A Trapping Approach Reveals Novel Substrates and Physiological Functions of the Essential Protease FtsH in Escherichia coli\textsuperscript{*}\textsuperscript{5}

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Results: New cytoplasmic and membrane-bound substrates of FtsH were trapped in vivo.

Conclusion: FtsH is involved in the sulfatation of molecules, \(\alpha\)-amino acid metabolism, and adaptation to anaerobiosis and stress conditions.

Significance: The novel FtsH substrates significantly expand our knowledge on the biological functions of this fundamentally important protease.

Proteolysis is a universal strategy to rapidly adjust the amount of regulatory and metabolic proteins to cellular demand. FtsH is the only membrane-anchored and essential ATP-dependent protease in \textit{Escherichia coli}. Among the known functions of FtsH are the control of the heat shock response by proteolysis of the transcription factor RpoH (\(\sigma^H\)) and its essential role in lipopolysaccharide biosynthesis by degradation of the two key enzymes LpxC and KdtA. Here, we identified new FtsH substrates by using a proteomic-based substrate trapping approach. An FtsH variant (FtsH\textsuperscript{trap}) carrying a single amino acid exchange in the proteolytic center was expressed and purified in \textit{E. coli}. FtsH\textsuperscript{trap} is devoid of its proteolytic activity but fully retains ATPase activity allowing for unfolding and translocation of substrates into the inactivated proteolytic chamber. Proteins associated with FtsH\textsuperscript{trap} and wild-type FtsH (FtsH\textsuperscript{WT}) were purified, separated by two-dimensional PAGE, and subjected to mass spectrometry. Over-representation of LpxC in the FtsH\textsuperscript{trap} preparation validated the trapping strategy. Four novel FtsH substrates were identified. The sulfur delivery protein IscS and the \(\alpha\)-amino acid dehydrogenase DadA were degraded under all tested conditions. The formate dehydrogenase subunit FdoH and the yet uncharacterized YfgM protein were subject to growth condition-dependent regulated proteolysis. Several lines of evidence suggest that YfgM serves as negative regulator of the RcsB-dependent stress response pathway, which must be degraded under stress conditions. The proteins captured by FtsH\textsuperscript{trap} revealed previously unknown biological functions of the physiologically most important AAA\textsuperscript{+} protease in \textit{E. coli}.

The cellular protein pool varies with changing conditions. Protein degradation is a common but costly mechanism to shape the cellular proteome. As it acts on already synthesized proteins, proteolysis is more efficient than delayed transcriptional or translational control mechanisms because it removes undesired proteins rapidly and irreversibly. In \textit{Escherichia coli}, the five AAA\textsuperscript{+} (ATPases associated with various cellular activities) proteases ClpAP/XP, HslUV, Lon, and FtsH play important roles in diverse regulatory networks (1, 2). Among these, FtsH is the only essential and the only membrane-bound protease in \textit{E. coli} (3, 4). It forms a homo-hexameric barrel-like structure (5). AAA\textsuperscript{+} proteases commonly consist of an ATPase and a protease domain, which can reside in a single polypeptide or in two separate polypeptides. The ATPase domain of FtsH contains the Walker A/B motifs and the second region of homology, which allow the binding and hydrolysis of ATP (6). In general, the ATPase domain is solely responsible for unfolding and translocation of the substrate into the proteolytic chamber, which is driven by conformational changes after hydrolysis of ATP (7, 8). The subsequent degradation reaction is carried out by the protease domain. FtsH is a metalloprotease that requires catalytic Zn\textsuperscript{2+} ions for functionality. The histidines in the \textit{HHEXXH}\textsuperscript{21} motif and a glutamic acid at position 495 are responsible for zinc binding. The imidazoles of these histidines are positioned by Glu\textsuperscript{479} in the correct conformation (9, 10). Substitution of either histidine against a tyrosine retained ATPase activity but impaired proteolytic activity (11). The FtsH protease is known to control several important physiological processes (12–14) and plays a major role in the quality control of membrane proteins (15). The essential function of FtsH in \textit{E. coli} is to degrade the lipopolysaccharide (LPS) biosynthesis enzymes LpxC and KdtA, thereby controlling production of lipid A, the hydrophobic anchor of LPS (3, 16). Altered LPS amounts are lethal because LPS in the outer leaflet of the outer membrane of Gram-negative bacteria form a crucial permeability barrier. FtsH guarantees a strict balance between LPS and phospholipids. An \(\text{ftsH}\) deletion mutant is viable only in the presence of a suppressor mutation within the \textit{fabZ} gene, resulting in a balance of LPS to phospholipids (3).

