

## SUPPLEMENTARY DATA

### Substrate recognition and cleavage-site selection by a single-subunit protein-only RNase P

**Nadia Brillante<sup>1,†</sup>, Markus Gößringer<sup>2,†</sup>, Dominik Lindenhofer<sup>1</sup>, Ursula Toth<sup>1</sup>,  
Walter Rossmannith<sup>1,\*</sup> and Roland K. Hartmann<sup>2,\*</sup>**

<sup>1</sup>Center for Anatomy & Cell Biology, Medical University of Vienna, 1090 Vienna, Austria

<sup>2</sup>Institute of Pharmaceutical Chemistry, Philipps-University Marburg, 35037 Marburg, Germany

\*To whom correspondence should be addressed. Email: walter.rossmanith@meduniwien.ac.at  
Correspondence may also be addressed to Roland K. Hartmann. Email: roland.hartmann@staff.uni-marburg.de

†The authors wish it to be known that, in their opinion, the first 2 authors should be regarded as joint First Authors.

**Supplementary Table S1. Oligonucleotides used for cloning and site-directed mutagenesis of PRORP3.**

Amino acid substitution	Forward	Reverse
none <sup>a</sup>	GGCTCTAGACCATGGCTGGTACTGAT	CGGCTCGAGTGAAGTCTGCCTTGTA
T113S	CTAATGAATCATCTGTCTCTGCAGTTG CACGACTAG	CTAGTCGTGCAACTGCAGAGACAGAT GATTCATTAG
T113N	CTAATGAATCATCTGTCAATGCAGTTG CACGACTAG	CTAGTCGTGCAACTGCATTGACAGAT GATTCATTAG
R145N	GTGTATCGGTCCTAATCTGAGAACTT ATGC	GCATAAGTTCTCAGATTAGGGACCGA TACAC
R145D	GTGTATCGGTCCTGATCTGAGAACTT ATGC	GCATAAGTTCTCAGATCAGGGACCGA TACAC

<sup>a</sup>Primer pair used for the cloning of the *A. thaliana* wild-type PRORP3 cDNA.

**Supplementary Table S2. Oligonucleotides used for site-directed mutagenesis and (PCR) cloning of RNA-substrate templates.**

