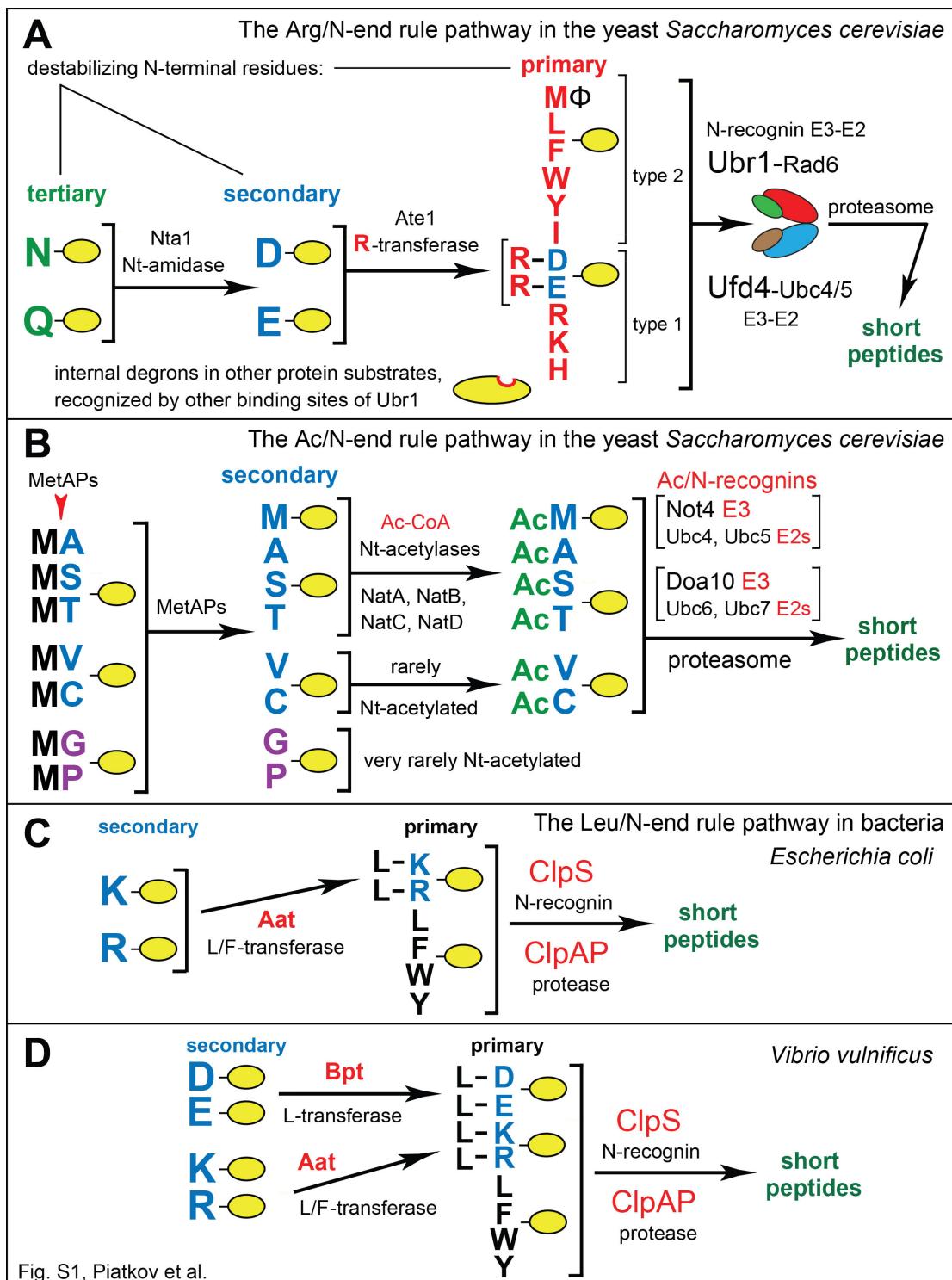


Supplemental Materials for Research Article in *Microbial Cell*:**Formyl-methionine as a degradation signal  
at the N-termini of bacterial proteins**Konstantin I. Piatkov<sup>1,3#</sup>, Tri T. M. Vu<sup>1,#</sup>, Cheol-Sang Hwang<sup>2</sup>, and Alexander Varshavsky<sup>1,\*</sup>#These authors contributed equally to this study.<sup>1</sup>Division of Biology, California Institute of Technology, Pasadena, CA 91125, USA<sup>2</sup>Department of Life Sciences, Pohang University of Science and Technology, Pohang,  
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Telephone: 626-395-3785. Email: [avarsh@caltech.edu](mailto:avarsh@caltech.edu)**These Supplemental Materials contain:**

Figure S1 and its legend.

