



**Figure 7 – figure supplement 4:** Amino acid alignment of GH25 sequences from different fungi (see attached list –‘GH25 with accession number’, for full length sequences). The protein sequences were obtained from the NCBI database. Alignment was achieved using the PRALINE multiple sequence alignment program with default parameters. The scoring scheme works from 0 for the least conserved alignment position, up to 10 (indicated by \*) for the most conserved alignment position. A conserved active-site DxE motif has been predicted for glycoside hydrolase family 25. Sequences tested from different basidiomycete, ascomycete and Chytrids, have the active site residue conserved (purple box).