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Citation

As Published
http://dx.doi.org/10.1016/j.jmb.2010.09.008

Publisher
Elsevier

Version
Author's final manuscript

Accessed
Mon Dec 31 05:38:36 EST 2018

Citable Link
http://hdl.handle.net/1721.1/98873

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Multiple sequence signals direct recognition and degradation of protein substrates by the AAA+ protease HslUV

Shankar Sundar1, Kathleen E. McGinness1,4, Tania A. Baker1,2, and Robert T. Sauer1,3
1 Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139
2 Howard Hughes Medical Institute, Massachusetts Institute of Technology, Cambridge, MA 02139

Abstract

Proteolysis is important for protein quality control and for the proper regulation of many intracellular processes in prokaryotes and eukaryotes. Discerning substrates from other cellular proteins is a key aspect of proteolytic function. The E. coli HslUV protease is a member of a major family of ATP-dependent AAA+ degradation machines. HslU hexamers recognize and unfold native protein substrates and then translocate the polypeptide into the degradation chamber of the HslV peptidase. Although a wealth of structural information is available for this system, relatively little is known about mechanisms of substrate recognition. Here, we demonstrate that mutations in the unstructured N-terminal and C-terminal sequences of two model substrates alter HslUV recognition and degradation kinetics, including changes in $V_{\text{max}}$. By introducing N- or C-terminal sequences that serve as recognition sites for specific peptide-binding proteins, we also show that blocking either terminus of the substrate interferes with HslUV degradation, with synergistic effects when both termini are obstructed. These results support a model in which one terminus of the substrate is tethered to the protease and the other terminus is engaged by the translocation/unfolding machinery in the HslU pore. Thus, degradation appears to consist of discrete steps, which involve the interaction of different terminal sequence signals in the substrate with different receptor sites in the HslUV protease.

Introduction

AAA+ proteases are responsible for quality-control surveillance of the proteome and for regulating key intracellular processes in all kingdoms of life.1,2 These ATP-fueled molecular machines recognize specific substrates, forcibly denature these proteins, and then spool the denatured polypeptide in a processive fashion through an axial channel and into a sequestered chamber for degradation.3 In the HslUV protease, for example, ring hexamers of HslU perform the recognition, unfolding, and translocation functions, whereas the double-ring HslV dodecamer degrades polypeptides that are translocated into its proteolytic chamber.4–7 Recent studies have shown that HslUV is an extremely powerful protein unfoldase when degrading proteins in the N-terminal to C-terminal direction but has modest denaturation activity when degradation initiates at the C-terminus of a substrate.8

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For all proteases, substrate recognition is critical in ensuring that the correct molecules are degraded. Exposed peptide sequences in specific substrates, called degrons or degradation tags, typically serve as recognition signals for bacterial AAA+ proteases. Peptide sequences can also target proteins for HslUV degradation, but relatively little is known about the underlying recognition events. Based on studies with related AAA+ proteases, it is clear that some degrons are bound by pore loops in the central translocation channel of the hexameric unfoldase, allowing these enzymes to grasp the attached substrate and to begin translocation-mediated unfolding. This mechanism is also likely to be important for HslUV degradation, because mutations in the highly conserved GYVG pore loop of HslU diminish or block degradation of specific substrates. Other degradation signals tether substrates to other parts of the protease, raising the effective concentration of the substrate relative to the enzyme and facilitating recognition of a weak degron elsewhere in the substrate. Indeed, there is growing evidence in both natural and engineered substrates that the existence of multiple degradation signals can play important roles in determining how well a protein is recognized and degraded by AAA+ proteases.

Although a handful of substrates for HslUV have been identified, relatively little is known about the ways in which sequence signals in these proteins influence degradation. To explore this issue, we employ two model substrates, the Arc repressor of phage P22 and the N-terminal domain of phage λ cI repressor. In solution, both proteins unfold in seconds but refold in milliseconds and thus maintain metastable structures. As a consequence, unfolding of these substrates is not a serious impediment to HslUV degradation. We find that mutations in the unstructured N-terminal or C-terminal sequences of both proteins alter the steady-state kinetics of HslUV proteolysis, including changes in the maximal rate of degradation. By introducing N- or C-terminal sequences that serve as recognition sites for specific peptide-binding proteins, we also demonstrate that blocking either substrate terminus by protein binding interferes with HslUV degradation. Our results support a model in which one terminus of the substrate is tethered to the protease and the other terminus is engaged by the translocation/unfolding machinery in the HslU pore. This model explains how mutations in either N- or C-terminal sequence can affect the maximal degradation rate and suggests that substrate recognition by HslUV consists of discrete steps, with the efficiency of degradation ultimately depending on the interplay of multiple sequence signals in the substrate with appropriate receptor sites in the protease.

