Supporting Information for

Cryo-EM structure of the fatty acid reductase LuxC-LuxE complex provides insights into bacterial bioluminescence

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Figure S1. Sequence alignment of LuxE from different luminous bacteria.

Figure S2. Sequence alignment of LuxC from different luminous bacteria.

Figure S3. Cryo-EM image processing of LuxCE.

Figure S4. Single-particle cryo-EM data analysis of LuxCE.

Figure S5. The final map and overall structure of LuxCE.
Figure S1. Sequence alignment of LuxE from different luminous bacteria. The critical residues are indicated by red star.
Figure S2. Sequence alignment of LuxC from different luminous bacteria. The catalytic cysteine is indicated by red star. The residues selected for mutagenesis are indicated by red dots.
Figure S3. Cryo-EM image processing of LuxCE. A) A representative micrograph of LuxCE. B) A flow chart for data processing of LuxCE.
Figure S4. Single-particle cryo-EM analysis of LuxCE. A) Local-resolution map of LuxCE. B) The gold-standard Fourier shell correlation (FSC) curve for the final map.
Figure S5. The final map and overall structure of LuxCE. Density of LuxC and LuxE are colored in pink and gray, respectively. Structures of LuxC (cyan) and LuxE (blue) are shown as cartoon.