

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.

Barber AE*, Weber M, Kaerger K, Linde J, Gölz H, Duerschmied D, Markert A, Guthke R, Walther G, Kurzai O (2019) Comparative genomics of serial *Candida glabrata* isolates and the rapid acquisition of echinocandin resistance during therapy. *Antimicrob Agents Chemother* 63(2), e01628-18.

Zoran T, Weber M, Springer J, White PL, Bauer J, Schober A, Löffler C, Seelbinder B, Hünninger K, Kurzai O, Scherag A, Schäuble S, Morton CO, Einsele H, Linde J, Löffler J (2019) Treatment with etanercept and low monocyte concentration contribute to the risk of invasive aspergillosis in patients post allogeneic stem cell transplantation. *Sci Rep* 9(1), 17231.

Conrad T*, Kniemeyer O, Henkel SG, Krüger T, Mattern DJ, Valiante V, Guthke R, Jacobsen ID, Brakhage AA, Vlaic S, Linde J (2018) Module-detection approaches for the integration of multilevel omics data highlight the comprehensive response of *Aspergillus fumigatus* to caspofungin. *BMC Syst Biol* 12(1), 88.

Sieber P, Voigt K, Kämmer P, Brunke S, Schuster S, Linde J (2018) Comparative study on alternative splicing in human fungal pathogens suggests its involvement during host invasion. *Front Microbiol* 9, 2313.

Wolf T, Kämmer P, Brunke S, Linde J (2018) Two's company: studying interspecies relationships with dual RNA-seq. *Curr Opin Microbiol* 42, 7-12. (Review)

Dix A, Czakai K, Leonhardt I, Schäferhoff K, Bonin M, Einsele H, Guthke R, Kurzai O, Löffler J, Linde J (2017) Specific and novel microRNAs are regulated as response to fungal infection in human dendritic cells. *Front Microbiol* 8, 270.

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 C2BB_e1. *Cellular Microbiology* 18(7), 889-904.

Czakai K, Leonhardt I, Dix A, Bonin M, Linde J, Einsele H, Kurzai O, Löffler J (2016) Krüppel-like Factor 4 modulates interleukin-6 release in human dendritic cells after *in vitro* stimulation with *Aspergillus fumigatus* and *Candida albicans* *Sci Rep* 6, 27990.

Dix A, Czakai K, Springer J, Fliesser M, Bonin M, Guthke R, Schmitt AL, Einsele H, Linde J, Löffler J (2016) Genome-wide Expression Profiling Reveals S100B as Biomarker for Invasive Aspergillosis. *Front Microbiol* 7, 320.

Dix A, Vlaic S, Guthke R, Linde J (2016) Use of systems biology to decipher host-pathogen

interaction networks and predict biomarkers. *Clin Microbiol Infect* 22(7), 600-606.

Freihorst D, Brunsch M, Wirth S, Krause K, Kniemeyer O, Linde J, Kunert M, Boland W, Kothe E (2016) Smelling the difference: Transcriptome, proteome and volatilome changes after mating. *Fungal Genet Biol* 112, 2-11.

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.

Guthke R, Gerber S, Conrad T, Vlaic S, Durmus S, Cakir T, Sevilgen E, Shelest E, Linde J (2016) Data-based reconstruction of gene regulatory networks of fungal pathogens. *Front Microbiol* 7, 570.

Hebecker B, Vlaic S, Conrad T, Bauer M, Brunke S, Kapitan M, Linde J, Hube B, Jacobsen ID (2016) Dual-species transcriptional profiling during systemic candidiasis reveals organ-specific host-pathogen interactions. *Sci Rep* 6, 36055.

