

SUPPLEMENTAL INFORMATION

Fig. S1 Sequence alignment of selected IclR proteins using CLUSTALW (1). Also shown are the secondary structures of BlcR determined in this study. Amino acid sequences are from the following bacteria: BlcR of this study, *Agrobacteria tumefaciens*; TM-IclR, *Thermotoga maritime*; IclR_E, YaiJ, GclR, and AllR, *E. coli*; IclR_Y, *Yersinia pestis*; KdgR, *Erwinia*; RexZ, *Erwinia sp*; TtgT, TtgV and PcaR, *Pseudomonas putida*; PcaU, *Acinetobacter*; TsaQ, *Comamonas testosteroni*.

Fig. S2 ITC studies of SSA binding to **A)** wild type BlcR, and **B)** BlcR^{C220A}. Panel descriptions are the same as Figure 3 C&D.

REFERENCES:

1. Chenna, R., Sugawara, H., Koike, T., Lopez, R., Gibson, T. J., Higgins, D. G., and Thompson, J. D. (2003) *Nucleic Acids Res* **31**, 3497-3500

Fig. S1

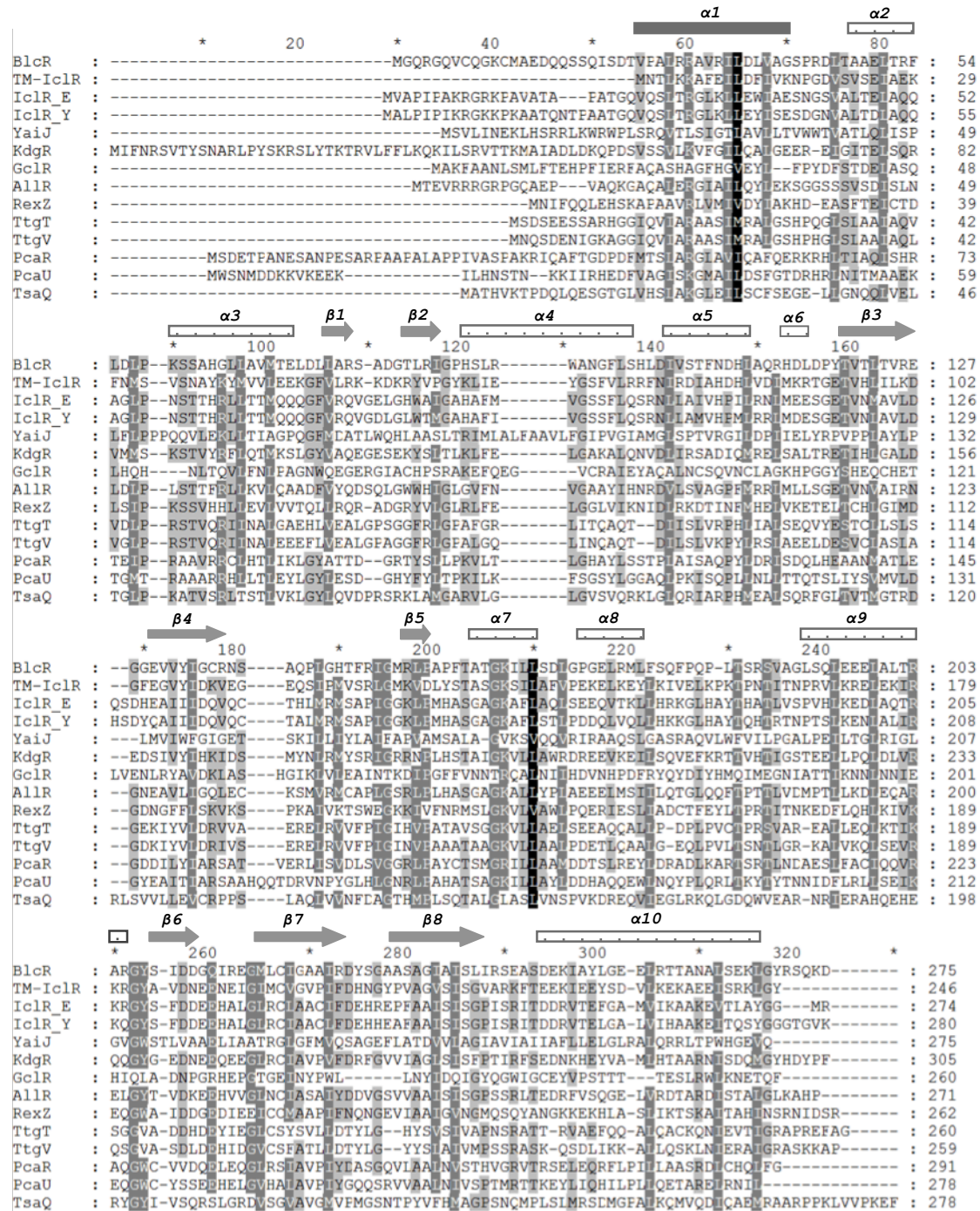


Fig. S2

