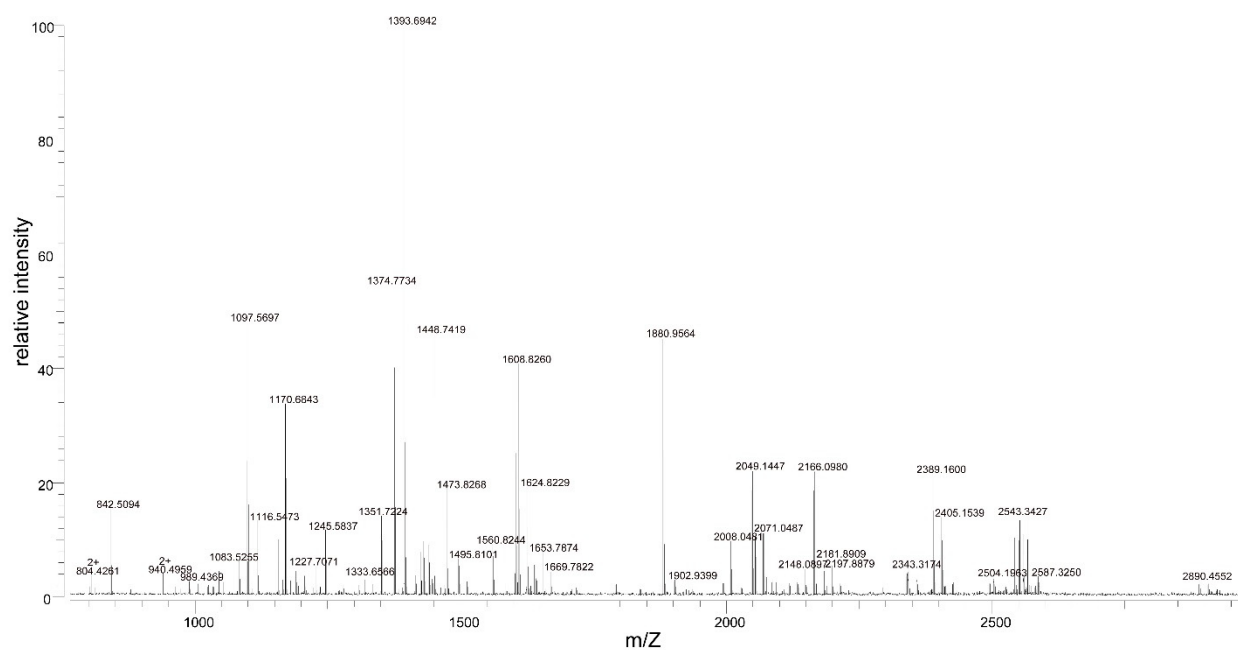


Supplementary S1. Alignment of the FtsZ amino acid sequence.

