**Protein architecture and evolution of the polyadenylation machinery in the fungal kingdom (and higher eukaryotes?)**

Questions of interest:

1. **What are the core components of the polyadenylation machinery in fungi?**
2. **What domains are conserved and which ones have changed (exon shuffling)?**
3. **What protein subunits have changed or are missing?** We already know that CFI 25/68 are not present in yeast. Hrp1 is not present in all fungi.
4. **Include microsporia fungi in the analysis** (The microsporidia constitute a phylum (Microspora) of spore-forming unicellular parasites. They were once thought to be protists but are now known to be fungi.) They have very small genome (3 Mb). I don’t know how many are publically available.
5. **any correlation with fungal lifestyles (pathogenic, symbiotic, saprophytic)?**
6. **Is it possible to predict in silico RNA sequences recognized by the polyadenylation machinery?** It will be important to check **structural features** conserved among protein subunits of the polyadenylation machinery – there is a paper about it. “Phylogenetic analysis of mRNA polyadenylation sites reveals a role of transposable elements in evolution of the 3’-end of genes Ju Youn Lee, Zhe Ji and Bin Tian “
7. **How do the RNA sequences recognized by the polyadenylation machinery differ among organisms?** **Correlation among sequences and domain structure?** (if it is possible to do this in silico…
8. Look in the literature reconstitution experiments for polyadenylation in vitro to know what proteins are sufficient for cleavage and polyadenylation. (there is a table with this information. I can pass it if you don’t have it)

Additional questions if time allows it:

- what happen in plants , animals and oomycetes?

- Are we looking at archaebacteria? (archaea possess genes and several metabolic pathways that are more closely related to those of eukaryotes: notably the enzymes involved in transcription and translation)