RNA substrate	Forward	Reverse
U <sub>1</sub> -A <sub>72</sub> <sup>a</sup>	TAGGATTTCCCTTTCTCGGGAGTAGCTCAGTC CAAGTCCCGTCTCCCGATCCAGTCACCGGATGTGC	GACTGAGCTACTCCCGAGAAAGGGAAAATCCTA GCACATCCGGTACTGGATCGGGAGACGGGACTTG
U <sub>-1</sub>	CTATAGGATTTCCCTTTGCGGGAGTAGCTCAGTCG	CGACTGAGCTACTCCCGCAAAGGGAAAATCCTATAG
G <sub>-1</sub> , A <sub>73</sub> <sup>a</sup>	TATAGGATTTCCCTTTGGCGGGAGTAGCTCAGTCG CAAGTCCCGTCTCCCGCACCAGTCACCGGATGTGC	CGACTGAGCTACTCCCGCAAAGGGAAAATCCTATA GCACATCCGGTACTGGTGCGGGAGACGGGACTTG
A <sub>-1</sub> , A <sub>73</sub> <sup>a</sup>	CTATAGGATTTCCCTTTAGCGGGAGTAGCTCAGTCG CAAGTCCCGTCTCCCGCACCAGTCACCGGATGTGC	CGACTGAGCTACTCCCGTAAAGGGAAAATCCTATAG GCACATCCGGTACTGGTGCGGGAGACGGGACTTG
A <sub>73</sub>	CAAGTCCCGTCTCCCGCACCAGTCACCGGATGTGC	GCACATCCGGTACTGGTGCGGGAGACGGGACTTG
G <sub>18</sub> →A <sub>18</sub>	GCGGGAGTAGCTCAGTCAGTAGAGCACGACCTTGC	GCAAGGTCGTGCTCTACTGACTGAGCTACTCCCGC
G <sub>19</sub> →A <sub>19</sub> , C <sub>56</sub> →U <sub>56</sub> <sup>a</sup>	TCGGGGTCGCGGGTTTAAAGTCCCGTCTCCCG GGAGTAGCTCAGTCGATAGACGACCTTGC	CGGGAGACGGGACTTAAACCCGCGACCCCGA GCAAGGTCGTGCTCTATCGACTGAGCTACTCC
C <sub>56</sub> →U <sub>56</sub>	TCGGGGTCGCGGGTTTAAAGTCCCGTCTCCCG	CGGGAGACGGGACTTAAACCCGCGACCCCGA
A <sub>57</sub> →C <sub>57</sub>	GGTCGCGGGTCCAGTCCCGTCTCC	GGAGACGGGACTGGAACCCGCGACC
U <sub>65</sub> →C <sub>65</sub> <sup>b</sup>	GGTCAAGTCCCGCTCCCGTCCAGT	ACTGGAGCGGGAGGCGGGACTTGAACC
Aa <sub>b1</sub> T <sup>c</sup>	TTCCCTTTGCGGGAGAGCGGGTTCAAGTC	GACTTGAACCCGCTCTCCCGCAAAGGGAA
Aa <sub>b4</sub> T <sup>d</sup>	TTCCCTTTGCGGGAGAGCTGCGGGTTCAAGTC GGAATTGTGAGCGGATAACA	GGTCTGCTTCAAGTAAAGCCAG GACTTGAACCCGAGCTCTCCCGCAAAGGGAA
Aa <sub>b9</sub> T <sup>d</sup>	TTCCCTTTGCGGGAGCCAGCTCTGCGGGTTCAAGTC GGAATTGTGAGCGGATAACA	GGTCTGCTTCAAGTAAAGCCAG GACTTGAACCCGAGGAGCTGGCTCCCGCAAAGGG AA
AaT	AATTCGAGCTCGCCTAATACGACTCACTATAGGATTTT CCCTTTGCGGGAGGCGGGTTCAAGTCCCGCTCCCG CTCCAGTACCGGATGTGCTTTCCGGTCTGATGAGTCC GTGAGGACGAACTGGTATG	GATCCATACCAGTTTCGTCTCACGGACTCATCAGACC GGAAAGCACATCCGGTACTGGAGCGGGAGGCGGG ACTTGAACCCGCTCCCGCAAAGGGAAAATCCTATA GTGAGTCGTATTAGGCGAGCTCG
Aa <sub>-2bp</sub> <sup>a</sup>	GTTCAAGTCCCGTCTCGCTCCAGTACCG ACTATAGGATTTCCCTTTGCGGAGTAGCTCAGTCGG	CGGTGACTGGAGCGAGACGGGACTTGAAC CCGACTGAGCTACTCGCAAAGGGAAAATCCTATAGT
Aa <sub>+2bp</sub> <sup>a</sup>	TCAAGTCCCGTCTCCGGCGCTCCAGTACCC TAGGATTTCCCTTTGCGCCGAGTAGCTCAGTC	GGTACTGGAGCGCCGAGACGGGACTTGA GACTGAGCTACTCCGGCGCAAAGGGAAAATCCTA

<sup>a</sup>Primer pairs for 2 rounds of site-directed mutagenesis.

<sup>b</sup>Used to generate the plasmid encoding pre-tRNA<sup>Gly</sup>-U<sub>65</sub>→C<sub>65</sub>, used as a template for further mutagenesis only.

<sup>c</sup>Plasmid encoding pre-tRNA<sup>Gly</sup>-U<sub>65</sub>→C<sub>65</sub> was used as a DNA template in the mutagenesis.

<sup>d</sup>Primer pairs to produce 2 overlapping PCR products from plasmid encoding pre-tRNA<sup>Gly</sup>-U<sub>65</sub>→C<sub>65</sub>.

**Supplementary Table S3. Oligonucleotides used for “inside-out” PCR mutagenesis of RNA-substrate templates.**

RNA substrate	Forward primer	Reverse primer
7-nt leader	AGGACGAAACGGTACCCGGTACCGTCCCCTTC GCGGGAGTAGCTCAGTCGGTAGAGCACGACC	CACGGACTCATCAGCCCTTCGCTCCTATAGTGAGTC GTATTAGGGCGAGCTCGAATTCGTAATCATGG
4-nt leader	AGGACGAAACGGTACCCGGTACCGTCTTTCGCG GGAGTAGCTCAGTCGGTAGAGCACGACC	CACGGACTCATCAGTTTCGCGGCTCCTATAGTGAGT CGTATTAGGGCGAGCTCGAATTCGTAATCATGG
2-nt leader	AGGACGAAACGGTACCCGGTACCGTCCCGCGG GAGTAGCTCAGTCGGTAGAGCACGACC	CACGGACTCATCAGCCGCGGGACTCCTATAGTGAGT CGTATTAGGGCGAGCTCGAATTCGTAATCATGG
1-nt leader	AGGACGAAACGGTACCCGGTACCGTCCCGGG AGTAGCTCAGTCGGTAGAGCACGACC	CACGGACTCATCAGCGGGGAGCTCCTATAGTGAGT CGTATTAGGGCGAGCTCGAATTCGTAATCATGG