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Identification of Novel FtsH Substrates

FtsH also controls heat shock gene expression by degrading the heat shock σ factor RpoH (σH) thereby adapting the cellular amount of the transcription factor to different temperatures (17, 18). Together with the Lon protease, FtsH participates in the shutdown of the superoxide stress response (19, 20). Furthermore, FtsH degrades a number of phage proteins and thereby takes part in the lysis/lysogeny decision of the phage λ (21–23).

Despite the importance of FtsH for bacterial survival, only a limited number of substrates are known to date as compared with other proteolytic machineries. Furthermore, the substrate recognition logics of FtsH are poorly understood and require further investigation. For example, proteolysis of LpxC depends on a length- and sequence-specific C-terminal degradation signal (24, 25). Although the replication inhibitor CspD carries a similar C-terminal sequence, it is not an FtsH but a Lon substrate (26). Degradation of RpoH requires an internal structural element composed of an α-helix and the chaperone systems DnaK/J and GroEL/ES (17, 27–30).

To fully comprehend the biological functions of FtsH and its substrate selection principles, we set out to identify new substrates of the protease by an experimental approach. Entirely unrelated recognition motifs in LpxC and RpoH and unknown degradation signals in other known substrates excluded in silico searches. Instead, we employed a substrate trapping approach as has been used for the AAA+ protease ClpXP (31). Here, we present the construction of FtsH<sup>H<sub>trap</sub></sup>, an ATPase-competent protease variant with an active-site mutation in the Zn<sup>2+</sup>-binding motif (H417Y). Proteomic-based identification of proteins co-purified with FtsH<sup>H<sub>trap</sub></sup> revealed 14 potential new FtsH substrates. Among these, four proteins were proven to be degraded by FtsH using in vivo degradation experiments. This study gives new insights into the extent of FtsH-dependent proteolysis in <i>E. coli</i> and provides a basis to further characterize the cellular functions and substrate selection of this unique protease.

**Experimental Procedures**

**Bacteria and Growth Conditions—**<i>E. coli</i> strains used in this study are listed in <sup>supplemental Table S1</sup>. Except for the ΔftsH strain, <i>E. coli</i> cells were grown aerobically in LB medium at 37 °C. ΔftsH cells were routinely cultivated at 30 °C. When needed, antibiotics were used as follows: ampicillin, 100 μg ml<sup>−1</sup>; chloramphenicol, 200 μg ml<sup>−1</sup>; kanamycin, 50 μg ml<sup>−1</sup>; tetracycline, 12.5 μg ml<sup>−1</sup>.

**Construction of Plasmids—**Plasmids used in this study are listed in <sup>supplemental Table S1</sup>. For mutagenesis of <i>ftsH</i>, a fragment of the gene (1024 bp) was cloned from pGST-FtsH into a pBCSK<sup>(+)</sup> derivative (pBO966) using the Acc65I and Ndel sites. The resulting plasmid was used as a template for QuikChange<sup>®</sup> PCR (oligonucleotides: H417Y-fw and H417Y-rv; E479D-fw and E479D-rv; <sup>supplemental Table S2</sup>) to generate the amino acid substitutions H417Y and E479D. Success of the QuikChange<sup>®</sup> PCR was analyzed by sequencing, and the mutated fragment was used to substitute the equivalent wild-type fragment in pMAL-C-FtsH. For construction of expression plasmids coding for putative FtsH substrates, the respective genes were amplified by PCR using <i>E. coli</i> K12 genomic DNA as a template. The coding regions were inserted into the backbone of pBO1199. The resulting expression plasmids code for proteins with an N-terminal hexahistidine (His<sub>6</sub>) sequence under the control of an inducible anhydrotetracycline promoter. For construction of a plasmid allowing constitutive expression of YfgM, a yfgM PCR product was inserted in pBO1750 using the SmaI and Bsp1407I sites.

