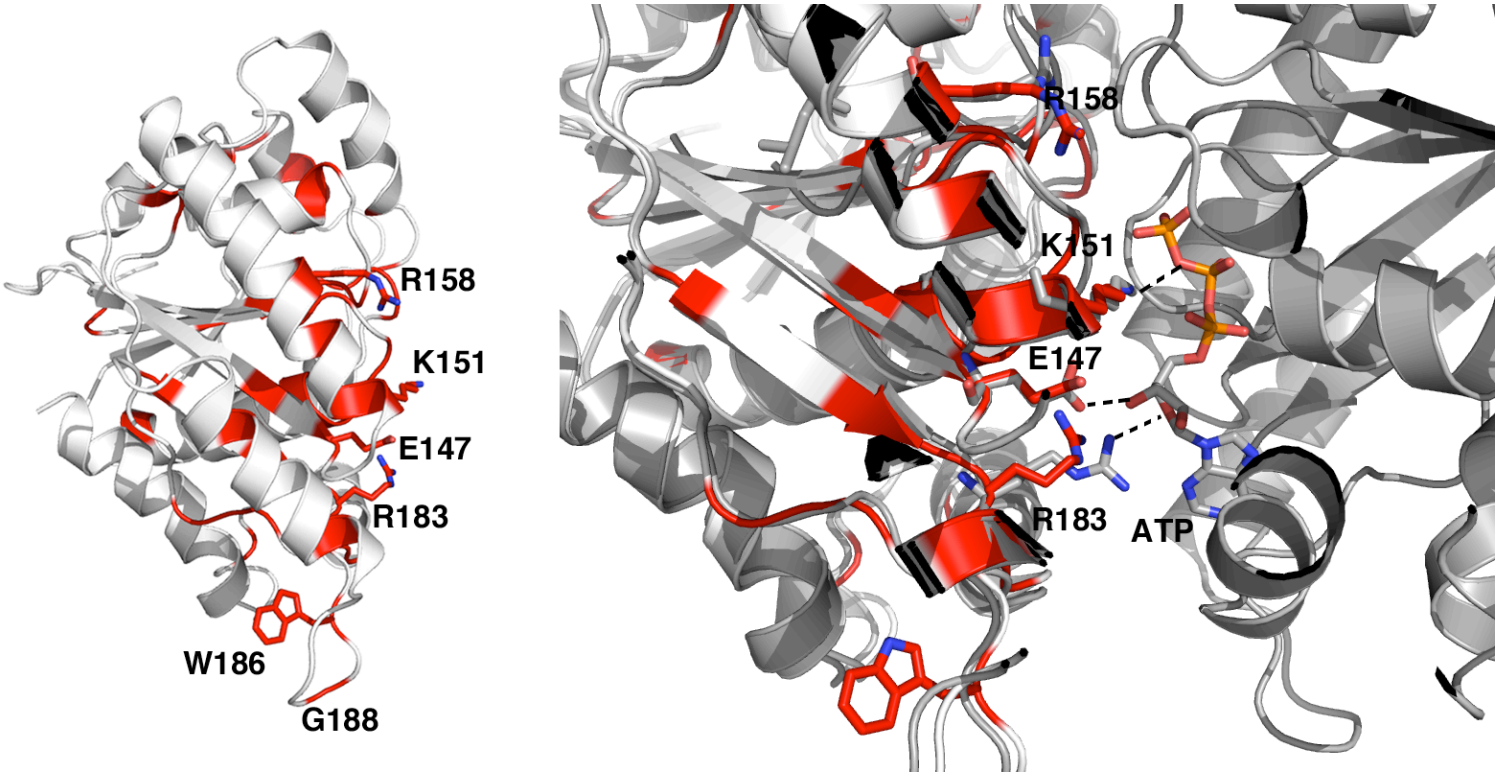

Figure S4: Mapping of conserved McdA residues that point into the solvent onto the McdA(D38A)-ATP structure. Surface exposed conserved McdA residues are colored red and labeled. Left shows overall location of the residues on a McdA monomer. Right shows the location of the residues in the context of the McdA nucleotide sandwich dimer. The residues make contacts to residues in the other subunit of the dimer and/or the ATP bound in the adjacent monomer, explaining their conservation.