**Supplementary Table S4. Oligonucleotides used to prepare RNA-substrate templates by PCR.**

RNA substrate	Forward primer	Reverse primer
(mature) CCA <sup>a</sup>	CTCGAGTAATACGACTCACTATAGG	TGGAGCGGGAGACGGGACTT
no trailer <sup>a</sup>	CTCGAGTAATACGACTCACTATAGG	AGCGGGAGACGGGACTT
40-nt trailer <sup>a</sup>	CTCGAGTAATACGACTCACTATAGG	TCCTCACGGACTCATCAG
ΔAc <sup>b</sup>	TAATACGACTCACTATAGG	TATTGGAGCGGGAGACG
ΔD <sup>b</sup>	TAATACGACTCACTATAGG	TATTGGAGCGGGAGACG
Aa <sub>b9</sub> T-U <sub>54</sub> →C <sub>54</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTTGAG CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T-U <sub>55</sub> →C <sub>55</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTTGGA CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T-C <sub>56</sub> →U <sub>56</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTTAAA CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T-A <sub>57</sub> →G <sub>57</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTCGAA CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T-A <sub>57</sub> →C <sub>57</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTGGAA CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T-A <sub>57</sub> →U <sub>57</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTAGAA CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T-A <sub>58</sub> →G <sub>58</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGACTGAA CCCGCAGGAGCTGGC
Aa <sub>b9</sub> T <sub>CCUUUUU</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGTAAAAGG CCCGCAGGAGCTGGC
Aa <sub>+2bp</sub> b <sub>9</sub> T <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGCCGAGCCAGCTCCTG	GACTGGAGCGCCGAGGCGGGACTTG AACCCGAGGAGCTGGC
Aa <sub>b9</sub> T <sub>+2bp</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGCCGACTTG AACCGCGCAGGAGCTGGC
Aa <sub>-2bp</sub> b <sub>9</sub> T <sub>+2bp</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGAGCCAGCTCCTG	GACTGGAGCGAGGCGCCGACTTGAAC CGGCGCAGGAGCTGGC
Aa <sub>b9</sub> T <sub>4loop</sub> <sup>c</sup>	CTCGAGTAATACGACTCACTATAGGATT TTCCTTTTCGCGGGAGCCAGCTCCTG	GACTGGAGCGGGAGGCGGGTTTCCCCG CAGGAGCTGGC
Aa <sub>+4bp</sub> <sup>b</sup>	CTCGAGTAATACGACTCACTATAGG	GACTGGAGCGCGCCGGAGA
Aa <sub>+m3GC</sub> <sup>b</sup>	CTCGAGTAATACGACTCACTATAGG	GACTGGAGCGAGCCGGAGA
Aa <sub>+m3AU</sub> <sup>b</sup>	CTCGAGTAATACGACTCACTATAGG	GACTGGAATAAGCCGGAGA
G <sub>-1</sub> -C <sub>73</sub> <sup>d</sup>	CTCGAGTAATACGACTCACTATAGG	GACTGGGGCGGGAGA
U <sub>-1</sub> -A <sub>73</sub> <sup>e</sup>	CTCGAGTAATACGACTCACTATAGG	GACTGGTGCGGGAGA
Aa <sub>+3AU</sub> <sup>a</sup>	CGAGTAATACGACTCACTATAGGATTTT CCCTTCAATGCGGGAGTAGC	GACTGGAATGCGGGAGAC

<sup>a</sup>Plasmid pSBpt3'hh was used as a template.

<sup>b</sup>Oligonucleotide template listed in Supplementary Table S6.

