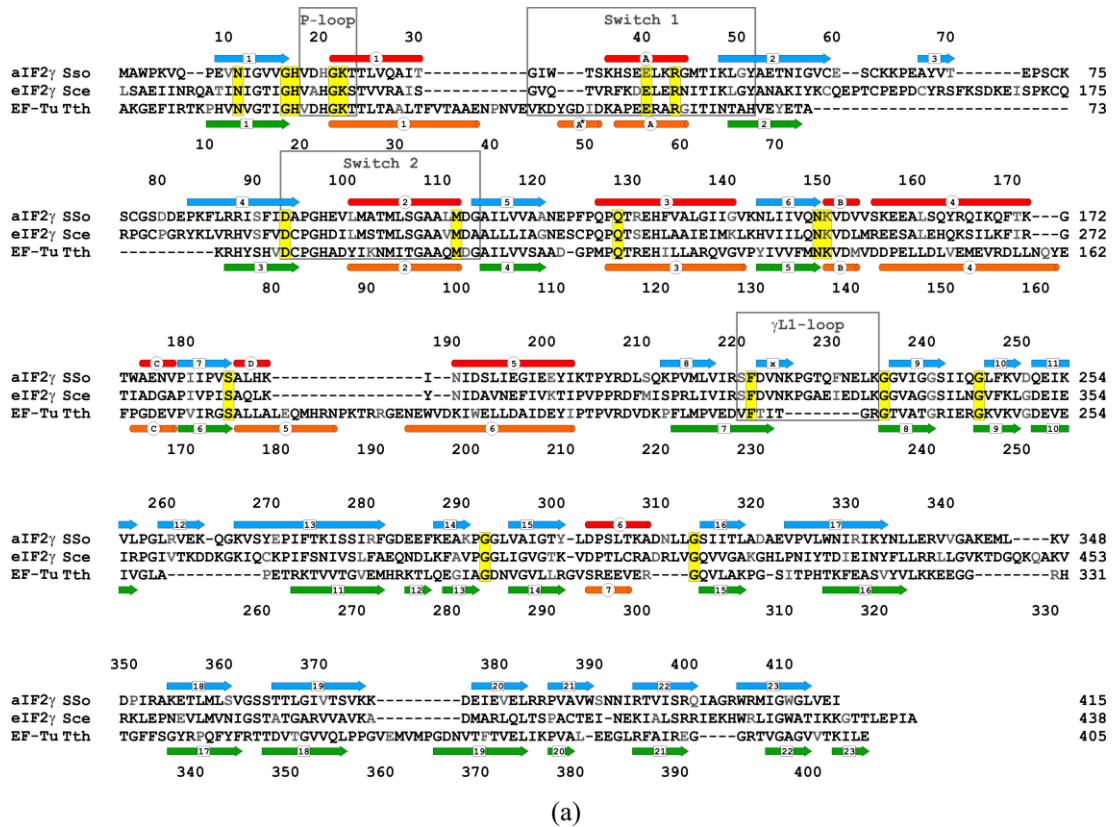
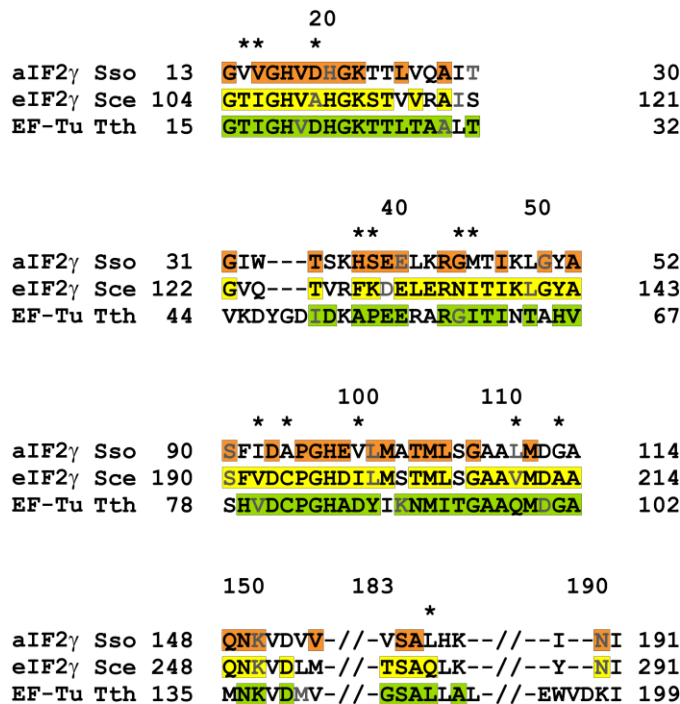


