

File name: Supplementary Information

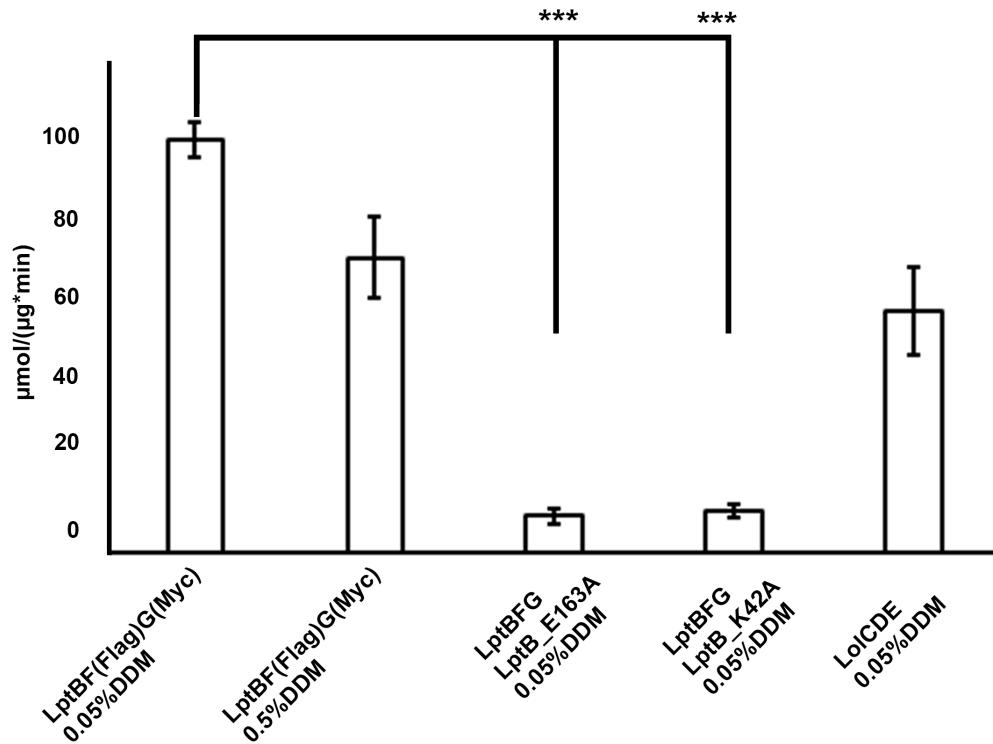
Description: Supplementary figures and supplementary tables.

File name: Supplementary Movie 1

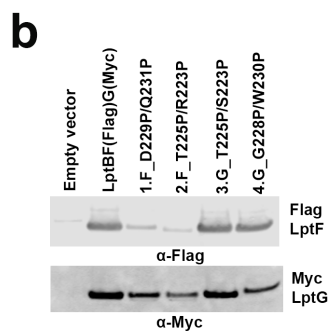
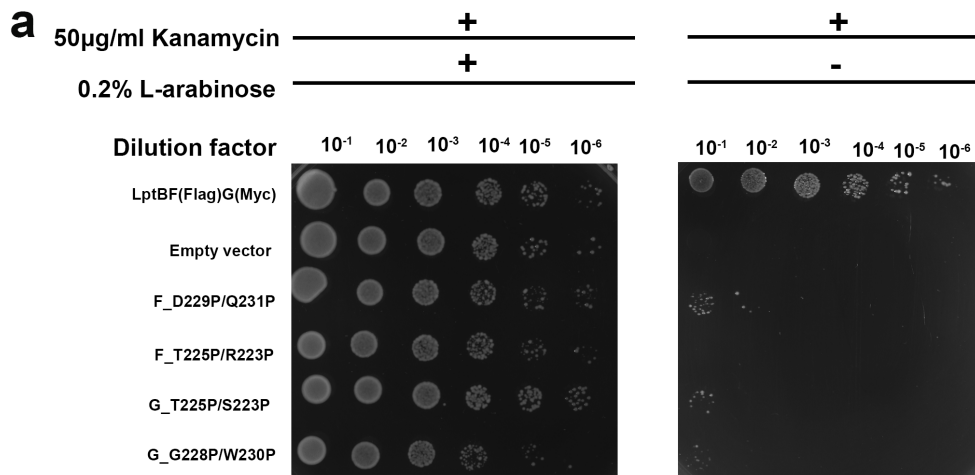
Description: The conformational changes from the LptB₂FG structure of *K. pneumoniae* to that of the LptB₂FG of *P. aeruginosa*. The side view of the lateral gate TM1F--TM5G. The periplasmic domains rotate around 90°, while the conformation of this lateral gate TM1F--TM5G is from the closed state (LptB₂FG of *K. pneumoniae*) to the open state (LptB₂FG of *P. aeruginosa*).

File name: Supplementary Movie 2

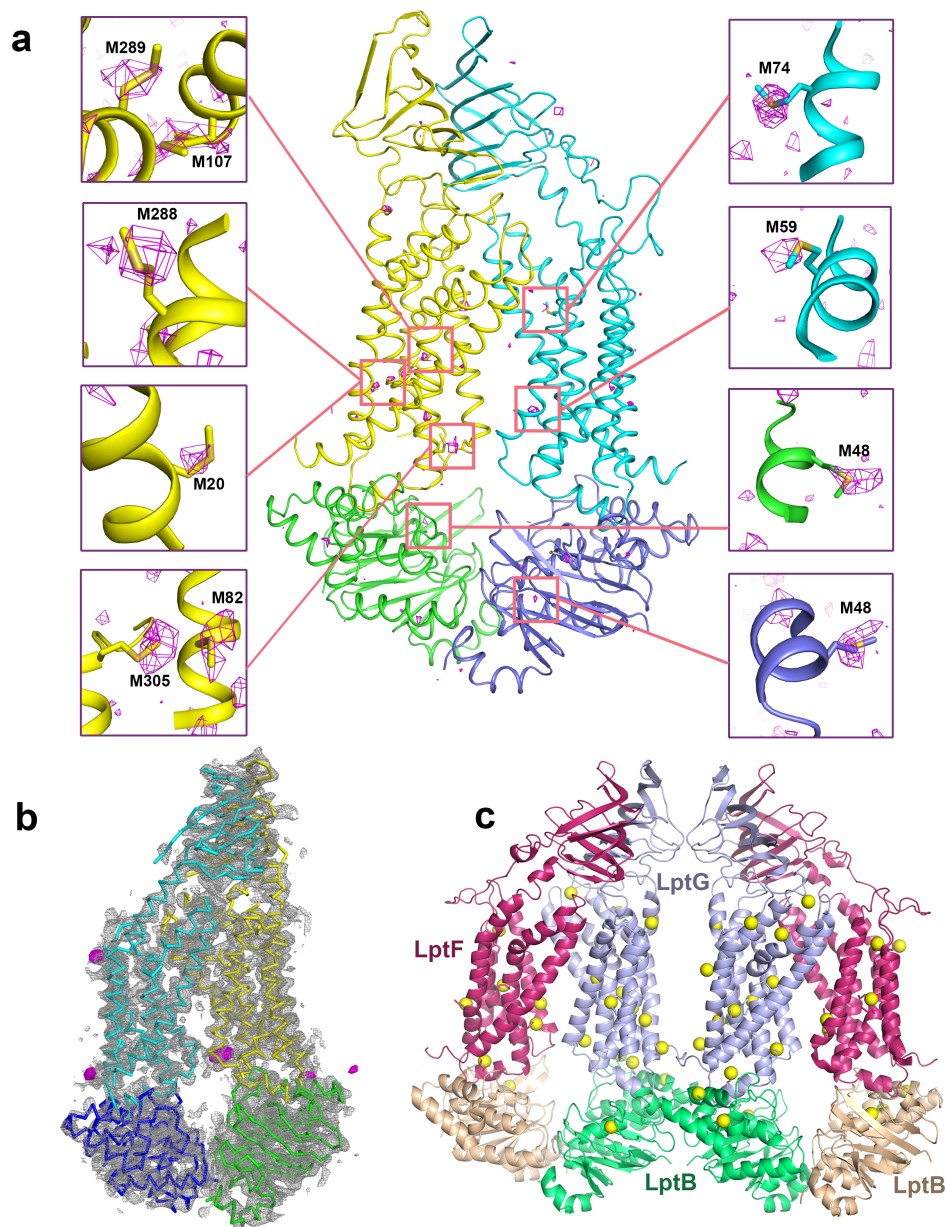
Description: The conformational changes from the LptB₂FG structure of *K. pneumoniae* to that of the LptB₂FG of *P. aeruginosa*. The side view of the lateral gate TM5F--TM1G. The periplasmic domains rotate toward to this lateral gate TM5F--TM1G, while the conformation of this lateral gate TM5F-TM1G is from the open state (LptB₂FG of *K. pneumoniae*) to the closed state (LptB₂FG of *P. aeruginosa*).



Supplementary Figure 1. Purified LptB₂FG has ATPase Activity. Purified *E. coli* LptBF(Flag)G(Myc) transporter has ATPase activity in different concentrations of detergent DDM. The *E. coli* LptB₂FG protein complex with LptB_E163A or LptB_K42A mutation shows significant lower ATPase activity than that of LptBF(Flag)G(Myc). *E. coli* lipoprotein transporter LoICDE is included in the ATPase activity assay as a system control. The detergent DDM has a minor affection on the ATPase activity of LptB₂FG. The data was analysed using one-way ANOVA, n=3; P<0.01; graphs show mean±S.E.M.

