Supplementary Figures

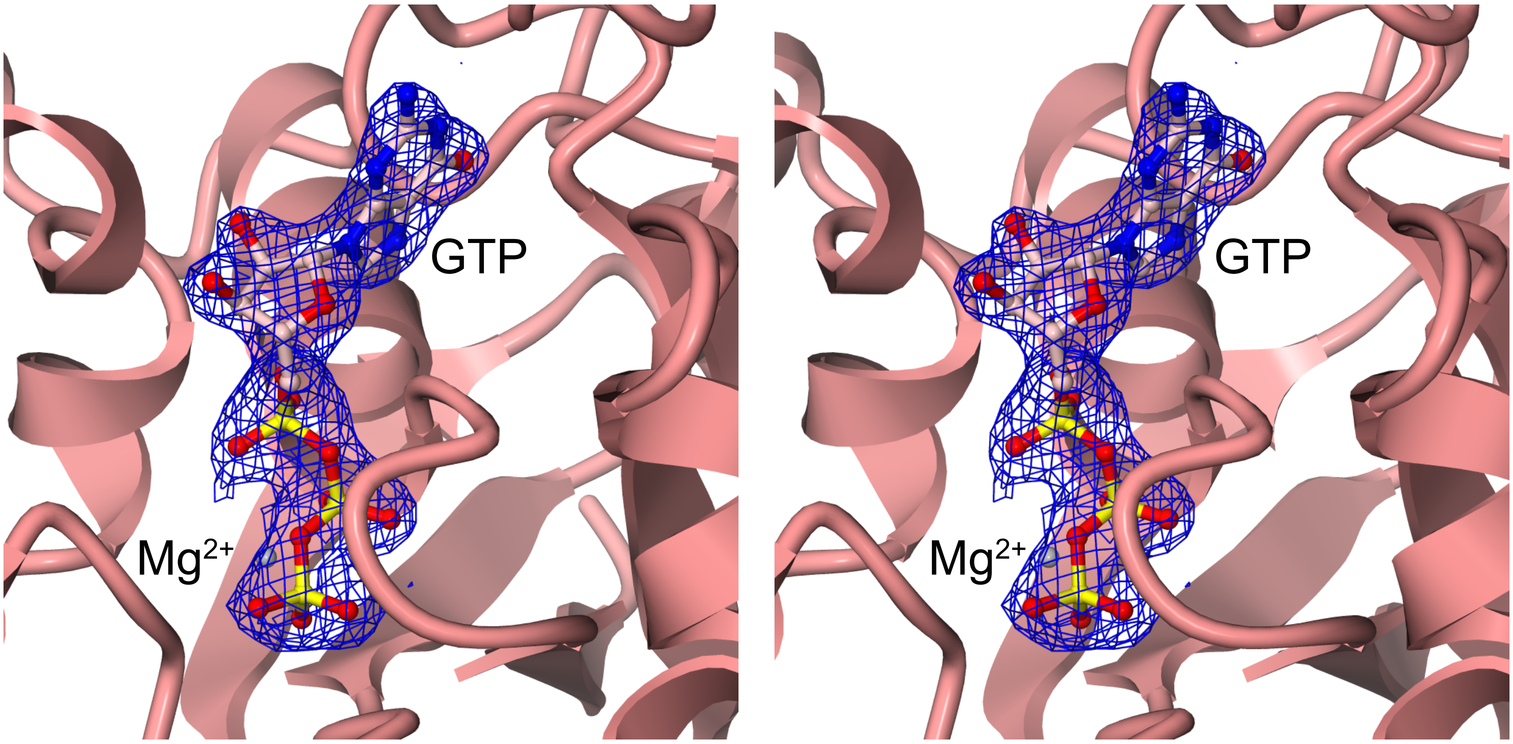
