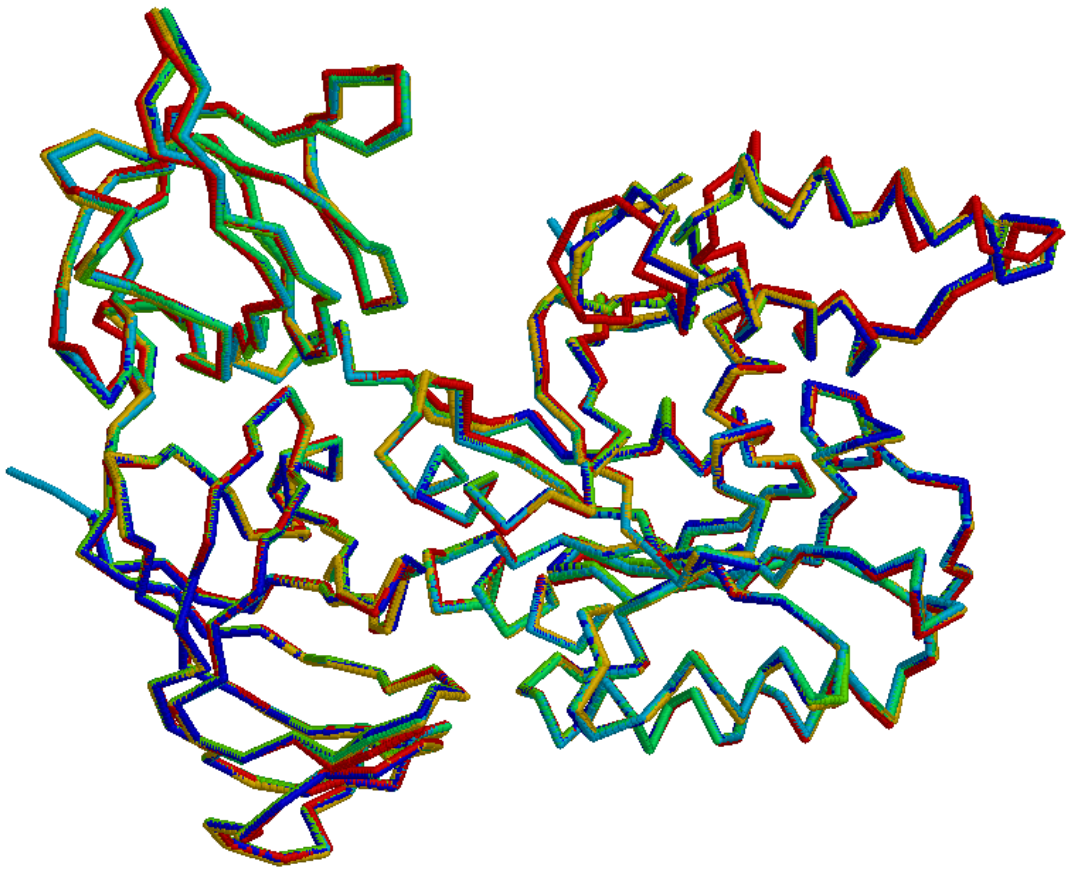
Supplementary file S1: Yeast crystal structure comparison.

(A)

PDB ID	Reference	Resolution	eEF1A	eEF1Bα	Ligand
1F60	[1]	1.67 Å	A: 2-441	B: 1117-1206	-
1G7C	[2]	2.05 Å	A: 4-443	B: 1117-1206	GDPnP
1IJE	[2]	2.4 Å	A: 4-441	B: 1117-1206	GDP
1IJF	[2]	3.0 Å	A: 2-441	B: 1117-1206	GDP-Mg^{2+}
2B7B	[3]	2.6 Å	A: 2-441	B: 1117-1206 (K205A)	GDP
2B7C	[3]	1.8 Å	A: 5-441	B: 1117-1206 (K205A)	-

(B)



(C)

PDB ID	1F60	1G7C	1IJE	1IJF	2B7B	2B7C
1F60						
1G7C	0.26 Å (438 aa)					
1IJE	0.27 Å (438 aa)	0.18 Å (438 aa)				
1IJF	0.13 Å (440 aa)	0.29 Å (438 aa)	0.30 Å (438 aa)			
2B7B	0.29 Å (440 aa)	0.33 Å (438 aa)	0.31 Å (438 aa)	0.32 Å (440 aa)		
2B7C	0.69 Å (437 aa)	0.68 Å (437 aa)	0.68 Å (437 aa)	0.72 Å (437 aa)	0.70 Å (437 aa)	

(A) Table depicting the six different yeast eEF1A crystal structures in the Protein Data Bank (PDB) [4], resolution, PDB chains and solved residue lengths, along with each of their corresponding interacting eEF1Bα proteins and ligands. **(B)** MultiProt [5,6] structural superposition of all six eEF1A crystal structures highlights the structural conservation among them. Each structure color-coded differently. **(C)** Table depicting the pair-wise structural comparisons for all vs. all yeast crystal structures. The Combinatorial Extension [7] calculated Cα root mean square deviation (RMSD) is shown in Angstroms Å along with the structural alignment length between the two proteins. The closeness of the structures is evident in this table.

References:

1. Andersen GR, Pedersen L, Valente L, Chatterjee I, Kinzy TG, et al. (2000) Structural basis for nucleotide exchange and competition with tRNA in the yeast elongation factor complex eEF1A:eEF1Balpha. Mol Cell 6: 1261-1266.
2. Andersen GR, Valente L, Pedersen L, Kinzy TG, Nyborg J (2001) Crystal structures of nucleotide exchange intermediates in the eEF1A-eEF1Balpha complex. Nat Struct Biol 8: 531-534.

3. Pittman YR, Valente L, Jeppesen MG, Andersen GR, Patel S, et al. (2006) Mg2+ and a key lysine modulate exchange activity of eukaryotic translation elongation factor 1B alpha. J Biol Chem 281: 19457-19468.
4. Berman HM, Westbrook J, Feng Z, Gilliland G, Bhat TN, et al. (2000) The Protein Data Bank. Nucleic Acids Res 28: 235-242.
5. Shatsky M, Nussinov R, Wolfson HJ (2002) MultiProt - A multiple protein structural alignment algorithm. Algorithms in Bioinformatics, Proceedings 2452: 235-250.
6. Shatsky M, Nussinov R, Wolfson HJ (2004) A method for simultaneous alignment of multiple protein structures. Proteins-Structure Function and Bioinformatics 56: 143-156.
7. Shindyalov IN, Bourne PE (1998) Protein structure alignment by incremental combinatorial extension (CE) of the optimal path. Protein Eng 11: 739-747.