

Isolation and amplification of fungal RNA for microarray analysis from host samples.

Lüttich A, Brunke S, Hube B (2012) Isolation and amplification of fungal RNA for microarray analysis from host samples. In: Brand AC, MacCallum DM (eds.) Methods in Molecular Biology. Host-fungus interactions. Methods and Protocols. 845, pp. 411-421. Humana Press (Springer).

[Details](#)



Abstract

Transcriptional profiling is a powerful tool to investigate the interplay between pathogens and their hosts. For several pathogenic fungi, like *Candida albicans*, genome-wide microarrays are now available, and alternative methods, such as Serial Analysis of Gene Expression (SAGE) or RNASeq, are becoming increasingly widespread. In other chapters of this book, in vitro models for studying fungal infections are described. Here, we provide information on methods to isolate fungal RNA from these models and to investigate transcriptional changes during experimental infections. The protocols focus on *C. albicans* but are applicable to many other fungi with minor modifications.

Beteiligte Forschungseinheiten

[Mikrobielle Pathogenitätsmechanismen](#) [Bernhard Hube](#) [Mehr erfahren](#)

Leibniz-HKI-Autor*innen



Sascha Brunke

[Details](#)



Bernhard Hube

[Details](#)



Anja Wartenberg

[Details](#)

Identifier

doi: 10.1007/978-1-61779-539-8

PMID: 22328391