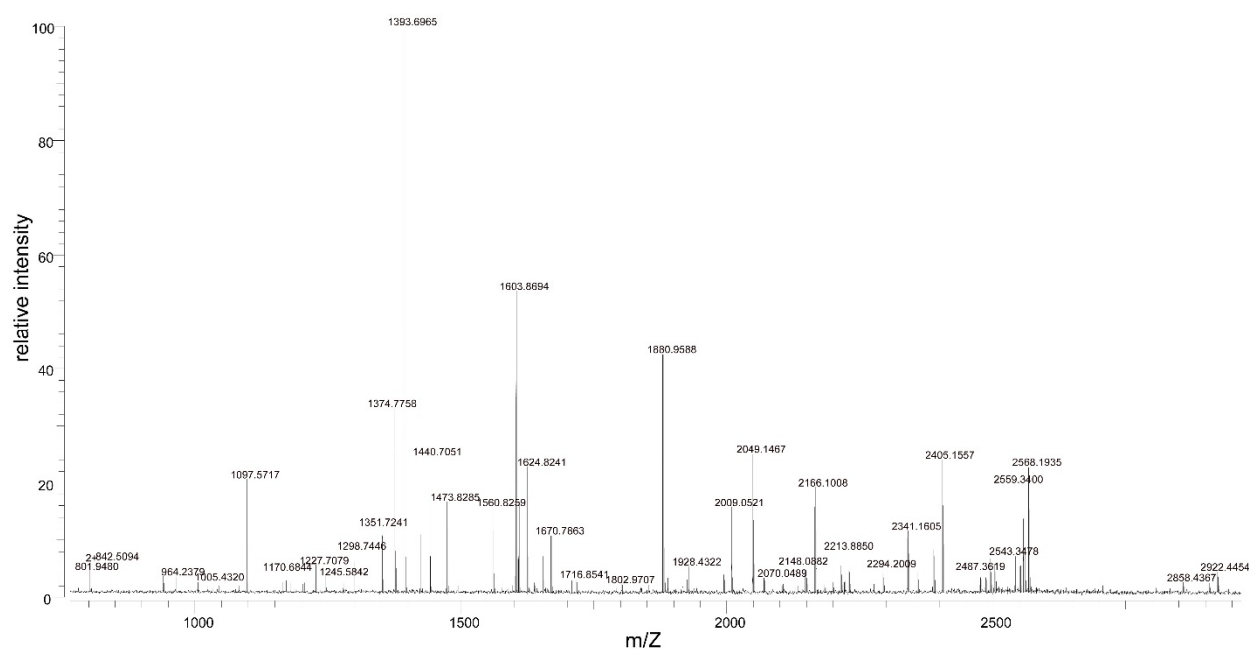
	1	10	20	30	40	50	60	70	80	90	100
S. proteanaculans	MFEPHMLTNDVYIKVIGVGGGGNAYEHMVRERIEGVFFAYNTDAAALRKTAVGQTIQIGSGITKGLGAGANPEVGRNSAEEDREALRAALDGADMY										
E. coli	MFEPHMLTNDVYIKVIGVGGGGNAYEHMVRERIEGVFFAYNTDAAALRKTAVGQTIQIGSGITKGLGAGANPEVGRNAEDRDALRAALEGADMY										
A. laidlawii	MVFGEFNDKPVYIKVIGVGGGGNAYNRHENDVRGVSVAHNTDAAALRKTAVGQTIQIGSGITKGLGAGANPEVGRNAEDRDALRAALEGADMY										
Consensus	..nfepnELt#daYIKVIGVGGGGnAY#hM!r#r!eGve%FAvNTDAAALrktavg#t.IQIGsgitKGLGAGANPe!Gr#AALEdrDaLRaalsgADMY										
	101	110	120	130	140	150	160	170	180	190	200
S. proteanaculans	FIRAGMGGGTGTGAAPVVAEVAKDLGILTVAVYTKPFNFEGKKRMFAEQGIAELSKHVDSLITIPNDKLLKVLGRGISLLDAFGAANDVYKGA VQGIAE										
E. coli	FIRAGMGGGTGTGAAPVVAEVAKDLGILTVAVYTKPFNFEGKKRMFAEQGITELSKHVDSLITIPNDKLLKVLGRGISLLDAFGAANDVYKGA VQGIAE										
A. laidlawii	FITAGMGGGTGTGAAPVVAEVAKDLGILTVAVYTKPFNFEGPLRMQAITGLEELKPNVDLTIVIPNERLFSIADRDHQLLDFAFRESOKVLRQGVQGI AE										
Consensus	FIRAGMGGGTGTGAAPVVAE!AK#LG!LT!a!YTKPFNFEGkkRMafaeqGieELskhVDSLtIPN#kLk!lgRgisLLDAFgaa#dVlkgavQGI AE										
	201	210	220	230	240	250	260	270	280	290	300
S. proteanaculans	LITRPGLMNVDFADYRTVMSEMGYAMHSGVACGEDRAEEAEMAISSPLLEDIDL SGARGVLYNITAGFDLRLDEFETVGNIRAFASDNATVYIGTSL										
E. coli	LITRPGLMNVDFADYRTVMSEMGYAMHSGVACGEDRAEEAEMAISSPLLEDIDL SGARGVLYNITAGFDLRLDEFETVGNIRAFASDNATVYIGTSL										
A. laidlawii	LITRPGLMNVDFADYRTVMSEMGYAMHSGVACGEDRAEEAEMAISSPLLEDIDL SGARGVLYNITAGFDLRLDEFETVGNIRAFASDNATVYIGTSL										
Consensus	LITrPG#nNVDFADYRTVMs#nGyA\$MGS GvASGE#RAeEAAEnAISpLLEd!dlsGArgvLYNItaGf#lRdEfEtvgntIRafasd#atv!iGtsl										
	301	310	320	330	340	350	360	370	380	388	
S. proteanaculans	DPEHNDLRVTYVATGIGMD-KRPEITLVTNKQV-SQPVMDHRYQQHGMSPLPQEVKPAKVVYNDPTAQPNKEPDYLDIPAFRLKQAD										
E. coli	DPEHNDLRVTYVATGIGMD-KRPEITLVTNKQV-SQPVMDHRYQQHGMSPLPQEVKPAKVVYNDPTAQPNKEPDYLDIPAFRLKQAD										
A. laidlawii	SVPLEDEMIYTIYATGYELRAKGNEVEKIAGDIFRNSTQQYKITDTGLEPLNNKEASGEDTKKRTLPSMLHRK										
Consensus	dpD\$#DE\$rVT!VATGig\$d.KrpE!tL!tnkqf.##pvn#vryq#hG\$ePLN#e#kpgakvvndtLPqulkepdyl dipaflrkqad										

High consensus (60%) is highlighted in red. Low consensus (30%) is highlighted in blue. Neutral is highlighted in black. Consensus symbols: “!” = IV, “\$” = LM, “%” = FY, “#” = NDQEBZ. The Multalin version 5.4.1 was used to build a consensus sequence.