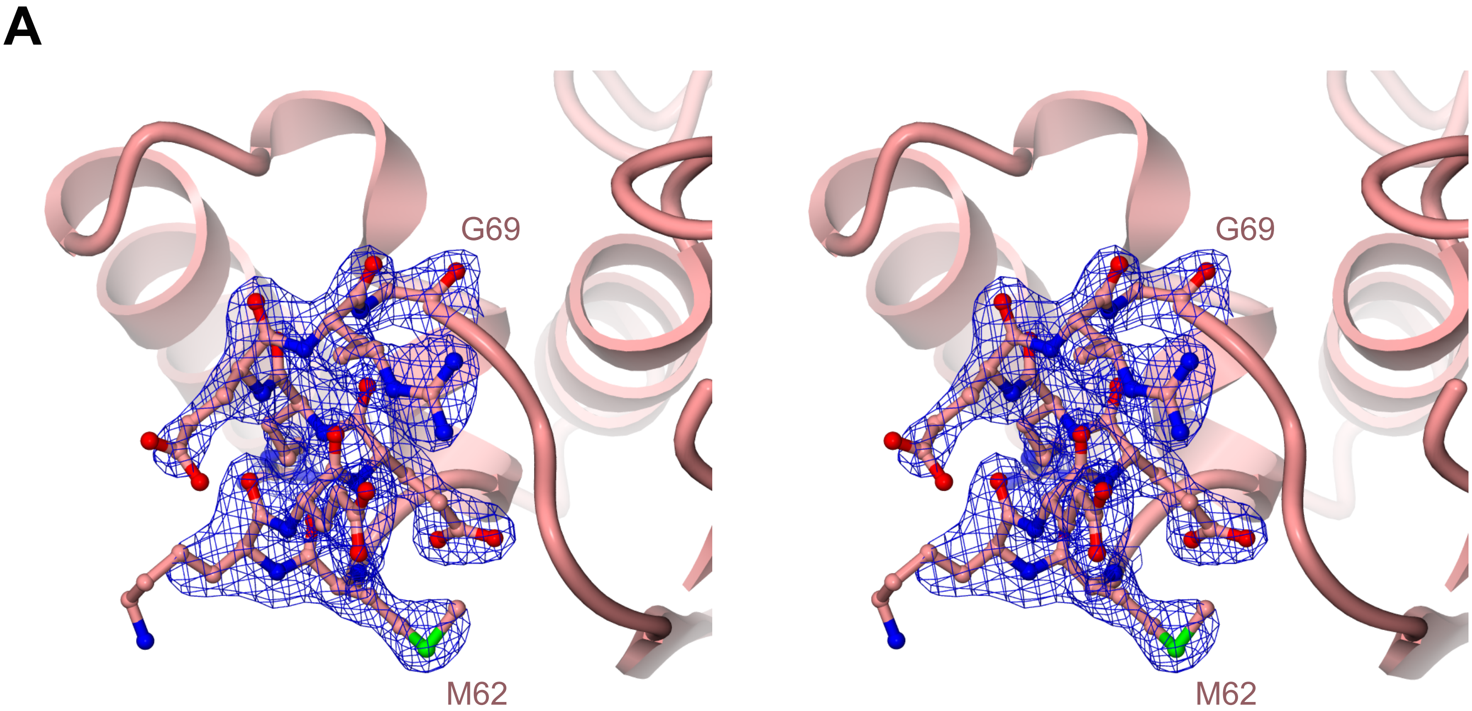
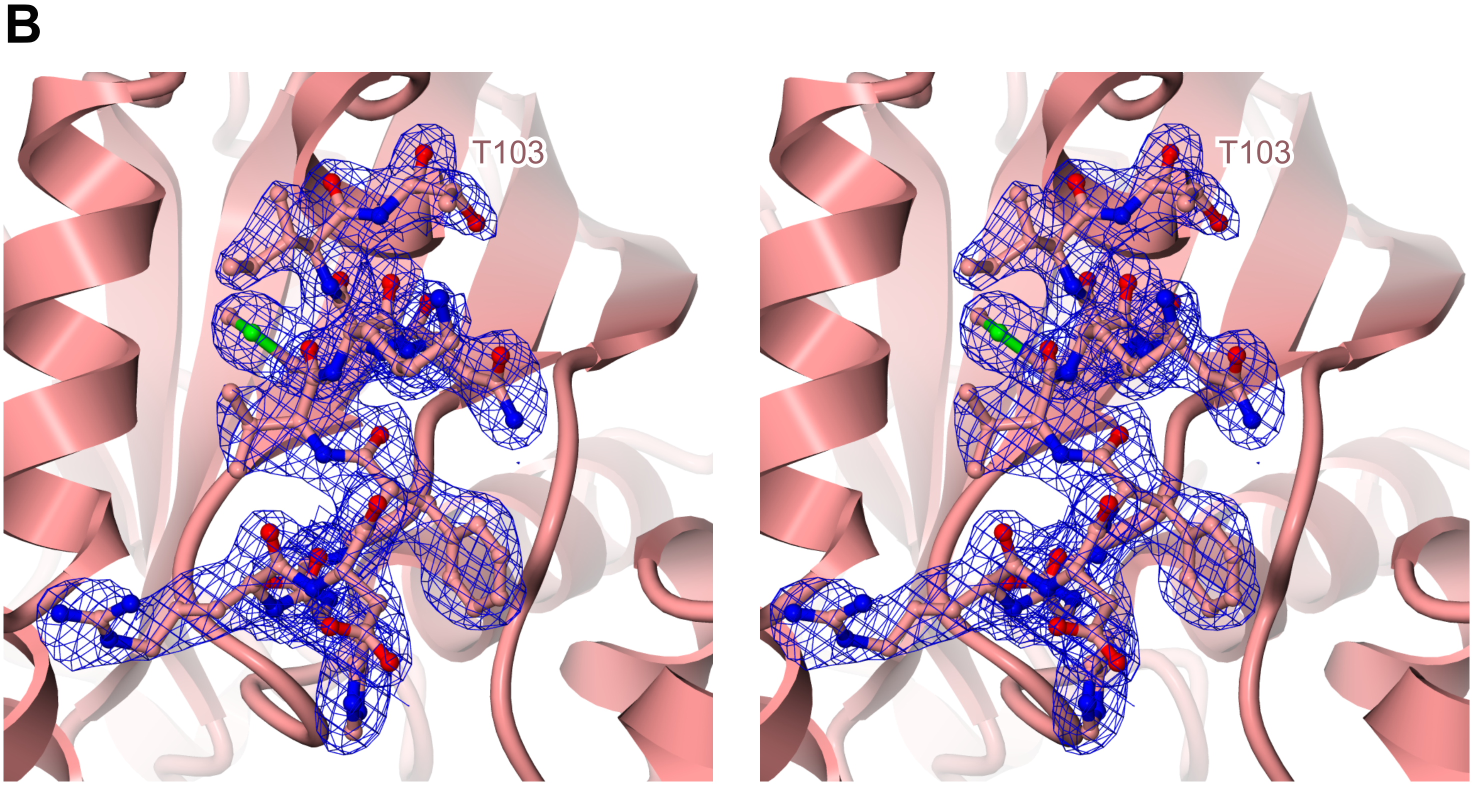