Results

Effects of terminal λcIN sequences on HslUV degradation

By screening a library in which five unstructured C-terminal residues of the N-terminal domain of λ cI repressor (residues 1–102; λcIN) had been randomized, Parsell et al. identified variants that were degraded rapidly in vivo. To determine if some of these proteins were substrates for Escherichia coli HslUV, we recloned the parental domain and several variants to add an N-terminal MGS2H6S3H tag (called ext1), purified these proteins, and assayed HslUV degradation by SDS-PAGE. We identified one variant in which the C-terminal sequence was changed from RSEYE to ISVTL (ext1-λcIN-ISVTL) that HslUV degraded faster than the parental protein (ext1-λcIN-RSEYE; Fig. 1A), suggesting that the altered C-terminal residues of this mutant make it a better substrate.

Although substrate degradation by HslUV is a multi-step reaction, simple Michaelis-Menten kinetics are observed, indicating that the overall reaction can be modeled by substrate binding and dissociation steps, and by a rate-limiting enzymatic step (kdeg), which could correspond to substrate engagement, unfolding, or translocation. Because degradation signals usually affect protease binding, we expected that the ISVTL sequence would reduce K_M for HslUV degradation when compared to degradation of the wild-type RSEYE.
sequence. Indeed, when we determined steady-state kinetic parameters for degradation of $^{35}$S-labeled proteins, a slight reduction in $K_M$ was observed (Fig. 1B; Table 1). Surprisingly, however, the major effect on degradation of the ISVTL substrate was a ~2-fold increase in $V_{\text{max}}$ (Fig. 1B; Table 1).

For inhibition experiments presented below, we changed the N-terminal residue of mature $\lambda cI^N$ from serine to leucine and/or changed the C-terminal sequence from RSEYE to RSYYF. Determination of the kinetic parameters for HslUV degradation of the S1L$\lambda cI^N$-RSYYF and S1L$\lambda cI^N$-RSEYE variants revealed a ~2-fold difference in $V_{\text{max}}$ and ~3-fold difference in $K_M$ (Fig. 1C; Table 1). Because this pair of substrates differs only at the final and antepenultimate amino acids, these C-terminal residues apparently affect both HslUV binding and the maximum velocity of degradation. $\lambda cI^N$ substrates with the same C-terminal sequences but different N-termini sequences were degraded by HslUV with similar kinetic parameters (Table 1).

We used another $\lambda cI^N$ variant to test if dimerization affected HslUV degradation. Monomers and dimers of $\lambda cI^N$ equilibrate rapidly in solution ($K_D \approx 300 \mu M$), but the I84S mutation reduces dimerization to undetectable levels. We introduced the I84S mutation into ext1-$\lambda cI^N$-ISVTL and determined kinetic parameters for HslUV degradation, which were within error of the parental protein (ext1-$\lambda cI^N$-ISVTL; Table 1). We conclude that $\lambda cI^N$ dimerization is not a prerequisite for HslUV degradation.

**Effects of terminal Arc sequences on degradation**

Arc repressor and variants, including those with C-terminal sequences of $\text{H}_6$KNQHD (st11 tag) and/or AANDENYALAA (ssrA tag), are substrates for the *E. coli* and *Haemophilus influenzae* HslUV enzymes. Using *E. coli* HslUV, we determined steady-state degradation parameters for Arc variants with a C-terminal ssrA tag (Arc-ssrA), the st11 and ssrA tags (Arc-st11-ssrA), or st11 and a mutant ssrA tag in which the terminal AA sequence was replaced by DD (Arc-st11-ssrA$^{DD}$) (Fig. 2; Table 1). $K_M$ for degradation of these substrates varied over a ~2-fold range (Table 1; Fig. 2). Importantly, HslUV degraded Arc-ssrA and Arc-st11-ssrA with $V_{\text{max}}$ values of 4.9 and 12 min$^{-1}$ enz$^{-1}$, respectively. Thus, inserting the st11 tag before the ssrA tag increased the maximum degradation rate more than 2-fold. Changing the C-terminal residues of Arc-st11-ssrA from AA to DD reduced $V_{\text{max}}$ from 12 to 7 min$^{-1}$ enz$^{-1}$. Hence, the C-terminal sequences of both $\lambda cI^N$ and Arc substrates influence binding as well as the maximal rate of HslUV degradation.

