Poster

Crystal structure of GajB protein in Gabija anti-phage defense

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Bacteriophages (phages) are viruses that infect prokaryotic hosts. The intense arms race between bacteria and phages have led to the development of sophisticated antiphage defense strategies in bacteria [1,2]. A number of novel antiphage defense systems have been identified, but few of them are thoroughly characterized at molecular level. Gabija system is an antiphage defense system in over 4000 prokaryotic genomes and consists of two proteins, GajA and GajB.

Here, we report the structural and functional analyses of GajB protein. The crystal structure of GajB revealed a UvrD-like domain architecture, comprising two RecA-like core and two accessory subdomains (Fig. 1A). However, local structural elements for helicase function of UvrD were not conserved in GajB (Fig. 1B).

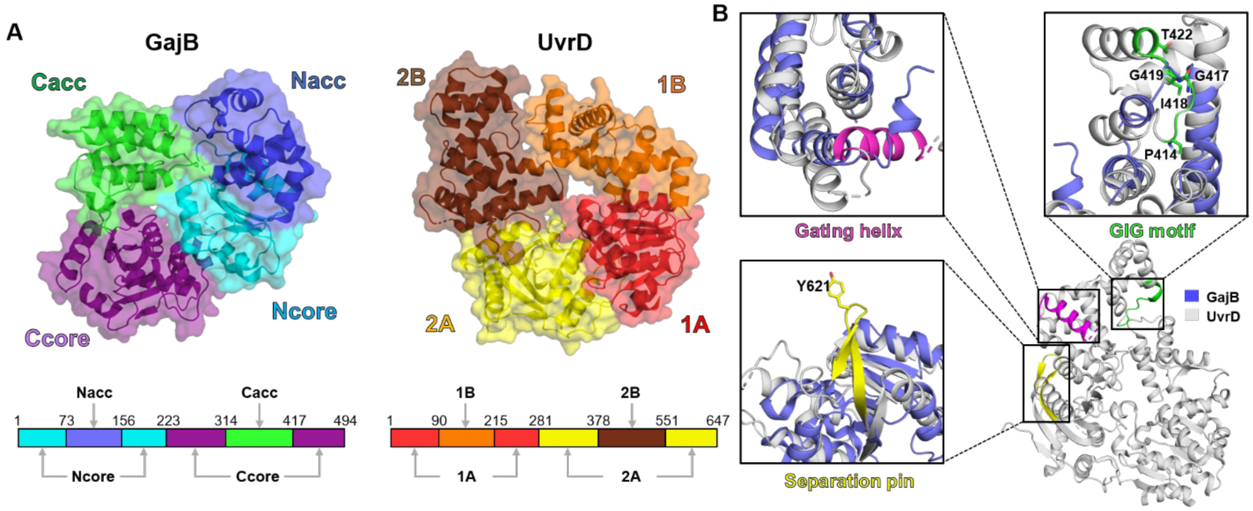

Figure 1 Crystal structure of GajB with UvrD (PDB ID:3LFU) (A) and structural alignments of local elements for helicase function (B).

In functional assays, GajB did not bind or unwind DNA (Fig. 2). Taken together, these results further our understanding of the molecular mechanism underlying the Gabija defense system.

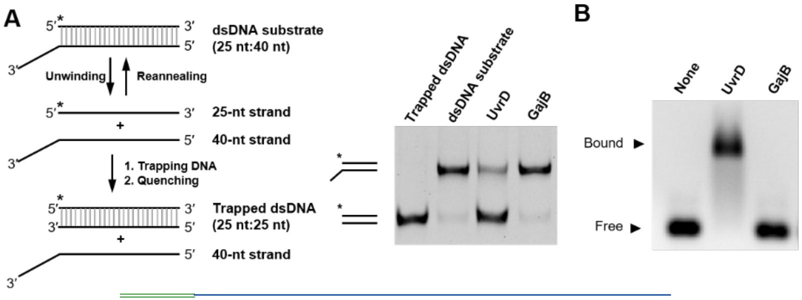

Figure 2 Helicase activity assay (A) and DNA binding assay (B) of GajB. UvrD was used as a positive control

[1] Hille, F. et al. (2018). *Cell*. **172**, 1239-1259.

[2] Brussow H. and Hendrix R. W. (2002). *Cell.* **108**(1):13-6.