**Protein Purification—**His<sub>6</sub>-MBP-FtsH<sup>WT</sup>, His<sub>6</sub>-MBP-FtsH<sup>H417Y</sup>, and His<sub>6</sub>-MBP-FtsH<sup>E479D</sup> were produced in <i>E. coli</i> ΔftsH. Cells were grown in 2× 500 ml of LB broth at 30 °C to an A<sub>590 nm</sub> of 0.5. The overexpression of the protein variants was induced by 1 mM isopropyl-1-thio-β-D-galactopyranoside for 18 h at 20 °C. Cells were harvested and resuspended in 12 ml of 140 mM NaCl, 2.7 mM KCl, 1.8 mM KH2PO<sub>4</sub>, 10 mM Na2HPO<sub>4</sub>, pH 7.3, 0.2 mg ml<sup>−1</sup> DNase, and 0.2 mg ml<sup>−1</sup> RNase. Cells were disrupted by a French press, and FtsH variants were purified using nickel-nitrilotriacetic acid columns (Qiagen) equilibrated with 0.5 mM KCl and 20 mM Tris-HCl, pH 7.9. For washing (W) and elution (E) of the column, increasing amounts of imidazole were used (W, 5–50 mM; E, 150 mM to 1 M). The elution fractions were stored in 0.2 M NaCl, 0.5% (v/v) Nonidet P-40, 20 mM monoethanolamine, 20% (v/v) glycerol, and 1 mM DTT at −80 °C. Protein concentrations were determined by Bradford assays (32).

**ATPase Activity Assay—**To measure ATPase activity, 1 μg of purified FtsH was mixed with 1 mM ATP, 50 mM Tris-HCl, pH 7.5, 5 mM MgCl<sub>2</sub>, 25 μM zinc acetate, 2.5 mM C<sub>2</sub>H<sub>5</sub>KO<sub>2</sub>, 1 mM DTT, and 0.1% (v/v) Nonidet P-40 in a total volume of 500 μl. The reaction was incubated at 37 °C. After 0, 30, 60, and 90 min, 120 μl of this mixture was added to 480 μl of detection solution (0.027% (w/v) malachite green, 0.1% (v/v) Triton X-100, 0.95% (w/v) ammonium molybdate) and 40 μl of 34% C<sub>6</sub>H<sub>5</sub>Na<sub>2</sub>O<sub>7</sub> solution. After 40 min of incubation at room temperature, the absorption was measured at 660 nm. Increasing concentrations of KH2PO4 were used as reference to calculate the amount of free phosphate. As controls, the assay was performed without addition of ATP or FtsH.

**In Vitro Degradation of β-Casein—**In vitro degradation of β-casein by purified FtsH variants was performed as described previously (10) with minor modifications. In a 100-μl reaction mix, 20 μg of His<sub>6</sub>-MBP-FtsH<sup>WT</sup> or His<sub>6</sub>-MBP-FtsH<sup>H417Y</sup> and 5 μg of β-casein were used and incubated at 42 °C. The reaction was started with 10 mM ATP, and samples were taken at different time points. Degradation of β-casein was quantified using the AlphaEaseFC (Alpha Innotech) software after SDS-PAGE and Coomassie staining.

**Two-dimensional PAGE and Mass Spectrometry—**Elution fractions of His<sub>6</sub>-MBP-FtsH<sup>WT</sup> and His<sub>6</sub>-MBP-FtsH<sup>H417Y</sup> were concentrated by chloroform/methanol precipitation (33) up to 600 μg ml<sup>−1</sup>. Isoelectric focusing and SDS-PAGE were performed as described previously (34). Protein solutions were loaded on Immobiline DryStrip pH 4–7, 24 cm (GE Healthcare). After isoelectric focusing, proteins were subjected to 12.5% SDS-PAGE, and the spots were visualized using RuBPS (C<sub>7</sub>H<sub>42</sub>N<sub>6</sub>Na<sub>4</sub>O<sub>18</sub>RuS<sub>6</sub>) staining. Protein spots were scanned using a Typhoon TRIO (GE Healthcare) and were quantified with the Delta two-dimensional software (version 4.0, Decodon). Selected protein spots were excised from the gel, and...
protein identification using mass spectrometry was performed by MALDI-TOF mass spectrometry as described previously (35).