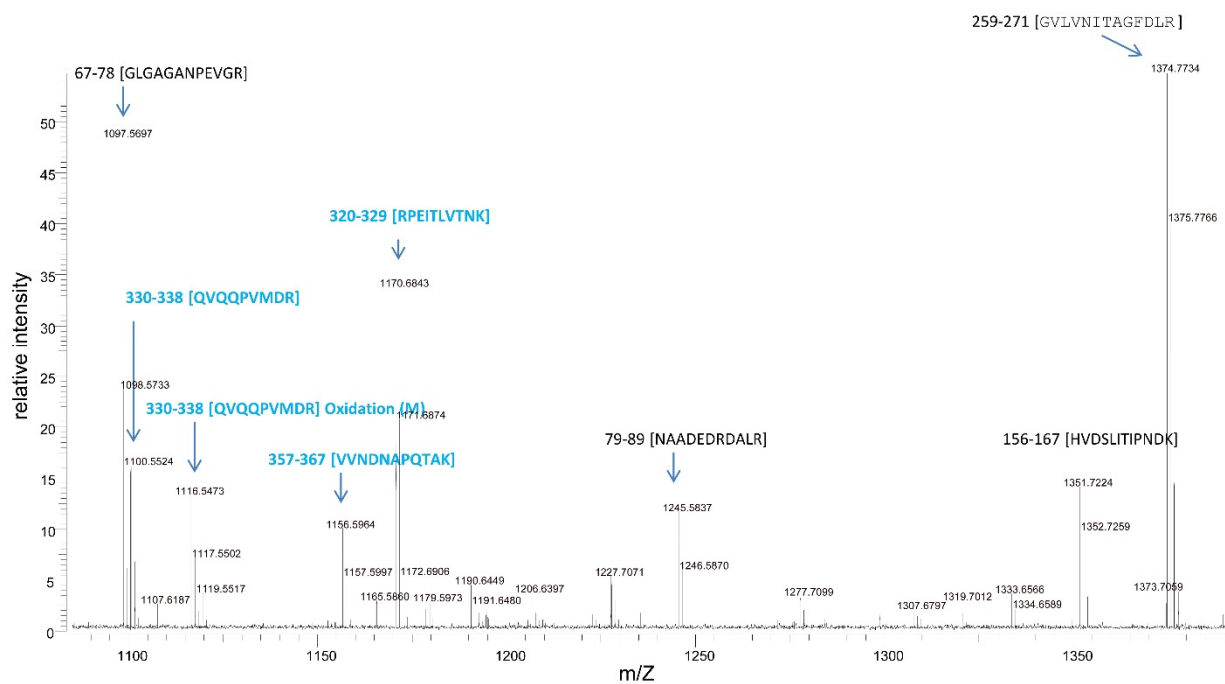
Supplementary S2. Examples of mass spectra.



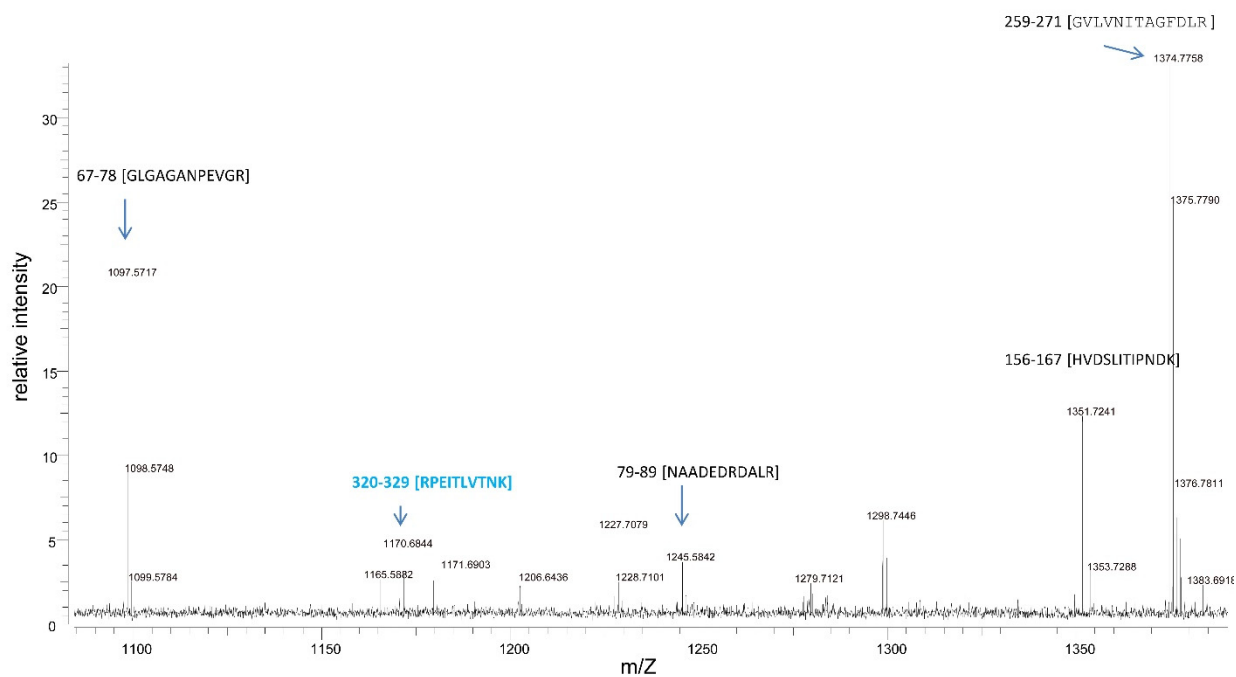
Spectrum of uncleaved *E. coli* FtsZ.



Spectrum of *E. coli* FtsZ cleaved by a protealysin.
Full mass range.