Hölzer M, Krähling V, Amman F, Barth E, Bernhart SH, Carmelo VAO, Collatz M, Doose G, Fallmann F, Feldhahn LM, Fricke M, Eggenhofer F, Ewald J, Linde J, Gebauer J, Gruber AJ, Hufsky F, Indrischek H, Mostajo NB, Ochsenreiter R, Riege K, Kanton S, Rivarola-Duarte L, Sahyoun AH, Saunders SJ, Seemann SE, Tanzer A, Vogel B, Wehner S, Wolfinger MT, Backofen R, Gorodkin J, Grosse I, Hofacker I, Hoffmann S, Kaleta C, Stadler PF, Becker S, Marz M (2016) Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells *Sci Rep* 6, 34589.

Horn F, Linde J, Mattern DJ, Walther G, Guthke R, Scherlach K, Martin K, Brakhage AA, Petzke L, Valiante V (2016) Draft genome sequences of fungus *Aspergillus calidoustus*. *Genome Announc* 4(2), e00102-16.

Manchanda H, Seidel N, Blaess MF, Claus RA, Linde J, Slevogt H, Sauerbrei A, Guthke R, Schmidtke M (2016) Differential Biphasic Transcriptional Host Response Associated with Coevolution of Hemagglutinin Quasispecies of Influenza A Virus *Front Microbiol* 7, 1167.

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

Altwasser R, Baldin C, Weber J, Guthke R, Kniemeyer O, Brakhage AA, Linde J, Valiante V (2015) Network Modeling Reveals Cross Talk of MAP Kinases during Adaptation to Caspofungin Stress in *Aspergillus fumigatus*. *PLOS One* 10(9), e0136932.

Brunsch M, Schubert D, Gube M, Ring C, Hanisch L, Linde J, Krause K, Kothe E (2015) Dynein Heavy Chain, Encoded by Two Genes in Agaricomycetes, Is Required for Nuclear Migration in *Schizophyllum commune*. *PLOS One* 10(8), e0135616.

Dix A, Hünninger K, Weber M, Guthke R, Kurzai O, Linde J (2015) Biomarker-based classification of bacterial and fungal whole-blood infections in a genome-wide expression study. *Front Microbiol* 6, 171.

Horn F, Habel A, Scharf DH, Dworschak J, Brakhage AA, Guthke R, Hertweck C, Linde J (2015) Draft Genome Sequence and Gene Annotation of the Entomopathogenic Fungus *Verticillium hemipterigenum*. *Genome Announc* 3(1), e01439-14.

- Horn F, Linde J, Mattern DJ, Walther G, Guthke R, Brakhage AA, Valiante V (2015) Draft Genome Sequence of the Fungus *Penicillium brasilianum* MG11. *Genome Announc* 3(5), e00724-15.
- Horn F, Üzüm Z, Möbius N, Guthke R, Linde J, Hertweck C (2015) Draft Genome Sequences of Symbiotic and Nonsymbiotic *Rhizopus microsporus* Strains CBS 344.29 and ATCC 62417. *Genome Announc* 3(1), pii: e01370-14.
- Linde J, Duggan S, Weber M, Horn F, Sieber P, Hellwig D, Riege K, Marz M, Martin R, Guthke R, Kurzai O (2015) Defining the transcriptomic landscape of *Candida glabrata* by RNA-Seq. *Nucleic Acids Res* 43(3), 1392-1406.
- 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.
- Priebe S, Kreisel C, Horn F, Guthke R, Linde J (2015) FungiFun2: a comprehensive online resource for systematic analysis of gene lists from fungal species. *Bioinformatics* 31(3), 445-446.
- Schleicher J(+), Conrad T(+), Gustafsson M, Cedersund G, Guthke R, Linde J (2015) Facing the challenges of multiscale modelling of bacterial and fungal pathogen-host interactions *Briefings in Functional Genomics* 2016, pii: elv064. (Review)
- 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.
- Wagner K, Linde J, Krause K, Gube M, Koestler T, Sammer D, Kniemeyer O, Kothe E (2015) *Tricholoma vaccinum* host communication during ectomycorrhiza formation. *FEMS Microbiol Ecol* 91(11),
- Hillmann F, Linde J, Beckmann N, Cyrulies M, Strassburger M, Heinekamp T, Haas H, Guthke R, Kniemeyer O, Brakhage AA (2014) The novel globin protein fungoglobulin is involved in low oxygen adaptation of *Aspergillus fumigatus*. *Mol Microbiol* 93(3), 539-553.
- Horn F, Schroeckh V, Netzker T, Guthke R, Brakhage AA, Linde J (2014) Draft genome sequence of *Streptomyces iranensis*. *Genome Announc* 2(4), e00616-14.
- Linde J, Schwartze V, Binder U, Lass-Flörl C, Voigt K, Horn F (2014) *De Novo* Whole-Genome Sequence and Genome Annotation of *Lichtheimia ramosa*. *Genome Announc* 2(5), e00888-14.
- Ramachandra S, Linde J, Brock M, Guthke R, Hube B, Brunke S (2014) Regulatory networks controlling nitrogen sensing and uptake in *Candida albicans*. *PLOS One* 9(3), e92734.
- Schwartze VU, Winter S, Shelest E, Marcet-Houben M, Horn F, Wehner S, Linde J, Valiante V, Sammeth M, Riege K, Nowrousian M, Kaerger K, Jacobsen ID, Marz M, Brakhage AA, Gabaldón T, Böcker S, Voigt K (2014) Gene expansion shapes genome architecture in the human pathogen *Lichtheimia corymbifera*: an evolutionary genomics analysis in the ancient terrestrial Mucorales (Mucoromycotina). *PLOS Genetics* 10(8), e1004496.
- Wartenberg A, Linde J, Martin R, Schreiner M, Horn F, Jacobsen ID, Jenull S, Wolf T, Kuchler K, Guthke R, Kurzai O, Forche A, d'Enfert C, Brunke S, Hube B (2014) Microevolution of *Candida albicans* in macrophages restores filamentation in a nonfilamentous mutant. *PLOS Genet* 10(12), e1004824.

