

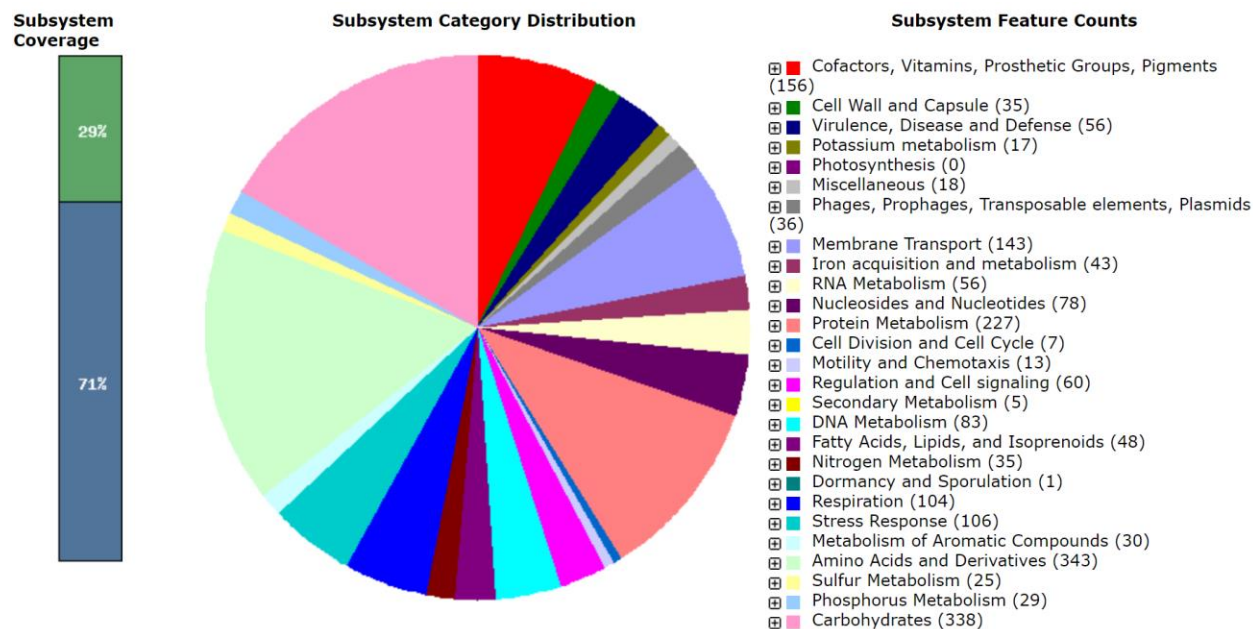


Figure S1. Subsystem distribution and feature counts of various category in *Enterobacter sp.* LR6 genome