Tables S1 and S2.

Supplemental References.



**Figure S1.** The Arg/N-End Rule Pathway and the Ac/N-End Rule Pathway. N-terminal residues are indicated by single-letter abbreviations. A yellow oval denotes the rest of a protein substrate.

The N-end rule pathway recognizes proteins containing N-terminal degradation signals called N-degrons, polyubiquitylates these proteins and thereby causes their degradation by the 26S proteasome. Recognition components of the N-end rule pathway are called N-recognins. Eukaryotic N-recognins are E3 ubiquitin (Ub) ligases that can target N-degrons. The main determinant of an N-degron is a destabilizing N-terminal residue of a protein. In eukaryotes, the N-end rule pathway consists of two branches, described in panels **A** and **B**.

**(A)** The Arg/N-end rule pathway in *S. cerevisiae* [1-5]. The prefix “Arg” in the pathway’s name refers to Nt-arginylation of N-end rule substrates. The Arg/N-end rule pathway targets specific unacetylated N-terminal residues. It is mediated by the Ubr1 N-recognin, a 225 kDa RING-type E3 Ub ligase and a part of the targeting complex containing the Ubr1-Rad6 and Ufd4-Ubc4/5 holoenzymes. The Ubr1 (N-recognin) component of this complex recognizes (binds to) the “primary” destabilizing N-terminal residues Arg, Lys, His, Leu, Phe, Tyr, Trp and Ile, as well as the unmodified N-terminal Met residue, if Met is followed by a bulky hydrophobic ( $\Phi$ ) residue [5]. The terms “secondary” and “tertiary” refer to the indicated enzymatic modifications of specific N-terminal residues. N-terminal Cys can be arginylylated by the Ate1 arginyltransferase (R-transferase) only after the oxidation of Cys to Cys-sulfinate or Cys-sulfonate, in reactions that involve nitric oxide (NO) and oxygen [2-4, 6, 7]. Regulated oxidation of N-terminal Cys takes place in multicellular eukaryotes but not in fungi such as *S. cerevisiae*, which apparently do not produce NO under normal conditions.

**(B)** The Ac/N-end rule pathway in *S. cerevisiae* [3, 5, 8-10]. This pathway recognizes substrates through their  $N^{\alpha}$ -terminally acetylated (Nt-acetylated) residues. The corresponding degradation signals and E3 Ub ligases are called Ac/N-degrons and Ac/N-recognins, respectively. Red arrow on the left indicates the removal of N-terminal Met by Met-aminopeptidases (MetAPs). N-terminal Met is retained if a residue at position 2 is larger than Val [11-13]. The term “secondary” refers to the requirement for a modification (Nt-acetylation) of a destabilizing N-terminal residue before a protein can be recognized by an Ac/N-recognin.

**(C)** and **(D)** The bacterial Leu/N-end rule pathway, in *Escherichia coli* **(C)** and in *Vibrio vulnificus* **(D)** [14-32]. The Aat L/F-transferase conjugates (largely) Leu to N-terminal Arg or Lys. N-end rule substrates bearing primary (bulky hydrophobic) destabilizing N-terminal residues are recognized by the ClpS N-recognin and are delivered for degradation to the ClpAP protease. In *V. vulnificus*, the Leu/N-end rule pathway contains both the Aat L/F-transferase and the Bpt L-transferase. As a result, N-terminal Asp and Glu, which are not destabilizing residues in *E. coli*, function as secondary destabilizing residues in *V. vulnificus* [16].

Regulated degradation of proteins or their natural fragments by the N-end rule pathway mediates a broad range of biological functions (refs. [2-5, 8-10, 31] and refs therein).

