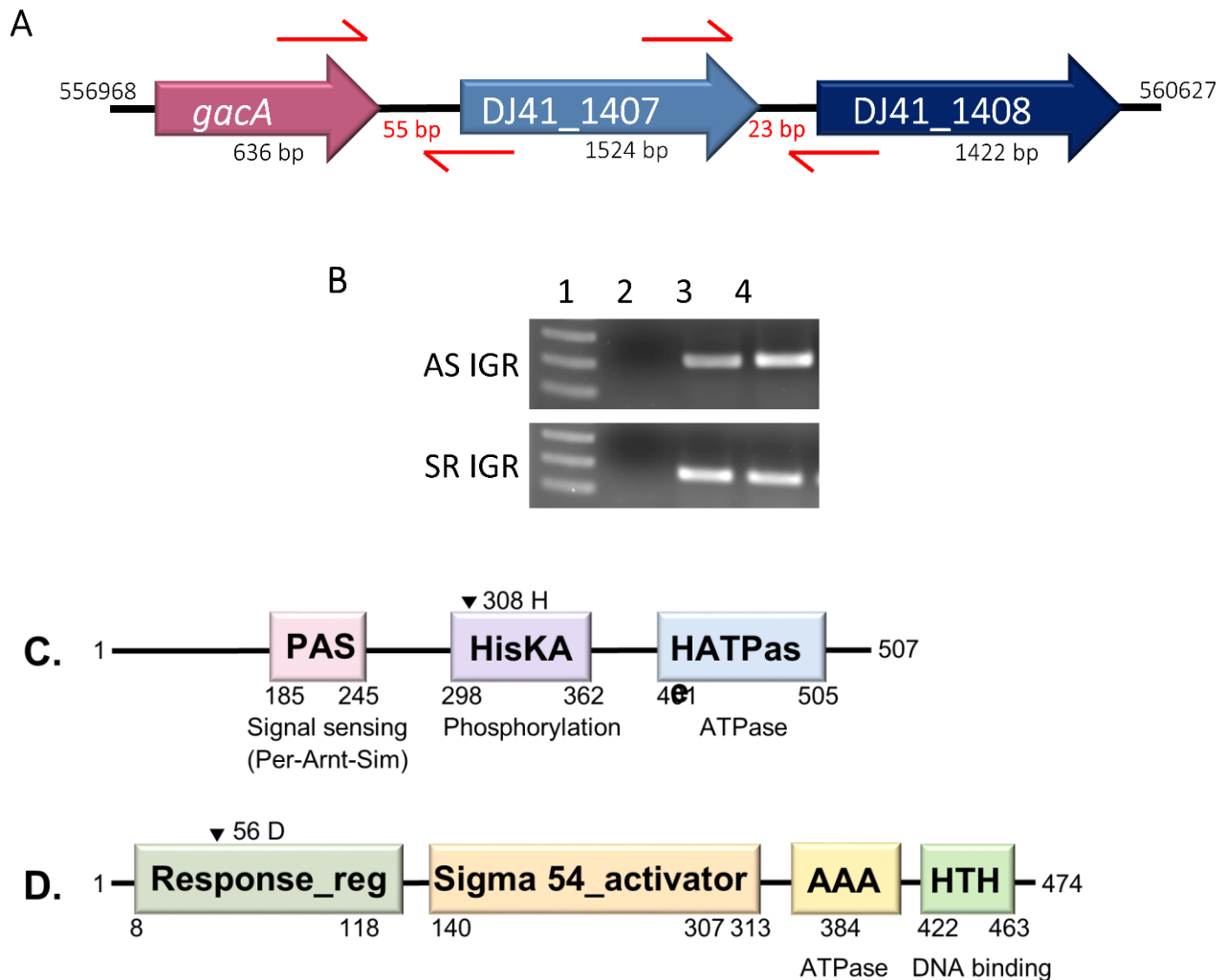


# Roles of DJ41\_1407 and DJ41\_1408 in *Acinetobacter baumannii* ATCC19606 aminoglycosides resistance and virulence

## Supplementary Material



**Figure S1.** (A) Genetic organization of *gacA*, DJ41\_1407 and DJ41\_1408 in the *A. baumannii* ATCC19606 genome. *gacA* (DJ41\_1406): 636 bp; DJ41\_1407: 1,524 bp; DJ41\_1408: 1,422 bp; distance between *gacA* and DJ41\_1407: 55 bp; distance between DJ41\_1407 and DJ41\_1408: 23 bp; red arrow: position of primers used to amplify the *gacA*, DJ41\_1407 and DJ41\_1408 intergenic region. (B) Analysis of the PCR products of *gacA*, DJ41\_1407, and the DJ41\_1408 intergenic region using 2% agarose gel. 1: 100 bp DNA marker, 2: Negative control, 3: *A. baumannii* chromosome as template (Positive control), 4: *A. baumannii* cDNA as template. AS IGR: *gacA* and DJ41\_1407 intergenic region amplification. SR IGR: DJ41\_1407 and DJ41\_1408 intergenic region amplification. Putative domains of DJ41\_1407 and DJ41\_1408 were analysed using CDvist. (C) DJ41\_1407 conserved domains. PAS: Per-Arnt-Sim for signal sensing, HisKA: Histidine kinase domain for phosphorylation, HATPas: ATPase domain. The possible phosphorylation site is the histidine residue at 308. (D) DJ41\_1408 conserved domains. Response\_reg: response regulator domain, Sigma 54\_activator: domain for transcription initiation, AAA: AAA type ATPase domain, HTH: Helix-turn-helix domain for DNA binding. The possible phosphorylation site is the aspartic acid residue at 56. CDvist links: <http://cdvist.zhulinlab.org/>

