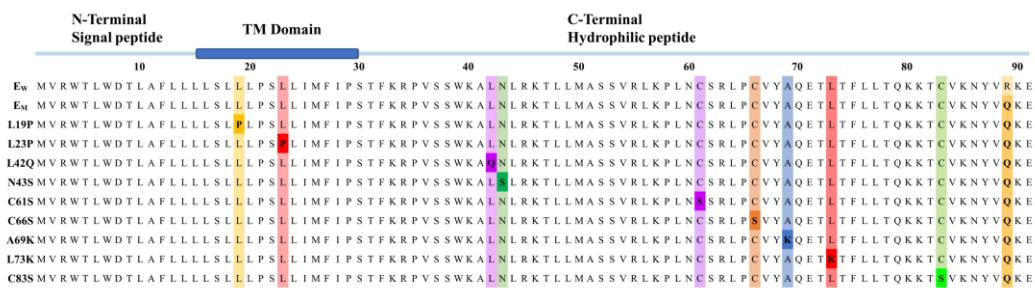
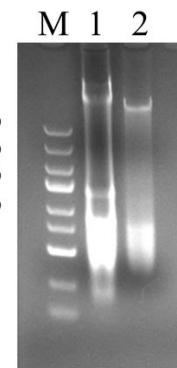


# Supplementary Materials: A Novel High-Efficient Method for Preparing Bacterial Ghosts in Large Quantities

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**Figure S1.** Alignment of lysis protein E and its mutants were listed. E<sub>w</sub> referred to wild-type lyase, and E<sub>m</sub> was the mutation of arginine at position 89 to glutamine. The mutation sites were marked in color. Transmembrane domain (TM Domain) from the 15th to 30th was labeled.



**Figure S2.** The genomic DNA in *E. coli* BL21 (DE3) before lysis (lane 1) and after lysis (lane 2) were analyzed by gel electrophoresis.

**Table S1.** Part of the primers used in this study.

Primers	Sequence (5'-3')
F-Ew	TTTAAGAAGGAGATATACCATGGATGGTACGCTGGACTTGTGG
R-Ew	CGGATCTCAGTGGTGGTGGTGGTGGCTCTTCTGGACATAATTCTTC
F-Em	TTTAAGAAGGAGATATACCATGG ATGGTGCCTGGACTTATGG
R-Em	CGGATCTCAGTGGTGGTGGTGGTGGCTCTTCTGGACATAATTCTTCAC
F <sub>M/L19P</sub>	TTAGTCTGCCATTGCCATCATTGTTAATTATGTTATCCCGAGCAC
R <sub>M/L19P</sub>	AATGATGGCAATGGCAGACTAAACACTTGCTTTCTTGCTGC
F <sub>M/L23P</sub>	TCTGCCATCACCATTAAATTATGTTATCCCGAGCACCTT
R <sub>M/L23P</sub>	AATTAATGGTATGGCAAGAGCAGACTAACAGCAAAGAA
F <sub>M/L42Q</sub>	AAGCACAGAACCTCGTAAAACGCTGCTCATGGCGTCTCGTT
R <sub>M/L42Q</sub>	TTTACGAAGGTTCTGTGCTTCCATGAGCTACAGGTCTCTT
F <sub>M/N43S</sub>	CTTAGTCTCGTAAAACGCTGCTCATGGCGTCTCGTT
R <sub>M/N43S</sub>	AGCGTTTACGAAGACTAACAGCTTCCATGAGCTTACAGG
F <sub>M/C61S</sub>	GCTTAAAACCTCTGAATTCTTCCGGTACCGTGC
R <sub>M/C61S</sub>	AGAATTCAGAGGTTAACGCAACCGAAGACGCCATGA
F <sub>M/C66S</sub>	ATTGTTCCCGTTACCGTCTGTTACGCCAAGAACATT
R <sub>M/C66S</sub>	AGACGGTAACCAGGAACAATTCAAGAGGTTAACGCAACC
F <sub>M/A69K</sub>	CGCTTACAAGCAAGAACATTAACATTCTACTGACGCAGAAG
R <sub>M/A69K</sub>	TGTTTCTGCTTGAAACGCACGGTAACCGGAACATT
F <sub>M/L73K</sub>	GAAACAAAGACATTCTACTGACGCAGAAGAACCTGCGT
R <sub>M/L73K</sub>	AGTAAGAATGTCTTGTCTGGCGTAAACGCACGGTA
F <sub>M/C83S</sub>	ACCTCTGTGAAGAATTATGTCCAGAAAGAGCACCAC
R <sub>M/C83S</sub>	ACATAATTCTCACAGAGGTCTTCTGCGTCAGTAAGAATG