

Poster

Insights into the molecular mechanism of ParABS system in chromosome partition by *HpParA* and *HpParB*Yuh-Ju Sun^{1,*} Chen-Hsi Chu¹, Min-Guan Lin² and Chwan-Deng Hsiao^{2,*}¹*Institute of Bioinformatics and Structural Biology, National Tsing Hua University, Hsinchu 300, Taiwan*, ²*Institute of Molecular Biology, Academia Sinica, Taipei 115, Taiwan**hsiao@gate.sinica.edu.tw*

The ParABS system [1, 2], composed of ParA (an ATPase), ParB (a DNA binding protein), and *parS* (a centromere-like DNA), regulates bacterial chromosome partition. The ParB-*parS* partition complex interacts with the nucleoid-bound ParA to form the nucleoid-adaptor complex (NAC) [3]. In *Helicobacter pylori*, ParA and ParB homologs are encoded as *HpSoj* and *HpSpo0J* (*HpParA* and *HpParB*), respectively. We determined the crystal structures of the ATP hydrolysis deficient mutant, *HpParAD41A*, and the *HpParAD41A*-DNA complex. We assayed the CTPase activity of *HpParB* and identified two potential DNA binding modes of *HpParB* regulated by CTP, one is the specific DNA binding by the DNA binding domain and the other is the non-specific DNA binding through the C-terminal domain under CTP.

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[2] Gallagher, K.A. and Brun, Y.V. (2021). *Curr Biol*, **31**, R1044-R1046.

[3] Havey, J.C., Vecchiarelli, A.G. and Funnell, B.E. (2012). *Nucleic Acids Res*, **40**, 801.