**Table S1.** Bacterial strains used in this study.

<i>E. coli</i> strains	Genotype	Source or Ref.
MG1655	<i>F</i> - $\lambda$ - <i>rph-1</i>	[33]
MG-D	<i>F</i> - $\lambda$ - <i>rph-1</i> $\Delta$ (def-fmt)::cm $\Delta$ <i>gloB</i> ::frt	Gift from D. Mazel
DH5 $\alpha$	$\varphi 80$ <i>lacZ</i> $\Delta$ <i>M15</i> <i>endA1</i> <i>recA1</i> <i>gyrA96</i> <i>thi-1</i> <i>hsdR17</i> ( $r_k^-$ , $m_k^-$ ) <i>relA1</i> <i>supE44</i> <i>deoR</i> $\Delta$ ( <i>lacZYA-argF</i> ) <i>U169</i>	Promega
CAG12184	$\lambda$ <i>rph-1</i> <i>tolC210::Tn10(tet)</i>	[34]
KPS73	$\lambda$ - <i>rph-1</i> <i>tolC210::Tn10(tet)</i> $\Delta$ fmt ::Km	This study
KPS74	$\lambda$ - <i>rph-1</i> <i>tolC210::Tn10(tet)</i> $\Delta$ def- $\Delta$ fmt ::Km	This study

**Table S2.** Plasmids used in this study.

Plasmid name	Description	Source or Ref.
pJT184	Cm <sup>R</sup> ; pACYC184-based plasmid with 2.8-kb BamHI/SalI insert containing <i>S. cerevisiae</i> Ubp1.	[14]
pBADET	Ap <sup>R</sup> ; pBAD2-based plasmid containing arabinose-inducible promoter and expanded multiple cloning site.	Gift from V. Ksenzenko
pACYC177	Ap <sup>R</sup> , Km <sup>R</sup> ; low copy vector containing p15A repl. origin.	[35, 36]
pKD46	Ap <sup>R</sup> ; ts replication (repA101ts); encodes lambda Red genes ( <i>exo</i> , <i>bet</i> , <i>gam</i> ); native terminator (tL3) after <i>exo</i> gene; arabinose-inducible promoter for expression ( <i>Para</i> ); encodes <i>araC</i> for repression of the <i>Para</i> promoter. This plasmid was used for chromosomal deletions of specific genes.	[37]
pKD3	Ap <sup>R</sup> , Cm <sup>R</sup> ; R6K origin-based plasmid containing <i>cat</i> -cassette flanked by FRT sites. This plasmid was used as a template in PCR to create gene-specific <i>cat</i> -cassettes.	[37]
pCH178	Ap <sup>R</sup> ; p314CUP1-based plasmid expressing Ub-CK-e <sup>K</sup> -ha-Ura3.	[9]
pKP249	Ap <sup>R</sup> ; pBADET-based plasmid expressing P1 <sup>T2</sup> -e <sup>K</sup> -ha-Ura3 from <i>Para</i> promoter.	This study
pKP250	Ap <sup>R</sup> ; pBADET-based plasmid expressing P1 <sup>T2D</sup> -e <sup>K</sup> -ha-Ura3 from <i>Para</i> promoter.	This study
pKP251	Ap <sup>R</sup> ; pBADET-based plasmid expressing Ub-P1 <sup>T2</sup> -e <sup>K</sup> -ha-Ura3 from <i>Para</i> promoter.	This study
pKP252	Ap <sup>R</sup> ; pBADET-based plasmid expressing Ub-P1 <sup>T2D</sup> -e <sup>K</sup> -ha-Ura3 from <i>Para</i> promoter.	This study
pKP257	Ap <sup>R</sup> ; pACYC177-based plasmid expressing P1 <sup>T2</sup> -e <sup>K</sup> -ha-Ura3 from P <sub>KmR</sub> promoter.	This study
pKP258	Ap <sup>R</sup> ; pACYC177-based plasmid	This study

	expressing P1 <sup>T2D</sup> -e <sup>K</sup> -ha-Ura3 from P <sub>KmR</sub> promoter.	
pKP286	Ap <sup>R</sup> ; pBADET-based plasmid expressing PpiB-8his-flag from <i>Para</i> promoter.	This study
pKP287	Ap <sup>R</sup> ; pBADET-based plasmid expressing PpiB <sup>V2D</sup> -8his-flag from <i>Para</i> promoter.	This study
pKP335	Ap <sup>R</sup> ; pBADET-based plasmid expressing PpiB-8his-flag-Ub-PpiB-8his-flag from <i>Para</i> promoter	This study
pKP458	Ap <sup>R</sup> ; pBADET-based plasmid expressing <sup>MVTV</sup> PpiB-8his-flag and <sup>MDDD</sup> PpiB-8his-flag-Ub from two identical and independent <i>Para</i> promoters.	This study
pKP459	Ap <sup>R</sup> ; pBADET-based plasmid expressing <sup>MVTV</sup> PpiB-8his-flag and <sup>MYFY</sup> PpiB-8his-flag-Ub from two identical and independent <i>Para</i> promoters.	This study

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