

Supporting information

LptD is a promising vaccine antigen and immunotherapeutic target for protection against Vibrio species infection

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Legends of Supplementary Figures

Fig. S1 Three dimensional structures showed linear antibody epitopes of (a) YLNSDKKYQDDS (286-297)(score of 0.77), (b) IPDETTNYS (585-593)(score of 0.648), and (c) LENLDT (656-661)(score of 0.507); epitope residues were in yellow. Epitopes were predicted by ElliPro based on the modelled three dimensional structure of LptD.

Fig. S2 Chart review of discontinuous B cell epitopes predicted by DiscoTope (<http://tools.immuneepitope.org/stools/discotope/discotope.do>) which was based on predicted three dimensional structure of LptD. Prediction threshold was set at -1.

Fig. S3 Homology alignment of top 5 score of CTL epitopes of *V. parahaemolyticus* LptD among different *Vibrio* species. The CTL epitopes were predicted by CTLPred server based on SVM methods. Identical residues were in red and strongly similar residues were in green. The epitopes were listed with score from high to low. Peptides boxed with dotted line were distributed inside of cell outer membrane.

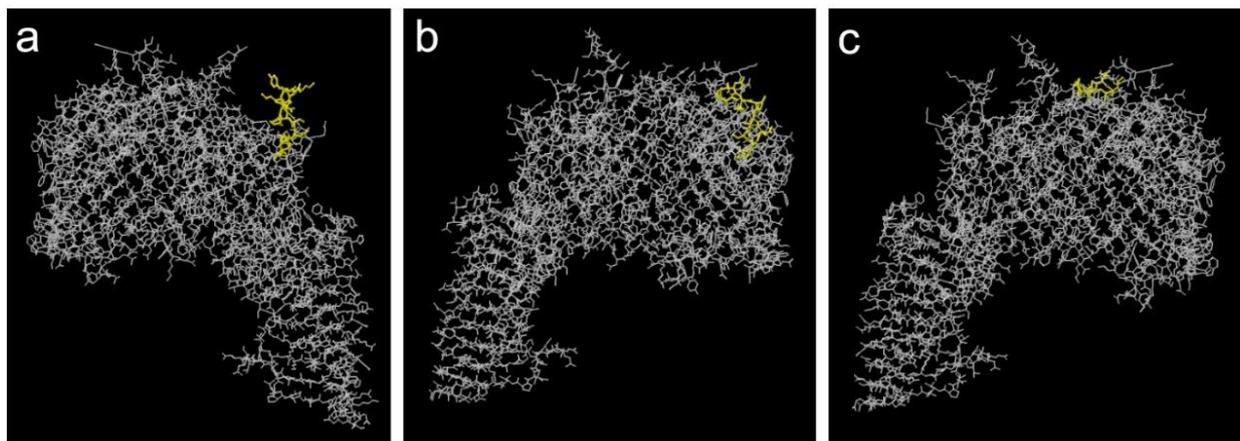


Fig. S1

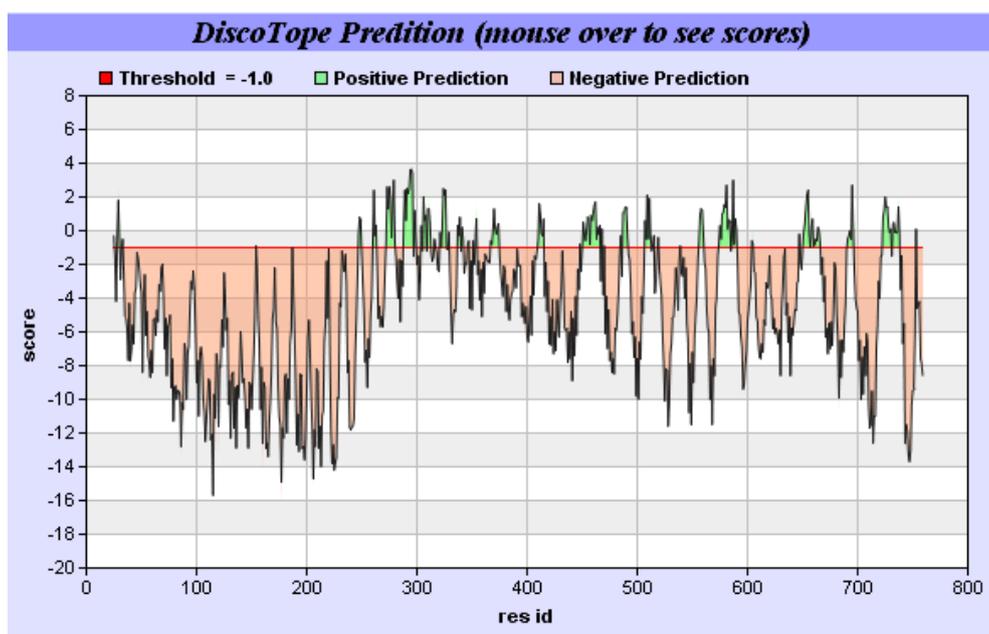


Fig. S2

	783	197	374	100	659
<i>V. parahaemolyticus</i>	 IKYGRPFYL	 IMDVPVFYV	 KEENRPYRL	 TLHQQDNVV	 EYIEDTIIL
<i>V. alginolyticus</i>	IKYGRPFYL	VLDVPVFYV	KEENRPYRL	TLHQQDNVV	EYIEDTIIL
<i>V. harveyi</i>	IKYGRPFYL	VLDVPVFYV	QEDNQPYRL	TLHQQDNVV	EYIEDTIIV
<i>V. campbellii</i>	IKYGRPFYL	ILDVPVFYV	EEDNQPYRL	VTLHQQDNV	EYIEDTIIV
<i>V. natriegens</i>	IKYGRPFYL	VLDVPIFYV	QEENKPYRL	TLHQQDNVV	EYIEDTIIL

Fig. S3