Figure S5

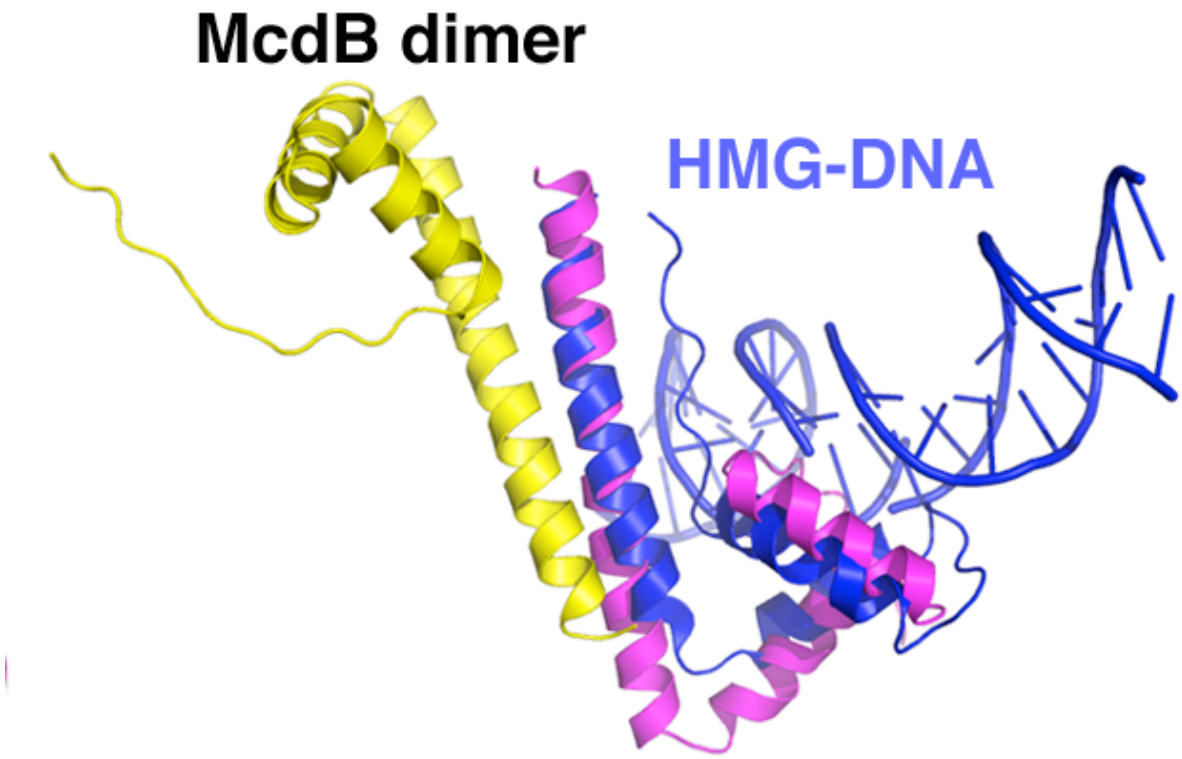

Figure S5: McdB shows weak structural homology to HMG proteins. The McdB dimer is colored as in Figure 6A. Shown is an overlay of one McdB subunit (magenta) onto the HMGB structure, 3NM9 (blue), which results in an rmsd of 4.4 Å. The other subunit of the McdB dimer is colored yellow. Note, the McdB is dimeric compared to the HMG monomer.