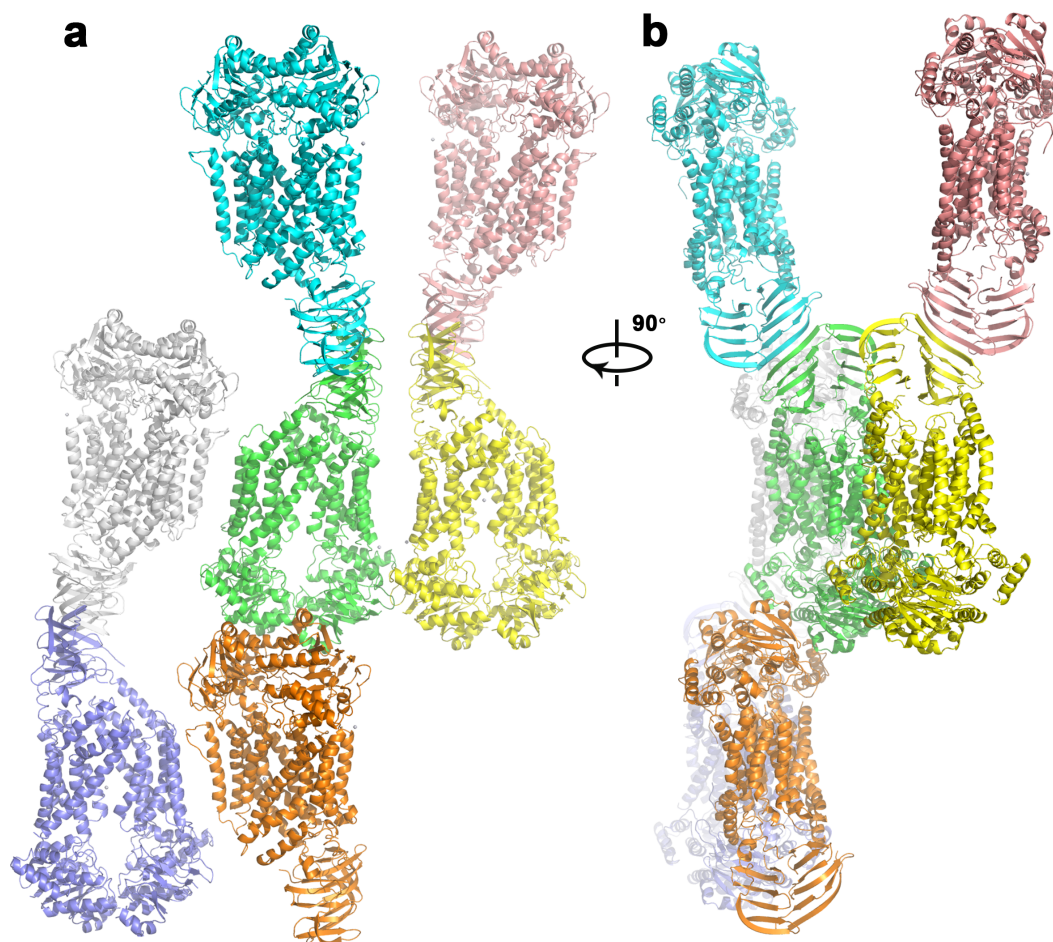


Supplementary Figure 2. Complementation assays of NR1113 with wild type and mutant LptB₂FG complexes. The NR1113 depletion strain expresses *lptFG* genes from an L-arabinose inducible promoter. a. Functional assays of the double proline mutants. NR1113 cells were transformed with empty vector (pTRC99a_Kan) or the vector encoding LptBF(Flag)G(Myc) as negative and positive controls, respectively, or with LptBF(Flag)G(Myc) double proline mutants. All bacterial cultures were adjusted to an OD_{600nm} = 0.5 with fresh medium, serially diluted 1:10 as indicated on the top of the figure and then replica plated in agar plates with (+) or without (-) 0.2% L-arabinose. b. Detection of protein expression levels of LptF(Flag)G(Myc) of the positive control, negative control, and the double proline mutants by Western blotting. The bacteria cells for Western blotting were cultured in the presence of 0.2% L-arabinose.

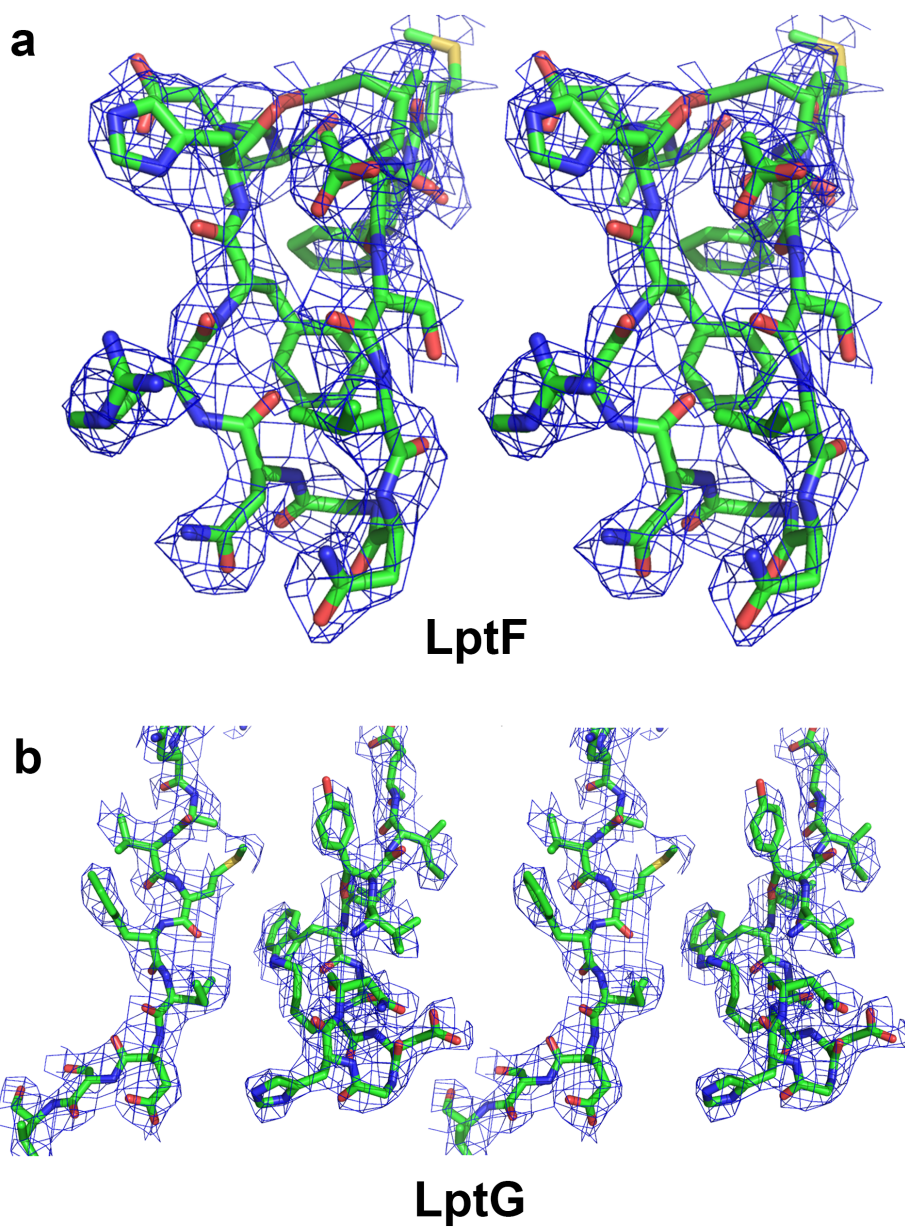


Supplementary Figure 3. LptB₂FG complex structure of *K. pneumoniae* was registered using sulfur data and *S. flexneri* Selenomethionine data. a. The anomalous difference Fourier map of sulfur contoured at 3σ is shown in pink. The map of sulphur was used for the model building. b. The final refined structure of LptB₂FG is shown as a Ca trace superimposed on the initial density modified experimental map (grey) contoured at 1.2σ . The anomalous difference Fourier map contoured at 7σ is shown in pink, highlighting the location of the Pt sites. Both maps were calculated from data that was corrected for anisotropy along the surface defined by $1/|\sigma| < 1.2$. c. The data from *S. flexneri* LptB₂FG selenomethionine (Se-Met) incorporated crystal are