**In Vivo Degradation Experiments in E. coli**—To analyze the stability of proteins, cells containing plasmids encoding for the proteins of interest were grown at 37 °C (ΔftsH at 30 °C) in a water bath shaker (180 rpm) to different growth phases. Protein expression was induced by the addition of 100–200 ng ml−1 anhydrotetracycline for 30 min. Then translation was blocked using 300 μg ml−1 spectinomycin. Samples were taken at different time points and were frozen in liquid nitrogen. To measure the effects of oxygen on degradation of His6–FdoH, anaerobic conditions were generated by incubating the cultures in hange tubes without oxygen and shaking. To analyze whether degradation of His6–YfgM is regulated by osmotic conditions, cells in exponential phase of a growth curve were shocked with 15% (w/v) sucrose.

**Preparation of Protein Extracts and Immunodetection**—Depending on their absorbance, cell pellets were resuspended in 15 ml of M9 medium (10 mM Tris-HCl, pH 8, 1 mM EDTA, 10 μM of TE buffer per A₅₈₀ nm of 1.0) and mixed with protein sample buffer (final concentrations of 2% SDS (w/v), 0.1% (w/v) bromophenol blue, 10% glycerol (v/v), 1% (v/v) β-mercaptoethanol, 50 mM Tris-HCl, pH 6.8). After incubation for 10 min at 100 °C, samples were centrifuged (1 min, 16,000 g) and the protein extract was subjected to SDS gel electrophoresis and Western transfer using standard protocols (36). Proteins containing His tag fusions were detected using a Penta-His-HRP conjugate (Qiagen). FtsH and RpoH were detected using a respective polyclonal antiserum derived from rabbit as the primary antibody. A goat anti-rabbit immunoglobulin G(H+L)-HRP conjugate (Bio-Rad) served as a secondary antibody. Protein signals were visualized using Luminata Forte Western HRP substrate (Millipore) and the ChemiImager Ready (Alpha Innotec). Half-lives of proteins were calculated with the AlphaEaseFC software (version 4.0.0, Alpha Innotec).

**Survival after Acidic Stress**—The survival rate after an acidic shock was determined as described previously (37). E. coli cells containing a plasmid mediating constitutive expression of YfgM as well as cells carrying the empty vector were grown to an A₅₈₀nm of 0.6 in M9 minimal medium with glucose (22.2 mM) and casamino acids (0.2% w/v), buffered with MOPS and MES. The cultures were centrifuged, and the pellets were resuspended in 15 ml of M9 medium (+ MOPS; pH 5.7) and incubated for 70 min in a water bath shaker at 37 °C. After centrifugation, cells were resuspended in 15 ml of M9 medium, pH 2.4, and incubated for 2 h in a water bath shaker at 37 °C. Cells were sedimented and resuspended in 15 ml M9 medium (+ MOPS; pH 7). 100 μl of serial dilutions (10⁻², 10⁻⁴, 10⁻⁶, and 10⁻⁸) were plated on LB agar plates. After incubation overnight at 37 °C, colonies were counted, and the survival rate was calculated. Serial dilutions of untreated cells were used as references. The survival rate of cells carrying the empty vector incubated in M9 medium (+ MOPS; pH 2.4) was set to 100%.