Figure S6

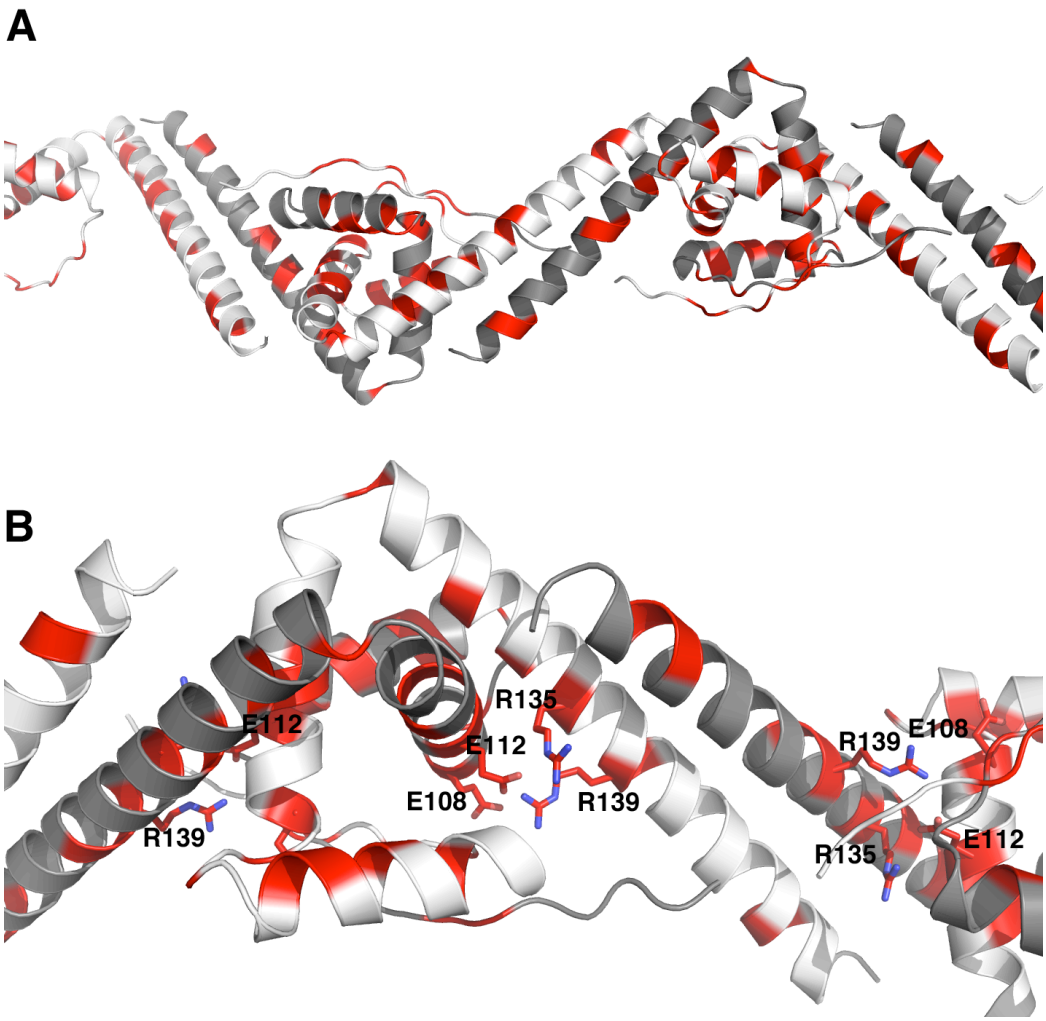

Figure S6: Mapping conserved McdB residues onto the structure. (**A**) overview of the location of the conserved residues (red) showing that they mainly correspond to regions that are involved in oligomer formation. (**B**) Highly conserved charged residues in the interface are labeled and shown to interact.

Figure S7

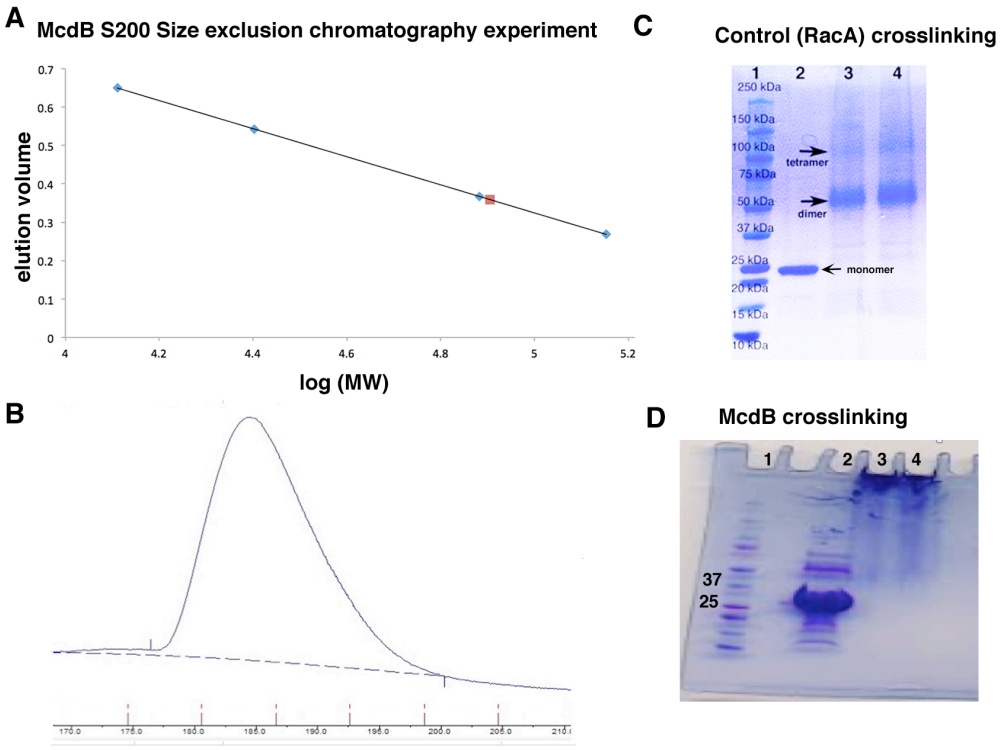

Figure S7: Analyses of McdB oligomer state. (**A**) Size exclusion chromatography (SEC) analyses of the *Cyanothece* McdB protein showing it elutes as a higher order oligomer on an S200 column. The y-axis is elution volume normalized for the column volume and the x-axis is log(MW). Controls are shown as blue diamonds and McdB as a red square. (**B**) The resultant McdB elution profile from the SEC run. (**C**) Control crosslinking experiment with *B. subtilis* RacA, a known dimer that can form tetramers. Glutaraldehyde crosslinking of FL RacA. Lane 1 is the MW marker, lane 2 corresponds to 0 time crosslinking and lanes 3 and 4 correspond to 5 min and 20 min after addition of 0.2% glutaraldehyde. The FL protein runs at a MW of 20 kDa and crosslinking primarily leads to the generation of a dimer at ~50 kDa. Weak tetramer bands are observed at ~95 kDa. (**D**) Glutaraldehyde crosslinking experiment of *Cyanothece* McdB. The McdB protein, which notably runs as a dimer (lane 2, note the position of the MW markers for 25 and 37 kDa bands) on SDS-PAGE, was crosslinked with 0.1% glutaraldehyde for 30 min (lane 3) and 3 hr (lane 4) revealing higher order oligomers near the top of the gel.