Previous studies demonstrated that N-terminal residues of Arc were important for HslUV degradation. Consistently, we found that addition of an 18-residue N-terminal extension (ext2; LA$_3$SGAG$_2$SEG$_2$TSGAT) to Arc-ssrA reduced $V_{\text{max}}$ and increased $K_M$ (Fig. 2; Table 1). Interestingly, extending the C-terminal region of Arc-ssrA by insertion of the st11 sequence increased $V_{\text{max}}$, whereas extending the N-terminal region decreased $V_{\text{max}}$. Thus, degradation efficiency is not a simple function of the total number of unstructured residues at the ends of a substrate.

**Terminal sequences do not alter substrate stability**

Sequences at the termini of $\lambda cI^N$ and Arc substrates might influence the kinetics of HslUV degradation by altering protein thermodynamic stability. However, no substantial differences in the melting temperatures of different $\lambda cI^N$ or Arc substrates were observed when thermal denaturation was monitored by changes in circular-dichroism ellipticity (Table 1). These results support a model in which interactions between the terminal sequences of these substrates and HslUV are responsible for the observed changes in degradation kinetics.
Protein binding to the C-terminus of substrates slows HslUV degradation

As noted above, λcIN variants were engineered to contain a C-terminal YYF sequence, which can be bound with sub-μM affinity by the PDZ domain of E. coli DegS. Saturating concentrations of the DegS PDZ domain inhibited HslUV degradation of S1L λcIN-RSYYF to ~10% of the uninhibited rate but inhibited degradation of the S1L λcIN-RSEYE control protein only marginally (Fig. 3A). Thus, inhibition by the PDZ domain is specific and depends on the C-terminal sequence of the substrate.

The E. coli SspB protein binds to the AANDENY segment of the ssrA tag with sub-μM affinity. At saturating concentrations, SspB slowed HslUV degradation of M1L Arc-ssrA to ~15% of the uninhibited value (Fig. 3B). SspB addition had a much smaller effect on degradation of an otherwise identical protein with a mutant ssrA N3A tag that binds SspB poorly. Again, these results show that SspB inhibits HslUV degradation in a substrate-specific fashion. Thus, blockade of the C-terminal sequences of λcIN and Arc substrates by protein binding prevents efficient HslUV degradation.

ClpS binding to the N-terminus of substrates inhibits HslUV degradation

E. coli ClpS binds with μM affinity to proteins with an N-terminal leucine, phenylalanine, tyrosine, or tryptophan but binds substantially more weakly to proteins with N-terminal methionine or other amino acids. To test if ClpS blockade of the N-terminus of λcIN or Arc influenced HslUV degradation, we engineered variants of these substrates containing N-terminal leucines. Addition of ClpS to an Arc variant with an N-terminal leucine (M1L Arc-ssrA) slowed HslUV degradation to ~20% of the uninhibited rate at saturation but did not inhibit degradation of an otherwise identical substrate with an N-terminal methionine (Fig. 4A). Thus, ClpS binding to the N-terminal leucine of M1L Arc-ssrA is responsible for slowing HslUV degradation.

We also observed strong ClpS inhibition of HslUV degradation of S1L λcIN-RSEYE and somewhat weaker inhibition of S1L λcIN-RSYYF (Fig. 4B). This difference may reflect the lower Km for HslUV degradation of the latter substrate (Table 1).

Synergistic effects of N- and C-terminal blocking

If protein binding to the N- and C-terminus of substrates inhibits HslUV degradation by independent mechanisms, then blocking both termini should produce greater inhibition than blocking just one terminus. Indeed, inhibition of HslUV degradation of M1L Arc-ssrA by the combination of SspB and ClpS was greater than inhibition by either protein alone (Fig. 5A, top). Similarly, inhibition of HslUV degradation of S1L λcIN-RSYYF was more severe in the presence of ClpS and the DegS PDZ domain than with either single protein (Fig. 5A, bottom).

