

Fig. S1. Purified native and refolded FtsE.(A) Refolded and purified FtsE protein, the SDS PAGE image for refolded FtsE in 0.5 M arginine, and purified from inclusion bodies. (B) Analytical size-exclusion chromatography profile for the refolded FtsE, eluting near to the void volume by using Superdex 200 10/300 GL column. (C) SDS PAGE image for soluble final purified FtsE. (D) Western blot with the anti-His antibody of FtsEduring steps of checking solubility and purification. In: Induced, TS:Total supernatant, FL:Flowthrough,W:Wash fraction, F1: Elution fraction 1, F2: Elution fraction 2, F3: Elution fraction 3.


Fig. S2. Molecular weight calculation, CD spectra and surface charge distribution of FtsE. (A) The SDS-PAGE image of final purified mutant FtsE proteins from the soluble fraction. (B) Molecular weight calculation of the final purified soluble FtsE by following the equation described in materials and methods. (C) CD spectrum of FtsE obtained in soluble form and purified revealing proper secondary structure and hence folding with approximately $36.9 \%$ helix, $28.9 \%$ betasheet, and $5.3 \%$ turn. (D) Surface charge distribution of modeled FtsE.


Fig. S3. ATPase activity of refolded FtsEand in silico interaction of ATP with FtsE. (A). Dendrogram showing the ATPase activity of refolded FtsE. (B)Western blot with the anti-His antibody showing the absence of dimerization of FtsE in the presence and absence of the bacterial cytoplasmic fraction. (C)Docking of FtsE modeled structure with ATP, showing its interaction with K41 residue.(D) Enlarged view of FtsEwith the docked ATP shows the interaction of lysine residue from the Walker-A motif and all the phosphate groups of ATP.


Figure S4. Uncropped western blots shown in the manuscript.Panel Ashows the original westernblot, from which Fig. 5A was made. Panel B and panel $\boldsymbol{C}$ show the western blot from which S1D and S3B were made. All lanes shown in the western blot were used.