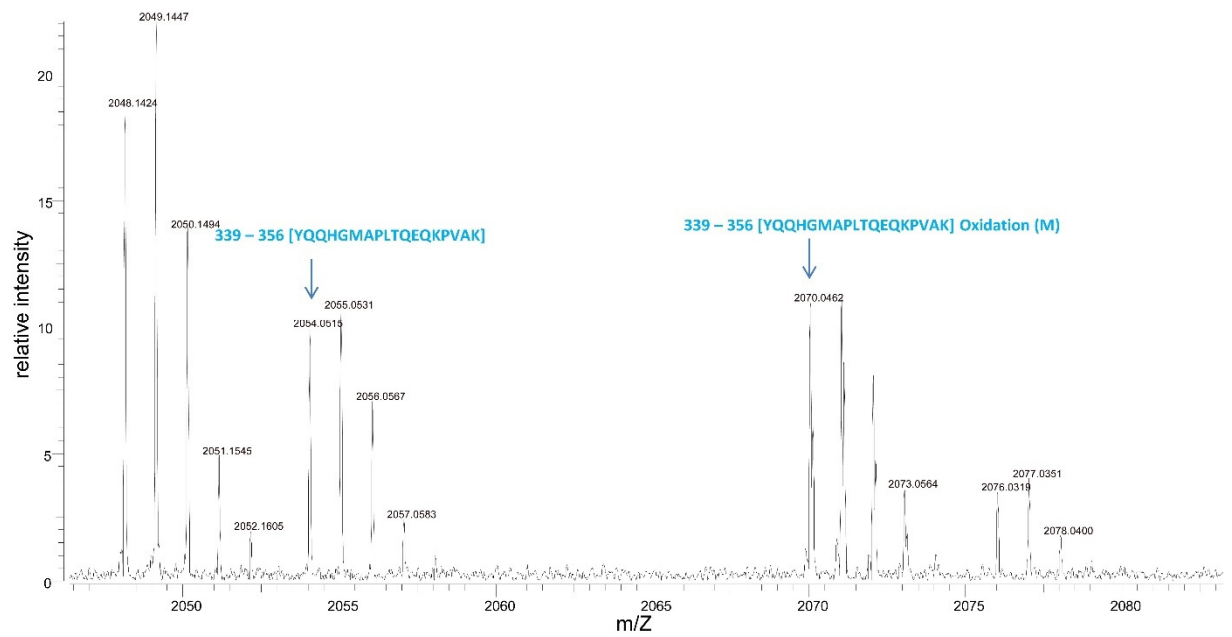


Spectrum of uncleaved *E. coli* FtsZ.

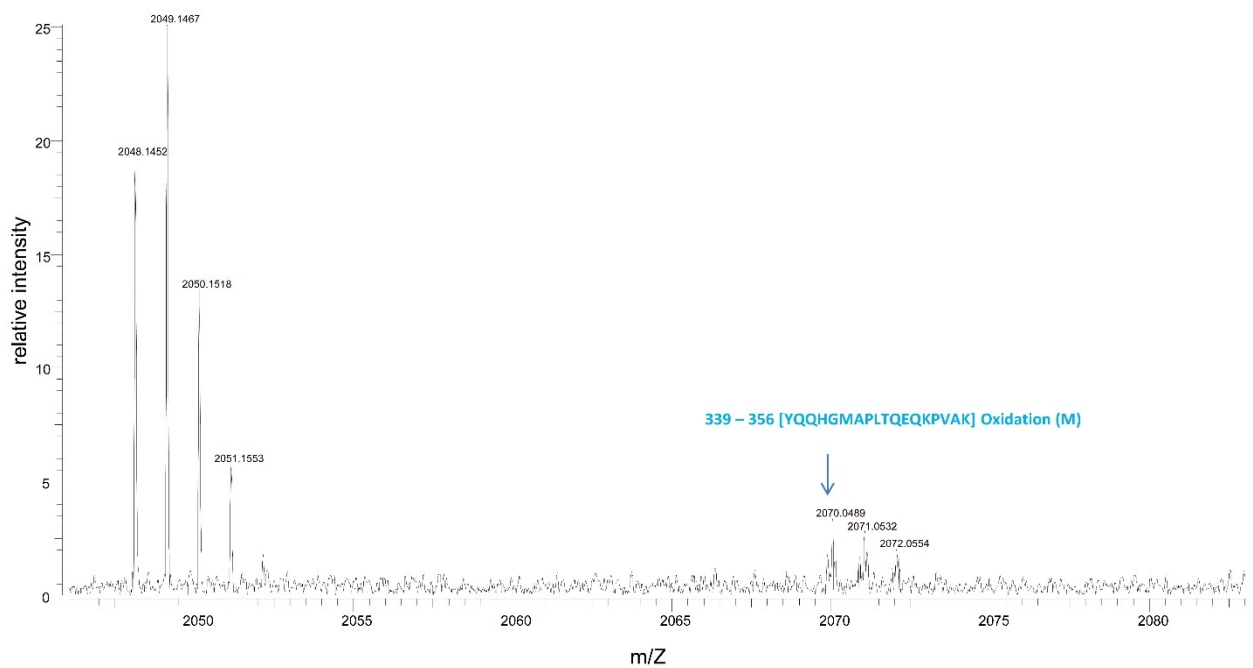


Spectrum of *E. coli* FtsZ cleaved by a protealysin.