**RESULTS**

**Validation of FtsHtrap for Substrate Identification**—A promising strategy for identification of new protease substrates was to capture proteins by an inactive protease that accepts and retains substrates but is unable to degrade them (31). To trap FtsH substrates, we constructed variants expected to have normal ATPase activity that promotes translocation of substrates into the proteolytic chamber but were deficient in proteolysis (Fig. 1A). The catalytic activity should be destroyed by a single point mutation exchanging the first histidine in the zinc-binding motif (HEXXH) to a tyrosine or by exchanging the glutamic acid at position 479 to an aspartic acid. To verify that the ATPase activity was not affected by the H417Y or the E479D exchange, we purified His₆-MBP-FtsHWT, His₆-MBP-FtsH417Y, and His₆-MBP-FtsH479D (from now on called FtsHWT, FtsH417Y, and FtsH479D) by nickel-nitriilotriacetic acid chromatography. Both proteins were subjected to an in vitro ATPase assay based on the photometric detection of free phosphate (Pᵢ) from ATP hydrolysis (Fig. 1B). FtsHWT, FtsH417Y, and FtsH479D were able to hydrolyze ATP in a
time-dependent manner, although there was no significant increase of free Pi in the absence of ATP or without FtsH. Full ATPase activity of FtsH^{H417Y} and FtsH^{E479D} suggested that they should be competent in substrate translocation.

Two independent assays were used to examine the proteolytic activity of these proteins. In an in vivo approach, we analyzed whether the heat shock σ factor RpoH could be degraded by FtsH\textsuperscript{WT}, FtsH\textsuperscript{H417Y}, and FtsH\textsuperscript{E479D}. Consistent with previous studies (11), RpoH accumulated in the ΔftsH strain (Fig. 2A). In contrast, the σ factor was not detectable by immunoblot analysis in the presence of plasmid-encoded FtsH\textsuperscript{WT} or FtsH\textsuperscript{E479D}. Equal amounts of FtsH\textsuperscript{H417Y} (from now on called FtsH\textsuperscript{trap}), however, were unable to degrade the σ factor suggesting that the mutated protein is impaired in proteolysis. A complementary in vitro approach showed that FtsH\textsuperscript{trap} was unable to degrade the standard protease substrate β-casein (Fig. 2B). Both assays thus confirmed the suitability of FtsH\textsuperscript{trap} for the trapping approach.

**Identification of Co-purified Proteins**—To identify putative substrates of FtsH, plasmid-encoded FtsH\textsuperscript{WT} and FtsH\textsuperscript{trap} were expressed in a ΔftsH strain. The FtsH preparations were subjected to two-dimensional PAGE. Dual-channel images of two-dimensional gels of representative elution fractions from FtsH\textsuperscript{WT} and FtsH\textsuperscript{trap} (Fig. 3) show proteins present in both preparations (yellow spots), and proteins that were over-represented in elution fractions of FtsH\textsuperscript{WT} (red spots; DnaK) or FtsH\textsuperscript{trap} (green spots). After data analysis of three replicates, 15 putative FtsH substrates were selected and identified by mass spectrometry. The presence of the known substrate LpxC among them supported the value of this approach. The other proteins that co-eluted with FtsH\textsuperscript{trap} fall into a wide variety of cellular functions (Table 1); for example, HisG, a histidine biosynthesis enzyme (38). PspA is a protein involved in phage shock and stress response (39, 40). Rsd, the anti-σ factor of the housekeeping σ factor RpoD (41) was not only trapped with FtsH but also with ClpXP (31).

Not All Proteins Co-purified with FtsH\textsuperscript{trap} Are Protease Substrates—To verify whether the trapped proteins are subject to FtsH-dependent proteolysis, we constructed expression plasmids coding for N-terminal His\textsubscript{6} tag fusions of a selection of
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TABLE 1
List of putative FtsH substrates that were co-purified by FtsH\textsuperscript{\textregistered}ap