Single-turnover inhibition

In principle, protein binding to the N- or C-terminal sequences of substrates could block substrate sequences required for HslUV binding or engagement. Alternatively, the protein-bound substrate could be recognized, engaged, unfolded, and translocated like the free substrate, but steady-state degradation could be slowed because of the inability of the enzyme to initiate the next cycle of degradation. The latter possibility could occur, for example, if the protein that was bound at the terminus (ClpS, SspB, or the DegS PDZ domain) had to dissociate or be enzymatically stripped in order to complete the last steps of degradation. By this model, the initial release of 35S-peptides from a substrate would occur faster than subsequent steps, and inhibition by bound protein might not be evident if enzyme were present in excess of substrate. Thus, we assayed single-turnover degradation of low concentrations of 35S-labeled substrate in the presence of excess enzyme and inhibitor.
Under these conditions, specific inhibition by ClpS, SspB, and the DegS PDZ domain was still observed (Fig. 5B), suggesting that inhibition affects an early step in degradation.

**Discussion**

The simplest mechanism of targeting substrates for degradation by specific AAA+ proteases is exemplified by the ssrA-tagging system, in which a short peptide signal targets a wide variety of proteins for ClpXP or ClpAP degradation.\(^{36-37}\) It is becoming evident, however, that substrate recognition mediated by a single tag or degron is generally the exception rather than the rule. Indeed, one substrate signal often mediates binding, whereas another signal ensures engagement by the translocation machinery of the AAA+ protease.\(^3\) The results presented here show that sequences at both the N- and C-terminal ends of Arc and \(\lambda cI^{N}\) substrates influence the rate of HslUV degradation and thus support a multi-degron model of recognition.

Unfolded monomers and native dimers of Arc equilibrate rapidly in solution, but the strong dimerization constant (~10 nM) ensures that most molecules are dimers at the concentrations used for degradation studies.\(^{25,38}\) Thus, each Arc substrate has two N-terminal sequences and two C-terminal sequences that potentially could interact with HslU. By contrast, the dimerization constant of \(\lambda cI^{N}\) is substantially weaker (~300 \(\mu\)M),\(^{28}\) and a mixture of monomers and dimers are present in our degradation assays. Importantly, however, a mutation (I84S) that weakens \(\lambda cI^{N}\) dimerization >30-fold did not cause significant changes in the steady-state kinetics of \(\lambda cI^{N}\) degradation (Table 1), suggesting that HslUV recognizes monomers and dimers of \(\lambda cI^{N}\) comparably.

HslUV degradation of Arc variants was initially suggested to depend exclusively on C-terminal sequences and was subsequently proposed to depend completely on N-terminal sequences.\(^{10-11}\) Our present studies resolve this apparent conflict, as mutational and inhibitor experiments demonstrate that both termini of Arc substrates need to be recognized for efficient HslUV degradation. Similar results with \(\lambda cI^{N}\) variants suggest that multi-degron recognition may be common for HslUV substrates. The terminal sequences of both Arc and \(\lambda cI^{N}\) variants are unstructured in the free proteins and could mediate binding/engagement by the translocation machinery of the HslU pore or tethering to an independent receptor site elsewhere in the enzyme. At present, we do not know which termini serve which function or even if one specific terminus always binds the pore while the other always serves a tethering role, but the results presented here should allow future experiments to address this question.

Fig. 6 shows a model with three types of HslUV-substrate complexes and provides a framework for understanding how sequence changes at either terminus of a substrate can alter \(K_M\) and \(V_{\text{max}}\) for degradation. In complex P, one terminus of the substrate binds to the enzyme pore. In complex T, the other terminus of the substrate binds to a distinct tethering site. In complex TP, both termini of the substrate bind to their respective sites in HslUV. Only complexes P and TP are proteolytically active, because binding to the pore is required for degradation. The distribution of these species depends on the equilibrium constants for binding the tethering site in a bimolecular reaction (\(K_1\)), binding the pore in a bimolecular reaction (\(K_2\)), binding the pore in a unimolecular reaction (\(K_3\)), and binding the tethering site in a unimolecular reaction (\(K_4\)). Because \(K_1K_3 = K_2K_4\), specifying three of these constants determines the fourth constant. Thus, the apparent \(K_M\) and the fraction of active enzymes at substrate saturation (\(f_{\text{act}}\)) can be expressed as a function of just \(K_1\), \(K_2\), and \(K_3\) (Fig. 6). In principle, changing the sequence at either terminus could alter \(K_M\) and the maximal rate of degradation (\(f_{\text{act}}k_{\text{deg}}\)). In practice, however, substantial sequence-dependent changes in either kinetic parameter would only be observed if the T complex is present in excess of the P and TP complexes, which requires stronger bimolecular binding to the tethering site than...
to the pore site ($K_1 < K_2$) and a $K_3$ value > 1. Under these conditions, mutations at either substrate terminus could alter both $K_M$ and $V_{max}$ by affecting binding to one of the enzyme sites (altering $K_1$ or $K_2$) and might also change these parameters by altering the length or flexibility of the terminal sequences (affecting $K_3$). Sequence changes at the substrate terminus that binds the pore of HslUV could also directly affect the efficiency of engagement by the translocation machinery and thus alter $V_{max}$ by changing $k_{deg}$ as well as $f_{act}$. Studies of adaptor-mediated delivery of substrates to the ClpXP protease provide general precedents for changing the steady-state kinetics of degradation via alterations in tethering sequences, pore-contact sequences, and the flexibility and geometry of intervening domains.21,39

