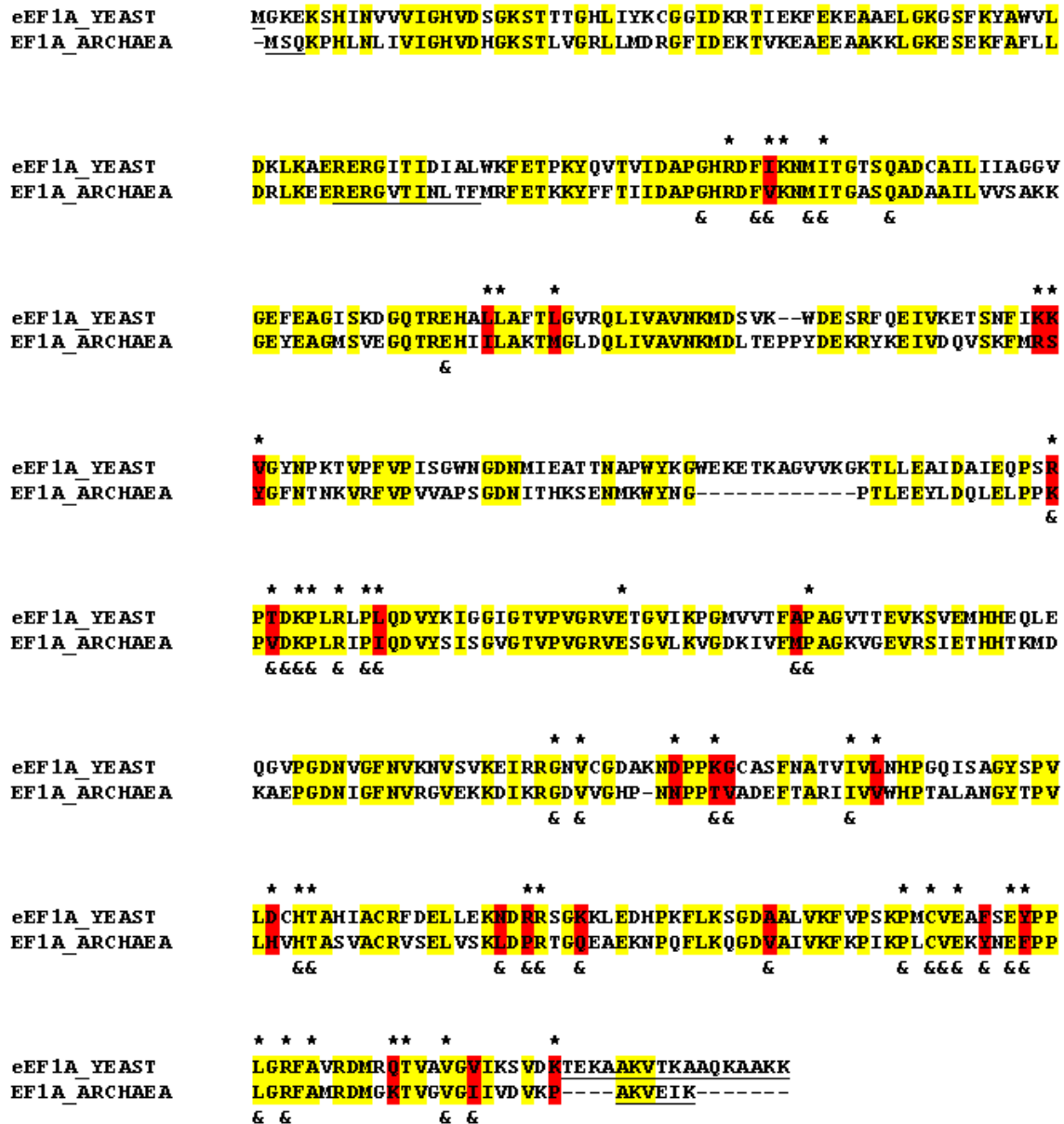


Supplementary file S4: Sequence alignment between archaeal EF1A (*Sulfolobus solfataricus*) and yeast (*Saccharomyces cerevisiae*) eEF1A.



Pair-wise sequence alignment between eEF1A from yeast vs. EF1A from archaea. From the structures of yeast and archaea, residues involved in domain-domain contacts are depicted as follows: \* = yeast amino acid residue involved in domain-domain contact, when bound to eEF1B $\alpha$ ; & = archaea amino acid residue involved in domain-domain contact, free of eEF1B $\alpha$ ; underlined residues = not present in the crystal structures. Identical positions in the alignment are shown with a yellow background; variable

positions involved in a domain-domain contact are highlighted with a red background. A total of 42 residues are involved in domain-domain contacts in the eEF1B $\alpha$ -bound yeast structure, 17 are non-identical at the equivalent position in the archaeal sequence, and conversely, there are 40 residues involved in domain-domain contacts within the unbound archaeal structure, 14 of which are non-identical in the yeast sequence.