Table S2. Crystallization, X-ray data collection and refinement statistics for structures of eIF5B(517-858) mutants

	eIF5B(517-858)D533A·GTPγS	**eIF5B(517-858)D533R·GTPγS**	**eIF5B(517-858)D533N·GTP·Na^+**
Crystallization			
Condition	100 mM HEPES (pH 7.3), 15% PEG 4000, 150 mM NaOAc	100 mM MES (pH 6.7), 13% PEG 8000, 225 mM NaOAc	100 mM HEPES (pH 7), 13% PEG 4000, 125 mM NaOAc
Temperature (°C)	20	20	20
Data Collection			
Space Group	$P2_1$	$P4_12_12$	$P2_1$
Unit Cell	a = 55.6 Å b = 115.8 Å c = 65.9 Å α = 90° β = 102.3° γ = 90°	a = 115.7 Å b = 115.7 Å c = 119.8 Å α = 90° β = 90° γ = 90°	a = 55.4 Å b = 115.9 Å c = 66.1 Å α = 90° β = 101.4° γ = 90°
Molecules/asym. unit	2	2	2
Resolution (Å)	1.58 (1.68-1.58)	2.75 (2.92-2.75)	1.5 (1.59-1.5)
Observed reflections	374970 (60270)	154138 (23582)	542902 (84681)
Unique reflections	110416 (17665)	21704 (3403)	131458 (20989)
Completeness (%)	98.8 (98.0)	99.8 (99.1)	99.2 (98.2)
$<I>/\sigma$	17.7 (2.2)	19.35 (3.11)	24.4 (2.9)
R_{sym} (%)	3.9 (51.5)	7.8 (56.8)	3.0 (46.3)
CC(1/2) (%)	99.9 (73.9)	99.9 (86.1)	100 (82.8)
Refinement			
R_{work} (%)	16.9	20.6	15.5
R_{free} (%)	19.4	25.7	18.2
Rmsd from Standard Stereochemistry			
Bond length (Å)	0.012	0.005	0.014
Bond angles (°)	1.5	1.0	1.6
Ramachandran Plot Statistics			
Most favored (%)	98.7	98.2	98.5
Allowed regions (%)	1.3	1.8	1.5
Disallowed regions (%)	0	0	0

Values in parentheses refer to the highest resolution shell.

R_{work} and R_{free} factors are calculated using the formula $R = \Sigma_{hkl} ||F(obs)_{hkl}| - |F(calc)_{hkl}||/\Sigma_{hkl} |F(obs)_{hkl}|$, where $F(obs)_{hkl}$ and $F(calc)_{hkl}$ are observed and measured structure factors, respectively. R_{work} and R_{free} differ in the set of reflections they are calculated from: R_{free} is calculated for the test set, whereas R_{work} is calculated for the working set.