SUPPLEMENTARY INFORMATION

Fingerloop activates cargo delivery and unloading during co-translational protein

targeting

Aileen R. Ariosa*, Stacy S. Duncan[†‡], Ishu Saraogi*, Xiaodong Lu[†], April Brown[†],

Gregory J. Phillips[†], and Shu-ou Shan*[§]

*Division of Chemistry and Chemical Engineering, California Institute of Technology,

Pasadena, CA 91125

[†]Department of Veterinary Microbiology, College of Veterinary Medicine, Veterinary

Medical Research Institute (VMRI), Iowa State University, Ames, IA 50011

[‡]Present Address: Department of Medicine, Division of Infectious Diseases, Vanderbilt

University, Nashville, TN 37232

[§]Corresponding author. E-mail: sshan@caltech.edu

Figure S1. Expression of *ffh* alleles analyzed by SDS-PAGE. Proteins were resolved and detected as described in Materials and Methods. Lanes 1-2: *ffh*PG→AA; 3-4: *ffh*ΔFL; 5-6: *ffh*$^+$, 7-8: *ffh*LM→AA. Lanes 1, 3 5, 7: + L-arabinose; 2, 4, 6, 8: − L-arabinose. Molecular weight standards are shown on the left, the relative positions of which were identified using a corresponding SDS-PAGE gel stained with Coomassie Brilliant Blue.

1   2   3   4   5   6   7   8

120—
85—
50—
35—
25—
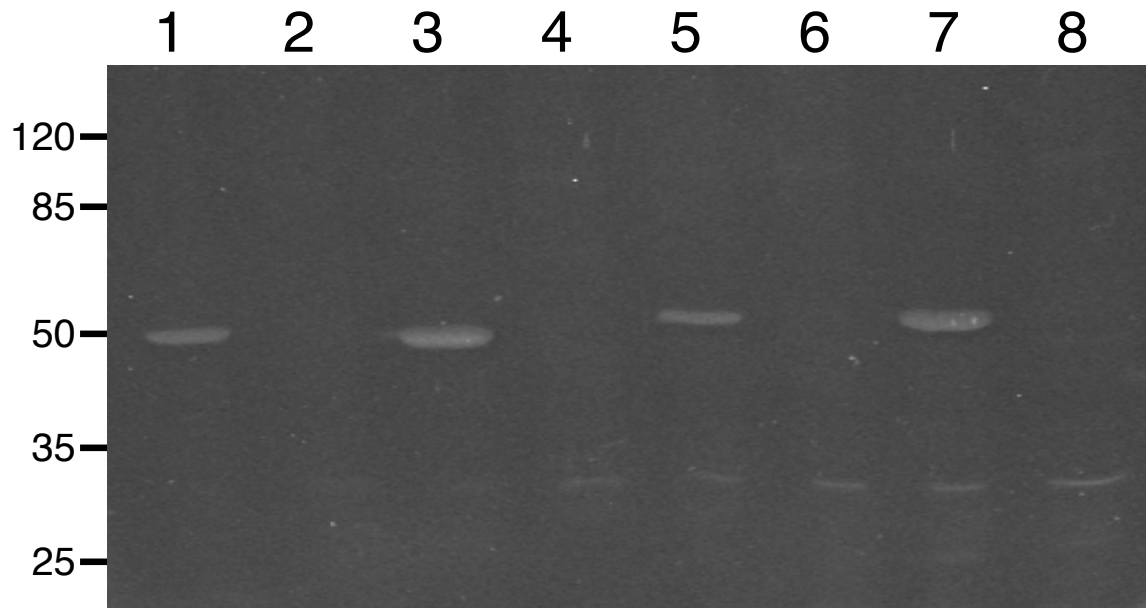
Figure S2. The effects of fingerloop mutants on SRP-FtsY complex assembly. Measurements of SRP-FtsY complex assembly kinetics of wild-type SRP (●), mutant SRP(ΔFL) (○) and mutant SRP(LM→AA) (◇) in the presence of Nikkol.
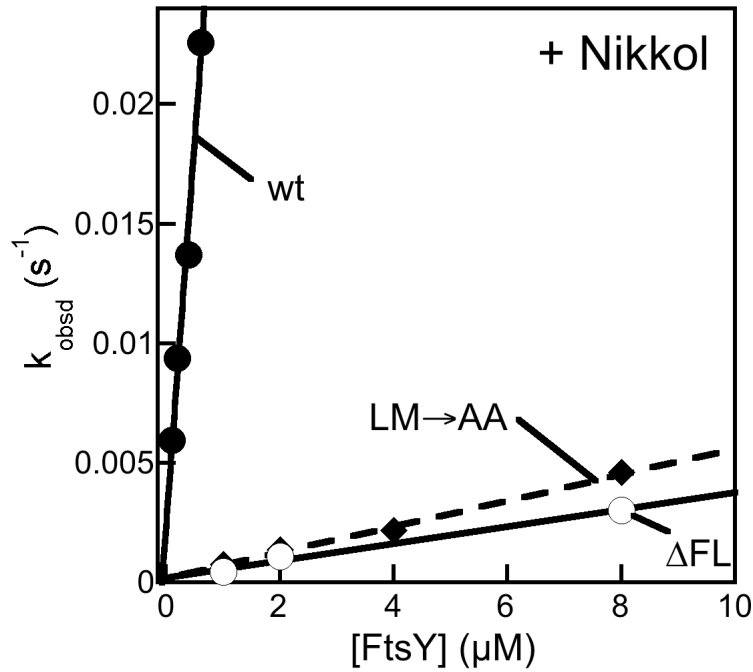

