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FIG 1 *P. aeruginosa* PAO1 ChiC does not encode an orthodox signal peptide. The amino acid sequence of *P. aeruginosa* PAO1 ChiC (NCBI RefSeq accession: NP_250990.1) was submitted to the SignalP 5.0 server (<https://services.healthtech.dtu.dk/service.php?SignalP-5.0>) to generate predictions for the presence of signal peptides. SignalP 5.0 predicted 0.0032 probability for lipoprotein signal peptides transported by the Sec translocon and cleaved by Signal Peptidase II (LIPO (Sec/SPII)); 0.0213 probability for Tat signal peptides transported by the Tat translocon and cleaved by Signal Peptidase I (TAT (Tat/SPI)); 0.0267 probability for secretory signal peptides transported by the Sec translocon and cleaved by Signal Peptidase I (SP (Sec/SPI)); and 0.9489 probability for no signal peptide (OTHER). CS represents predicted cleavage site (only reported when there is a predicted signal peptide).

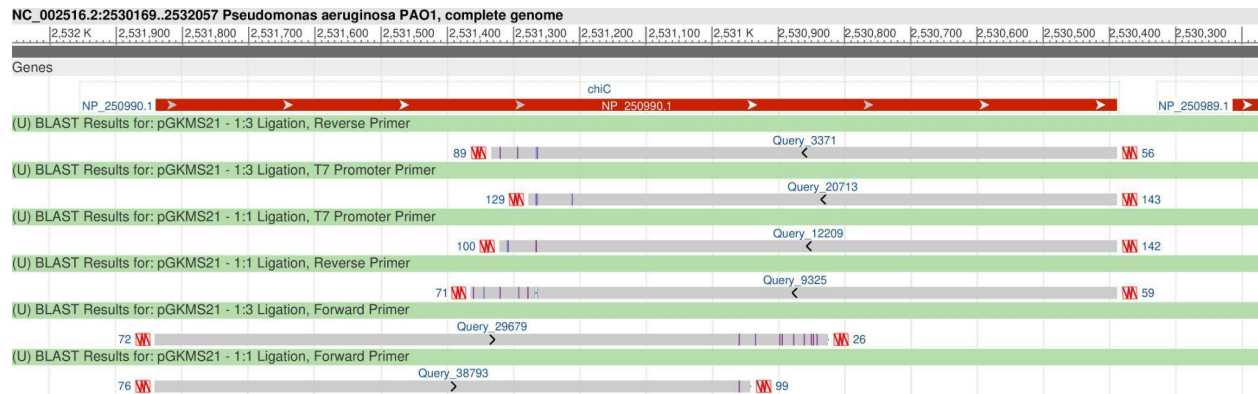


FIG 2 Nucleotide sequence of pGKMS21 plasmid insert aligned to the published nucleotide sequence of *chiC* from *P. aeruginosa* PAO1. Sanger sequencing results of the plasmids isolated from two colonies of cells transformed using pGKMS21 ligation mixtures with 1% DMSO PCR product revealed that the full *chiC* gene was present in both pGKMS21 plasmids and showed high sequence similarity with published *chiC*. Link to above view:

https://www.ncbi.nlm.nih.gov/nuccore/110645304?report=graph&tkey=KQ9HMiFESAnFhskCBk0IBpZgJlw7y72Dfkq3RryPsMzexmKvSCojMvwNOSTUeqK9LKLjvTu&assm_context=GCF_000006765.1&v=2530170:2532057&c=FFFFF99&gflip=1&select=null&slim=0