

Title	Functional environmental screening of a metagenomic library identifies stlA; a unique salt tolerance locus from the human gut microbiome
Authors	Culligan, Eamonn P.;Sleator, Roy D.;Marchesi, Julian R.;Hill, Colin
Publication date	2013
Original Citation	Culligan EP, Sleator RD, Marchesi JR, Hill C (2013) Functional Environmental Screening of a Metagenomic Library Identifies stlA; A Unique Salt Tolerance Locus from the Human Gut Microbiome . PLoS ONE 8(12): e82985. doi:10.1371/journal.pone.0082985
Type of publication	Article (peer-reviewed)
Link to publisher's version	<a href="https://doi.org/10.1371/journal.pone.0082985">10.1371/journal.pone.0082985</a>
Rights	© 2015 Culligan et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited - <a href="http://creativecommons.org/licenses/by/4.0/">http://creativecommons.org/licenses/by/4.0/</a>
Download date	2024-04-23 17:46:03
Item downloaded from	<a href="https://hdl.handle.net/10468/2350">https://hdl.handle.net/10468/2350</a>



**Figure S5.** Multiple sequence alignment of StIA protein sequence with HMP and MetaHit homologues

**Figure S5. Multiple protein sequence alignment of StlA and homologous sequences from Human Stool Microbiome from Human Microbiome Project (HMP) and MetaHit.** Black shading indicates regions of 100% amino acid identity. Putative transmembrane regions for StlA, predicted by TMHMM, are indicated with red boxes. Truncated or partial sequence fragments from HMP were not included (n=4). Information on the protein sequences (A) – (L) is indicated in the legend below.

**Legend:**

(A) = StlA protein sequence (B) SRS053214\_LANL\_scaffold\_17021\_gene\_42707 (C) SRS024549\_LANL\_scaffold\_1815\_gene\_4559 (D) C3406971\_gene\_199744 (E)  
SRS018656\_WUGC\_scaffold\_544\_gene\_591 (F) SRS015217\_WUGC\_scaffold\_30292\_gene\_65222 (G) SRS077730\_LANL\_scaffold\_24345\_gene\_72567 (H)  
SRS024075\_LANL\_scaffold\_21370\_gene\_63545 (I) Baylor\_scaffold\_22757\_gene\_50812 (J) C2121591\_gene\_151559 (K) MetaHit\_MH0011\_GL0108025  
[Complete] locus=scaffold6530\_52:7938:8564 (L) MetaHit\_V1\_GL0100177 [Complete] locus=scaffold36986\_1:2178:2888