

# Proteome analysis for pathogenicity and new diagnostic markers for *Aspergillus fumigatus*.

Kniemeyer O, Lessing F, Brakhage AA (2009) Proteome analysis for pathogenicity and new diagnostic markers for *Aspergillus fumigatus*. *Med Mycol* 47 Suppl 1, S248-S254.

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## Abstract

With the completion of the *Aspergillus fumigatus* genome it is now possible to study protein regulation on a global scale. One of the most suitable protein separation techniques is based on 2D-gel electrophoresis, which allows the separation of proteins based on their charge and size in a gel matrix. In addition, gel-free proteomics techniques based on liquid-chromatography coupled with mass spectrometry have gained importance. With the application of proteomic tools a comprehensive overview about the proteins of *A. fumigatus* present or induced during environmental changes and stress conditions can be obtained. For *A. fumigatus*, several proteomic studies have already been published including the response of the fungus to oxidative stress that induced the up-regulation of many proteins including catalases and thioredoxin peroxidase. Since many of the identified proteins/genes were apparently regulated by a putative *Saccharomyces cerevisiae* Yap1 homolog, the corresponding gene of *A. fumigatus* was identified, designated *Afyap1* and further characterized. In addition, some of the gene products expressed under stress conditions are also known fungal antigens, such as the thioredoxin peroxidase *AspF3*. Thus, besides pathogenicity studies, proteomics also delivers the tools to screen for new

antigens which could improve the diagnosis of diseases caused by *A. fumigatus*.

## Beteiligte Forschungseinheiten

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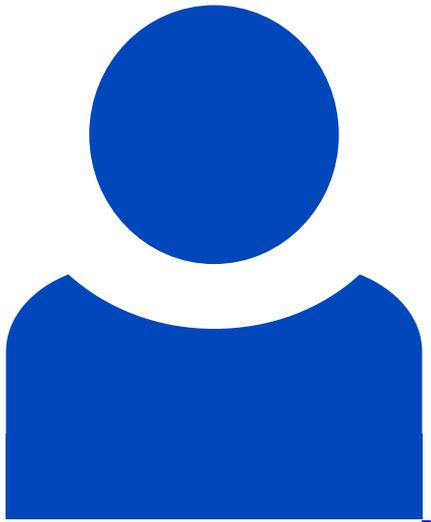
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