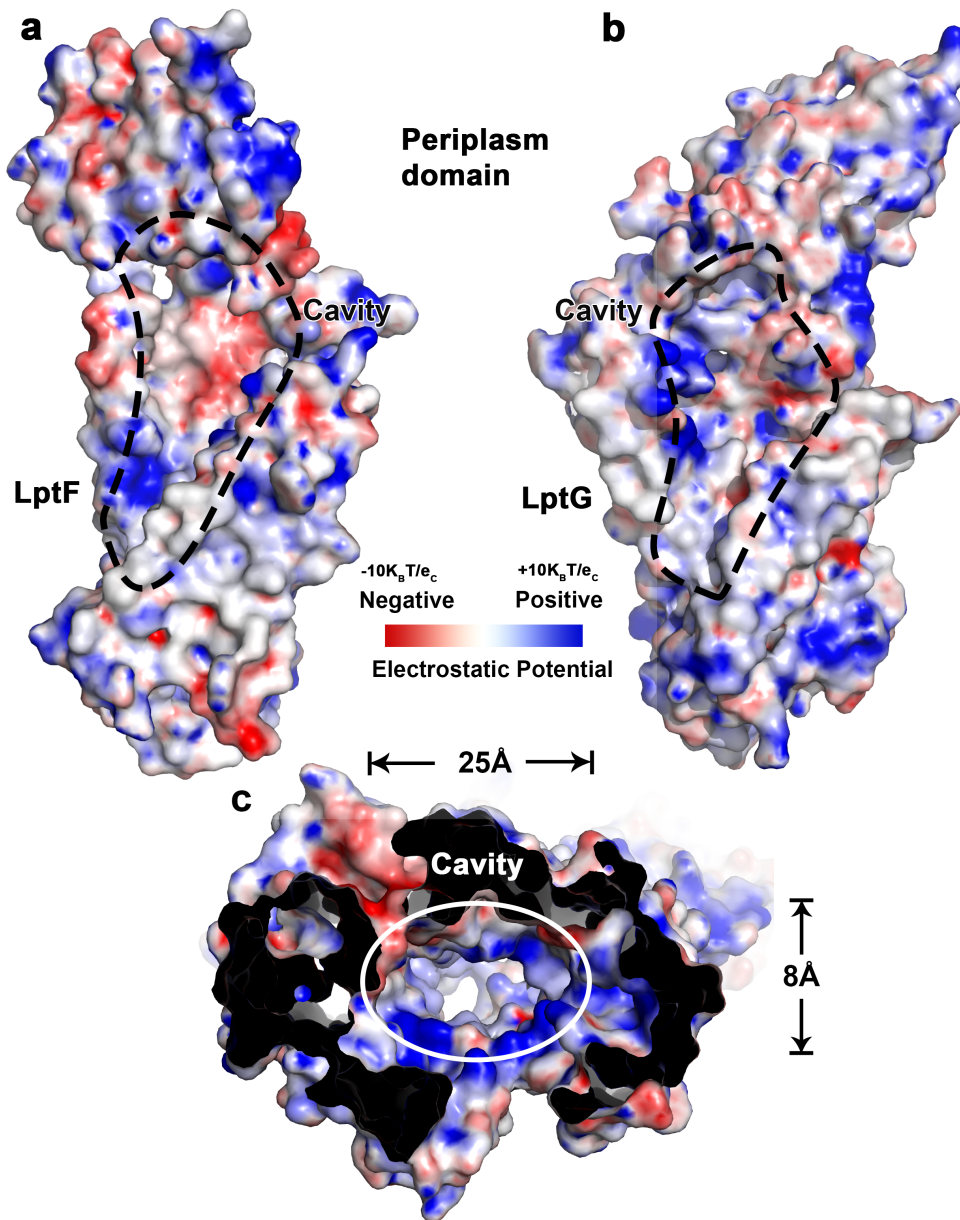
collected and the anomalous signal map is generated for amino acids sequence registry. The yellow spheres display the Se-Met sites identified by phaserEP from the Se-Met incorporated crystal dataset per asymmetric unit. The Se-Met incorporated crystal belongs to space group $P212121$. There are two transporters per asymmetric unit. LptF and LptG are shown in raspberry and slate respectively. The two copies of LptB are shown in lime green or light orange.



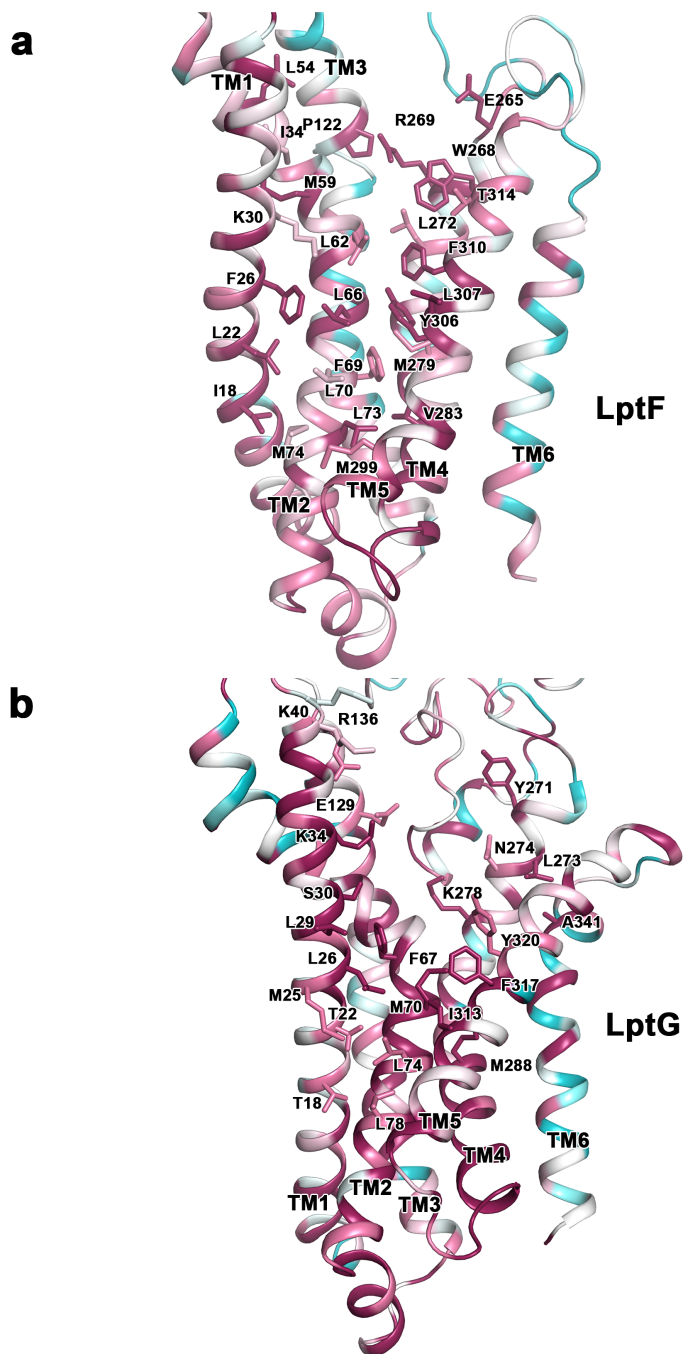
Supplementary Figure 4. Crystal packing of LptB₂FG. a. The LptB₂FG molecules are packed in the crystals via interactions of the neighbouring LptF periplasmic domains, neighbouring LptB molecules, and neighbouring LptG TM domains. The transporters are in cyan, raspberry, grey, green, yellow, slate and orange. b. Rotation of 90° of Figure A along Y-axis. The neighbouring periplasmic domains of LptF stack against each other.



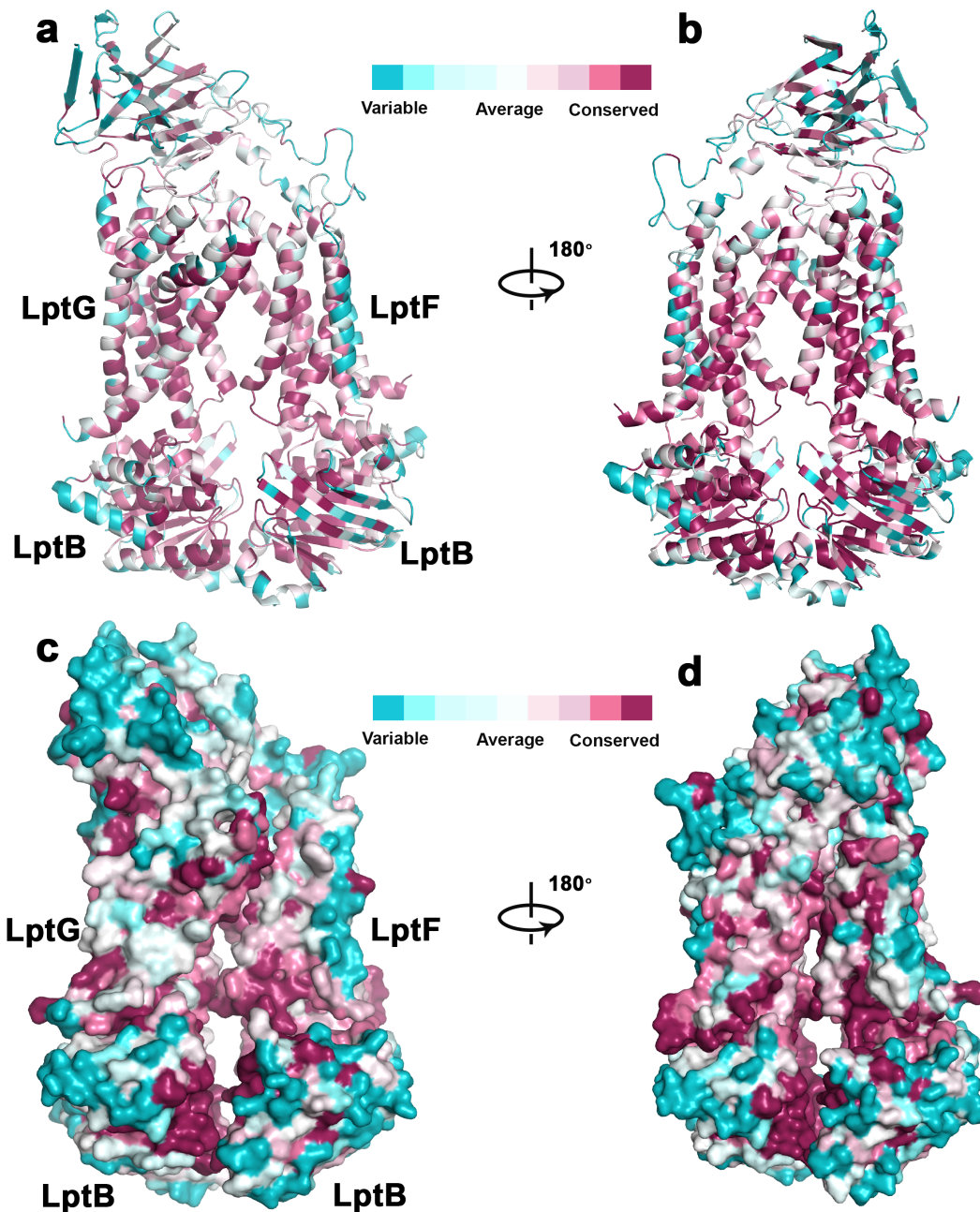
Supplementary Figure 5. The stereo electron density map of parts of LptB₂FG. The 2Fo-Fc electron density map is shown, contoured at 1 σ . a. a stereo electron density map of a part of LptF. b. a stereo electron density map of a part of LptG.



