

Table S1. Data Collection and Refinement Statistics, Related to Figure 1

Data collection	
Space group	P2 ₁ 2 ₁ 2 ₁
Cell dimensions	
a, b, c (Å)	47.6, 76.2, 219.8
Resolution (Å)	47.6 - 2.5 (2.6 - 2.5) ^a
R _{merge} (%)	7.5 (62.3)
I / σ	14.5 (1.5)
Completeness (%)	93.8 (58.8)
Redundancy	5.0 (2.2)
Refinement	
Resolution (Å)	45.0 - 2.5
No. reflections	25,452
R _{work} / R _{free} (%)	22.4 / 27.5
No. atoms	5517
Protein	4,985
RNA / SO ₄	424 / 5
Water	103
B-factors (Å ²)	34.4
Protein	35.0
RNA / SO ₄	27.8 / 60.0
Water	28.5
Ramachandran analysis	
Favored	94.2
Additionally allowed	4.8
Not favored	1.0
R.m.s. deviations	
Bond lengths (Å)	0.01
Bond angles (°)	1.3

^a Highest resolution shell is shown in parenthesis.

Table S2. Primers for Mutagenesis, Related to Figure 5

GGCCAATGGAGGCTGCCattCTTTTCTCAAGTTCCTGTTGGAGC	T55I
GCTCCAACAGGAACCTTGAGAAAAAGaatGGCAGCCTCCATTGGGCC	
CAGCCCATTAAACCAAGAAATTACgcaTTAGAGCTTGCTTTGCCTGC	Q247A
GCAGGCAAAGCAAGCTCTAAAtgcGTAATTTCTTGGTTAAATGGGCTG	
GGGAATTTGGAACACAGAAATATGAAgcaTGGATTGTTACAGTTCAGAAAGCATGCATGG	Q511A
CCATGCATGCTTTCTGAACTGTAACAATCCAAtgcTTCATATTTCTGTGTTCCAAATTCCC	
GGATTGTTACAGTTCAGAAAGCAgcaATGGTGTTCAGATGCCAGAC	C520A
GTCTGGCATCTGGAACACCATTggcTGCTTTCTGAACTGTAACAATCC	
TGATGAATGACTCTATTTTACGCCTTgcaACATGGGACGAAGCAGTATTTAGGG	Q769A
CCCTAAATACTGCTTCGTCCCATGTggcAAGGCGTAAAATAGAGTCATTCATCA	
CTATTTTACGCCTTCAGACATGGGACgcaGCAGTATTTAGGGAAAAGATTCTGC	E773A
GCAGAATCTTTCCCTAAATACTGctgcGTCCCATGTCTGAAGGCGTAAAATAG	
GCAGTATTTAGGGAAAAGATTCTGCATATAgcaACTCATGAAAAATTCATCAGAGATAGTCAAGAAAAACC	Q784A
GGTTTTCTTGACTATCTCTGATGAATTTTTCATGAGTggcTATATGCAGAATCTTTCCCTAAATACTGC	
CATGAAAAATTCATCAGAGATAGTCAAGAAAAACCAAAAAGATAAGGAAAATAAAAAACTGCTCTGCAGAA AGTGCAAAGCC	ΔPVP ₇₉₉₋₈₀₁
GGCTTTGCACTTTCTGCAGAGCAGTTTTTTATTTTCCTTATCTTTGGTTTTTCTTGACTATCTCTGATGAATT TTTCATG	
CATGAAAAATTCATCAGAGATAGTCAAGAAAAACCAAAAagcagcagcaGATAAGGAAAATAAAAAACTGCTCT GCAGAAAAGTGCAAAGCC	PVP ₇₉₉₋₈₀₁ :AAA
GGCTTTGCACTTTCTGCAGAGCAGTTTTTTATTTTCCTTATCtgcctgcTTTTGGTTTTTCTTGACTATCTCTGAT GAATTTTTCATG	