Fig. S1



Switch I



Switch II

Fig. S2

Supplementary Figure Legends

Fig. S1

Stereo view of the electron density map of the GTP bound to aEF1α. The $2F_O$-F_C electron density map of GTP bound to aEF1α, contoured at 1.5 σ, is shown. The GTP and Mg^{2+} ion are depicted by ball-and-stick models.

Fig. S2

Stereo views of the electron density maps of the switch regions of aEF1α.

(A) The $2F_O$-F_C electron density map of the switch I region of aEF1α, contoured at 1.5 σ. Residues 62-69 of aEF1α are depicted by ball-and-stick models.

(B) The $2F_O$-F_C electron density map of the switch II region of aEF1α, contoured at 1.5 σ. Residues 93-103 of aEF1α are depicted by ball-and-stick models.

Tables

Table S1

Data collection statistics

Data collection statistics	**Native**
X-ray source	SPring-8 BL32XU
Wavelength (Å)	1.0
Space group	$C2$
Unit cell dimensions (Å, °)	$a = 176.6$, $b = 55.2$, $c = 90.7$ $\alpha = \gamma = 90$, $\beta = 101.6$
Resolution (Å)	50–2.30 (2.34–2.30)
Unique reflections	38,192 (1,866)
Redundancy	5.7 (3.9)
Completeness (%)	98.9 (97.2)
$I/\sigma(I)$	37.7 (3.82)
R_{sym}	0.063 (0.282)

The numbers in parentheses are for the last shell.

Table S2

Structure refinement statistics

Refinement statistics	
Resolution (Å)	46.498–2.30
No. of reflections (all/test)	37988/1906
$R_{\text{work}}/R_{\text{free}}$	0.2013/0.2606
No. of atoms	
Protein	5961
Ligand	33
Ion	5
Water	162
RMSD of	
Bond length (Å)	0.009
Bond angle (°)	1.202
Average *B* factor (Å)	
Protein	50.9
Ligand	40.9
Ion	61.6
Water	46.7
Ramachandran plot	
Favored (%)	98.58
Outliers (%)	0.00