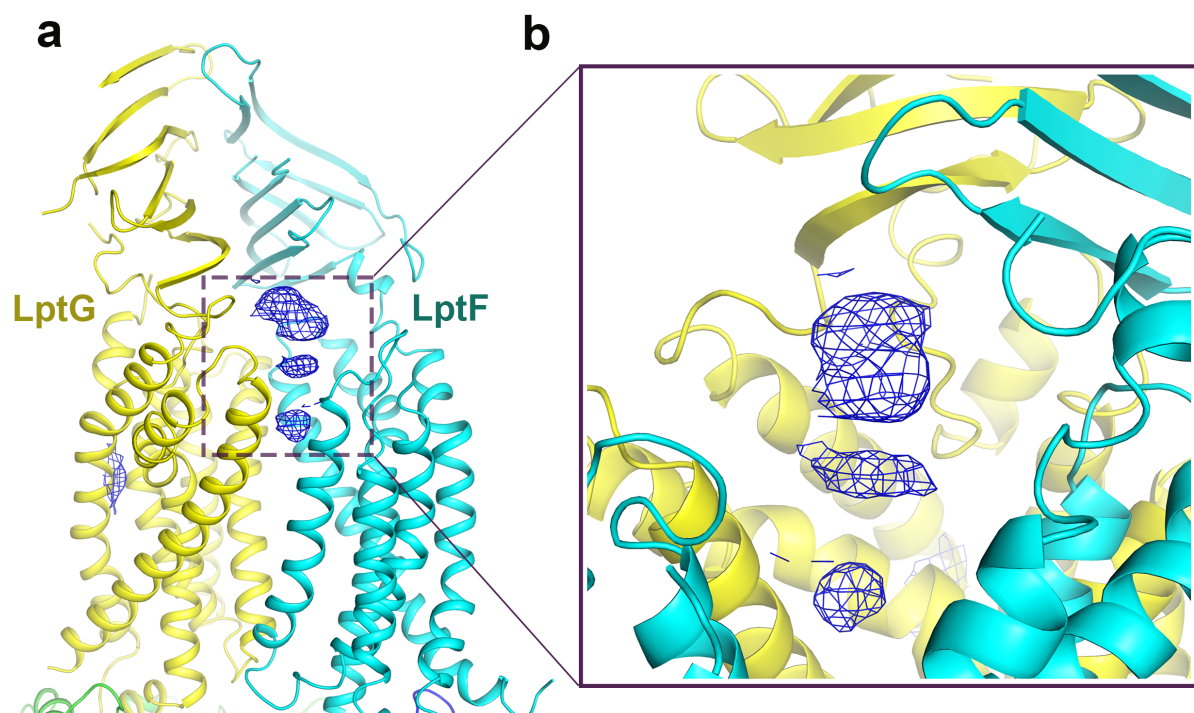
Supplementary Figure 6. Electrostatic potential map of LptF, LptG and LptB₂FG. The cavity of LptB₂FG, shown in the dotted circular lines (black). The cavity in the membrane section is very hydrophobic, while the cavity in the periplasm is highly positively charged. This feature may be important for LPS binding, as the lipid A of LPS is hydrophobic, while the core oligosaccharide is highly negatively charged. a. The electrostatic potential map of LptF. b. The electrostatic potential map of LptG. c. The electrostatic potential map of the cavity of LptB₂FG. The cavity is about 25 Å in length and 8 Å in width. The cavity is shown in the circular line (white). The figures were colored by electrostatic charge from red ($-10K_B T/e_c$, in which K_B is the Boltzmann Constant, T is temperature and e_c is the electron charge) to blue ($+10 K_B T/e_c$).



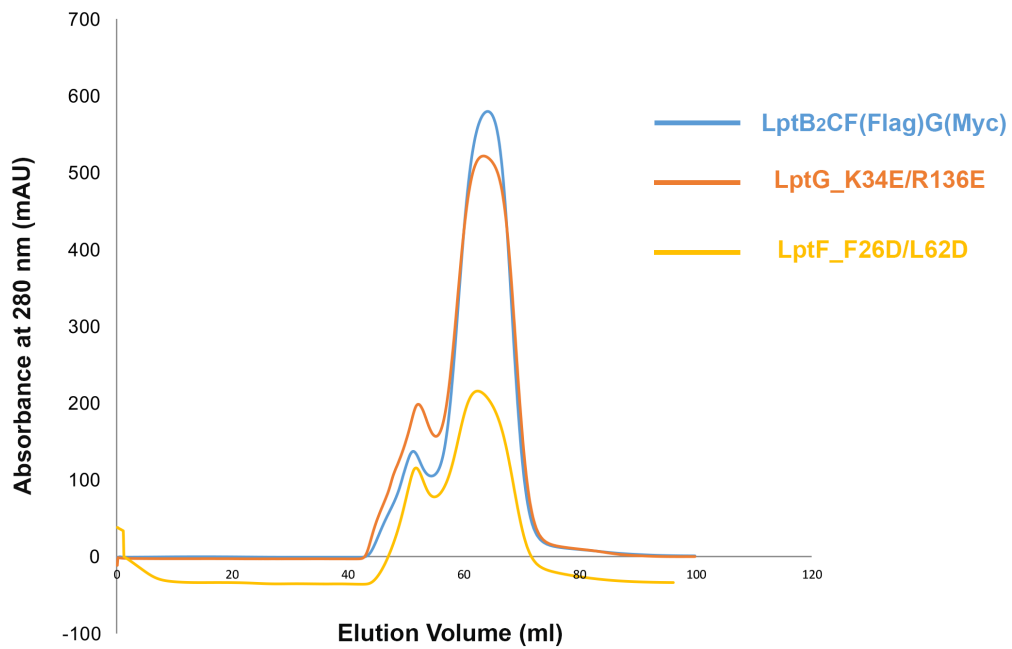
Supplementary Figure 7. The highly conserved residues in the cavity. The conserved residues of LptB₂FG were analysed using the Consurf server. The conserved residues were identified from 150 homologues of LptF and LptG. The most variable residues are in cyan, and the most conserved residues are in dark red. The highly conserved residues of a. LptF; b. LptG.



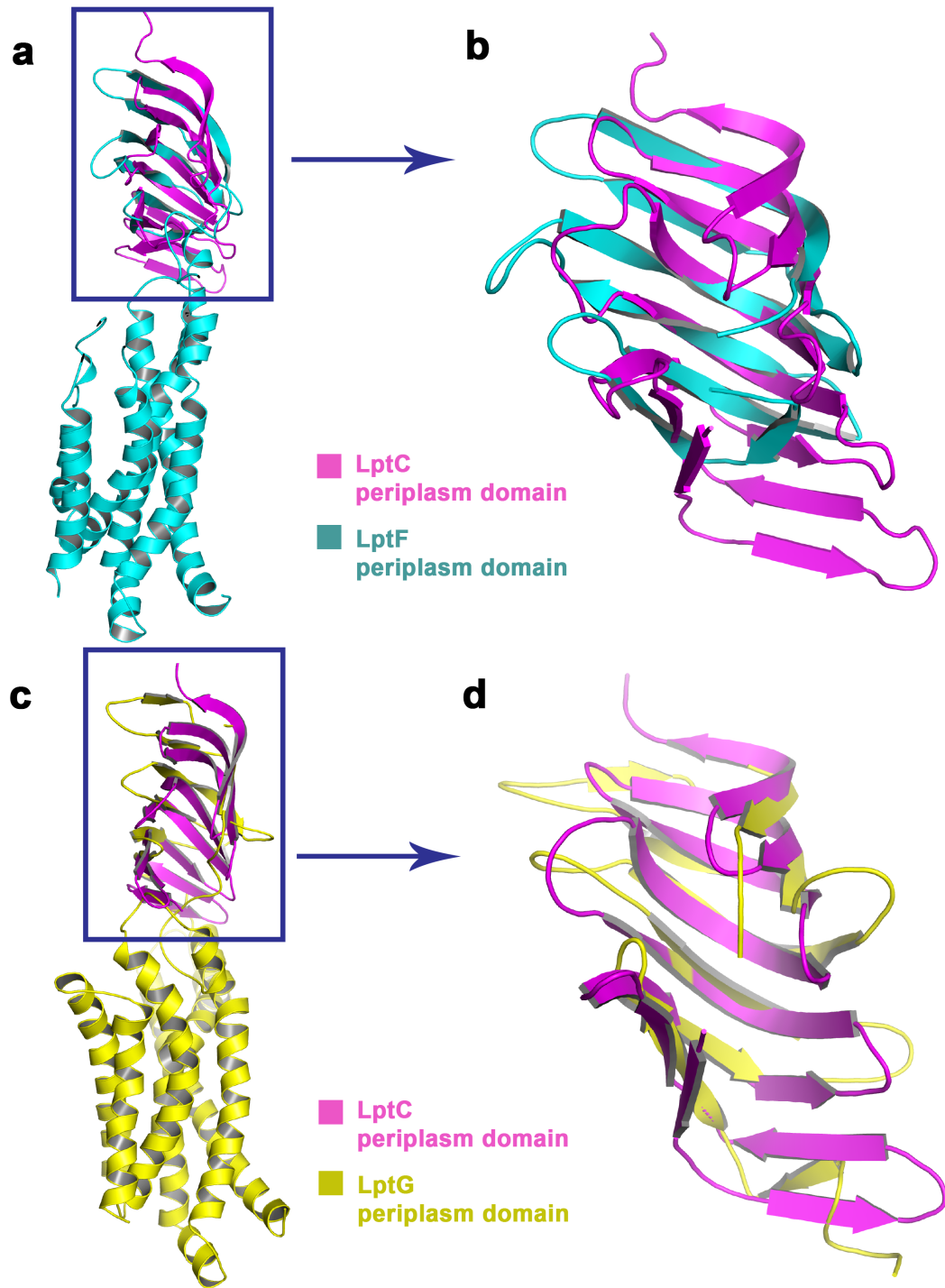
Supplementary Figure 8. Conserved residues of the LptB₂FG. The conserved residues of LptB₂FG were analysed using the ConSurf server. The conserved residues were identified from 150 homologues of LptF and LptG and 52 homologues of LptB. The most variable residues are in cyan, and the most conserved residues are in dark red. The LptB₂FG transporter is shown as a cartoon (a and b) and as a surface (c and d) renderings.