From a biological perspective, multi-degron degradation permits combinatorial control of proteolysis through masking of one or both degrons in a substrate, as demonstrated by our observation that protein binding to the N- and C-terminal sequences of Arc and $\lambda_{cI}^N$ substrates inhibits HslUV degradation. Such effects can be readily rationalized in terms of the model of Fig. 6, as substrates with proteins bound to their terminal sequences would be expected to have different $K_1$, $K_2$, and/or $K_3$ values. Many proteins are multimeric, and it is straightforward to envision regulatory strategies in which two degrons are properly displayed only in a monomer or only in a multimer, allowing just one species to be targeted for degradation.9 Degrons could also be masked by a protein’s native structure and only be revealed when the protein unfolds at high temperatures. In this regard, we note that HslUV is a heat-shock protease and that degradation signals in the interior of protein sequences have been shown to act as recognition signals for other AAA+ proteases,19,22,40,41

AAA+ proteases are allosteric machines that undergo continual cycles of ATP-powered conformational changes, even in the absence of substrate. As a consequence, it may be more difficult for the translocation machinery to bind and engage a degron in a single concerted step, but easier if the substrate is first tethered to the protease and engagement occurs subsequently. The latter situation could be viewed analogously to mid-air refueling, in which the speeds and general orientations of two airplanes are matched in one step and the fuel-transfer machinery is engaged in a subsequent step. We propose that HslUV carries out degradation in a similar multistep manner.

Materials & Methods

Protein expression and purification

Genes encoding protein substrates were constructed by standard methods of molecular biology using the polymerase-chain reaction and/or site-directed mutagenesis. $\lambda_{cI}^N$ substrates contained varied N-terminal sequences, a common core corresponding to residues 2–97 of $\lambda$ ci repressor, and C-terminal sequences of RSEYE (residues 98–102 of $\lambda$ ci repressor), RSYYF, or ISVTL.

The initiator methionine of wild-type $\lambda$ repressor is removed post-translationally,42 leaving Ser1 as the N-terminal residue. Variants designated ext1-$\lambda_{cI}^N$ had an additional N-terminal extension (MG5H6S3H3; glycine at N-terminus after processing of initiator methionine), which was derived from the pACYCDuet-1 expression vector (Novagen). Variants designated $S1L\lambda_{cI}^N$ were initially cloned, expressed, and purified as fusions to an N-terminal H6-tagged SUMO domain in a pET23b vector (Novagen), and the fusion protein was then purified and cleaved with Ulp1 protease to generate the mature substrate with Leu1 at the N-terminus.43 Arc substrates contained variable N-terminal sequences, a common core consisting of residues 2–53 of P22 Arc repressor, and C-terminal sequences including the st11 sequence (H6KNQHD), ssrA tag (AANDENYALAA), ssrA$^{DD}$ tag (AANDENYAL$^{DD}$), or ssrA$^{N3A}$ tag (AAADENYALAA). The wild-type N-terminus of
Arc variants were expressed as H6-SUMO fusions from pET23b, purified, and cleaved to generate Leu1 at the N-terminus. Substrates designated ext2-Arc contained the N-terminal extension LA3SGAG2SEG2TSGAT and were also purified as SUMO fusions and processed by Ulp1 cleavage.

H6-tagged variants of E. coli HslU6 and HslV12 were purified essentially as described (Burton et al., 2005), except buffer B (pH 8.0) contained 50 mM NaHPO4, 300 mM NaCl, and 250 mM imidazole, and buffer C (pH 7.5) contained 20 mM Tris-HCl, 100 mM NaCl, 1 mM EDTA, and 10% (v/v) glycerol. Pooled HslU6 or HslV12 fractions after Ni2+-NTA chromatography were chromatographed on a Sephacryl-300HR26/60 gel filtration column (GE Healthcare) and then on an HR16/10 Q-Sepharose column (GE Healthcare), developed with a gradient from 0.1 M to 1 M NaCl in buffer C. Appropriate fractions were pooled, concentrated, and exchanged into buffer B using Amicon Ultra-15 centrifugation filters.