Palige K, Linde J, Martin R, Böttcher B, Citiulo F, Sullivan DJ, Weber J, Staib C, Rupp S, Hube B, Morschhäuser J, Staib P (2013) Global transcriptome sequencing identifies chlamydospore specific markers in *Candida albicans* and *Candida dubliniensis*. *PLoS One* 8(4), e61940.

Altwasser R, Linde J, Buyko E, Hahn U, Guthke R (2012) Genome-wide scale-free network inference for *Candida albicans*. *Front Microbiol* 3, 51.

Guthke R, Linde J, Mech F, Figge MT (2012) Systems biology of microbial infection. *Front Microbiol* 3, 328.

Linde J, Hortschansky P, Fazius E, Brakhage AA, Guthke R, Haas H (2012) Regulatory interactions for iron homeostasis in *Aspergillus fumigatus* inferred by a Systems Biology approach. *BMC Syst Biol* 6, 6.

Tierney L, Linde J, Müller S, Brunke S, Molina JC, Hube B, Schöck U, Guthke R, Kuchler K (2012) An interspecies regulatory network inferred from simultaneous RNA-seq of *Candida albicans* invading innate immune cells. *Front Microbiol* 3, 85.

Vlaic S, Schmidt-Heck W, Matz-Soja M, Marbach E, Linde J, Meyer-Baese A, Zellmer S, Guthke R, Gebhardt R (2012) The extended TILAR approach: a novel tool for dynamic modeling of the transcription factor network regulating the adaption to in vitro cultivation of murine hepatocytes. *BMC Syst Biol* 6, 147.

Priebe S, Linde J, Albrecht D, Guthke R, Brakhage AA (2011) FungiFun: A web-based application for functional categorization of fungal genes and proteins. *Fungal Genet Biol* 48(4), 353-358.

Linde J, Wilson D, Hube B, Guthke R (2010) Regulatory network modelling of iron acquisition by a fungal pathogen in contact with epithelial cells. *BMC Syst Biol* 4, 148.

Linde J, Olsson B, Lubovac Z (2009) Network Properties for Ranking Predicted miRNA Targets in Breast Cancer. *Adv Bioinformatics* , 182689-182689.

*equal contribution #corresponding author