Comparison of transcriptome technologies in the pathogenic fungus *Aspergillus fumigatus* reveals novel insights into the genome and MpkA dependent gene expression.

Müller S, Baldin C, Groth M, Guthke R, Kniemeyer O, Brakhage AA, Valiante V (2012) Comparison of transcriptome technologies in the pathogenic fungus *Aspergillus fumigatus* reveals novel insights into the genome and MpkA dependent gene expression. *BMC Genomics* 13, 519.

Details

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Abstract

The filamentous fungus Aspergillus fumigatus has become the most important airborne fungal pathogen causing life-threatening infections in immuno-compromised patients. Recently developed high-throughput transcriptome and proteome technologies, such as microarrays, RNA deep-sequencing, and LC-MS/MS of peptide mixtures, are of enormous value for systematically investigating pathogenic organisms. In the field of infection biology, one of the priorities is to collect and standardise data, in order to generate datasets that can be used to investigate and compare pathways and gene responses involved in pathogenicity. The

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Topics

RNA-Seq data analysis and modeling

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