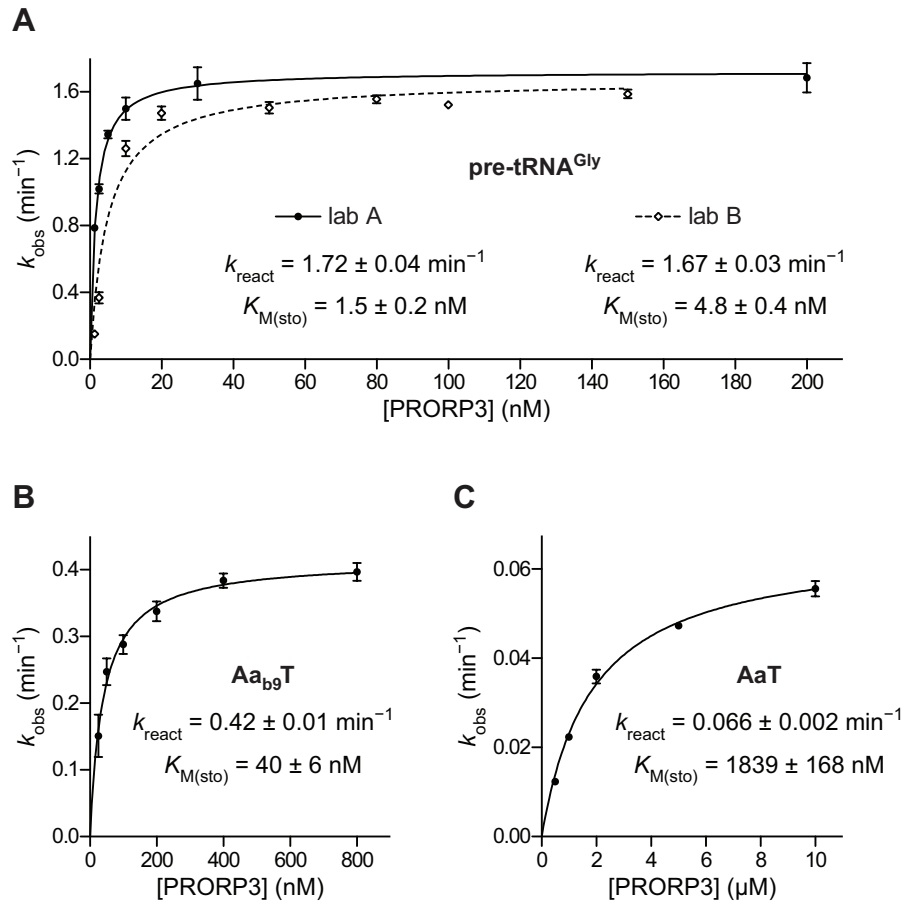
<sup>c</sup>Overlapping primers (no extra template).

<sup>d</sup>Pre-tRNA<sup>Gly</sup>-G<sub>-1</sub> was used as a template.

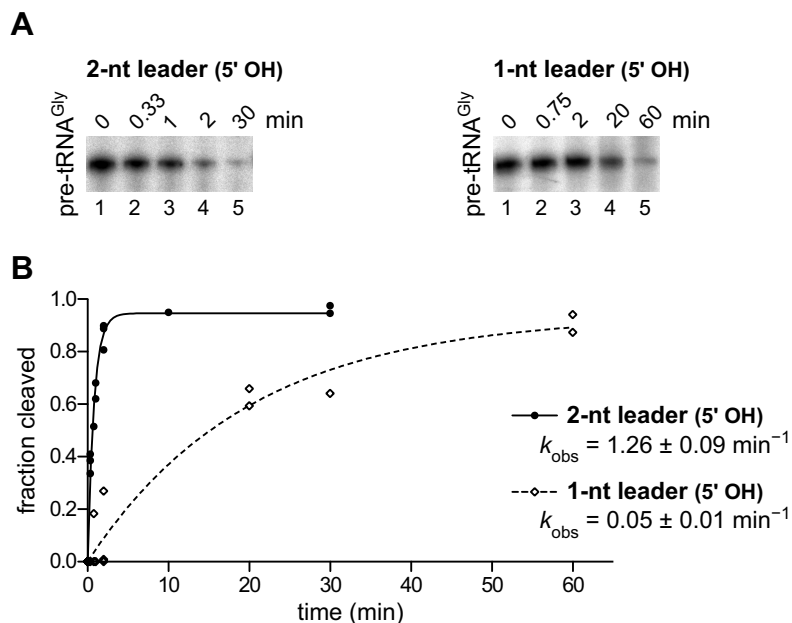
<sup>e</sup>Pre-tRNA<sup>Gly</sup>-U<sub>-1</sub> was used as a template.

**Supplementary Table S5. Oligonucleotide templates used for PCR of RNA-substrate templates.**

RNA substrate	Oligonucleotide template
Aa <sub>+4bp</sub> & Aa <sub>+m3GC</sub>	TAATACGACTCACTATAGGATTTTCCCTTTCGCGCGCCGGAGTAGCTCAGTCGGTAGAGC ACGACCTTGCCAAGGTCGGGGTCGCGGGTTCAAGTCCCGTCTCCGGCGCGCTCCAGTC
Aa <sub>+m3AU</sub>	TAATACGACTCACTATAGGATTTTCCCTTTCATACGCCGGAGTAGCTCAGTCGGTAGAGCA CGACCTTGCCAAGGTCGGGGTCGCGGGTTCAAGTCCCGTCTCCGGCGTATTCCAGTC
ΔD	TAATACGACTCACTATAGGATTTTCCCTTTCGCGGGAGTAGACCGACCTTGCCAAGGTCG GGTCGCGGGTTCAAGTCCCGTCTCCCGCTCCAATA
ΔAC	TAATACGACTCACTATAGGATTTTCCCTTTCGCGGGAGTAGCTCAGTCGGTAGAGCACCTT CGGGGGTTCGCGGGTTCAAGTCCCGTCTCCCGCTCCAATA

