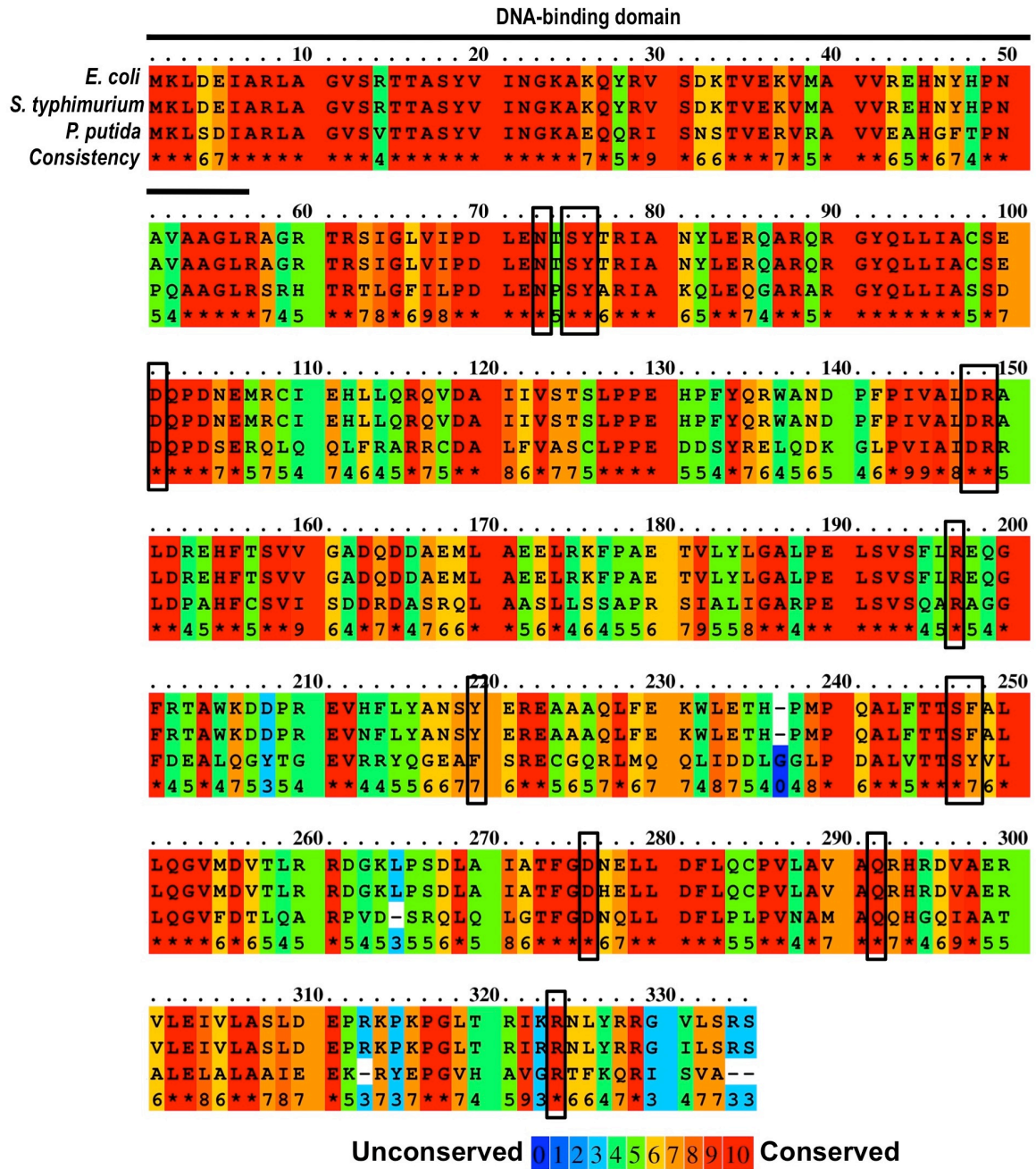


1 **Supplemental Figure S2.** Alignment of Cra proteins from *E. coli*, *S. typhimurium* and *P. putida* KT2440.

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4

5 The *P. putida* Cra protein has 74% similarity and 48% identity with the *E. coli* counterpart. Identity  
6 increases to 70% in the predicted DNA binding domain of the proteins. The DNA binding module is  
7 located in the N-terminal side and it is formed by the first 57 amino acids of the proteins (indicated with a  
8 black line). Amino acids that form the effector-binding pocket are marked with black boxes. Note that 85%

1 of the amino acids that form the pocket of the *P. putida* protein are identical (100% similar) to those of *E.*  
2 *coli* and *S. typhimurium*. The only changes are Phe220 (Tyr in *E. coli*) and Tyr 248 (Phe in *E. coli*). The  
3 alignment and the conservation score were carried out with the PRALINE software. The scoring ranks  
4 (consistency values) from 0 for the least conserved alignment position, up to 10 for the most conserved  
5 alignment position.

6