Figure S2 Phylogeny of *A. fumigatus* and *S. cerevisiae* protein phosphatases. The optimal tree for the *A. fumigatus* and *S. cerevisiae* phosphatases is represented. The tree was inferred using the Neighbourg-Joining Method. The bootstrap values calculated on 500 replicates are indicated on the tree branches. When homologues are available, *A. fumigatus* proteins were named according to the *S. cerevisiae* protein names (see http://www.yeastgenome.org) (see Table 1). Sequences were aligned with ClustalW and the tree was constructed by using MEGA6. Sequences are available in File S1.