

BaeS <i>E. coli</i> K12	MKFWRPGITGKLFVLAIFATCIVLLISMHWAVRISFFERGFIDYIKHGNEQRLQLLSDALGE	60
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	MKFWRPGITGKLFVAIFATCIVLLITMHWAVRISFFERGFIDYIKHGNEQRLQGLSDALSE	60
	*****.*.*****.*****.*****.*****.*****.	
BaeS <i>E. coli</i> K12	QY AQHGNWRFLRNDRFVFQILRSFEHDNSEDKPGPGMPPHGWRTOFWVVDQNNKVLVGF	120
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	QY AQHGNWRFLRNDRFVFQILRSLEHDTGDGDRPGPGMPPHGWRTOFWVIDQDMRTL VGF	120
	*****.*****.*****.*.:*****.*****.*****.:**.*.*****.	
BaeS <i>E. coli</i> K12	RAP I PPDGTRRP I LVNGAEV GAV I ASPVERL TRNTD I NFDK QQR QTS	180
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	RAP I PPDGTRRA I KVNNATVGWV I ASPVERL TRNTD I NFD R QQR QTS	180
	*****.*.*.*.*****.*****.*****.:*****.*****.*****.	
BaeS <i>E. coli</i> K12	ATFLLARGLLAPVKRLVDGTHKLAAGDFTTRVTP TSEDELGKLAQDFNQLASTLEKNQQM	240
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	ATFPLARGLLAPVKRLVEGTHKLAAGDFTTRVDTRS QDELGKLAQDFNQLASTLEKNQQM	240
	.**.*****.*****.*.:*****.*****.*****.	
BaeS <i>E. coli</i> K12	RRDFMADISHELRTP LAVLRGELEAIQDGVRKFTPETVASLQAEVGT LTKLVDDLHQLSM	300
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	RRDFMADISHELRTP LAVLRGELEAIQDGVRQFTPESVASLQAEVGT LTKLVDDLHQLSM	300
	*****.*.:*****.*****.*****.:*****.*****.*****.	
BaeS <i>E. coli</i> K12	SDEGALAYQKAPVDLIPLLEVAGGAFRERFASRGLKLQFSLPDSITVFGDRDRMLQLFNN	360
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	SDEGALAYQKAPVDVINILEVISGAFRERFASRNLIKIDLSLPDSAVVFGDKDRMLQLFNN	360
	*****.*.:***.*****.*.:*.:*****.*****.:*****.	
BaeS <i>E. coli</i> K12	LLENSLRYTDSGGSLQISAGQ RDKTVRLTFADSAPGVSDDQLQKLFERFYRTEGSRNRAS	420
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	LLENSLRYTDSGGGLHISGRQENGRFALT FADSAPGVQDAQLEKLFERFYRTEGSRNRAS	420
	*****.*.:*.*.*.:.*****.* *.:*****.*****.	
BaeS <i>E. coli</i> K12	GGSGGLG LAICLNIVEAHNGRI IAAHSPFGGVSITVELPLERDLQREV	467
BaeS <i>E. cloacae</i> subsp. <i>cloacae</i> ATCC 13047	GGSGGLG LAICV NIVEAHNGTIRAAHSPFGGVSITVELPLERDLSREV	467
	*****.*.:*****.* * *****.*****.	

FIG S1 Protein sequence comparison of BaeS from *E. coli* K12 and *E. cloacae* subsp. *cloacae* ATCC 13047 (amino acid identity = 87%). The different domains are indicated by different colors according to UniProt (accession no. P30847): cytoplasmic (yellow), transmembrane (pink), and periplasmic (green). The autocatalytic histidine residue (His₂₅₀) is also indicated (in grey) as well as the position of the Thr175Pro change (in white). Multiple-sequence alignment was performed with Clustal Omega software (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).