The spectra are shown with the selected mass range, in which the peaks of the cleaved protein disappear from the spectrum or the intensity of which is greatly reduced. Their corresponding peptides are marked in blue.

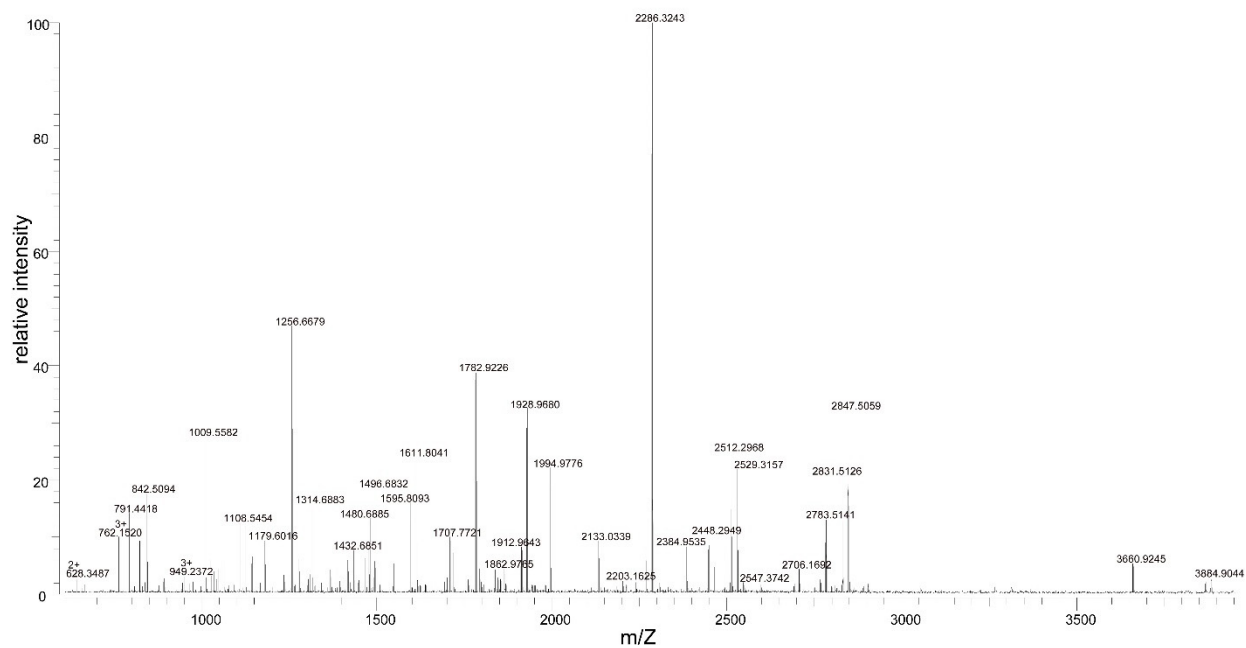


Spectrum of uncleaved *E. coli* FtsZ.

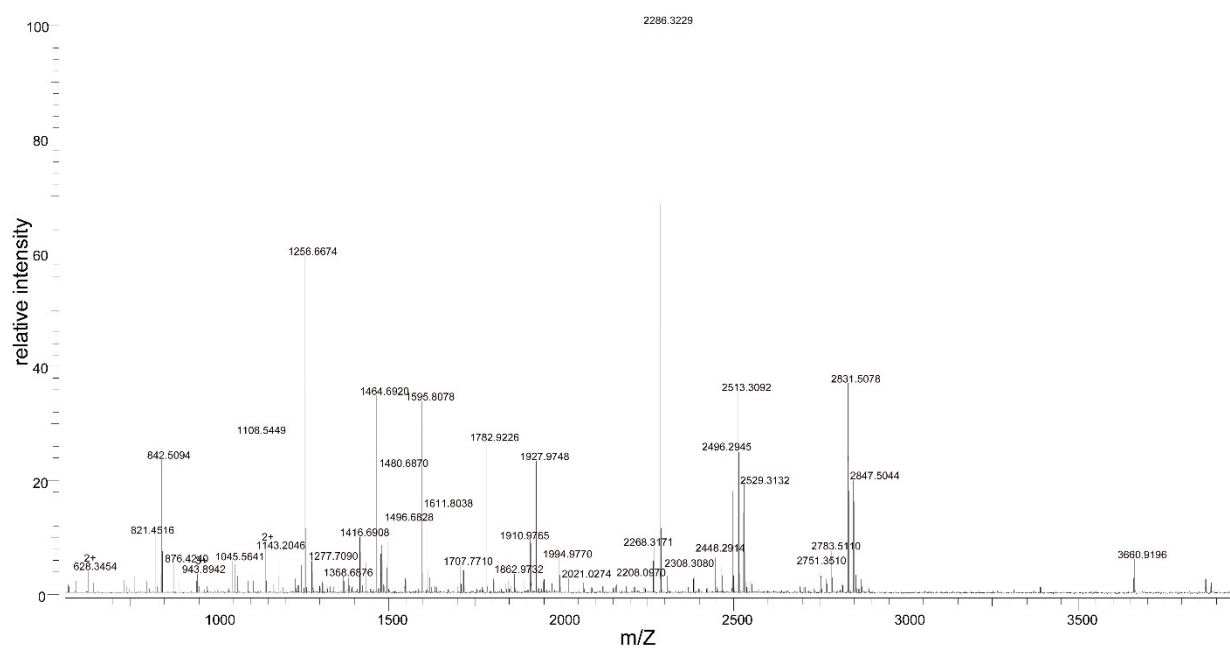


Spectrum of *E. coli* FtsZ cleaved by a proteolysin.