Supplementary Figure 9. Extra-electron densities in the cavity of LptB₂FG. The Fo-Fc electron density contoured at 2.5σ . a. The unassigned electron densities in the cavity of LptB₂FG. b. The close view of the electron densities.

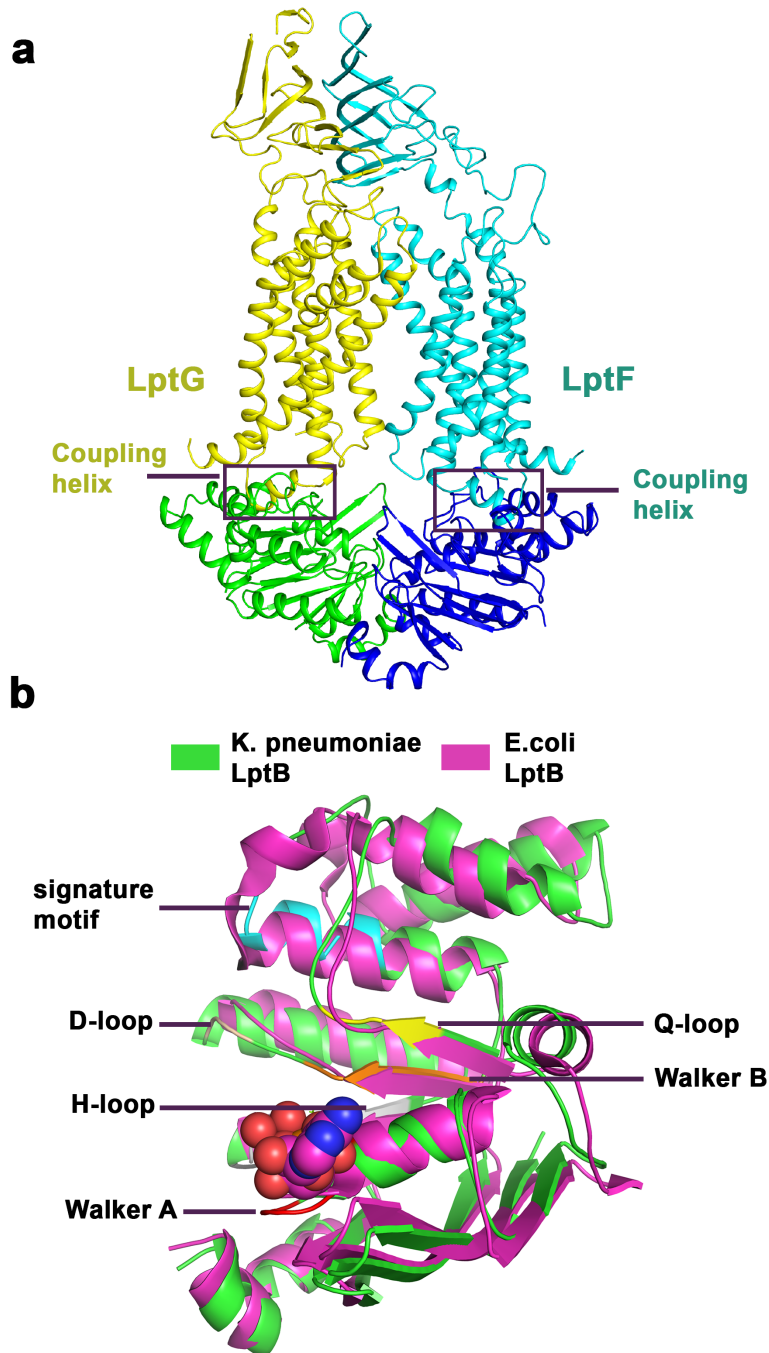


Supplementary Figure 10. Size-exclusion chromatography measurements of wild-type LptB₂CFG, LptB₂CFG mutant LptF_F26D/L62D and LptB₂CFG mutant LptG_K34E/R136E. *E. coli* wild-type LptB₂CFG, mutant LptF_F26D/L62D and mutant LptG_K34E/R136E were expressed, and the protein complexes were purified by a nickel column. The protein complexes were analysed by size-exclusion chromatography using a HiLoad 16/600 Superdex 200 pg column. The two mutant complexes were eluted at the same elution volume as that of the wild-type, suggesting that the two mutants are folded.

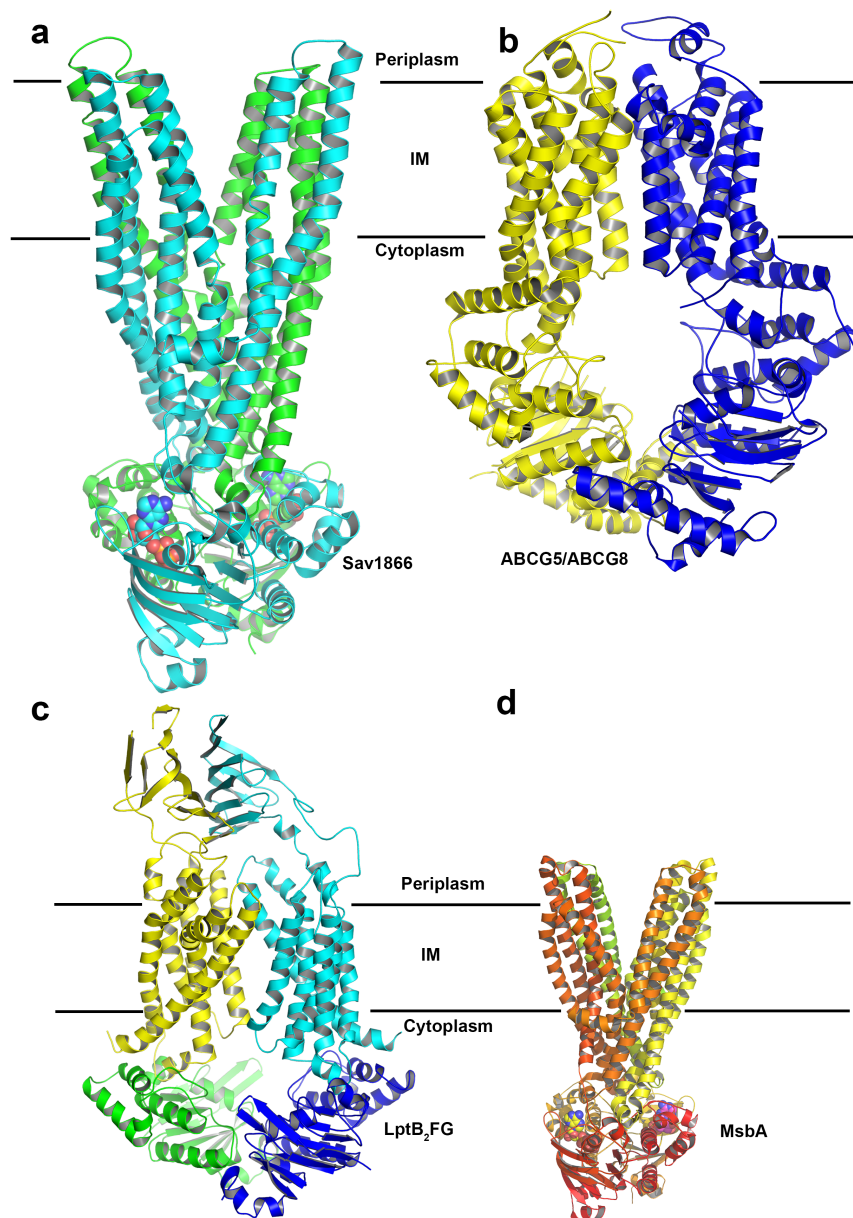


Supplementary Figure 11. Periplasmic domains of LptF and LptG resemble LptC.

