

Table S1. Predicted secretion signal likelihood of putative hydrolytic enzymes

Enzyme / Genus / COG ID	Signal Peptide Likelihood ¹	Predicted secretion signal
NlhH / <i>Pseudomonas</i> / COG0657	0.9983	MNIKKTAAASLLALSIGNAFA
EstA / <i>Bacillus</i> / COG1075	0.9958	MRLMRRCVALLIVFFIMAPTISTNVQA
PlpD / <i>Pseudomonas</i> / COG1752	0.9909, 0.9835	MRLLFCFLLVLTSFTAIA
FrsA / <i>Bacillus</i> / COG1073	0.7467*	LKRKFYFYMISGIVLVLLI
EstP / <i>Pseudomonas</i> / COG3240	0.7259	MRKAPLLRFTLASLALACSQALA
EstA / <i>Pseudomonas</i> / COG4625	0.6909	MIKQTLFVPLAGCLLAMACAQANA

¹The SignalP 5.0 server utilizes a deep convolutional and recurrent neural network

architecture to predict the presence and location of cleavage of Sec/SPI, Sec/SPII*, and Tat/SPI

signal peptides.