# Supporting Information



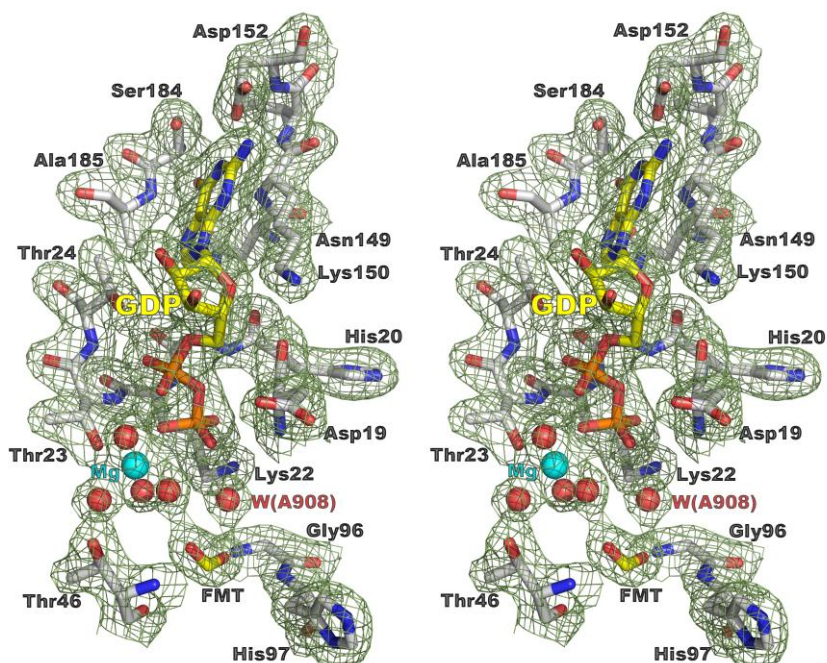
(a)



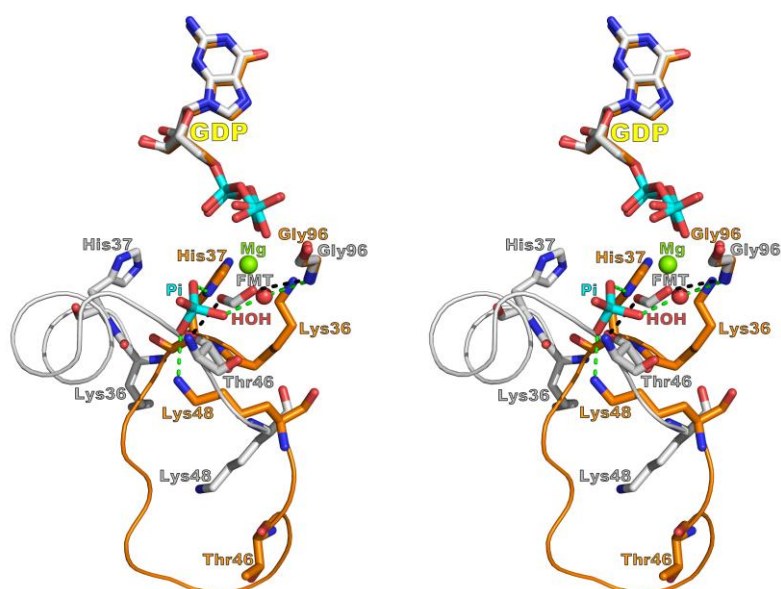
(b)

**Figure S1.** (a) Sequence alignments of the a/eIF2  $\gamma$  subunits and EF-Tu. The numbering of the secondary structure elements is indicated. The functionally important  $\gamma$ L1, P loop, switch 1, and switch 2 regions are boxed. The strongly conserved residues are shown in yellow. Every 10-th amino acid residue is shown in grey. (b) Sequence alignments of the a/eIF2  $\gamma$  subunits and EF-Tu

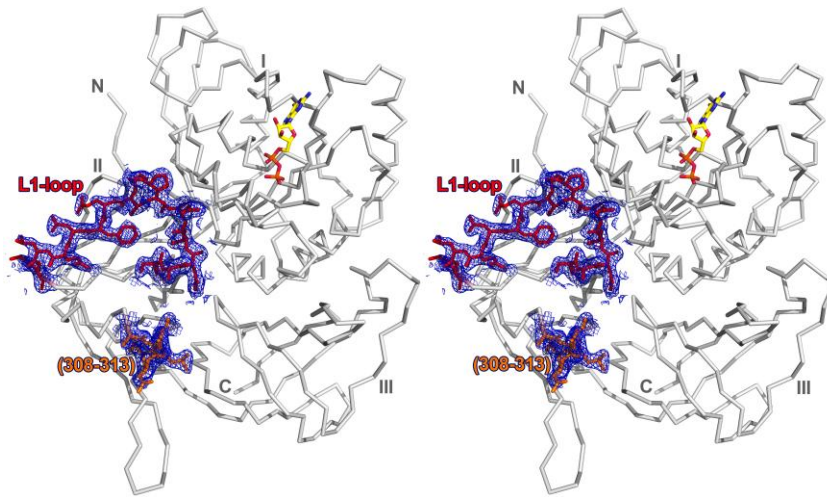
nucleotide binding pockets and surrounding regions. The conserved residues are shown in orange for archaea, yellow for eukaryotes and light green for EF-Tu. Every 10-th amino acid residue is shown in grey.



