Supplemental Material

Transcription of lncRNA *prt*, clustered *prt* RNA sites for Mmi1 binding, and RNA polymerase II CTD phospho-sites govern the repression of *pho1* gene expression under phosphate-replete conditions in fission yeast

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Table S1

Figures S1 and S2

Table S1

Crystallographic data and refinement statistics

	SeMet-Mmi1(311–488)	Mm1(311–488)	Mmi1(319–488)
Data collection			
Beamline	APS 24-ID-C	APS 24-ID-E	APS 24-ID-E
Space group	$P2_12_12_1$	$P2_12_12_1$	$P3_12_1$
Cell dimensions			
a, b, c (Å)	49.8, 79.7, 196.0	49.8, 79.6, 195.2	58.0, 58.0, 370.8
α, β, γ (°)	90, 90, 90	90, 90, 90	90, 90, 120
Resolution (Å)	50–2.05 (2.1–2.05)	50–1.75 (1.8–1.75)	50–1.95 (2.00–1.95)
Wavelength (Å)	0.9795	0.9792	0.9792
R_{pim}	0.056 (0.985)	0.022 (0.115)	0.040 (0.362)
CC(1/2)	0.995 (0.466)	0.998 (0.969)	0.996 (0.652)
<I>/<σI>	15.2 (1.1)	24.4 (4.3)	24.8 (2.9)
Completeness (%)	98.2 (94.8)	99.7 (98.4)	86.3 (58.0)
Redundancy	3.3 (3.2)	6.5 (5.5)	3.3 (2.7)
Unique reflections	49667	78868	46677
Phasing			
Number of Se sites	24		
Figure of merit	0.55		
Refinement			
R_{work} / R_{free}		0.187 / 0.205 (0.219 / 0.237)	0.205 / 0.251 (0.257 / 0.291)
B-factors (Å^2) Average/Wilson		29.8 / 21.1	34.2 / 26.4
RMS deviations			
bond lengths (Å)		0.005	0.008
bond angles (°)		0.797	1.01
Ramachandran plot			
% favored		97.8	98.8
% allowed		2.2	1.2
outliers		none	none
Model contents			
Protomers / ASU		4	4
Protein residues		687	668
Water		846	471
PDB ID		5H8A	5HFZ

Values in parentheses refer to the highest resolution shell.

R_{free} set consists of 5% of data chosen randomly against which structures were not refined.

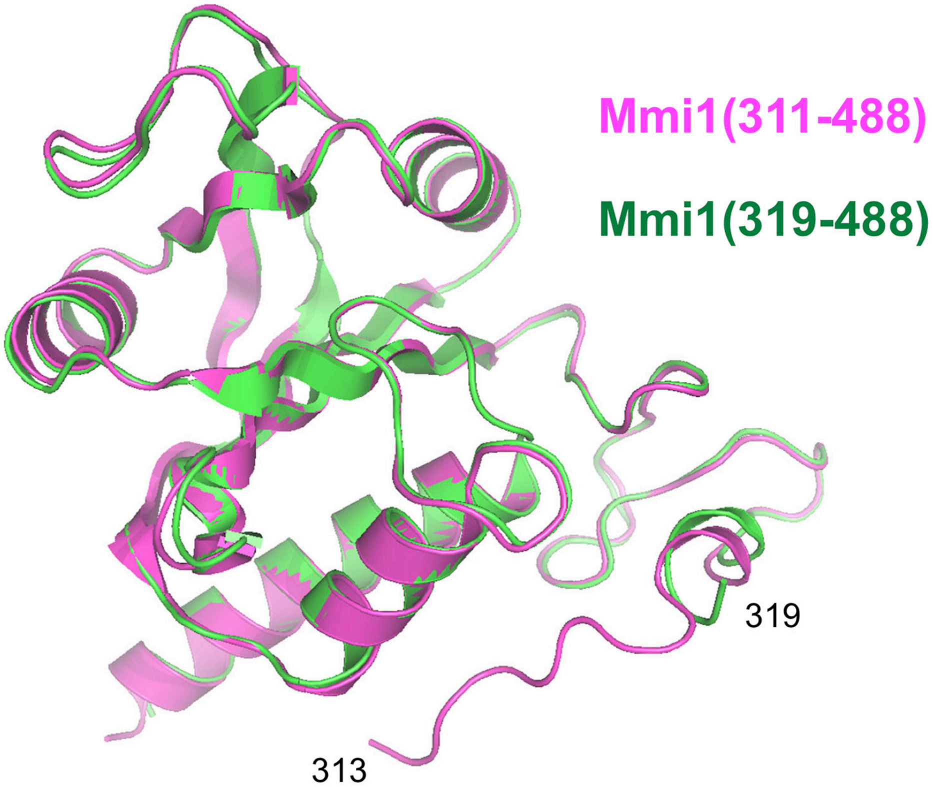

Figure S1. **Superposition of the structures of Mmi1(311-488) and Mmi1(319-488)**. Although the shorter YTH domain Mmi1(319-488) crystallized in a different lattice than Mmi1(311-488), the two structures were virtually identical. In particular, subtraction of the ^{311}STPPPLNF^{318} peptide had no apparent effect on the structure of the residual N peptide from aa 319 to 347.

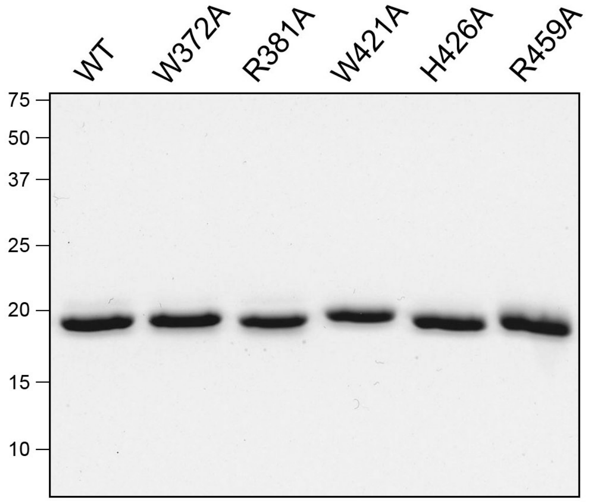

Figure S2. **Recombinant Mmi1 YTH domain mutants**. Purified wild-type Mmi1(319-488) and the indicated alanine mutants were analyzed by SDS-PAGE. The Coomassie blue-stained gel is shown. The positions and sizes (kDa) of marker polypeptides are indicated on the left.