FIG S1 Functional tests of SUMO-tagged proteins. The indicated strains were grown under SPI1-inducing conditions and analyzed via β-gal assay. A) Strains used: JS749, JS749 with pET-SUMO or pHilE, JS2103, JS2103 with pHilE, pET-SUMO, or pET-SUMO::*hilE*. B) Strains used: JS749, JS749 with pET-SUMO or pET-SUMO::*hilD*, JS2075, JS2075 with pET-SUMO or pET-SUMO::*hilD*. C) Strains used: JS749, JS749 with pET-SUMO or pET-SUMO::*hilC*, JS2075, JS2075 with pET-SUMO or pET-SUMO::*hilC*.
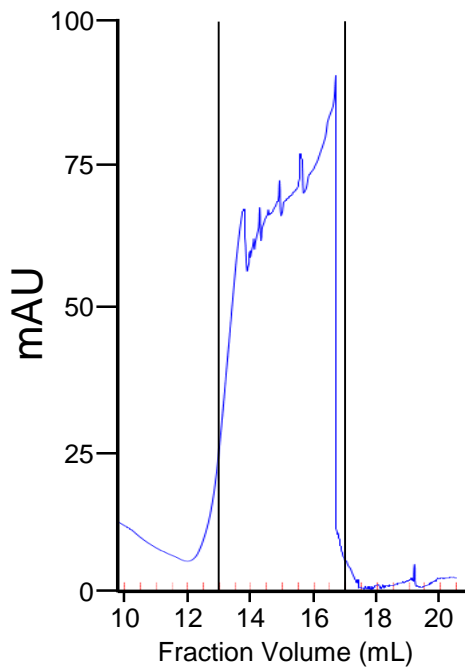
FIG S2 Elution profile of HilE. HilE was purified via size exclusion chromatography performed over a Superose 12-HR 10/30 column. Absorbance was monitored at 280 nm. The peaks are consistent with predicted molecular masses of 16 kDa (monomer) to 100 kDa (hexamer). Vertical lines indicate fractions pooled for use in subsequent assays.

TABLE S1. Bacterial strains and plasmids used in this study.

Strain	Genotype	Reference[a]
S. enterica		
14028	Wild-type serovar Typhimurium	ATCC[b]
JS749	*att*λ::pDX1::*hilA'-lacZ*+	1
JS953	*att*λ::pDX1::*hilA'-lacZ*+ *zjg*8118::*tetRA-rtsA*	2
JS2075	ΔSPI1::FRT Δ*rtsA5*::FRT *att*λ::pDX1::*hilA'-lacZ*+	3
JS2103	*att*λ::pDX1::*hilA'-lacZ*+ Δ*hilE115*::Cm	
JS2104	*att*λ::pDX1::*hilA'-lacZ*+ *zjg*8118::*tetRA-rtsA* Δ*hilD114*::Cm	
JS2105	*hilE115*::SPA-Kn *att*λ::pDX1::hilA'-lacZ+	
JS2106	*zjg8118*::*tetRA-hilC* Δ*hilCD2915*::FRT Δ*rtsA5*::FRT Δ*fliZ8042*::Kn Δ*hilE115*::Cm *att*λ::pJG1	
JS2107	*zjg8118*::*tetRA-hilD* Δ*hilCD2915*::FRT Δ*rtsA5*::FRT Δ*fliZ8042*::Kn Δ*hilE115*::*Cm* *att*λ::pJG1	
JS2108	Δ*lon*::Kn Δ(*wza-wcaM*)4201 *zjg*8118::*tetRA-hilD*-3xFLAG *att*λ::pDX1::*hilA'-lacZ*+ / pWKS30	2
JS2109	Δ(*wza-wcaM*)*4201 zjg*8118::*tetRA-hilD*-3xFLAG *att*λ::pDX1::*hilA'-lacZ*+ / pWKS30	
JS2110	Δ(*wza-wcaM*)*4201 zjg*8118::*tetRA-hilD*-3xFLAG *att*λ::pDX1::*hilA'-lacZ*+ Δ*hilE115*::Cm / pWKS30	
JS2111	Δ*lon*::Kn Δ*(wza-wcaM)4201 zjg*8118::*tetRA-hilD*-3xFLAG Δ*hilE115*::Cm *att*λ::pDX1::*hilA'-lacZ*+ / pWKS30	
JS2112	Δ(*wza-wcaM*)*4201 zjg*8118::*tetRA-hilD*-3xFLAG *att*λ::pDX1::*hilA'-lacZ*+ / pHilE	
JS2113	Δ*lon*::Kn Δ(*wza-wcaM*)*4201 zjg*8118::*tetRA-hilD*-3xFLAG *att*λ::pDX1::*hilA'-lacZ*+ / pHilE	
JS2115	Δ*fliZ*8042::Kn	
JS2116	Δ*fliZ8042*::Kn Δ*hilE115*::Cm	
JS135	*zjg8118*::*tetRA*	4
JS996	Δ*hilE115*::Cm	5
E. coli		
SU101	λRS45::p*sulA-lac*+ *lexA71*::Tn5 (Def)*sulA211* Δ(*lac*)*U169*/F'::Tn9 *lacI*q Δ(*lacZ*)*M15*	6
SU202	λRS45::p*sulA*op408/+-*lac*+ *lexA71*::Tn5 (Def)*sulA211* Δ(*lac*)*U169*/F'::Tn9 *lacI*q Δ(*lacZ*)*M15*	6
	(NOTE: SU101 and SU202 differ in the LexA operator sequence controlling *lacZ* expression. SU101 is wt operator and SU202 is a half-mutant operator sequence)	
BL21(DE3)	F– *ompT gal dcm lon hsdSB*(rB–mB–) λ(DE3 [*lacI lacUV5-T7p07 ind1 sam7 nin5*]) [*malB*+]K-12(λS)]	7
Plasmids	**Relevant genotype**	
pLS118	*bla* P$_{BAD}$ *hilD-myc*-His pACYC184 *ori*	8
pLS119	*bla* P$_{BAD}$ *hilC-myc*-His pACYC184 *ori*	8
pCE81	*bla* P$_{BAD}$ λ*att*B1 *myc-rtsA* λ*att*B2 pACYC184 *ori*	9
pWKS30	pSC101 *ori* Ap^r	10
pHilE	pWKS30::*hilE*+	9
pSR658	ColE1 *ori* Tc^r lexA-DBD(wt)	11
pSR659	p15A *ori* Ap^r lexA-DBD(mut)	11
pMS604	pSR658::*fos*	6
pDP804	pSR659::*jun*	6
pDD506	pSR658::*cat*	6
pET-SUMO	pBR322 *ori* Kan^r	Invitrogen

a This study unless otherwise noted; b American Type Culture Collection

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