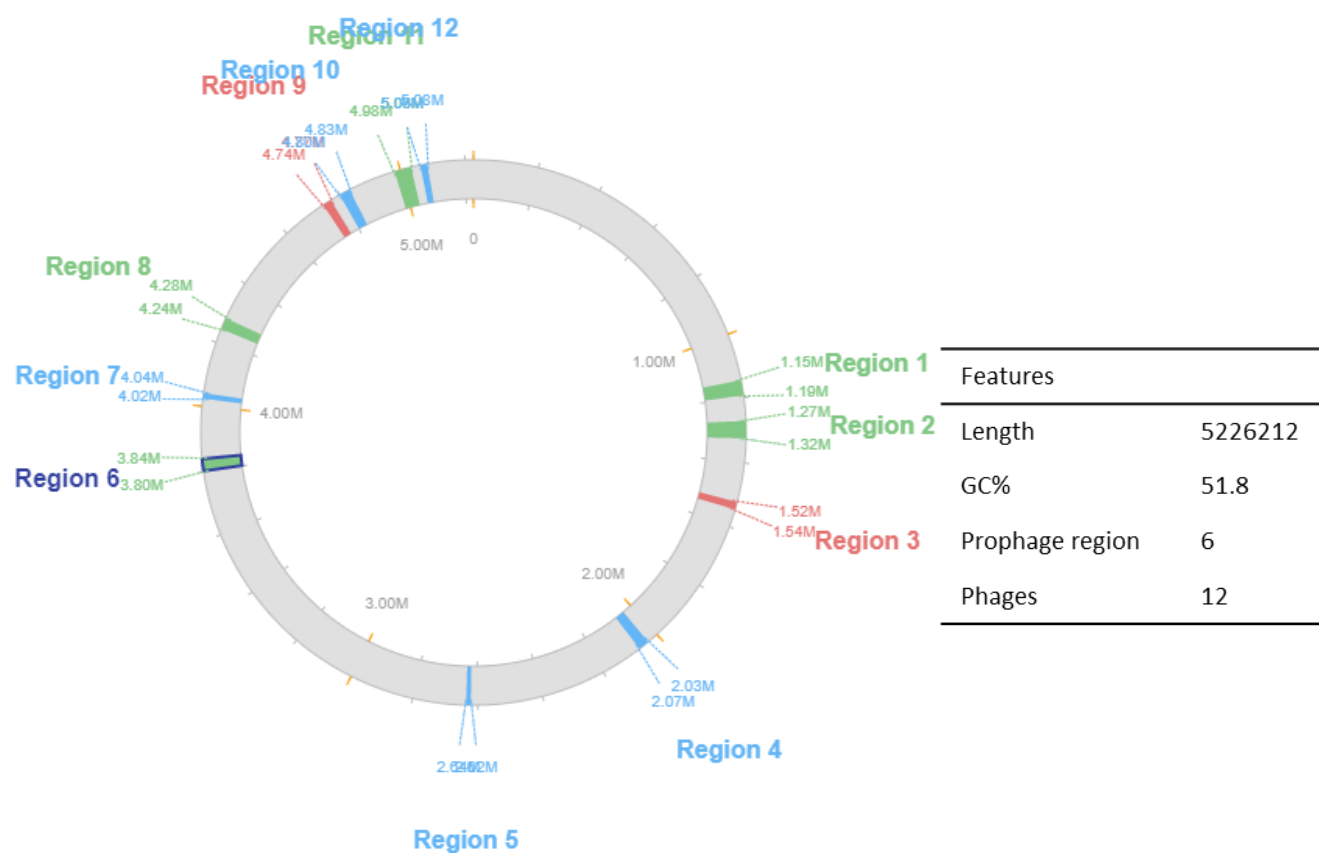


Figure S2. The view of detected prophage area in the genome of *Enterobacter* sp. LR6 by using PHASTER tool. The green region on genome map represent the complete, blue relatively complete and red represent the incomplete prophage area.

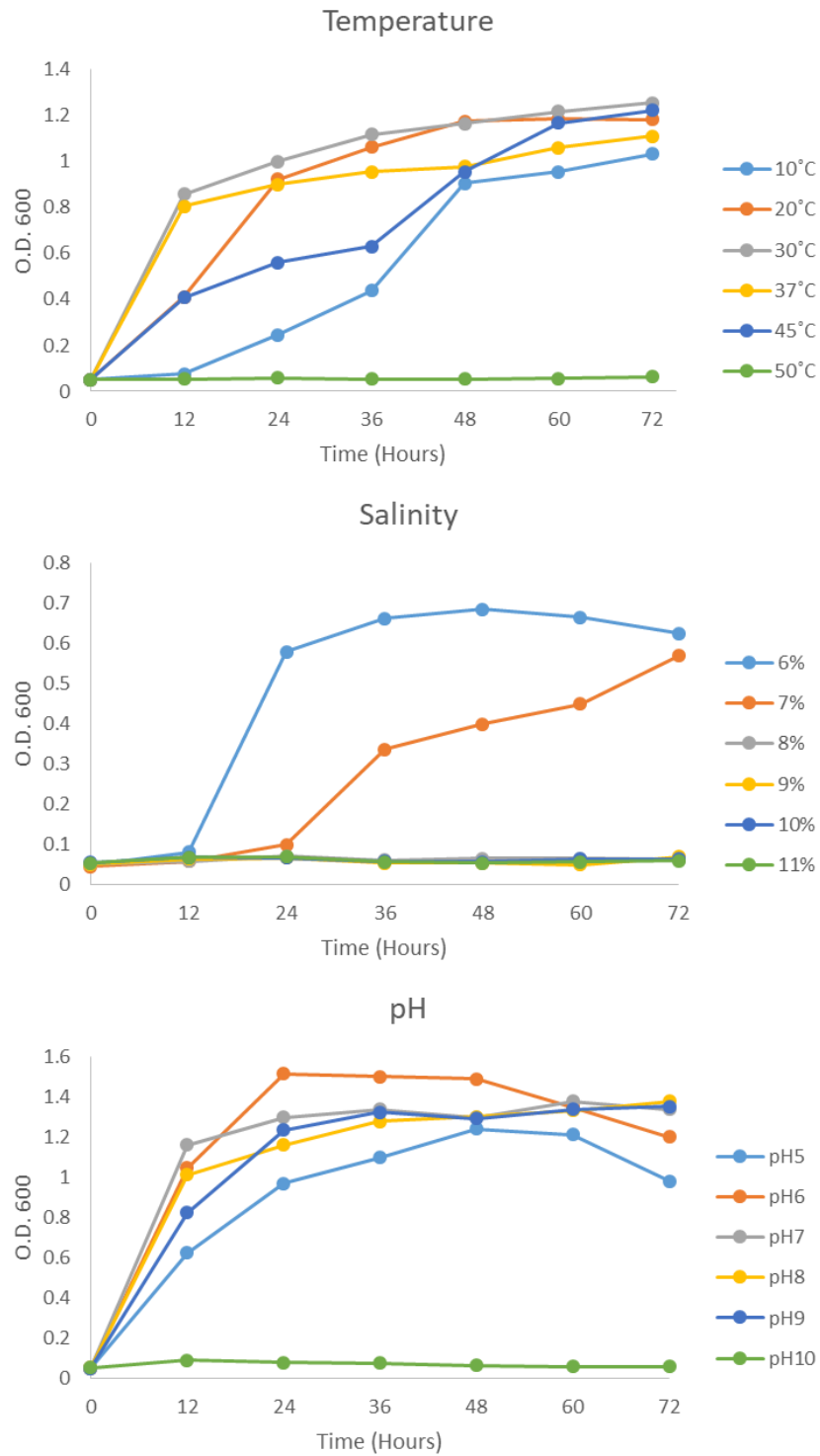


Figure S3. Growth optimization of *Enterobacter Sp. LR6* at different temperature (a), salinity (b), and pH (c).



Figure S4. Pathogenicity testing using sheep blood agar plate, the absence of hemolytic zone around colony indicate LR6 is nonpathogenic

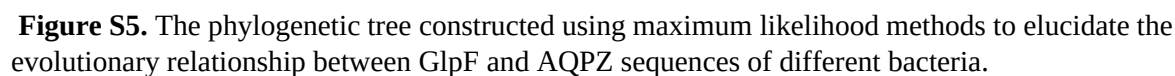


Figure S5. The phylogenetic tree constructed using maximum likelihood methods to elucidate the evolutionary relationship between GlpF and AQPZ sequences of different bacteria.