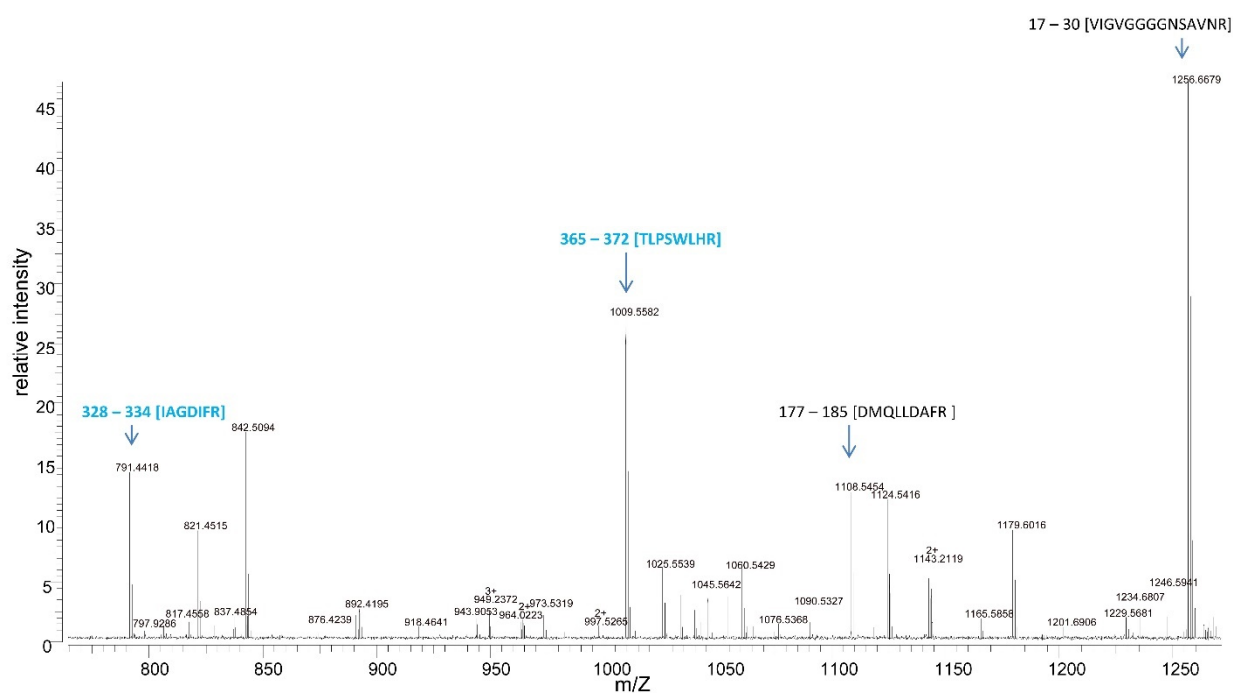
The spectra are shown with the selected mass range, in which the peaks of the cleaved protein disappear from the spectrum or the intensity of which is greatly reduced. Their corresponding peptides are marked in blue.



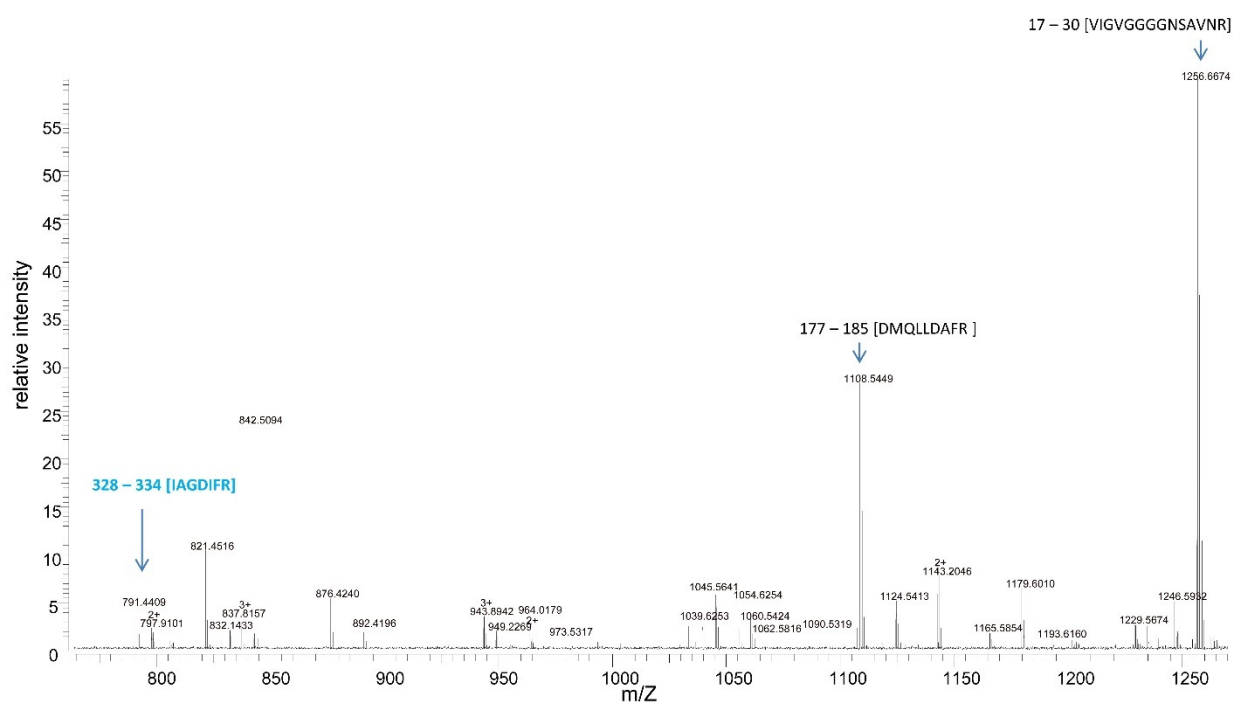
Spectrum of uncleaved *A. laidlawii* FtsZ.