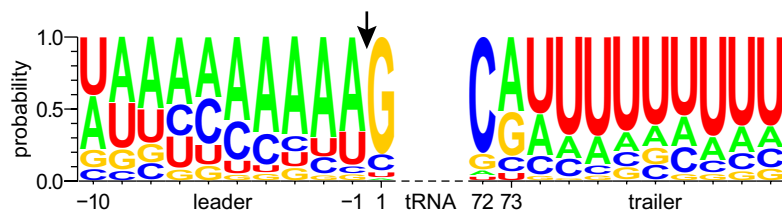


**Supplementary Figure S1. Single-turnover cleavage kinetics of representative substrates.** First-order rate constants of cleavage ( $k_{\text{obs}}$ ) obtained at different PRORP3 concentrations were plotted against the enzyme concentration and fit by nonlinear regression to a “Michaelis-Menten-like” enzyme kinetics model to derive the maximal rate constant  $k_{\text{react}}$  and the single-turnover Michaelis constant  $K_{\text{M(sto)}}$ . Data points represent the mean of at least 3 replicates with SEM (error bars display only if SEM exceeds the size of the data point in the graph). **(A)** Kinetic analysis of pre-tRNA<sup>Gly</sup> cleavage by PRORP3 independently performed by the two labs. **(B)** Kinetic analysis of the cleavage of the minimal substrate Aa<sub>b9</sub>T by PRORP3. **(C)** Kinetic analysis of the cleavage of the stem-loop substrate AaT by PRORP3.



**Supplementary Figure S2. Cleavage analysis of pre-tRNA<sup>Gly</sup> variants with a short 5'-hydroxyl-end leader.** (A) Unlabeled pre-tRNA<sup>Gly</sup> variants with a 5'-hydroxyl-end leader of 1 or 2 nt were cleaved with PRORP3 under presumably enzyme-saturated conditions (80 nM). Aliquots of the reactions were withdrawn at indicated times, and the RNA <sup>32</sup>P-5'-end labeled and resolved by denaturing PAGE. The panels show the substrate RNA remaining after the reaction time indicated. (B) First-order rate constants of cleavage ( $k_{\text{obs}}$ ; best-fit values  $\pm$  standard error) for the two substrates were derived from the data of three experiments each. Individual data points are shown ("substrate remaining" converted to "fraction cleaved"; note: in the three replicate experiments some sampling time points differed).





**Supplementary Figure S3. Nucleotide frequencies of the 5'-leader and 3'-trailer sequences of the nucleus-encoded pre-tRNAs of *A. thaliana*.**

Nucleotides upstream of the 5' end and downstream of the 3' end of the mature tRNA, including the first base pair of the tRNAs' nucleotides 1 and 72, and the discriminator position 73, were aligned, and a logo derived from the alignment of the 598 sequences. An arrow indicates the canonical RNase P cleavage site.

**Supplementary Table S6. Base-pair frequencies at the RNase P cleavage site of the nucleus-encoded pre-tRNAs of *A. thaliana*.**

Base-paired positions <sup>a</sup>	G-C/C-G bp	A-U/U-A/G-U/U-G bp	G-C/C-G as 1 <sup>st</sup> or 2 <sup>nd</sup> upstream bp <sup>b</sup>
+1 - 72	92.0%	7.0%	
-1 - 73	1.0%	22.9%	
-2 - 74			
-1 - 73	0.0%	8.5%	1.5%
-3 - 75			
-2 - 74	0.0%	3.5%	0.4%
-1 - 73			
-4 - 76			
-3 - 75			
-2 - 74	0.0%	1.8%	0.0%
-1 - 73			

<sup>a</sup>Numbering according to convention with the exception of positions 74–76, which do not indicate the CCA end of the mature tRNA, but the first 3 nt of the trailer of the pre-tRNA (see also Supplementary Figure S3); nucleotides of the 5' leader carry negative numbers starting from the nucleotide closest to the RNase P cleavage site with -1.

<sup>b</sup>Extensions of the acceptor stem with a single G-C base pair at the first or second upstream position; the other base pairs of the extension are either A-U or G-U.