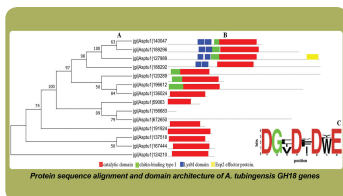

About the Cover



The photo depicts the protein sequence alignment and domain architecture of the GH18 (glycoside hydrolase family 18) genes of *Aspergillus tubingensis*, a common fungal species. The GH18 genes of *A. tubingensis* and another species, *Daldinia eschscholzii*, were found to contain variability in amino acid sequences and additional domain architectures. Moreover, both have been proven capable of rapidly degrading chitin within 3–5 days of incubation. Such properties make these fungi ideal sources of chitinases for enzyme mechanistic studies and biotechnology applications (*e.g.*, shell waste management in the crustacean processing industry). To learn more, go to page 575–582.

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