<table>
<thead>
<tr>
<th>Trapped protein</th>
<th>Function</th>
<th>Degradation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Known substrates</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LpxC</td>
<td>Key enzyme in LPS biosynthesis</td>
<td>Yes</td>
</tr>
<tr>
<td><strong>Putative substrates</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>OmpA</td>
<td>Outer membrane protein</td>
<td>Not determined (ND)</td>
</tr>
<tr>
<td>FtsZ</td>
<td>Cell division protein</td>
<td>No (70)</td>
</tr>
<tr>
<td>ThrC</td>
<td>Threonine synthase</td>
<td>ND</td>
</tr>
<tr>
<td>PurA</td>
<td>De novo synthesis of purine nucleotides</td>
<td>ND</td>
</tr>
<tr>
<td>PspA</td>
<td>Regulator of phage shock and stress response</td>
<td>No</td>
</tr>
<tr>
<td>Rsd</td>
<td>Anti-σ factor of RpoD (σ\textsuperscript{E})</td>
<td>No</td>
</tr>
<tr>
<td>AroG</td>
<td>Biosynthesis of 3-deoxy-D-arabino-heptulosonate 7-phosphate</td>
<td>No</td>
</tr>
<tr>
<td>Add</td>
<td>Deamination of adenosine</td>
<td>No</td>
</tr>
<tr>
<td>YeiE</td>
<td>Putative transcription activator</td>
<td>No</td>
</tr>
<tr>
<td>HisG</td>
<td>Biosynthesis of histidine</td>
<td>No</td>
</tr>
<tr>
<td>DadA</td>
<td>Oxidative deamination of d-amino acids</td>
<td>Yes</td>
</tr>
<tr>
<td>IscS</td>
<td>Sulfatation of molecules</td>
<td>Yes</td>
</tr>
<tr>
<td>YfgM</td>
<td>Unknown function</td>
<td>Yes (growth phase-dependent)</td>
</tr>
<tr>
<td>FdoH</td>
<td>Adaptation to anaerobic conditions</td>
<td>Yes (oxygen-dependent)</td>
</tr>
</tbody>
</table>

these proteins. Because degradation of many protease substrates depends on the actual growth conditions, stability of the putative FtsH substrates was assayed by \textit{in vivo} degradation experiments at different time points along a growth curve of \textit{E. coli} at 37 and 20 °C. PspA, Rsd, HisG, Add, AroG, and YeIE were stable under all tested conditions (Fig. 4). Consistent with this, PspA has recently been shown not to be an FtsH substrate (42). Rsd, the anti-σ factor of the housekeeping σ factor RpoD, was also stable after a sudden shift from stationary phase to log phase, when inhibition of RpoD is not needed anymore (data not shown).

Validation of Four New FtsH Substrates—In contrast to the six proteins that did not seem to be prone to proteolytic control, the cytosolic protein IscS was subject to proteolysis (Fig. 5A). In an \textit{E. coli} W3110 (WT) strain, IscS decayed in all growth phases with half-lives of about 40 min. IscS is an FtsH substrate as it was stabilized in the ΔftsH background.

Another novel FtsH substrate is DadA, which is an inner membrane protein able to deaminate d-amino acids. Like IscS, DadA was degraded in all growth phases but with shorter half-lives around 25 min (Fig. 5B). Stabilization in the ΔftsH strain indicated FtsH-dependent degradation of DadA.

FdoH and YfgM are also inner membrane proteins, which are directed to proteolysis. FdoH is part of the formate dehydrogenase complex FDH-O that is responsible for the adaptation to a sudden shift from aerobic to anaerobic conditions. The protein was slowly degraded with half-lives of about 70 min in the early, middle, and late logarithmic phase (Fig. 6A). Turnover increased significantly in the stationary phase. Here, FdoH was degraded with a half-life of 15 min. Slow degradation of FdoH in stationary phase cultures of ΔftsH and Δlon strains suggested an involvement of both proteases (Fig. 6B). To address whether degradation of FdoH was affected by the availability of oxygen, stationary overnight cultures were split into two new cultures and subjected to either aerobic and anaerobic conditions (Fig. 6C). In an aerated shaken culture, FdoH was degraded with a half-life of 15 min. In the absence of oxygen, however, FdoH was stable indicating an important role of O\textsubscript{2} for regulation of FdoH proteolysis. Consistent with these findings under two extreme situations, intermediate oxygen levels correlated with intermediate FdoH stabilities (data not shown).

A general decrease in FtsH activity under oxygen-limited conditions can be excluded because the YfgM protein was degraded by FtsH under both aerobic and anaerobic conditions (data not shown).

