

Table S3. PGN_1234 PSI-BLAST matches to WbpS and WbqG compared to AsnB

Species	^a NCBI	^b Uniprot	Name	^c E-value	^d % cov, % id	^e CD top hit
<i>P. aeruginosa</i>	WP_012613869.1	Q9RHD2_PSEAI	WbpS	6E ⁻⁷⁹	92, 17.3	eps_aminotran_1
<i>E. coli</i>	WP_032178609.1	J3RWI0_ECOLX	WbqG	6E ⁻⁷⁶	97, 17.2	eps_aminotran_1
<i>P. aeruginosa</i>	WP_003115546.1	Q9I231_PSEAE	AsnB	3E ⁻⁶¹	88, 14.3	AsnB
<i>E. coli</i>	WP_000337077.1	ASNB_ECOLI	AsnB	1E ⁻⁴³	92, 15.1	AsnB

BLAST settings: PSI-BLAST, 2 iterations; taxonomy = gamma proteobacteria; max # hits = 10,000; Database = NCBI nr; Input sequence = PGN_1234.

^aThe NCBI accessions are non-redundant sequences that match to the same protein from many different strains.

^bThe uniprot accessions are unique and match the protein name provided

^cE-value = Expect Value

^d% cov = coverage of sequence (%); % id = level of sequence identity (%)

^eThe top hit to the conserved domain database (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>)