

Publications

Mirhakkak MH^{*}, Chen X^{*}, Heinekamp T, Sae-Ong T, Xu LL, Ni Y, Kurzai O, Barber AE, Brakhage AA, Boutin S, Schäuble S[#], Panagiotou G[#] (2023) Genome-scale Metabolic modeling of *Aspergillus fumigatus* strains reveals growth dependencies on the lung microbiome. *Nat Commun* 14(1), 4369.

Schruefer S, Pschibul A, Wong SSW, Sae-Ong T, Wolf T, Schäuble S, Panagiotou G, Brakhage AA, Aimanianda V, Kniemeyer O, Ebel F (2023) Distinct transcriptional responses to fludioxonil in *Aspergillus fumigatus* and its Δ tcsC and Δ skn7 mutants reveal a crucial role for Skn7 in the cell wall reorganizations triggered by this antifungal. *BMC Genomics* 24(1), 684.

Barber AE^{*}, Sae-Ong T^{*}, Kang K, Seelbinder S, Li J, Walther G, Panagiotou G[#] & Kurzai O[#] (2021) *Aspergillus fumigatus* pan-genome analysis identifies genetic variants associated with human infection. *Nat Microbiol* 6(12), 1526-1536.

Barber AE, Riedel J, Sae-Ong T, Kang K, Brabetz W, Panagiotou G, Deising HB, Kurzai O (2020) Effects of agricultural fungicide use on *Aspergillus fumigatus* abundance, antifungal susceptibility, and population structure. *mBio* 11(6), e02213-20.

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