Arc and λcIN proteins were expressed in E. coli strain X90 (λDE3). Cells were grown at 37 °C to an OD600 of ~0.8, and shifted to room temperature. Expression was induced by the addition of 1 mM IPTG, and cells were harvested 4 h later, lysed by sonication, and cleared lysates were applied to a Ni2+-NTA column as described for the HslU6 and HslV12 purifications. The Arc-st11-ssrA, Arc-st11-ssrA-DD, ext1-λcIN-ISVTL and ext1-λcIN-RSEYE proteins were subjected to additional purification on a HiLoad 16/60 Superdex-100 gel-filtration column (GE Healthcare) equilibrated in buffer D (20 mM Tris (pH 7.5), 200 mM NaCl, 1 mM EDTA). Appropriate fractions were pooled and concentrated using Amicon Ultra-15 centrifugation filters. Following the Ni2+-NTA step, substrates expressed as H6-SUMO fusions were exchanged into 50 mM NaHPO4 (pH 8.0), 100 mM NaCl, and 20 mM imidazole and cleaved with Ulp1 protease (a gift from J. Davis and J. Kaplan, MIT) at 37 °C overnight. Cleaved samples were re-applied to a Ni2+-NTA column, and the flow-through fraction, which contained the desired product, was pooled and chromatographed on a HiLoad 16/60 Superdex-100 gel-filtration column (GE Healthcare) equilibrated in buffer D. Appropriate fractions were pooled and concentrated using Amicon Ultra-15 centrifugation filters. 35S-substrates were expressed and purified as described (Burton et al., 2005), with additional steps of Ulp1 cleavage, Ni2+-NTA re-purification, and S100 purification for substrates expressed as H6-SUMO fusions.

An E. coli SspB expression clone was a gift from Igor Levchenko (MIT) and an E. coli ClpS expression clone (pET23b-H6-SUMO-ClpS) was a gift from G. Román-Hernández (MIT). SspB was purified as described. ClpS was purified by the protocol used for all SUMO-fusion proteins. The purified E. coli DegS PDZ domain was a gift from Jungsan Sohn (MIT). Protein concentrations were determined by absorbance at 280 nm using extinction coefficients calculated from the amino-acid sequence.

**Degradation assays**

For degradation assays monitored by SDS-PAGE, substrates (10 μM) were incubated at 37 °C for different times with 300 nM E. coli HslU6, 800 nM E. coli HslV12, and an ATP regeneration system (5 mM ATP, 16 mM creatine phosphate, 10 μg/mL creatine kinase). Steady-state HslUV degradation of 35S-labeled proteins at 37 °C was carried out as described, using 100 nM HslU6, 300 nM HslV12, and the ATP regeneration system. Aliquots were quenched at appropriate time points by adding ice-cold trichloroacetic acid (TCA) to a final concentration of 10% (w/v) and were separated into pellet and supernatant fractions by centrifugation. Radioactivity in the acid-soluble fraction was used as a measure of degradation. For experiments probing the inhibitory effects of SspB, ClpS, or the DegS PDZ domain, each protein was mixed with 35S-labeled substrate for 5 min at 37 °C before addition of 500 nM HslU6, 1.5 nM HslV12, and the ATP regeneration mix. At different times, degradation was assayed by acid-soluble radioactivity as described above. For
degradation of $^{35}$S-labeled proteins under single turnover conditions, each reaction contained 2 μM substrate, 5 μM HslU$_{6}$, 6 μM HslV$_{12}$, and the ATP regeneration system, and degradation was assayed as described above for steady-state kinetic experiments.

**Thermal denaturation**

Denaturation experiments were monitored by changes in circular-dichroism ellipticity at 222 nm using an AVIV Model 60DS spectrometer. Proteins (2 μM) in 10 mM KPO$_{4}$ (pH 6.8), 200 mM NaCl were heated from 25 to 95 °C in 2 °C steps, the sample was allowed to equilibrate for 1 min at each temperature, and the ellipticity was averaged for 30 s and recorded. Melting data were fit to a two-state model in which the intercepts and slopes of the native and denatured baselines, $T_M$, and $\Delta H_U$ were determined by a non-linear least squares fitting protocol.

