

Supplemental Figure legends

SUPPLEMENTAL FIGURE 1: Physical and genetic map of the *papA* and *papB* region in the *R. palustris* genome. ORFs and their directions of transcription are represented by arrows. The possible Shine-Dalgarno sequence (SD) for PapB translation is boxed. There are only four nucleotides between the stop codon for *papA* and the SD sequence for *papB*, indicating that *papA* and *papB* are co-transcribed.

SUPPLEMENTAL FIGURE 2: Superimposition of the modeled PapB/PapA complexes onto the BlrP1 crystal structure (colored gray). The PapB monomers are colored in magenta and green, and the PapA monomers are colored in blue and yellow. The qualities of the models were evaluated and ranked according to the ZDOCK values (46), which are 1223.506 (Rank 1), 1196.064 (Rank 2), 1158.475 (Rank 3), 1111.783 (Rank 4) and 1111.605 (Rank 5).

SUPPLEMENTAL FIGURE 3: Amino-acid sequence alignments of (A) the PapB and BlrP1 BLUF domains and (B) the PapA and BlrP1 EAL domains. The conserved arginines in the BLUF domains and the conserved leucines in the EAL domains are boxed. The roles of these residues are discussed in the text.