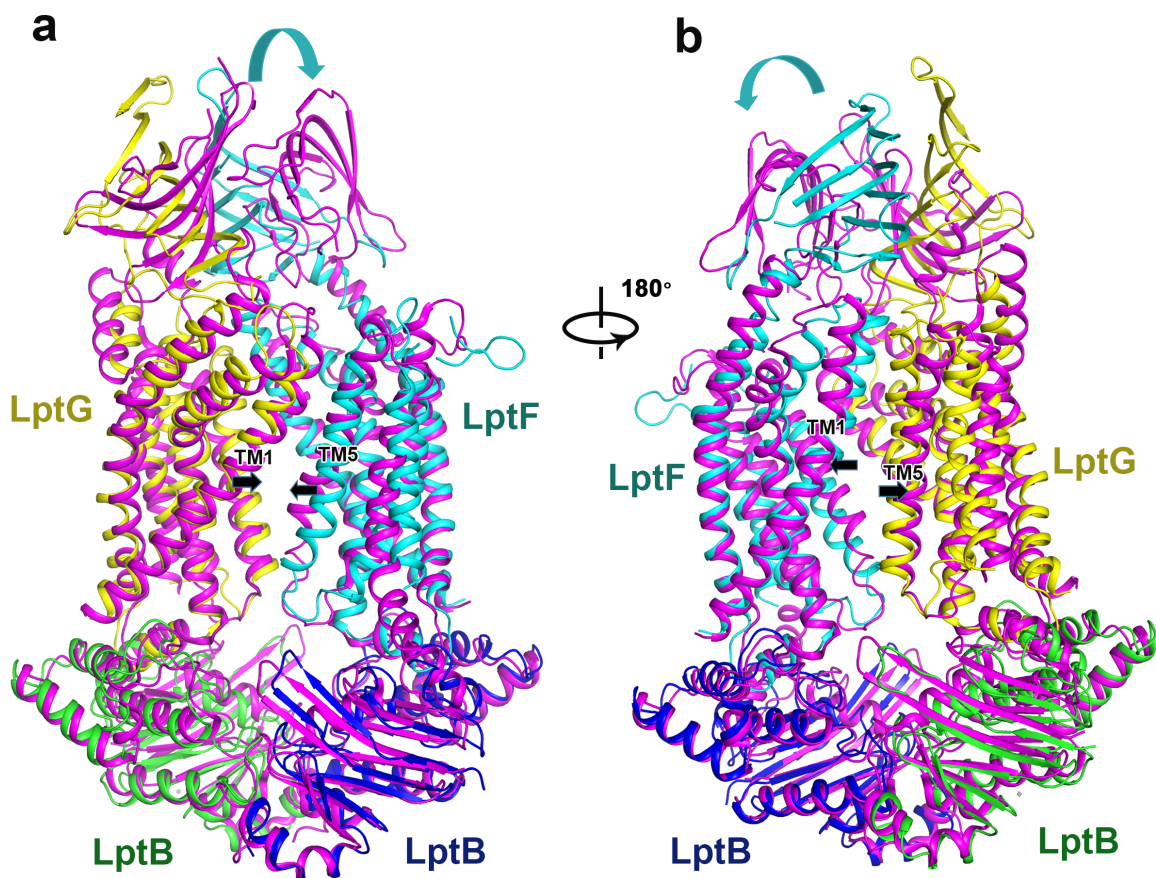
LptF, LptG and LptC molecules are in cyan, yellow and magenta, respectively. a. The periplasmic domain of LptC (PDB code 3MY2) is superimposed to the periplasmic domain of LptF. b. A close view of the superimposition of LptC and the periplasmic domain of LptF. c. The LptC is superimposed to the periplasmic domain of LptG. d. A close view of the superimposition of LptC and the periplasmic domain of LptG.



Supplementary Figure 12. LptB structures of the *E. coli* and *K. pneumoniae* and the coupling helices of LptF and LptG. LptB of *E. coli* was only crystallized in presence of nucleotide (ATP, ADP or AMP). The ATP-free LptB structure of *K. pneumoniae* was determined. a. The coupling helices of LptF and LptG. b. Superimposition of structures of *E. coli* LptB (magenta) (PDB code 4QC2) and *K. pneumoniae* LptB (green). The conformational changes were observed when ATP bound. The sequence identity of *E. coli* LptB and *K. pneumoniae* LptB is 95.85%.



Supplementary Figure 13. Crystal structures of ABC transporters in different conformations. a. The multidrug transporter Sav1866 in complex with ADP is in an outward-facing conformation (PDB code 2HYD). The NBDs is in “close contact”. b. Crystal structure of human sterol transporter ABCG5/ABCG8 (PDB code 5DO7). The structure is in an inward-facing conformation. The NBDs are ATP-free and in “loose contact”. c. Crystal structure of LptB₂FG. The lateral gate TM5F-1G is in an open conformation, while the NBDs are in ATP-free and in “loose contact”. The ATP-binding and hydrolysis may fully open the lateral gate TM5F-1G and drive LPS transport. d. MsbA in complex with AMP-PNP is in the outward-facing conformation (PDB code 3B60).



Supplementary Figure 14. The structure of LptB₂FG from *K. pneumoniae* is in a totally different conformation from that of LptB₂FG from *P. aeruginosa*. The colour scheme of LptB₂FG from *K. pneumoniae* is the same as that of the Fig 2 (LptF and LptG are in cyan and yellow, respectively). The LptB₂FG of *P. aeruginosa* is in magenta. The two transporter structures are superimposed. a. By comparing to the structure of LptB₂FG of *K. pneumoniae*, the periplasmic domains of LptB₂FG from *P. aeruginosa* rotate around 90° toward to the lateral gate TM5F-TM1G, whereas the lateral gate TM5F-TM1G is from an open conformation (*K. pneumoniae*) to a closed conformation (*P. aeruginosa*). The arrows showed that the lateral gate TM5F-TM1G is from the open conformation to the closed conformation. b. By comparing to the structure of LptB₂FG of *K. pneumoniae*, the conformations of the periplasmic domains of LptB₂FG of *P. aeruginosa* have changed, whereas the lateral gate TM1F-TM5G is from a closed conformation (*K. pneumoniae*) to an open conformation (*P. aeruginosa*). The arrows showed the conformational changes of the TM1F-TM5G.

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1      10      20      30      40      50      60
F_Shig MIIIRYLVRETLLKSQLAILFILLIFFCQKLVRI LGAAVDGDIPANLVLSLLGLGVPEMA
F_Ecoli MIIIRYLVRETLLKSQLAILFILLIFFCQKLVRI LGAAVDGDIPANLVLSLLGLGVPEMA
F_Kleb  MIIIRYLVRETLLKSQLAILFILLIFFCQKLVRI LGAAVDGDIPANLVLSLLGLGVPEMA
consensus>50 MIIIRYLVRETLLKSQLAILFILLIFFCQKLVRI LGAAVDGDIPANLVLSLLGLG!PEMA

70      80      90      100     110     120
F_Shig QLILPLSLF LGLLMTLGKLYTESEITVMHACGLSKAVLVKAAMILAVFTAIVAAVNVMMWA
F_Ecoli QLILPLSLF LGLLMTLGKLYTESEITVMHACGLSKAVLVKAAMILAVFTAIVAAVNVMMWA
F_Kleb  QLILPLSLF LGLLMTLGKLYTESEITVMHACGLSKAVLVKAAMILAVFTAIVAAVNVMMWA
consensus>50 QLILPLSLF LGLLMTLGKLYTESEITVMHACGLSKAVL!KAAMILAVFTAiVAAVNVMMWA

130     140     150     160     170     180
F_Shig GPWSSRHQDEVLA EAKANPGMAALAQGFQQA TNGSSVLFIESVDGSDFKDVF LAQIRPK
F_Ecoli GPWSSRHQDEVLA EAKANPGMAALAQGFQQA TNGSSVLFIESVDGSDFKDVF LAQIRPK
F_Kleb  GPWSSRHQDEVLA EAKANPGMAALAQGFQQA SGNAMVFIESVNGNRFDHVF LAQLRPK
consensus>50 GPWSSRHQDEVLA EAKANPGMAALAQGFQQA t#Gssv$FIESV#GsdFkDVF LAQiRPK

190     200     210     220     230     240
F_Shig GNARPSVVVADSGH LTLQLRDGSQVVTLNQ GTRFEGTALLRDFRITDFQDYQAIIGHQAVA
F_Ecoli GNARPSVVVADSGH LTLQLRDGSQVVTLNQ GTRFEGTALLRDFRITDFQDYQAIIGHQAVA
F_Kleb  GNARPSVVVADSGE LTLQKQKDG S QVVTLNK GTRFEGTALLRDFRITDFN NNYQAIIGHQAVS
consensus>50 GNARPSVVVADSGhLtQl rDGSQVVTLNqGTRFEGTAL$LRDFRITDF##YQAIIGHQAVA

250     260     270     280     290     300
F_Shig LDPNDTQMDMRTLWN TDTDRARAELNWRITLVV TVFMALMVVPLSVVNPRQGRVLSML
F_Ecoli LDPNDTQMDMRTLWN TDTDRARAELNWRITLVV TVFMALMVVPLSVVNPRQGRVLSML
F_Kleb  ADPDDEQMDMRTLW KTH TDRARAELHWRFTLVATVFI MALMVVPLSVVNPRQGRVLSML
consensus>50 lDP#DT#QMDMRTLWnTdTDRARAELnWRiTLV .TVFmALMVVPLSVVNPRQGRVLSML

310     320     330     340     350     360
F_Shig PAMLLYLFFLIQTS LKSNNGGKGDPTLWMWTVNLIYLALAVLNLNLDWTVPVRRIRAS F
F_Ecoli PAMLLYLFFLIQTS LKSNNGGKGDPTLWMWTVNLIYLALAVLNLNLDWTVPVRRIRAS F
F_Kleb  PAMLLYLFFLIQTS LKSNNGGKGDPAIWMWA NLLYFALAVLNLNLDWTVPMRRFRAR F
consensus>50 PAMLLYLlFFLiQTSlKSNNGGKGD$DpTLWMWt!NliYlAlA!vLNLDWTVpVRRlRAsF

F_Shig SRKGAV
F_Ecoli SRKGAV
F_Kleb  N.KGAA
consensus>50 srKGAV

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Supplementary Figure 15. The sequence alignment of LptF from *S. flexneri* (Shig), *E. coli* (Ecoli) and *K. pneumonia* (Kleb). The LptF amino acid sequences from these three species are highly conserved. The bottom is the consensus sequence (Consensus > 50). Uppercase is identity; lowercase is consensus level >0.5; ! is anyone of IV; \$ is anyone of LM; % is anyone of FY; # is anyone of NDQEBZ.


