

A genome-wide functional genomics approach identifies susceptibility pathways to fungal bloodstream infection in humans.

Jaeger M, Matzaraki V, Aguirre-Gamboa R, Gresnigt MS, Chu X, Johnson MD, Oosting M, Smeekens SP, Withoff S, Jonkers I, Perfect JR, van de Veerdonk FL, Kullberg BJ, Joosten LAB, Li Y, Wijmenga C, Netea MG, Kumar V (2019) A genome-wide functional genomics approach identifies susceptibility pathways to fungal bloodstream infection in humans. *J Infect Dis* 220(5), 862-872.

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Abstract

Candidemia, one of the most common causes of fungal bloodstream infection, leads to mortality rates up to 40% in affected patients. Understanding genetic mechanisms for differential susceptibility to candidemia may aid in designing host-directed therapies.

Leibniz-HKI-Authors



Mark Gresnigt

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Topics

[Immunology of Fungal Infections](#)

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