

Dr. Franziska Gerwien

Alumni

Publications

Böttcher B, Driesch D, Krüger T, Garbe E, Gerwien F, Kniemeyer O, Brakhage AA, Vylkova S (2022) Impaired amino acid uptake leads to global metabolic imbalance of *Candida albicans* biofilms. *NPJ Biofilms Microbiomes* 8(1), 78.

[Details](#)



Brandt P, Gerwien F, Wagner L, Krüger T, Ramírez-Zavala B, Mirhakkak MH, Schäuble S, Kniemeyer O, Panagiotou G, Brakhage AA, Morschhäuser J, Vylkova S (2022) *Candida albicans* SR-like protein kinases regulate different cellular processes: Sky1 is involved in control of ion homeostasis, while Sky2 is important for dipeptide utilization. *Front Cell Infect Microbiol* 12, 850531.

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Garbe E, Gerwien F, Driesch D, Müller T, Böttcher B, Gräler M, Vylkova S (2022) Systematic metabolic profiling identifies *de novo* sphingolipid synthesis as hypha associated and essential for *Candida albicans* filamentation. *mSystems* 7(6), e0053922.

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Garbe E, Miramón P, Gerwien F, Ueberschaar N, Hansske-Braun L, Brandt P, Böttcher B, Lorenz M, Vylkova S (2022) GNP2 encodes a high-specificity proline permease in *Candida albicans*. *mBio* 13(1), e0314221.

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Mogavero S, Höfs S, Lauer AN, Müller R, Brunke S, Allert S, Gerwien F, Groth S, Dolk E, Wilson D, Gutschmann T, Hube B (2022) Candidalysin is the hemolytic factor of *Candida albicans*. *Toxins (Basel)* 14(12), 874.

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Kämmer P, McNamara S^{*}, Wolf T, Conrad T, Allert S, Gerwien F, Hänniger K, Kurzai O, Guthke R, Hube B, Linde J, Brunke S (2020) Survival strategies of pathogenic *Candida* species in human blood show independent and specific adaptations. *mBio* 11(5), e02435-20.

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Gerwien F, Skrahina V, Kasper L, Hube B, Brunke S (2018) Metals in fungal virulence. *FEMS Microbiol Rev* 42(1), fux050. (Review)

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Gerwien F, Safyan A, Wisgott S, Brunke S, Kasper L, Hube B (2017) The fungal pathogen *Candida glabrata* does not depend on surface ferric reductases for iron acquisition. *Front Microbiol* 8, 1055.

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Gerwien F, Safyan A, Wisgott S, Hille F, Kämmer P, Linde J, Brunke S, Kasper L, Hube B (2016) A novel hybrid iron regulation network combines features from pathogenic and non-pathogenic yeasts. *mBio* 7(5), e01782-16.

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