Spectrum of *A. laidlawii* FtsZ cleaved by a protealysin.
Full mass range.



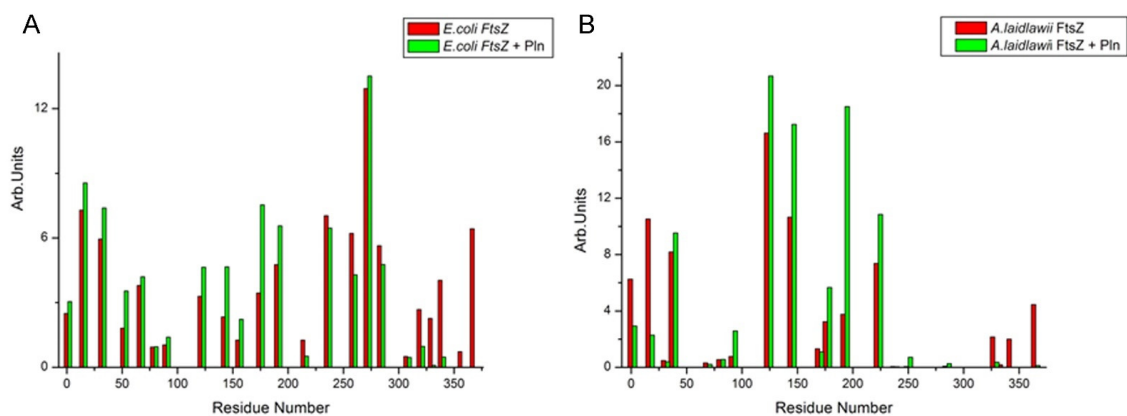
Spectrum of uncleaved *A. laidlawii* FtsZ.



Spectrum of *A. laidlawii* FtsZ cleaved by a proteolysin.

The spectra are shown with the selected mass range, in which the peaks of the cleaved protein disappear from the spectrum or the intensity of which is greatly reduced. Their corresponding peptides are marked in blue.

Supplementary S3. Peak intensities determined by mass spectrometry.



The abscissa shows the first amino acids numbers of the found peptides. The y-axis shows the average peak intensities corresponding to the found peptides in the spectra of the uncleaved FtsZ (red) and in the spectra of the FtsZ cleaved by a protealysin (green).

Supplementary S4. Peptides detected by mass spectrometry.

1	<u>M</u> FEP <u>M</u> ELTND	AVIK <u>V</u> IGVGG	GGGNAVEH <u>M</u> V	<u>R</u> ERIEGVEFF	AVNTDAQAL <u>R</u>
51	<u>K</u> TAVGQTIQI	GSGIT <u>K</u> GLGA	GANPEVGR <u>N</u> A	ADEDR <u>D</u> ALRA	ALEGADMVFI
101	AAGMGGGTGT	GAAPVVAEVA	<u>K</u> DLGILTAV	VT <u>K</u> PFNFEG <u>K</u>	<u>K</u> RMAFAEQGI
151	TELS <u>K</u> HVDSL	ITIPND <u>K</u> LL <u>K</u>	VLGR <u>G</u> ISLLD	AFGAANDV <u>L</u> K	GAVQGIAELI
201	TRPGLMNVD <u>F</u>	ADV <u>R</u> TVMSEM	GYAMMGSGVA	SGEDRAEEAA	EMAISSPLLE
251	DIDLSGARGV	LVNITAGFDL	<u>R</u> LDEFETVGN	TIRAFASDNA	TVVIGTSLDP
301	DMNDEL <u>R</u> VTV	VATGIGMD <u>K</u> R	PEITLVTN <u>K</u> Q	VQQPVMD <u>R</u> YQ	QHGMAPLTQE
351	QKPVA <u>K</u> VVND	NAPQTAKEPD	YLDIPAFL <u>R</u> K	QAD	

Uncleaved *E. coli* FtsZ.