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1      10      20      30      40      50      60
G_Shig M Q P F G V L D R Y I G K T I F T I M M T L F M L V S L S G I I K F V D Q L K K A G Q G S Y D A L G A G M Y T I L S V
G_Ecoli M Q P F G V L D R Y I G K T I F T I M M T L F M L V S L S G I I K F V D Q L K K A G Q G S Y D A L G A G M Y T I L S V
G_Kleb  M Q A F G V L D R Y I G K T I F N T I M M T L F M L V S L S G I I K F V D Q L K K S G Q G S Y D A L G A G L Y T I L S V
consensus>50 M Q P F G V L D R Y I G K T I F t T I M M T L F M L V S L S G I I K F V D Q L K K a G Q G S Y D A L G A G $ Y T I L S V

70      80      90      100     110     120
G_Shig P K D V Q I F F P M A A L L G A L L G L G M L A Q R S E L V V M Q A S G F T R M Q V A L S V M K T A I P L V L L T M A I
G_Ecoli P K D V Q I F F P M A A L L G A L L G L G M L A Q R S E L V V M Q A S G F T R M Q V A L S V M K T A I P L V L L T M A I
G_Kleb  P K D I Q I F F P M A A L L G A L L G L G M L A Q R S E L V V M Q A S G F T R L Q V A L A V M K T A I P L V L L T M A I
consensus>50 P K D ! Q I F F P M A A L L G A L L G L G M L A Q R S E L V V M Q A S G F T R $ Q V A L s V M K T A I P L V L L T M A I

130     140     150     160     170     180
G_Shig G E W V A P Q G E Q M A R N Y R A Q M Y G G S L L S T Q Q G L W A K D G N N F V Y I E R V K G D E V L G G ! S I Y A F
G_Ecoli G E W V A P Q G E Q M A R N Y R A Q M Y G G S L L S T Q Q G L W A K D G N N F V Y I E R V K G D E E L G G ! S I Y A F
G_Kleb  G E W V A P Q G E Q M A R N Y R A Q M Y G G S L L S T Q Q G L W A K D G H N F V Y I E R V K G N D E L G G V S I Y A F
consensus>50 G E W V A P Q G E Q M A R N Y R A Q a M Y G G S L L S T Q Q G L W A K D G n N F V Y I E R V K G # # e L G G ! S I Y A F

190     200     210     220     230     240
G_Shig N E N R R L Q S V R Y A A T A K F D P E H K V W R L S Q V D E S D L T N P K Q I T G S Q T V S G T W K T D L T P D K L G
G_Ecoli N E N R R L Q S V R Y A A T A K F D P E H K V W R L S Q V D E S D L T N P K Q I T G S Q T V S G T W K T N L T P D K L G
G_Kleb  N P E R R L Q S V R Y A A S A K F D S E N K V W R L S Q V D E S D L T D P K Q V T G S Q M V S G T W K T N L T P D K L G
consensus>50 N e # R R L Q S V R Y A A t A K F D p E h K V W R L S Q V D E S D L T # P K Q ! T G S Q t V S G T W K T # L T P D K L G

250     260     270     280     290     300
G_Shig V V A L D P D A L S I S G L H N Y V K Y L K S S G Q D A G R Y Q L N M W S K I F Q P L S V A V M M L M A L S F I F G P L
G_Ecoli V V A L D P D A L S I S G L H N Y V K Y L K S S G Q D A G R Y Q L N M W S K I F Q P L S V A V M M L M A L S F I F G P L
G_Kleb  V V A L D P D A L S I S G L H N Y V K Y L K S S G Q D P A G R Y Q L N M W S K I F Q P L S V A V M M L M A L S F I F G P L
consensus>50 V V A L D P D A L S I S G L H N Y V K Y L K S S G Q D a G R Y Q L N M W S K I F Q P L S V A V M M L M A L S F I F G P L

310     320     330     340     350     360
G_Shig R S V P M G V R V V T G I S F G F V F Y V L D Q I F G P L T L V Y G I P P I I G A L L P S A S F F L I S L W L M R K S
G_Ecoli R S V P M G V R V V T G I S F G F V F Y V L D Q I F G P L T L V Y G I P P I I G A L L P S A S F F L I S L W L M R K S
G_Kleb  R S V P M G V R V V T G I S F G F I F Y V L D Q I F G P L T L V Y G I P P I I G A L L P S A S F F L I S L W L M R K A
consensus>50 R S V P M G V R V V T G I S F G F ! F Y V L D Q I F G P L T L V Y G I P P I I G A L L P S A S F F L I S L W L $ M R K s

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Supplementary Figure 16. The sequence alignment of LptG from *S. flexneri* (Shig), *E. coli* (Ecoli), and *K. pneumonia* (Kleb). The LptG amino acid sequences from these three species are highly conserved. The bottom is the consensus sequence (Consensus > 50). Uppercase is identity; lowercase is consensus level >0.5; ! is anyone of IV; \$ is anyone of LM; % is anyone of FY; # is anyone of NDQEBZ.

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1      10      20      30      40      50      60
B_Shig MATLTAKNLAAYKGRVVEDVSLTVNSGEIVGLLGPNAGKTTTFYMVVGI VPRDAGNI
B_Ecoli MATLTAKNLAAYKGRVVEDVSLTVNSGEIVGLLGPNAGKTTTFYMVVGI VPRDAGNI
B_Kleb MATLTAKNLAAYKGRVVEDVSLTVNSGEIVGLLGPNAGKTTTFYMVVGI VPRDAGNI
consensus>50 MATLTAKNLAAYKGRVVEDVSLTVNSGEIVGLLGPNAGKTTTFYMVVGI VPRDAGNI

70      80      90      100     110     120
B_Shig IIDDDDISLLPLHARARRGIGYLPQEASIFRRLSVYDNLMAVLQIRDDLSAEQREDRANE
B_Ecoli IIDDDDISLLPLHARARRGIGYLPQEASIFRRLSVYDNLMAVLQIRDDLSAEQREDRANE
B_Kleb IIDDEDISLLPLHARARRGIGYLPQEASIFRRLSVYDNLMAVLQIRDDLTSEQREDRAKE
consensus>50 IIDD#DISLLPLHARARRGIGYLPQEASIFRRLSVYDNLMAVLQIRDDLsAEQREDRANE

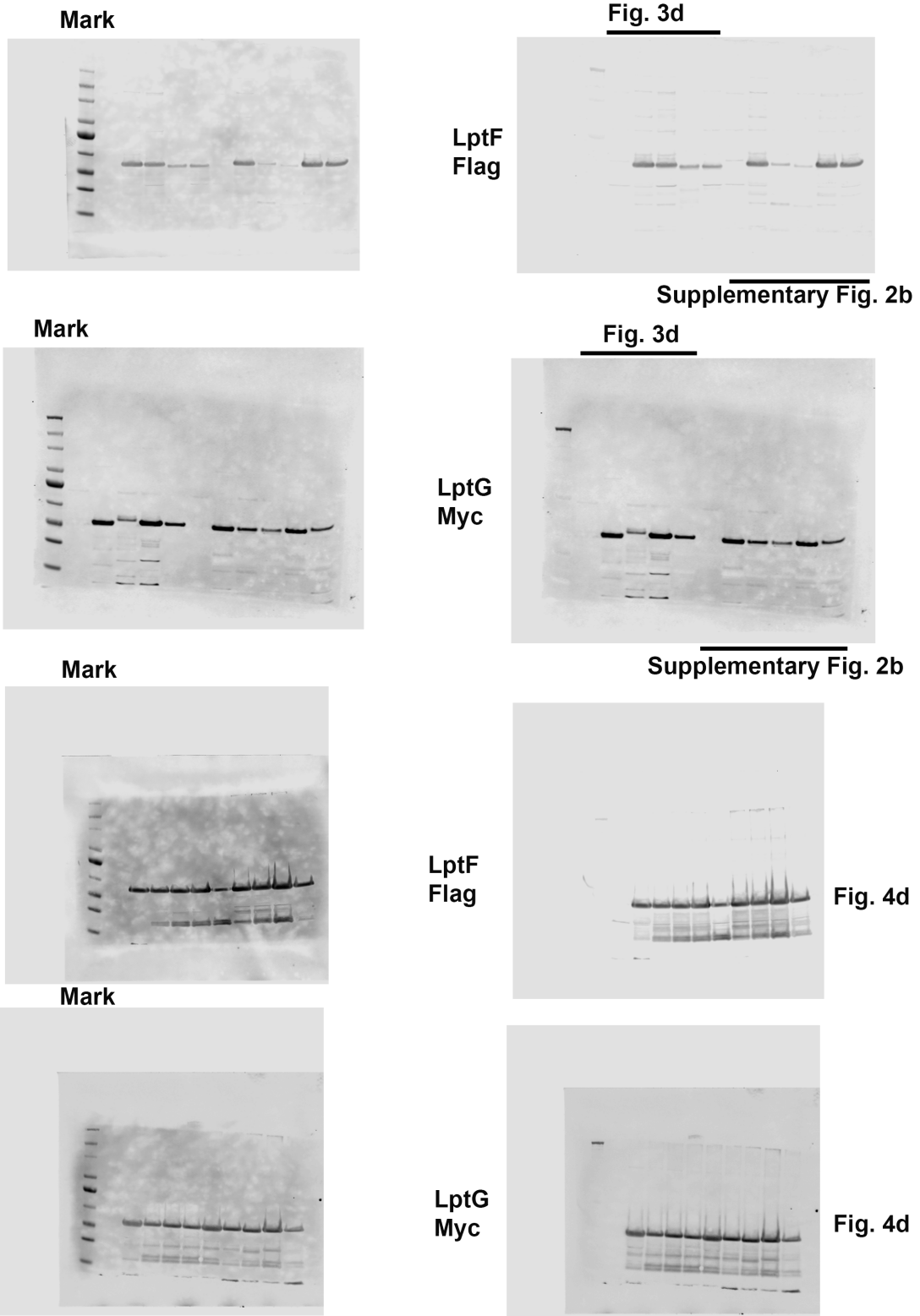
130     140     150     160     170     180
B_Shig LMEEFHIEHLRDSMQSLSGGERRRVEIARALAANPKFILLDEPFAGVDPI SVIDIKRII
B_Ecoli LMEEFHIEHLRDSMQSLSGGERRRVEIARALAANPKFILLDEPFAGVDPI SVIDIKRII
B_Kleb LMEEFHIEHLRDSIQALSGGERRRVEIARALAANPKFILLDEPFAGVDPI SVIDIKRII
consensus>50 LMEEFHIEHLRDS$GQsLSGGERRRVEIARALAANPKFILLDEPFAGVDPI SVIDIKRII