Figure S3. Effects of the fingerloop on the equilibrium stability of the early complex in the presence of RNC$_{FtsQ}$.
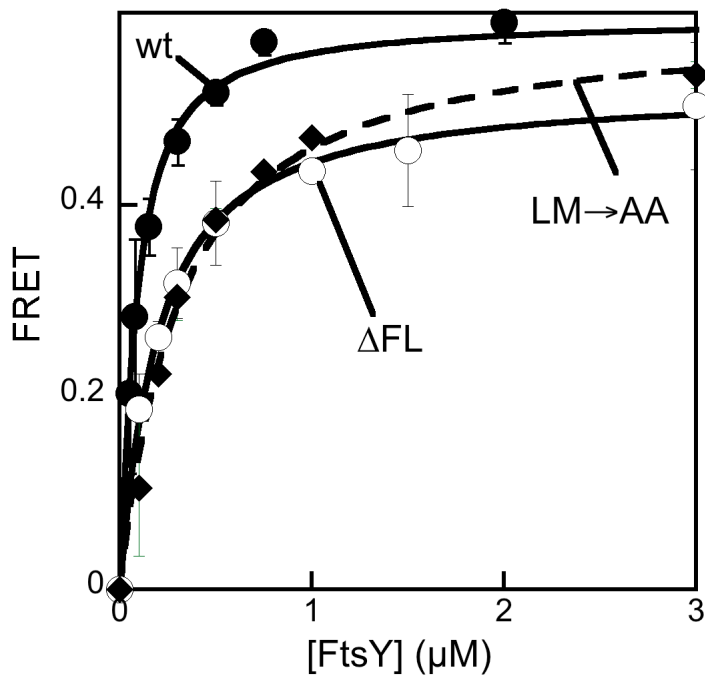
Figure S4. Rate constants for formation of the stable complex starting from a preformed RNC•SRP•FtsY early complex using either (A) SRP(ΔFL) or (B) SRP(LM→AA).
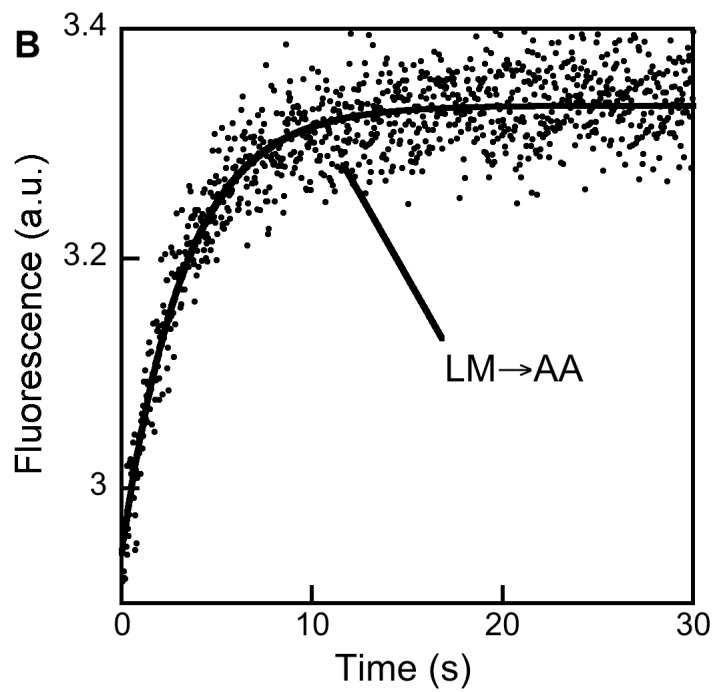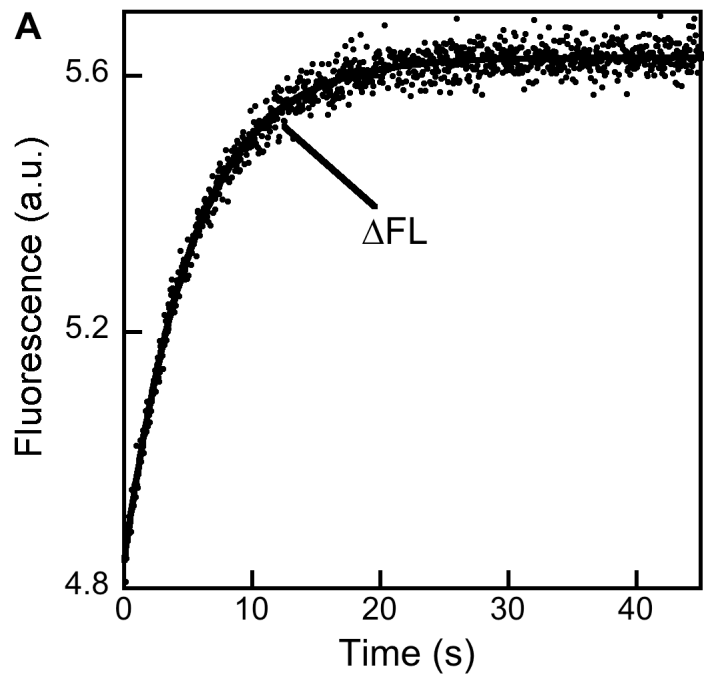
Figure S5. Deletion of the fingerloop results in inefficient GTPase activation. (A) The reciprocally stimulated GTPase reaction between SRP and FtsY were determined for wild-type SRP (●) and mutants SRP(LM→AA) (◇) and SRP(ΔFL) (○). The data were fit to Eq. 3 in the *Methods*. (B) Summary of the k_{cat} and K_m values from the data in part A.

