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High complexity of Glutamine synthetase regulation in *Methanosarcina mazei*: Small protein 26 interacts and enhances glutamine synthetase activity

WILEY

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Supplemental Material:

Supplemental figures 1+2

Supplemental Table 1 + 2



Suppl. Fig. 1. Annotated spectra for the proteotypic peptide KNLADSMMSPMSSEAR (MH+: 1754.78093 Da; +2 monoisotopic m/z: 877.89410 Da (-3.46 ppm) from sp26 identified by C-MS/MS after tryptic digestion of the *M. mazei* proteome [8]. The peptide was identified with high confidence at the peptide level (peptide level FDR <1%), the inferred identification of sp26 had a protein level FDR of <5%. Inserted peptide sequence showing the b and y ion fragmentation positions identified for the peptide.



Suppl. Fig. 2: Schematic plasmid maps of expression vectors: (a) pRS1209 containing His₆-sORF26 in pEX (gene synthesis, Eurofins Scientific, Nantes). (b) pRS1228 containing SUMO-sP26 for heterologous expression in *E. coli*. (c) pRS1229 containing SUMO-His₆-sP26 for heterologous expression in *E. coli* and pulldown experiments. (d) pRS1242 containing His₆-sP26 for expression in *M. mazei*. (e) pRS1245 containing His₆-sP26 for heterologous expression in *E. coli*. TTTT, transcriptional terminator for *M. mazei*; T7 TT, transcriptional terminator T7 RNA polymerase.

suppl. Table 1: GlnA₁ activity determined as described in Methods using purified proteins of independent purifications

Experimental		App. spec. activity	activation (n-fold)
conditions		(U/mg)	
+ His ₆ -sP26	$0.472 \ \mu mol \ GlnA_1$	0.0175	1.00
	+ 2.2 μmol sP26	0.0460	2.64
	+ 4.4 μmol sP26	0.115	6.60
	+ 8.8 μmol sP26	0.172	9.82
	0.95 μmol GlnA1	0.035	1.00
	+ 2.2 μmol sP26	0.047	1.36
	+ 8.8 µmol sP26	0.055	1.60
	0.95 μmol GlnA1	0.04	1.00
	+ 2.2 μmol sP26	0.05	1.20
	+ 17.9 μmol sP26	0.08	2.10
	0.95 μmol GlnA ₁	0.008	1.00
	+ 1.6 μmol sP26	0.029	3.50
	0.95 μmol GlnA ₁	0.013	1.00
	+ 2.9 μmol μg sP26	0.0292	2.22
+ 5 mM 2-0G	0.11 μmol GlnA ₁ + 2-		
	OG	4.80	1.00
+ His ₆ -sP26	+ 2.2 μmol μg sp26	10.60	2.20
	0.95 μmol GlnA ₁ + 2-		
	OG	0.55	1.00
	+ 2.2 μmol μg sP26	0.70	1.28
	+ 17.9 μmol sP26	2.78	5.07
	0.95 μmol GlnA ₁ + 2-		
	OG	1.17	1.00
	+ 2.9 µmol sP26	2.47	2.12
+ His ₆ -sP26			
	0.95 μmol GlnA1	0.008	1.00
+ His₀-GlnK₁	+ 3.3 μmol GlnK1	0.026	3.16
	+ 3.3 μmol GlnK1		
	+ 1.6 µmol sP26	0.042	5.10
	0.95 μmol GlnA1	0.013	1.00
	+ 0.65 μmol GlnK1	0.025	1.91
	+ 0.65 μmol GlnK ₁		
	+ 2.9 µmol sP26	0.043	3.29
+ 5 mM 2-0G			
	0.11 μmol GlnA1 + 2-		
	OG	4.82	1.00
+ His ₆ -GlnK ₁	+ 0.54 μmol GlnK ₁	7.61	1.58
	+ 0.54 μmol GlnK ₁		
+ His ₆ -sP26	+ 2.2 μmol sP26	11.76	2.44
	0.95 μmol GlnA ₁ + 2-		
	OG	1.17	1.00
	+ 0.65 μmol GlnK ₁	1.45	1.24
	+ 0.65 μmol GlnK ₁		
	+ 2.9 μmol sP26	2.54	2.17

suppl.	Table	2. S	trains	and	pla	smids	used
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Strain or plasmid	Genotype or description	Source of reference
Strains		
Methanosarcina mazei strain	wild type; DSM No. 3647	DSMZ, Braunschweig,
Gö1		Germany
Escherichia coli BL21 (DE3)	general expression strain	Invitrogen, Carlsbad,
		USA
Escherichia coli BL21-	general expression strain	Stratagene, La Jolla,
CodonPlus [®] -RIL	containing the pRIL plasmid (ileW,	USA
	leuY, proL)	
Plasmids		
pET28a	general cloning vector providing	Merck KGaA,
	N-terminal His₀-tag	Darmstadt, Germany
pET-SUMO	general cloning vector providing	Invitrogen, Carlsbad,
	N-terminal SUMO-tag	USA
pCR [®] II –TOPO [®] vector	general cloning vector	Life Technologies,
		Darmstadt, Germany
pRS196	<i>MM0964</i> (<i>glnA</i> ₁) under the control	[32]
	of T7 in pET28a	
pRS203	MM0732 (glnK ₁) under the control	[32]
	of T7 in pET28a	
pRS375	pRS196 with exchanged His ₆ -Tag	this work
	by Strep-tag	
pRS1209	His_6 -sORF26 under the control of	Eurofins Scientific,
	<i>pmcr</i> B in pEX	Nantes, Luxemburg
pRS1228	SUMO-sORF26 under the control	this work
	of T7 in pET-SUMO	
pRS1229	SUMO-His ₆ -sORF26 under the	this work
	control of T7 in pET-SUMO	
pRS1242	His_6 -sORF26 under the control of	this work
	pmcrB in pWM321	
pRS1244	sORF26 in pCR®II-TOPO®	this work
pRS1245	His_6 -sORF26 under the control of	this work
	T7 in pET28a	