**Acknowledgments**

We thank J. Davis, J. Kaplan, I. Levchenko, G. Román-Hernández, and J. Sohn for materials and helpful discussion. T.A.B. is an employee of the Howard Hughes Medical Institute. Supported by NIH grant AI-16892.

**References**


Figure 1.
C-terminal \( \lambda cI^N \) sequences alter HslUV degradation. (A) Degradation of \( \lambda cI^N \) variants (10 \( \mu \)M) bearing RSEYE or ISVTL C-terminal sequences by 300 nM HslU\(_6\), 800 nM HslV\(_{12}\) was analyzed by SDS-PAGE. (B, C) Rates of steady-state degradation of different concentrations of \( ^{35}S-\lambda cI^N \) variants by 100 nM HslU\(_6\), 300 nM HslV\(_{12}\) were determined by assaying acid-soluble radioactivity. Lines represent non-linear-least-squares fits to the Michaelis-Menten equation: rate = \( V_{max} \cdot [S]/([S]+K_M) \). Kinetic parameters are listed in Table 1.
Figure 2.
C- and N-terminal sequences of Arc substrates affect HslUV degradation. Steady-state rates of HslUV degradation of $^{35}$S-Arc variants were determined as described in the Fig. 1 legend. Lines are fits to the Michaelis-Menten equation; kinetic parameters are listed in Table 1.
Figure 3.
Occluding the C-terminus of λcIN and Arc substrates inhibits HslUV degradation. (A) Degradation of 35S-labeled λcIN substrates (50 μM) by 0.5 μM HslU6, 1.5 μM HslV12 was measured at different concentrations of the DegS PDZ domain, which binds strongly to the C-terminal tripeptide YYF but weakly to EYE. Rates are expressed as a percentage of the rate with no PDZ domain. (B) Degradation of 35S-labeled Arc variants (4 μM) by 0.5 μM HslU6, 1.5 μM HslV12 was measured at different concentrations of SspB, which binds strongly to the wild-type ssrA tag but weakly to the ssrA N3A mutant. Rates are expressed as a percentage of the rate with no SspB.
Figure 4.
ClpS binding to the N-terminus of Arc or λclN substrates slows HslUV degradation. (A) Proteolysis of 35S-labeled Arc variants (4 μM) by 0.5 μM HslU6, 1.5 μM HslV12 was measured at different concentrations of ClpS, which binds strongly to the N-terminal leucine of M1L-Arc-ssrA but weakly to the N-terminal methionine of Arc-ssrA. (B) ClpS inhibits HslUV (0.5 μM HslU6, 1.5 μM HslV12) degradation of λclN substrates (50 μM) with N-terminal leucines (S1L-λclN-RSYYF – open circles; S1L-λclN-RSEYE – closed circles) more efficiently than variants with an N-terminal serine (λclN-RSYYF – open squares) or glycine (ext1-λclN-RSEYE – closed squares).
Figure 5.
Combinatorial and single-turnover inhibition. (A) (top) A combination of SspB and ClpS inhibited degradation of $^{35}$S-M1L-Arc-ssrA (15 μM) by 0.5 μM HslU$_6$, 1.5 μM HslV$_{12}$ to a greater extent than either individual protein. (bottom) A combination of the DegS PDZ domain and ClpS also inhibited degradation of $^{35}$S-S1L-λcl$_{N}$-RSYYF (50 μM) by 0.5 μM HslU$_6$, 1.5 μM HslV$_{12}$ more than either single protein alone. (B) Degradation of different $^{35}$S-labeled substrates (2 μM) by 5 μM HslU$_6$, 6 μM HslV$_{12}$ was assayed in the presence the indicated concentrations of SspB, ClpS, or the DegS PDZ domain.
Figure 6.
Model of HslUV recognition of a substrate (S) with degrons at each terminus. One degron (shown as a triangle) binds to a tethering site on the HslUV enzyme (E). The other degron (shown as a circle) binds to a site in the translocation pore of HslU. Because binding to the pore is a prerequisite for degradation, the enzyme-substrate complexes marked P and TP are proteolytically active but the T complex is inactive. $K_1 ([E][S]/[T])$, $K_2 ([E][S]/[P])$, $K_3 ([T]/[TP])$, and $K_4 ([P]/[TP])$ are equilibrium dissociation constants. Note that $K_1 K_3 = K_2 K_4$. If the rate of substrate dissociation is fast compared to $k_{\text{deg}}$, then the apparent $K_M ([S]$ at half maximal velocity) is $1/(1/K_1+1/K_2+1/(K_1 K_3))$. At substrate saturation, the fraction of active enzymes ($f_{\text{act}}) = ([P]+[TP])/([T]+[P]+[TP]) = (1/K_2+1/(K_1 K_3))/((1/K_1+1/K_2+1/(K_1 K_3))$.

