

# Redox Proteomic Analysis Reveals Oxidative Modifications of Proteins by Increased Levels of Intracellular Reactive Oxygen Species during Hypoxia Adaptation of *Aspergillus fumigatus*.

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## Projects

Investigation of the stress response system of *A. fumigatus* by redox proteomics  
[Details](#)

## Abstract

*Aspergillus fumigatus* faces abrupt changes in oxygen concentrations at the site of infection. An increasing number of studies has demonstrated that elevated production of intracellular reactive oxygen species (ROS) under low oxygen conditions plays a regulatory role in modulating cellular responses for adaptation to hypoxia. To learn more about this process in *A. fumigatus*, intracellular ROS production during hypoxia has been determined. The results confirm increased amounts of intracellular ROS in *A. fumigatus* exposed to decreased oxygen levels. Moreover, nuclear accumulation of the major oxidative stress regulator AfYap1 is observed after low oxygen cultivation. For further analysis, iodoTMT labeling of redox-sensitive cysteine residues is applied to identify proteins that are reversibly oxidized. This analysis reveals that proteins with important roles in maintaining redox balance and protein folding, such as the thioredoxin Asp f 29 and the disulfide-isomerase PdiA, undergo substantial thiol modification under hypoxia. The data also show that the mitochondrial respiratory complex IV assembly protein Coa6 is significantly oxidized by hypoxic ROS. Deletion of the corresponding gene results in a complete absence of hypoxic growth, indicating the importance of complex IV during adaptation of *A. fumigatus* to oxygen-limiting conditions.

## Identifier

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