Supplementary materials

Fig. S1

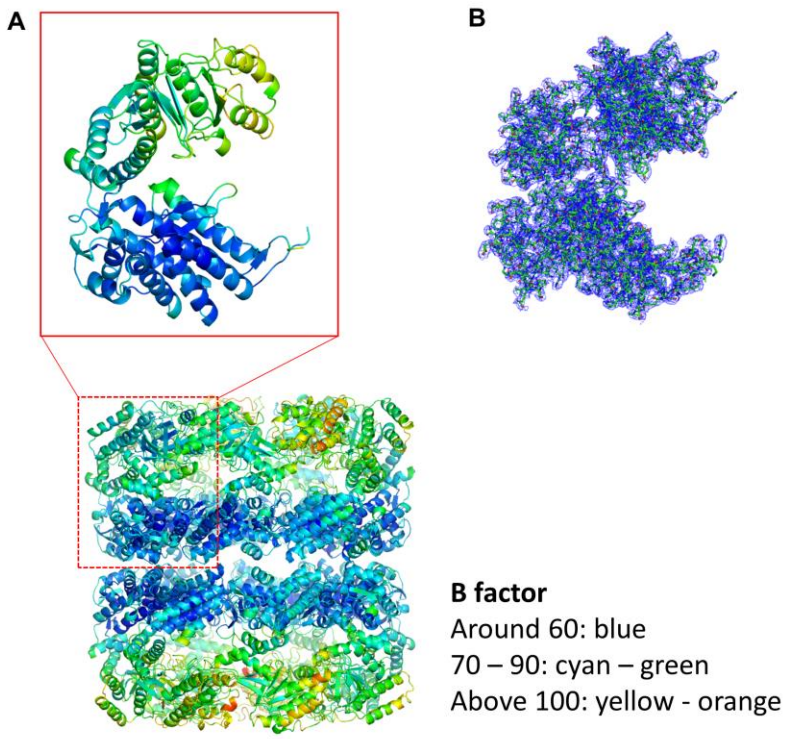

Figure S1. The B factor of XoGroEL protomers in crystal and the 2FoFc map of XoGroEL protomer.

Fig. S2

Figure S2. The sequence alignment of crystal structure determined chaperonin GroELs: XoGroEL, EcGroEL from *E. coli* (PDB ID: 4PKN, NCBI Reference Sequence: WP_000729117.1), PdGroEL from *Paracoccus denitrificans* (PDB ID: 1IOK, WP_011749890.1), CtGroEL from *Chlorobaculum tepidum* (PDB ID: 5DA8, WP_010932217.1), and TtGroEL from *Thermus thermophilus* (PDB ID: 1WE3, WP_011174077.1). Apical domain is shaded in pale blue; Intermediate domain, orange; Equatorial domain, grey.

Fig. S3

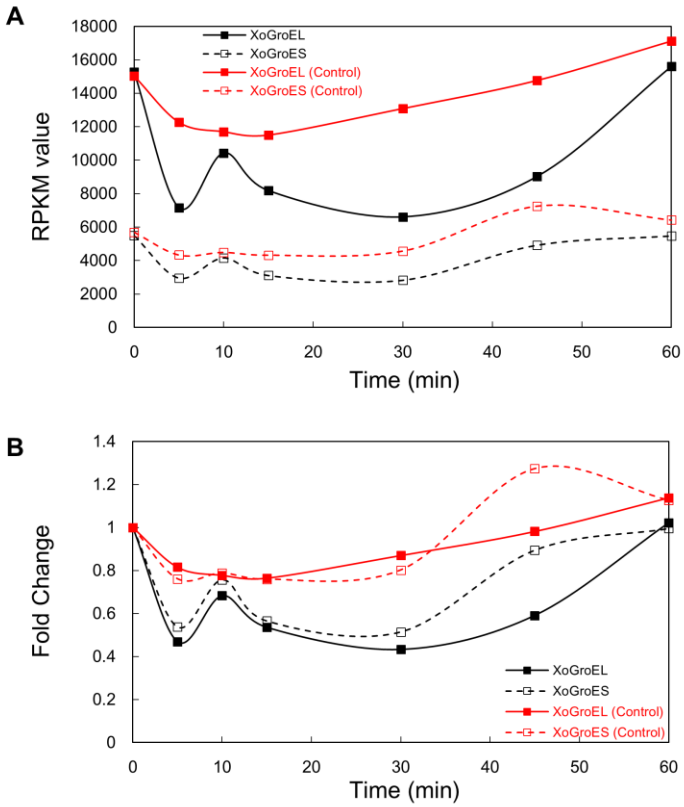

Figure S3. Time-resolved transcriptional expression of *XoGroEL* (*Xoo4288*) and *XoGroES* (*Xoo4289*) genes of Xoo on rice leaf extract (RLX) treatment. (A) RPKM values of *XoGroEL* and *XoGroES* genes (B) Fold change in the expression level of *XoGroEL* and *XoGroES* genes Transcriptional expression levels were measured in a time-dependent manner via RNASeq in RLX treated and control Xoo cells. Relative transcript abundance was calculated by counting the number of reads per kilobase per million mapped sequence reads (RPKM). In the fold change comparison of gene expression level, the expression levels at each time-points were divided by that at the zero time-point. Accordingly, all the expression levels of *XoGroEL* and *XoGroES* genes started uniformly from 1 at the zero time-point, which simplifies the comparison of expression level changes.