

Publications

Kämmer P, McNamara S*, Wolf T, Conrad T, Allert S, Gerwien F, Hünninger 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.

Magnusson R, Mariotti GP, Köpsén M, Lövfors W, Gawel DR, Jörnsten R, Linde J, Nordling TEM, Nyman E, Schulze S, Nestor CE, Zhang H, Cedersund G, Benson M, Tjärnberg A, Gustafsson M (2017) LASSIM—A network inference toolbox for genome-wide mechanistic modeling. *PLOS Comput Biol* 13(6), e1005608.

Böhringer M, Pohlers S, Schulze S, Albrecht-Eckardt D, Piegsa J, Weber M, Martin R, Hünninger K, Linde J, Guthke R, Kurzai O (2016) *Candida albicans* infection leads to barrier breakdown and a MAPK/NF- κ B mediated stress response in the intestinal epithelial cell line C2BB₇. *Cellular Microbiology* 18(7), 889-904.

Schulze S, Schleicher J, Guthke R, Linde J (2016) How to Predict Molecular Interactions between Species? *Front Microbiol* 7, 442.

Linde J, Schulze S, Henkel SG, Guthke R (2015) Data- and knowledge-based modeling of gene regulatory networks: An update *EXCLI Journal - Experimental and Clinical Sciences* 14, 346-378.

Schulze S, Henkel SG, Driesch D, Guthke R, Linde J (2015) Computational prediction of molecular pathogen-host interactions based on dual transcriptome data *Front Microbiol* 6, 65.

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