

Table S1

residue	mutant amino acid	protein level relative to wild-type ^a	dominance test ^b		mixed trimer test in UU1623	
			UU2377 (R69E)	UU2378 (T156K)	jamming ^c	rescue ^d
K215	P	0.8	+	+	no	no
S217	P	1.0	+	+	no	R1
L218	E	1.4	+	+	no	no
	K	1.1	+	+	no	(R2)
	N	1.3	+	+	no	R2
	P	0.9	0	0	E1	no
P221	R	1.1	+	+	no	(R2)
	F	0.9	+	+	E2	no
	I	0.6	+	+	no	R1
	L	0.7	+	+	no	R1
M222	W	0.7	+	+	no	R2
	D	0.9	+	+	no	no
	E	1.0	+	+	no	no
	N	1.3	+	+	no	no
	P	1.3	+	+	no	no
	Q	1.4	+	+	E1	no
L225	R	1.1	0	0	E1	no
	C	1.5	+	+	no	R2
	D	1.5	+	+	no	no
	G	1.0	+	+	no	(R2)
	K	1.0	+	+	no	no
	P	0.9	0	0	no	no
	Q	1.9	+	+	no	R2
I226	R	1.4	+	+	no	(R1)
	S	2.0	+	+	no	R2
	P	0.9	+	+	no	no
	D227	M	0.2	ND	ND	no
S228	P	0.1	ND	ND	no	no
	P	0.7	+	+	no	R2
I229	A	1.0	+	+	E1	(R2)
	D	1.0	0	0	no	no
	E	0.6	+	+	no	no
	P	0.9	+	+	no	no
	R	1.1	0	0	no	no
	S	0.8	+	+	E1	R2
I232	D	2.1	0	0	no	no

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	E	1.1	+	+	no	no
	G	1.6	+	+	no	no
	H	1.4	+	+	no	(R2)
	K	1.6	+	+	no	no
	N	0.8	+	+	no	no
	P	0.9	+	+	E1	no
	R	2.0	+	+	no	no
	S	1.6	+	+	no	(R2)
A233	C	0.9	+	+	no	R2
	F	0.7	+	+	no	R2
	I	0.9	+	+	no	R2
	L	0.9	+	+	E2	no
	N	0.7	+	+	E1	no
	P	1.0	+	+	no	R1
	V	0.7	+	+	E1	no
E248	G	0.8	+	+	no	R2
	H	1.1	+	+	no	R2
	I	0.9	+	+	no	R1
	K	1.1	+	+	E1	no
	L	1.0	+	+	E2	no
	M	0.8	+	+	E2	no
	N	0.8	+	+	no	R1
	P	0.8	+	+	no	R2
	Q	1.0	+	+	no	R2
	R	1.4	+	+	E1	no
	T	1.1	+	+	no	R2
	V	1.1	+	+	no	R1
M249	D	0.6	+	+	no	no
	E	0.7	+	+	no	no
	G	0.8	+	+	no	(R2)
	K	1.0	+	+	no	no
	Q	1.3	+	+	no	(R2)
	R	1.0	+	+	no	no
G250	P	1.0	+	+	E1	no
	W	0.8	+	+	no	R3
Q251	P	1.1	+	+	no	R1
L252	E	0.7	0	0	no	no
	H	0.5	+	+	no	no
	K	1.5	0	0	E1	no
	N	0.9	0	0	no	no
	P	0.6	+	+	no	no

Supporting Information - Zhou *et al.*

	R	0.9	0	0	no	no
	S	1.0	+	+	no	no
A253	D	1.0	+	+	no	no
	I	0.6	+	+	no	no
	K	0.8	+	+	no	(R1)
	P	1.0	+	+	E1	no
	R	1.1	+	+	no	R1
E254	P	0.8	+	+	no	no
S255	L	1.0	+	+	E1	R1
	P	1.2	+	+	no	(R2)
L256	A	0.7	+	+	E1	(R2)
	E	1.0	0	0	E3	no
	G	2.0	+	+	E3	no
	K	1.0	0	0	no	no
	N	1.9	0	0	no	no
	P	1.7	0	0	E3	no
	Q	0.7	0	0	E3	no
	R	0.7	0	0	E3	no
	S	0.6	+	+	E3	no
	T	0.6	+	+	E1	(R2)
	Y	1.0	+	+	E2	(R2)
R257	P	0.9	0	0	E1	no
H258	P	1.2	0	0	E1	no
M259	D	1.1	0	0	no	no
	E	1.0	0	0	no	no
	F	2.6	+	+	E1	(R2)
	H	1.1	+	+	E3	no
	I	0.8	0	0	E3	no
	K	1.8	+	+	E3	no
	P	1.1	+	+	E1	no
	Q	1.1	+	+	no	(R2)
	R	0.8	0	0	E3	no
	T	0.8	+	+	E3	(R2)
	V	0.9	0	0	E3	no
Q260	D	0.6	+	+	E1	no
	F	0.8	±	+	no	R1
	P	0.7	0	0	E1	no
G261	P	0.6	0	0	E1	no
E262	I	0.8	±	+	E2	R2
	L	1.0	0	0	E2	R2
	P	0.8	+	+	E1	R2

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L263	A	0.7	+	+	E1	(R2)
	C	0.6	+	+	E1	(R2)
	E	0.9	0	0	E3	no
	G	1.0	+	+	E3	no
	N	0.9	+	+	no	no
	P	0.8	0	0	E3	no
	R	0.8	0	0	E3	no
	S	0.7	+	+	E3	no
	T	0.8	+	+	E1	(R2)
	Y	0.8	+	+	no	R2
M264	P	0.9	0	0	E1	no
	Y	0.0	ND	ND	no	no
R265	P	1.0	+	+	E1	no

^a Values are rounded to one decimal place.

^b Results of complementation tests between plasmid-borne *tsr*-HAMP null mutations and strains with a recessive *tsr* serine-binding lesion (R69E or T156K); 0 = no complementation (Tsr^-); + = complementation (Tsr^+); ND = not done due to low expression level of mutant protein.

^c Results of Tar function tests in UU1623 ($\Delta tsr tar^+$) cells carrying plasmid-borne *tsr*-HAMP null mutations. Tar-jamming effects, if any, were classified from least to most severe on a scale (E1-E3) based on the level of Tsr^* expression needed for the effect (Ames *et al.*, 2002).

^d Results of Tsr function tests in UU1623 ($\Delta tsr tar^+$) cells carrying plasmid-borne *tsr*-HAMP null mutations. Rescue of Tsr function, if any, was classified from least to most effective on a scale (R1-R3) based on the level of Tsr^* expression needed for the effect (Ames *et al.*, 2002). Rescue effects shown in parentheses occurred at 30°C, but not at 32.5°C.