PylSn and the homologous N-terminal domain of pyrrolysyl-tRNA synthetase bind the tRNA that is essential for the genetic encoding of pyrrolysine*

Supplemental materials

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*Running title: *A protein specifically binding the pyrrolysine tRNA*

Name	Sequence
PylSnF	CCATGGGCATGAGAGGAGTGTCCCAGGCTTCTGAGGAAAAG
PylSnR	GCGGCCGCTTAGTGGTGATGATGGTGATGCCGCCGAAGATGTGAGCCATAATGCTGGC
92SF	CATATGGTGAAAGTTAGGGTAG
92SR	CTCGAGCAGATTGGTTGAAATCCC
FusCF	CCATGGAGGAGGATATCTCTGTTTCTGCAAAGGC
FusCR	GGATCCTTAGTGGTGATGATGGTGATG CAGATTGGTTGAAATCCC
FusNF	CCATGGAGAGAGGAGTGTCCCAGG
FusNR	GATATCAAGATGTGAGCCATAATGCTGG
PylTF	TCTAGACCCATTTCCAGCTGCTCC
PylTR	TCTAGACCCATTTCCAGCTGCTCC

Supplementary Table 1. Primers used in this report.

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PylSn    1 MRGVSQASEEKKRYYRKNVDFFNLVEKIKLWPSRSGTLHGIKAMTRRGNTAEIVTHCNRRFIIYNSKHSRAARW
PylS     1 -------------MDKKPLDV--LISATGLGMSRTGTLHKIKHHEVSRSKIYIEMACGDHLVVNNSRSCRTARA
PylSc    1 ----------------------------------------------------------------------------

PylSn   75 LRNKLHFGVCPHCRIPEWKLQKYSSTVMSQHYGSHL------------------------------------
PylS    60 FRHHKYRKTCKRCRVSDEDINNFLTRSTESKNSVKVRVVSAPKVKKAMPKSVSRAPKPLENSVSAKASTNTSRS
PylSc    1 ----------------------------------------------------------------------------

PylSn  110 ----------------------------------------------------------------------------
PylS   134 VPSPAKSTPNSSVPASAPAPSLTRSQLDRVEALLSPEDKISLNMAKPFRELEPELVTRRKNDFQRLYTNDREDY
PylSc    1 ---------LSS--FWTKVQYQRLKELNASGEQLEMGFSDALSRDRAFQGIEHQLMSQGKRHLEQLRTVKHRPA

PylSn      ----------------------------------------------------------------------------
PylS   208 LGKLERDITKFFVDRGFLEIKSPILIPAEYVERMGINNDTELSKQIFRVDKNLCLRPMLAPTLYNYLRKLDRIL
pylSc   64 LLELEEGLAKALHQQGFVQVVTPTIITKSALAKMTIGEDHPLFSQVFWLDGKKCLRPMLAPNLYTLWRELERLW

PylSn      ----------------------------------------------------------------------------
PylS   282 PGPIKIFEVGPCYRKESDGKEHLEEFTMVNFCQMGSGCTR--ENLEALIKEFLDYLEI-DFEIVGDSCMVYGDT
pylSc  137 DKPIRIFEIGTCYRKESQGAQHLNEFTMLNLTELGTPLEERHQRLEDMARWVLEAAGIREFELVTESSVVYGDT

PylSn      ----------------------------------------------------------------
PylS   353 LDIMHGDLELSSAVVGPVSLDREWGIDKPWIGAGFGLERLLKVMHGFKNIKRASRSESYYNGISTNL 419
pylSc  211 VDVMKGDLELASGAMGPHFLDEKWEIVDPWVGLGFGLERLLMIREGTQHVQSMARSLSYLDGVRLNIN 280
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Supplementary Figure 1. Protein sequences alignment of *D. hafniense* PylSn, PylSc and *M. barkeri* MS PylS. Sequences were aligned with clustalW2. Parts of the alignments were then adjusted and optimized manually. Identical residues were shown in red, conserved residues were shown in blue.