$V_{\text{max}}/[E_{\text{total}}]$ equals $f_{\text{act}} k_{\text{deg}}$. The $K_3-k_{\text{deg}}$ pathway of degradation corresponds to single-degron recognition.
Table 1

Properties of λcIN and Arc substrates.

<table>
<thead>
<tr>
<th>substrates</th>
<th>$V_{\text{max}}$ ($\text{min}^{-1}$)</th>
<th>$K_M$ (μM)</th>
<th>$V_{\text{max}}/K_M$ (μM$^{-1}$)min$^{-1}$</th>
<th>$T_m$ (°C)</th>
<th>SpB</th>
<th>DegS PDZ</th>
<th>ClpS</th>
</tr>
</thead>
<tbody>
<tr>
<td>ext1-λcIN-RSEYE</td>
<td>4.3 ± 0.1</td>
<td>120 ± 19</td>
<td>0.04</td>
<td>56.7</td>
<td>no</td>
<td>no</td>
<td>no</td>
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<tr>
<td>ext1-λcIN-ISVTL</td>
<td>9.9 ± 1.1</td>
<td>89 ± 12</td>
<td>0.11</td>
<td>56.1</td>
<td>no</td>
<td>no</td>
<td>no</td>
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<tr>
<td>ext1-λcIN(B4S)ISVTL</td>
<td>9.9</td>
<td>79</td>
<td>0.13</td>
<td>50.5</td>
<td>no</td>
<td>no</td>
<td>no</td>
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<tr>
<td>S11-λcIN-RSEYE</td>
<td>3.5 ± 0.3</td>
<td>120 ± 24</td>
<td>0.03</td>
<td>56.5</td>
<td>no</td>
<td>no</td>
<td>yes</td>
</tr>
<tr>
<td>S11-λcIN-RSYYF</td>
<td>7.1 ± 1.0</td>
<td>40 ± 5.0</td>
<td>0.18</td>
<td>55.5</td>
<td>no</td>
<td>yes</td>
<td>yes</td>
</tr>
<tr>
<td>λcIN-RSYYF</td>
<td>5.7 ± 0.6</td>
<td>54 ± 6.7</td>
<td>0.11</td>
<td>54.5</td>
<td>no</td>
<td>yes</td>
<td>no</td>
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<tr>
<td>Arc-ssrA</td>
<td>4.9 ± 0.1</td>
<td>24 ± 1.4</td>
<td>0.20</td>
<td>58.6</td>
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<td>no</td>
<td>no</td>
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<tr>
<td>Arc-st11-ssrA</td>
<td>12 ± 1.9</td>
<td>31 ± 0.9</td>
<td>0.38</td>
<td>56.5</td>
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<tr>
<td>Arc-st11-ssrA DD</td>
<td>7.0 ± 0.3</td>
<td>51 ± 4.8</td>
<td>0.14</td>
<td>59.3</td>
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<td>no</td>
<td>no</td>
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<tr>
<td>ext2-Arc-ssrA</td>
<td>3.0 ± 0.5</td>
<td>55 ± 1.3</td>
<td>0.06</td>
<td>58.2</td>
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<td>no</td>
<td>no</td>
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<td>MIL-Arc-ssrA</td>
<td>4.7 ± 1.5</td>
<td>21 ± 4.0</td>
<td>0.22</td>
<td>56.9</td>
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<td>no</td>
<td>yes</td>
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<tr>
<td>MIL-Arc-ssrA NOA</td>
<td>5.7 ± 0.5</td>
<td>23 ± 7.7</td>
<td>0.25</td>
<td>56.3</td>
<td>no</td>
<td>no</td>
<td>yes</td>
</tr>
</tbody>
</table>

$V_{\text{max}}$ values are expressed as turnover numbers (the degradation rate at substrate saturation divided by the total enzyme concentration). $V_{\text{max}}$ and $K_M$ values are generally averages of two determinations (error estimated as $\sqrt{\frac{\sum (\text{value} - \text{mean})^2}{n}}$). Values with no error are from a single experiment.