1	<u>M</u> FEP <u>M</u> ELTND	AVIK <u>V</u> IGVGG	GGGNAVEH <u>M</u> V	<u>R</u> ERIEGVEFF	AVNTDAQAL <u>R</u>
51	<u>K</u> TAVGQTIQI	GSGIT <u>K</u> GLGA	GANPEVGR <u>N</u> A	ADEDR <u>D</u> ALRA	ALEGADMVFI
10	AAGMGGGTGT	GAAPVVAEVA	<u>K</u> DLGILTAV	VT <u>K</u> PFNFEG <u>K</u>	<u>K</u> RMAFAEQGI
151	TELS <u>K</u> HVDSL	ITIPND <u>K</u> LL <u>K</u>	VLGR <u>G</u> ISLLD	AFGAANDV <u>L</u> K	GAVQGIAELI
201	TRPGLMNVD <u>F</u>	ADV <u>R</u> TVMSEM	GYAMMGSGVA	SGEDRAEEAA	EMAISSPLLE
251	DIDLSGARGV	LVNITAGFDL	<u>R</u> LDEFETVGN	TIRAFASDNA	TVVIGTSLDP
301	DMNDEL <u>R</u> VTV	VATGIGMD <u>K</u> R	PEITLVTN <u>K</u> Q	<u>V</u> QQP <u>V</u> M <u>D</u> RYQ	<u>Q</u> HGM <u>A</u> PLTQE
351	<u>Q</u> KPVA <u>K</u> VVND	NAPQTAKEPD	YLDIPAFL <u>R</u> K	QAD	

E. coli FtsZ cleaved by a protealysin.

1	<u>M</u> VFGFNDEFN	QKPVI <u>K</u> VIGV	GGGGNSAV <u>N</u> R	MIENDV <u>R</u> GV	YVAMNTDAQV
51	<u>L</u> KVSKADERI	QLGK <u>K</u> L <u>R</u> GL	GAGAKPAIG <u>K</u>	QAALESEDDI	<u>R</u> EVLSADAMV
101	FITAGMGGGT	GTGAAPV <u>V</u> AR	IA <u>K</u> ELGVLT	GIVTKPFVFE	G <u>P</u> L <u>R</u> MQHAI
151	GLEELKPNVD	TLVIPNERL	FSIAD <u>R</u> DMQL	LDA <u>F</u> RESD <u>K</u> V	L <u>R</u> QGVQIAE
201	IIAVPGMINV	DFADV <u>R</u> TVME	N <u>K</u> GTALMGIG	MASGEN <u>R</u> AIE	AAR <u>K</u> AIH <u>S</u> KL
251	LEVSIDGATD	AIVNISSGAE	VT <u>L</u> FEIEAAL	TEI <u>R</u> NATESD	LNVIYGH <u>T</u> VS
301	VDLEDEMIVT	IVATGYEL <u>R</u> A	<u>K</u> GNEVE <u>K</u> IAG	DIFRNNSTQQ	V <u>K</u> ITDTGLEP
351	LNN <u>K</u> EASGED	<u>T</u> K <u>K</u> R <u>T</u> LP <u>S</u> WL	<u>H</u> R <u>K</u>		

Uncleaved *A. laidlawii* FtsZ.

1	<u>M</u> VFGFNDEFN	QKPVI <u>K</u> VIGV	GGGGNSAV <u>N</u> R	MIENDV <u>R</u> GV	YVAMNTDAQV
51	<u>L</u> KVSKADERI	QLGK <u>K</u> L <u>R</u> GL	GAGAKPAIG <u>K</u>	QAALESEDDI	<u>R</u> EVLSADAMV
101	FITAGMGGGT	GTGAAPV <u>V</u> AR	IA <u>K</u> ELGVLT	GIVTKPFVFE	G <u>P</u> L <u>R</u> MQHAI
151	GLEELKPNVD	TLVIPNERL	FSIAD <u>R</u> DMQL	LDA <u>F</u> RESD <u>K</u> V	L <u>R</u> QGVQIAE
201	IIAVPGMINV	DFADV <u>R</u> TVME	N <u>K</u> GTALMGIG	MASGEN <u>R</u> AIE	AAR <u>K</u> AIH <u>S</u> KL
251	LEVSIDGATD	AIVNISSGAE	VT <u>L</u> FEIEAAL	TEI <u>R</u> NATESD	LNVIYGH <u>T</u> VS
301	VDLEDEMIVT	IVATGYEL <u>R</u> A	<u>K</u> GNEVE <u>K</u> IAG	D <u>I</u> FRNNSTQQ	<u>V</u> K <u>I</u> TD <u>T</u> GLEP
351	LNN <u>K</u> EASGED	<u>T</u> K <u>K</u> R <u>T</u> LP <u>S</u> WL	<u>H</u> R <u>K</u>		

A. laidlawii FtsZ cleaved by a protealysin.

Peptides found by mass spectrometry are highlighted in color. Underlining indicates the amino acids after which the protein is cleaved by trypsin. Blue indicate peptides whose peak intensity in the spectrum of the cleaved FtsZ is 10 or more times lower than the intensity of these peaks in the spectrum of the uncleaved protein (Supplementary S2, S3). Examples of amino acids before which protealysin can cleave protein are highlighted in yellow [19].