

## Supplementary Information

### STRUCTURE AND FUNCTIONAL ANALYSIS OF LPTC, A CONSERVED MEMBRANE PROTEIN INVOLVED IN THE LIPOPOLYSACCHARIDE EXPORT PATHWAY IN *ESCHERICHIA COLI*

An X. Tran<sup>1</sup>, Changjiang Dong<sup>2</sup>, and Chris Whitfield<sup>1\*</sup>

From the <sup>1</sup>Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, N1G 2W1, Canada, and <sup>2</sup> Biomedical Sciences Research Complex, School of Chemistry, University of St Andrews, Fife KY16 9ST, UK

• **These authors contributed equally to this work**

\*Corresponding author: C. Whitfield at Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, N1G 2W1, Canada; E-mail: cwhitfie@uoguelph.ca, Telephone: 519-824-4120 ext. 53361, Fax: 519-837-180

#### Legend for Supplemental Figures

Fig. S1. Determination of the molecular weight and composition of purified His<sub>6</sub>-LptC<sub>(24-191)</sub>. The molecular weight and subunit composition of purified His<sub>6</sub>-LptC<sub>(24-191)</sub> was determined by analytical ultracentrifugation. Purified His<sub>6</sub>-LptC<sub>(24-191)</sub> at 0.5 mg/mL in buffer C was centrifuged in a Beckman Coulter Optima XL-1 analytical ultracentrifuge at 45,000 rpm for 16 hr at 16 °C. A<sub>280 nm</sub> measurements were carried out 5 min intervals during the ultracentrifugation.

Fig. S2. ClustalW alignments of LptA and LptC. *Panels A* and *B* provide primary and secondary structure alignments of LptA and LptC, respectively. Residue numbering corresponds to LptA from *E. coli* K-12 (without gaps). *Panels C* and *D* provide the primary structure alignments of LBP-14, a synthetic fragment derived from the LPS binding protein, to LptA and LptC, respectively. Alignments were performed with ClustalW (<http://www.ebi.ac.uk/Tools/clustalw2/index.html>) (1). Residues with high sequence identity are colored, and non-conserved residues are shown as black letters. The residues within the loops regions are indicated.

#### Reference:

1. Thompson, J., Higgins, D., and Gibson, T. (1994) *Nucleic Acids Res* **22**, 4673-4680

Figure S1

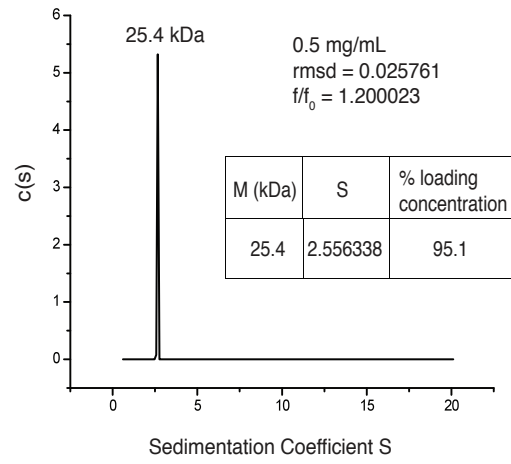


Figure S2

A

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LptA  MKFKTNKLSL  NLVLAASSLLA  ASIPAFAVTG  DTDQPIHIES  DQQLDMQGN  VVFTGNVIV  TQGTIKINAD  KVVVTRPGGE  80
LptC  --MSKARRWV  IIVLSLAVLV  MIGINMAEKD  DTAQVVVNNN  DPTYKSEHTD  TLVYNPEGAL  SYRLIAQHVE  YYSDAQVSWF  78

LptA  QGKEVIDGYG  KPATFYQMVD  NGKPVVEGAS  QMHYELAKDF  VVLTGNAYLQ  QVDSNIKGDK  ITYLVKEQKM  QAFSDKGKRV  160
LptC  TQPVLTTFDK  DKIPTWSVKA  DKAKLTNDRM  LYLYGHVEVN  ALVPDSQLRR  ITDINAQINL  VTQDVTSEDL  VTLYGTTFNS  158

LptA  TTVLVPSQLQ  DKN---NKG  QTPAQKKN-  ---  185
LptC  SGLKMRGNLR  SKNAELIEKV  RTSYEQNKQ  TQP  191
    
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B

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LptA sec pred  CCCCHHHHHH  HHHHHHHHHH  HHHHHHCCCC  CCCCC-----  -----EEEEEE  EEEEOCCCCE  EEEEEEEEEEE  -----CEEEE  67
LptC sec pred  CC--HHHHH  HHHHHHHHHH  HHHHECCCC  CCCCCCCCCC  CCCEEEEEE  EEEEOCCCCE  EEEEEEEEEEE  EECCCEEEE  78

LptA sec pred  EEEEEEEEC  CCCCC---  -EEEEEOCE  EEE---EE-  --CCCCCEE  EEEEEEEEO  CCCCCEEEC  EEEEEEOCE  136
LptC sec pred  ECEEEEEEC  CCCCCEEEE  CEEEOCCCC  EEEEOCCC  EEEEOCEE  CCCEEECEE  EEEEEEEEO  CCCCCEEEC  EEEEEEOCE  158

LptA sec pred  EEEEEEEEC  CCCCCEEEC  CCCCCEEEC  CCCCCCCC  CCCCCCCCC  185
LptC sec pred  EEEEEEEEC  CCCCCEEEC  ---EEEEEC  CCCCC---  -----  191
    
```

C

```

LptA  MKFKTNKLSL  NLVLAASSLLA  ASIPAFAVTG  DTDQPIHIES  DQQLDMQGN  VVFTGNVIV  TTTTINID  KVVVTRPGGE  80
LBP-14  R-----  -----  -----  -----  -----  VRRVVR-  -----  10

LptA  QGKEVIDGYG  KPATFYQMVD  NGKPVVEGAS  QMHYELAKDF  VVLTGNAYLQ  QVDSNIKGDK  ITYLVKEQKM  QAFSDKGKRV  160
LBP-14  -----  -SFK-----  -----  -----  -----  -----  -----  14

LptA  TTVLVPSQLQ  DKNNKGQTPA  QKKN  185
LBP-14  -----  -----  -----  14

          Loop 1          Loop 7          Loop 2
          |-----|          |-----|          |-----|
          40             60             80
    
```

D

```

LptC  MSKARRWV  IIVLSLAVLVM  GINMAEKDDT  AQVVVNNNDP  TYKSEHTDTL  VYNPEGALS  YRLIAQHVEY  SDQAVSWFTQ  80
LBP-14  -----  -----  -----  -----  -----  -----  -----  10

LptC  PVLTTFDKDK  IP-TSSKID  KAKLTNDRML  YLYGHVEVNA  LVPDSQLRR  ITDINAQINLV  TQDVTSEDLV  TLYGTTFNSS  159
LBP-14  -----  -RQGRKRS-  -----  -FFK-----  -----  -----  -----  14

LptC  GLKMRGNLRS  KNAELIEKVR  TSYEQNKQT  QP  191
LBP-14  -----  -----  -----  14

          Loop 7          Loop 2          Loop 6          Loop 3          Loop 5          Loop 1
          |-----|          |-----|          |-----|          |-----|          |-----|          |-----|
          100             120             140             160             180             80
    
```