190     200     210     220     230     240
B_Shig EHLRDSGLGVLI TDHNVRET LAVCERAY IVSQGHLIAHGTPTEILDEHVKRVYLGEDFR
B_Ecoli EHLRDSGLGVLI TDHNVRET LAVCERAY IVSQGHLIAHGTPTEILDEHVKRVYLGEDFR
B_Kleb EHLRDSGLGVLI TDHNVRET LAVCERAY IVSQGHLIAHGTPQQILDEHVKRVYLGEDFR
consensus>50 EHLRDSGLGVLI TDHNVRET LAVCERAY IVSQGHLIAHGTPt#IL#DHEVKRVYLGEDFR

B_Shig L
B_Ecoli L
B_Kleb L
consensus>50 L

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Supplementary Figure 17. The sequence alignment of LptB from *S. flexneri* (Shig), *E. coli* (Ecoli), and *K. pneumonia* (Kleb). The LptB amino acid sequences from these three species are highly conserved. The bottom is the consensus sequence (Consensus > 50). Uppercase is identity; lowercase is consensus level >0.5; ! is anyone of IV; \$ is anyone of LM; % is anyone of FY; # is anyone of NDQEBZ.



Supplementary Figure 18. The original western blots of Figure 3d, supplementary Figure 2b and Figure 4d.

Supplementary Table 1. Primers used for generating constructions.

Shigella_lptB_EcoRI_F	ATATGAATTCATGGCAACATTAAGTAACTGCAAAGAACCTTGC
Shigella_lptB_KpnI_8.HIS_R	ATATGGTACCTCAGTGATGGTGATGGTGATGGTGATGGAGTCTGAAG TCTTCCCCAAGGTATACAC
Shigella_lptFG_KpnI_F	ATAT GGTACC TTTTACGGGCGTATTTAAAGTGATAATC
Shigella_lptFG_XbaI_R	ATAT TCTAGA TTACGATTTTCTCATTAAACAGCCACAG
Klebsiella_lptB_EcoRI_F	ATAT GAATTC ATGGCAACCTTAAGTAACTGCGAAGAATCTCG
Klebsiella_lptB_KpnI_8.HIS_R	ATAT GGTACC TCA GTGATGGTGATGGTGATGGTGATG GAGTCTGAAGTCTTCCCCAAG
Klebsiella_lptFG_KpnI_F	ATATGGTACCTTTTTACGGGCGTATTTATAGTGATAATCATAAGATATC TGGTTCG
Klebsiella_lptFG_XbaI_R	ATAT TCTAGA TTA GGCCTTGCGCATCATCAGCC
K12_F230_Flag_F	GATTACAAAGATGACGACGATAAA CAGGCGATCATTGGTCACCAGGC
K12_F230_Flag_R	TTTATCGTCGTCATCTTTGTAATCATAATCCTGGAAGTCCGTAATGCG GAAATCACG
K12_G228_Myc_F	GAACAAAACTCATCTCAGAAGAGGATCTG ACCTGGAAAACCAACCT CACGCC
K12_G228_Myc_R	CCTCTTCTGAGATGAGTTTTTGTTC GCCGCTCACCGTCTGCGAAC
K12_F138_Flag_F	GATTACAAAGATGACGACGATAAA CCTGGCATGGCGGCGCTG
K12_F138_Flag_R	TTTATCGTCGTCATCTTTGTAATC GTTCGCTTTCGCTTCTGCTAACAC TTCATCCTG
K12_G144_Myc_F	GAACAAAACTCATCTCAGAAGAGGATCTG TTGCTCTCTACCCAGCA AGGCTTATGG
K12_G144_Myc_R	CCTCTTCTGAGATGAGTTTTTGTTC CGAGCCGCCGTACATCGCC

Supplementary Table 2. Primers used for mutagenesis.

G_K34E_F	GGCATTATC GAA TTTGTCTGAT CAGCTGAAAAAGCCGGGCAGG
G_K34E_R	ATCGACAAA TTC GATAATGCC CGACAGCGACACCAGCATGAAC
G_R136E_F	GTAAC TACGAAGCGCAG GCGATGTACGGCGGCTCG
G_R136E_R	CTGCGCTTCGTAGTTAC GCGCCATCTGCTCGCC
G_K40E_K41E_F	ATCAGCTGGAAGAAGCCG GGCAGGGGAGTTACGACGCG
G_K40E_K41E_R	CGGCTTCTTCCAGCTGAT CGACAACTTGATAATGCCCGACAGCG
F_F26D_F	CTTTTGATCGATTTCTGTCAAAAGT TAGTGAGGATCCTCGGCGCAGC
F_F26D_R	ACTTTTGACAGAAATCGATCAAAAG CAAGATGAAGAGTATCGCCAGCT GGC
F_L62D_F	AAATGGCGCAGGATATCCT GCCATTAAGCCTGTTCTCGGG
F_L62D_R	AGGATATCCTGCGCCATTT CCGGCACGCCCAACCC
F_D229P_F	TTCCAGCCGTATCAGG CGATCATTGGTCACCAGGCGGTG
F_D229P_R	CCTGATACGGCTGGAA GTCCGTAATGCGGAAATCACGTAACAATG
F_Q231P_F	GGATTATCCGGCGATCAT TGGTACCAGGCGGTGGCGCTC
F_Q231P_R	ATGATCGCCGGATAATCC TGGAAGTCCGTAATGCGGAAATCACG
F_R223P_F	TGATTTCCCGATTACGGA CTTCCAGGATTATCAGGCGATCATTGGTC
F_R223P_R	TCCGTAATCGGGAAATCA CGTAACAATGCAGTGCCTTCGAAGC
F_T225P_F	TCCGCATTCCGGACT TCCAGGATTATCAGGCGATCATTGGTC
F_T225P_R	AGTCCGGAATGCGGA AATCACGTAACAATGCAGTGCCTTCG
G_S223P_F	TTACCGGTCCGCAGAC GGTGAGCGGCACCTGGAAAACC
G_S223P_R	GTCTGCGGACCGGTAATCTGTTTCGGATTGGTCAGATCAGATTCATCA AC
G_T225P_F	TTCGCAGCGGGTGA GCGGCACCTGGAAAACCAACCTC
G_T225P_R	TCACCCGCTGCGAA CCGGTAATCTGTTTCGGATTGGTCAGATC
G_G228P_F	GCCCGACCTGGAAAA CCAACCTCACGCCGGACAAAC
G_G228P_R	TTTTCCAGGTCGGGC ATCTGACCAATCCGAAACAGATTACCGGTTT
G_W230P_F	GCACCCGGAAAACCAA CCTCACGCCGGACAAACTGG
G_W230P_R	TTGGTTTTCCGGGTGC CGCTCACCGTCTGCGAACCGG
F_D229P_Q231P_F	AGCCGTATCCGGCG ATCATTGGTCACCAGGCGGTGG
F_D229P_Q231P_R	CGCCGGATACGGCT GGAAGTCCGTAATGCGGAAATCACGTAAC
F_R223P_T225P_F	TTTCCCGATTCCGGACTTC CAGGATTATCAGGCGATCATTGGTCACCAG
F_R223P_T225P_R	GAAGTCCGGAATCGGGAAA TCACGTAACAATGCAGTGCCTTCGAAG
G_S223P_T225P_F	GTCCGCAGCCGGTGAG CCGCACCTGGAAAACCAACCTCAC
G_S223P_T225P_R	CTCACCGGCTGCGGAC CGGTAATCTGTTTCGGATTGGTCAGATCAGATTC
G_G228P_W230P_F	AGCCCGACCCCGAAAA CCAACCTCACGCCGGACAAAC
G_G228P_W230P_R	TTTTCGGGGTCCGGCT CACCGTCTGCGAACCGGTAATCTG