As the Y designation indicates, the exact function of the FtsH substrate YfgM is unknown. Similar to FdoH, YfgM was poorly degraded during exponential growth and showed the shortest half-lives in stationary phase (t\textsubscript{1/2} ≈ 10 min; Fig. 7A). Degradation of YfgM was mediated by FtsH as the protein was stabilized in all growth phases in the ΔftsH strain (Fig. 7B; note that the ΔftsH mutant reaches lower optical densities in stationary phase than the WT strain). Moreover, turnover of YfgM was influenced by osmotic conditions, because an osmotic shock with 15% sucrose (v/v) induced a 4-fold faster degradation in the exponential phase (Fig. 7C).

Phenotypes Caused by YfgM Overproduction—To approach a possible biological function of YfgM, we analyzed the effects of constitutive YfgM expression and observed several striking phenotypes. For example, elevated amounts of YfgM led to a drastic defect in cell division resulting in filamentous cells (Fig. 8A). The cells showed an elongated lag phase and a much earlier entry into the stationary phase compared with cells without constitutive YfgM expression (Fig. 8B). Moreover, the resistance against acidic stress was affected by YfgM. Overproduction of the protein decreased survival after an acidic shock to a pH of 2.4 about 100 times (Fig. 8C).
To extend our knowledge on the physiological functions of FtsH, the only essential protease in *E. coli*, we established a substrate trapping approach based on an ATPase-competent but protease-deficient FtsH variant. Differential proteomics of protein preparations associated with FtsHWT and FtsHtrap revealed four proteins that were authentic substrates of the *E. coli* FtsH protease. This expands the collection of known targets from 11 to 15 (Fig. 9). Compared with other proteases, this seems like a limited number. Many more substrates have been reported for ClpXP (31, 43) and the Lon protease (44). Nonetheless, it is unlikely that the number of undiscovered FtsH substrates is going to increase substantially. The previously reported poor unfoldase activity of the protease (45) might severely restrict the repertoire of proteins susceptible to degradation by FtsH.

Among the newly identified FtsH substrates were two that have also been trapped with ClpXP, namely IscS and DadA (31).
Fusion of the 11 N-terminal amino acids of IscS to a stable reporter protein rendered it unstable in vitro with a half-life of 13 min suggesting that the N-terminal end of IscS carries a recognition motif for the ClpX ATPase. DadA was proposed to carry a similar N-terminal motif. It is quite common that bacterial proteins are subject to proteolysis by several proteases (19). How and when they are directed to one or the other protease is unknown. IscS is the only newly identified FtsH target (19). How and when they are directed to one or the other protease is unknown. IscS is the only newly identified FtsH target (19).

Because of its unique location in the cytoplasmic membrane, FtsH is well suited for the quality control and regulated proteolysis of membrane proteins (15). We identified DadA as membrane-integrated FtsH substrate that was degraded in all growth phases with a moderate half-life of about 25 min. DadA has been implicated in the oxidative deamination of a broad range of D-amino acids into their corresponding ketoacid (48). Bacterial growth on D-amino acids should only be allowed when these non-proteinogenic amino acids are abundant. Otherwise, DadA would deplete the pool of certain D-amino acids required as building blocks for peptidoglycan biosynthesis, in particular in stationary phase when D-amino acids play a major role in cell wall remodeling (49). This suggests that either the activity or the amount of DadA in the cell needs to be under control. The flavin-dependent enzyme is predicted to form a heterodimeric complex with an unidentified partner protein (50). As we expressed epitope-tagged DadA to facilitate its immunodetection, it is possible that DadA is directed to proteolysis whenever it is not bound to its partner protein. Similar turnover in the absence of interaction partners is known for other membrane substrates like PspC, F0,6, and SecY (40, 51, 52).

The final two novel FtsH substrates were degraded in a strictly condition-dependent manner. To our knowledge, this is the first report of growth phase-regulated proteolysis of membrane-bound FtsH substrates. FdoH is likely degraded by FtsH and the Lon protease, as it has been described for SoxS (19, 20). FdoH is a subunit of one of two formate dehydrogenases (FDH) in E. coli. FDH enzymes catalyze the proton-translocating oxidation of formate at the expense of nitrate reduction to nitrite. FDH-N, the more effective enzyme, is induced by nitrate (53, 54). FDH-O, consisting of FdoG, FdoH, and FdoI, is constitutively expressed and only slightly induced by nitrate. This enzyme complex permits adaptation to a shift from aerobicism to anaerobiosis until a sufficient level of the inducible FDH-N pathway is reached (55–58). Assuming that FdoH might be stabilized in cells challenged with sudden anaerobiosis, we indeed found that the exposure of a stationary overnight culture to oxygen-limited conditions completely prevented proteolysis of FdoH. When growing cultures reach stationary phase, bacteria are adapted to oxygen deprivation by synthesis of FDH-N. In that case, FdoH was removed from the cell probably to avoid competition between FDH-N and the much less effective FDH-O complex.