A
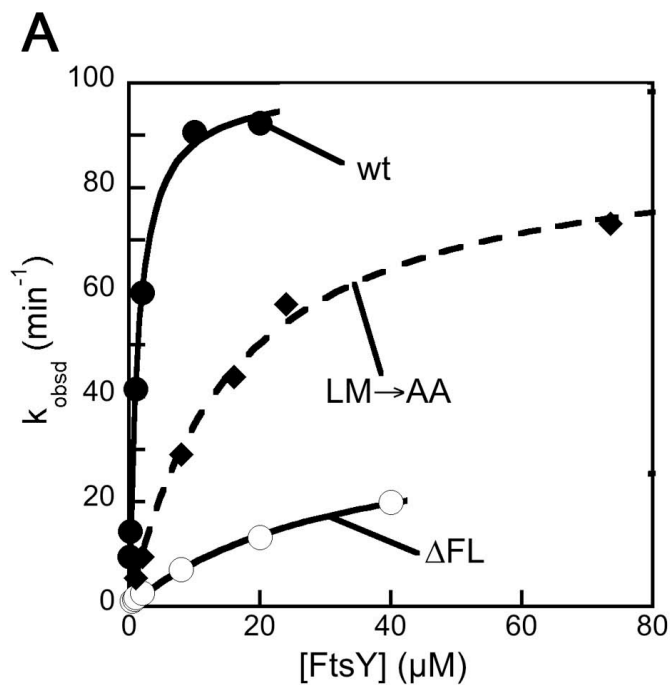
B

	SRP	ΔFL	LM→AA
k_{cat} (min⁻¹)	100 (1)	36 (0.36)	90 (0.90)
K_M (μM)	1.3 (1)	32 (25)	6 (4.6)
k_{cat}/K_M (μM⁻¹min⁻¹)	77 (1)	1.1 (0.01)	15 (0.19)