

Supplementary Fig. 10

Supplementary Fig. 10. A phylogenetic tree of *A. nidulans* PrmB orthologues. A maximum likelihood phylogenetic tree built from the protein sequence of *A. nidulans* PrmB and its orthologues from fungi (in blue), metazoa (in magenta) and bacteria (in turquoise). The SH+aRT support (%) / ultrafast bootstrap support (%) values at each node are given in the parentheses. Four major clades – Clade A, B, C and Clade D are indicated.