**Cover letter**

* Many new functions of PPOs are continuously being discovered
* We put them into context – how are all the characterized PPOs related to each other sequence-wise
* We describe a deep gene duplication that led to the two overall types of PPO
* We investigate the genomic distribution
* We give an overview of the conserved residues
* Detailed analysis of the short fungal – different genomic distribution in ascos and basidios

How our methodology is different from the Aguilera paper:

* It is difficult to capture all the diversity of the PPOs and have a small enough number of sequences to produce a phylogenetic tree. We used one proteome from each taxonomic class to get a representative set of proteomes. Using a Blast search based on characterized proteins to retrieve PPO sequences from the proteomes creates a bias, and may exclude some proteins that are distant from the seed sequences. Instead, we included all hits of Pfam PF00264 from the proteomes. Thus observed several groups, that were not shown in the Aguilera paper: b (cnidaria), c (oomyetes), d and e (zoopagomycetes), f (fungal short PPOs)
* Aguilera only defined two groups of the PF00264 domain. Only one of them is monophyletic: the gamma subgroup.