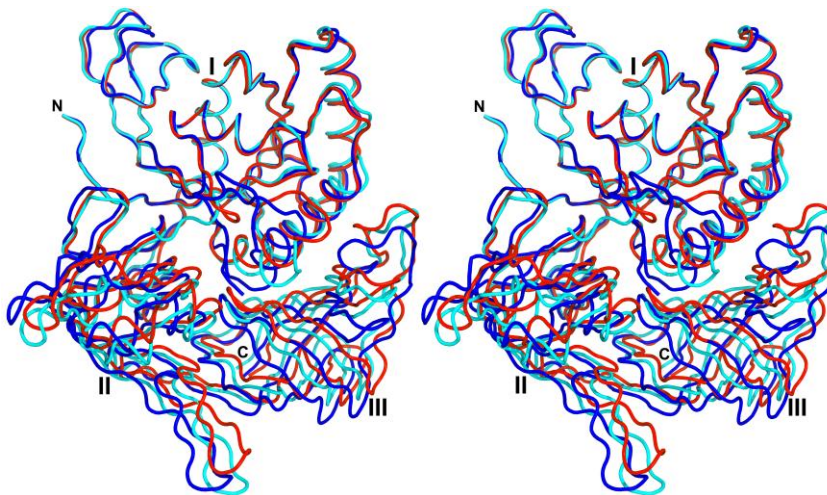
**Figure S2.** The nucleotide-binding pocket of the aIF2 $\gamma$ •GDP•formate complex. The orientation of the molecule is identical to that shown in Fig.4. The electron density was contoured at the level of 1 $\sigma$ . The formate ion is clearly visible on the map.



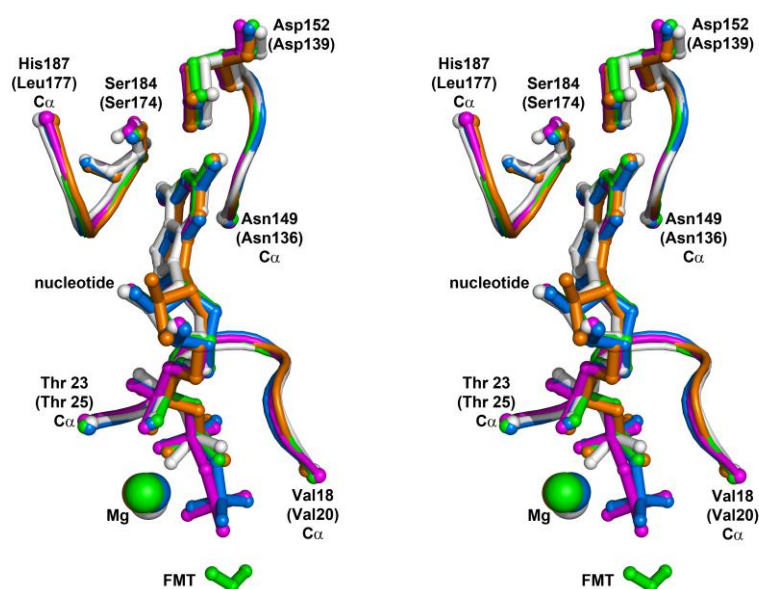
**Figure S3.** The superposition of the nucleotide-binding pockets of the S2 (grey) and Sso aIF2 $\alpha$ 3 $\beta$  $\gamma$  structures (Yatime *et al.*, 2007) (orange) both in the GDP-bound ON state. Hydrogen bonds formed by the formate and Pi ions are shown by dotted lines (cyan for Pi and black for formate). Conformations of the switch 1 regions are dramatically different.



**Figure S4.** The new conformation of the  $\gamma$ L1 and 308-313 loops in the S2 structure. The electron density was contoured at the level of  $1\sigma$ . Positions of both loops in the wild-type and mutant (F221A, K225A and R280A) aIF2 $\gamma$ •GDP•formate complexes are identical.



**Figure S5.** Superposition of the S1, S3 and S4 structures (ON, OFF, and nucleotide-free states, correspondingly). The S1, S3 and S4 structure are shown in red, blue and cyan, correspondingly. The C $\alpha$  atoms of the domain I  $\beta$ -sheet were superimposed. In the S4 structure, domain arrangement is intermediate between that in the active and inactive states.



**Figure S6.** Superposition of the conserved parts of the nucleotide-binding pockets of aIF2 $\gamma$  (structures S1 (magenta), S2 (green) and S3 (orange)) and EF1A (PDB code 1EXM (ON- state, blue) and PDB code 1TUI (OFF- state, light grey)). The switch 1 and switch 2 region are not shown.