YfgM has been reported to interact with PpiD and RcsB (59, 60). Interestingly, both proteins reside in separate compartments of the cell. PpiD is a periplasmic chaperone (61) suggesting that YfgM might be involved in the extracytoplasmic stress response. RcsB as interaction partner suggests that YfgM is involved in the general stress response. RcsB is the response regulator of the RCS phosphorelay system. Phosphorylated RcsB induces the expression of genes to survive an acidic or osmotic shock, to adapt to stationary phase, and to induce capsule biosynthesis (37, 62–64). In stationary phase, RcsB activates expression of the small RNA RprA, which promotes translation of the rpoS mRNA leading to increased amounts of RpoS ensuring adaptation to starvation (65). Based on the interaction of YfgM with RcsB, we speculated that it might act as an

2 The abbreviation used is: FDH, formate dehydrogenase.
inhibitor of the RcsB pathway. Fully consistent with a functional link between RcsB and YfgM, an osmotic shock induced the RCS phosphorelay system (64) as well as a faster degradation of YfgM (Fig. 7C). As one might expect for an inhibitor of a stress response pathway, an yfgM deletion strain did not reveal any obvious phenotypic defects (data not shown). In contrast, elevated levels of YfgM drastically decreased the acid resistance (Fig. 8C) much like the lack of RcsB (37). Our findings might explain why YfgM is proteolytically removed from the cell upon entry into stationary phase and under certain stress conditions to release the response regulator RcsB, which activates expression of RcsB-dependent genes.

The proteins degraded by FtsH are surprisingly diverse in their cellular localization, topology, and biological function (Fig. 9). It is unlikely that they are recognized and degraded by a unifying concept. In fact, individual principles seem to apply for different substrates. Although degradation of LpxC depends on conserved non-polar residues in the C-terminal tail (25), the mechanism of KdtA degradation, another FtsH substrate acting in the very same biosynthesis pathway as LpxC, is different and still unknown (16). Proteolysis follows another route for the entry into stationary phase and under certain stress conditions to release the response regulator RcsB, which activates expression of RcsB-dependent genes.

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Heat shock sigma factor RpoH, which bears internal recognition sites and requires the contribution of chaperones for degradation (66). Misfolded membrane proteins destined for degradation are recognized via exposed N or C termini (67). Intriguingly, the newly discovered FtsH substrates YfgM and FdoH differ entirely in their topology. Both span the cytoplasmic membrane by one transmembrane helix, but YfgM contains a short N terminus (20 amino acids) in the cytoplasm and more than 200 amino acids in the periplasm (60), whereas more than 250 N-terminal amino acids of FdoH reside in the cytoplasm and 20 C-terminal amino acids are exposed to the periplasm (68). Differences in topology and the fact that FdoH but not YfgM was stabilized under anaerobic conditions suggest that they are degraded by unrelated pathways.

Diverse recognition mechanisms for FtsH substrates are contrasted by more unifying concepts in the case of other proteases. Lon prefers degrons rich in aromatic and hydrophobic residues (68). Proteolysis mediated by ClpXP tends to use N- or C-terminal motifs that can be divided in five distinct classes (31). Many ClpAP substrates follow the N-end rule with N-terminal Phe, Leu, Trp, or Tyr residues (69). The fact that the known FtsH substrates share no obvious structural features emphasizes the need for unbiased global strategies to identify new substrates. Our trapping approach has proven successful to elucidate previously unknown substrates and biological functions of FtsH. Exploiting the FtsHtrap protein as bait under different growth conditions might help reveal even more substrates of this versatile protease.

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