

## Publications

Chao YY, Puhach A, Frieser D, Arunkumar M, Lehner L, Seeholzer T, Garcia-Lopez A, van der Wal M, Fibi-Smetana S, Dietschmann A, Sommermann T, Ćiković T, Taher L, Gresnigt MS, Vastert SJ, van Wijk F, Panagiotou G, Krappmann D, Groß O, Zielinski CE (2023) Human TH17 cells engage gasdermin E pores to release IL-1 $\alpha$  on NLRP3 inflammasome activation. *Nat Immunol* 24(2), 295-308.

Chen J<sup>\*</sup>, Leal Siliceo S<sup>\*</sup>, Ni Y, Nielsen HB, Xu A, Panagiotou G (2023) Identification of robust and generalizable biomarkers for microbiome-based stratification in lifestyle interventions. *Microbiome* 11(1), 178.

Csader S<sup>\*</sup>, Chen X<sup>\*</sup>, Leung H<sup>\*</sup>, Männistö V, Pentikäinen H, Tauriainen MM, Savonen K, El-Nezami H, Schwab U<sup>#</sup>, Panagiotou G<sup>#</sup> (2023) Gut ecological networks reveal associations between bacteria, exercise and clinical profile in non-alcoholic fatty liver disease patients. *mSystems* [Epub ahead of print]

Faessler E, Hahn U<sup>#</sup>, Schäuble S<sup>#</sup> (2023) GePI: large-scale text mining, customized retrieval and flexible filtering of gene/protein interactions. *Nucleic Acids Res* 51((W1)), W237-W242.

Häder A<sup>#</sup>, Schäuble S<sup>#</sup>, Gehlen J, Thielemann N, Buerfent BC, Schüller V, Hess T, Wolf T, Schröder J, Weber M, Hünninger K, Löffler J, Vylkova S, Panagiotou G, Schumacher J, Kurzai O (2023) Pathogen-specific innate immune response patterns are distinctly affected by genetic diversity. *Nat Commun* 14(1), 3239.

Kelani AA, Bruch A, Riviaccio F, Visser C, Krüger T, Weaver D, Pan X, Schaeuble S, Panagiotou G, Kniemeyer O, Bromley MJ, Bowyer P, Barber AE, Brakhage AA, Blango MG (2023) Disruption of the *A. fumigatus* RNA interference machinery alters the conidial transcriptome. *RNA* 29(7), 1033-1050.

Leung H, Xiong L, Ni Y, Busch A, Bauer M, Press AT, Panagiotou G (2023) Impaired flux of bile acids from the liver to the gut reveals microbiome-immune interactions associated with liver damage. *NPJ Biofilms and microbiomes* 9(1), 35.

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

Ni Y<sup>\*</sup>, Qian L<sup>\*</sup>, Leal Siliceo S<sup>\*</sup>, Long X<sup>\*</sup>, Nychas E, Liu Y, Ismaiah MJ, Leung H, Zhang L, Gao Q, Wu Q, Zhang Y, Jia Xi, Liu S, Yuan R, Zhou L, Wang X, Li Q, Zhao Y, El-Nezami H, Xu A, Xu G<sup>#</sup>, Li H<sup>#</sup>, Panagiotou G<sup>#</sup>, Jia W<sup>#</sup> (2023) Resistant starch decreases intrahepatic triglycerides in NAFLD patients via gut microbiome alterations. *Cell Metab* 35(9), 1530-1547.

Refisch A<sup>#</sup>, Sen ZD, Klassert TE, Busch A, Besteher B, Danyeli LV, Helbing D, Schulze-Späte U, Stallmach A, Bauer M, Panagiotou G, Jacobsen ID, Slevogt H, Opel N, Walter M (2023) Microbiome and immuno-metabolic dysregulation in patients with major depressive disorder with atypical clinical presentation. *Neuropharmacology* 235, 109568. (Review)

Schruefer S, Pschibul A, Wong SSW, Sae-Ong T, Wolf T, Schäuble S, Panagiotou G, Brakhage AA, Amanianda V, Kniemeyer O, Ebel F (2023) Distinct transcriptional responses to fludioxonil in

Aspergillus fumigatus and its  $\Delta$ tcsC and  $\Delta$ skn7 mutants reveal a crucial role for Skn7 in the cell wall reorganizations triggered by this antifungal. *BMC Genomics* 24(1), 684.

Seelbinder B<sup>#</sup>, Lohinai Z<sup>\*</sup>, Vazquez-Urbe R, Brunke S, Chen X, Mirhakkak M, Lopez-Escalera S, Dome B, Megyesfalvi Z, Berta J, Galfy G, Dulka E, Wellejus A, Weiss GJ, Bauer M, Hube B, Sommer MOA, Panagiotou G (2023) *Candida* expansion in the gut of lung cancer patients associates with an ecological signature that supports growth under dysbiotic conditions. *Nat Commun* 14(1), 2673.

Soll D, Arunkumar M, Alkhalaf M, Sun S, Nguyen T, Chu C, Lutz V, Schäuble S, Garcia-Ribelles I, Mueller M, Michalke B, Panagiotou G, Schatzlmaier P, Stockinger H, Schamel W, Huber M, Zielinski C (2023) Sodium chloride in the tumor microenvironment enhances T-cell metabolic fitness and cytotoxicity. *BioRxiv* [Preprint]

Allert S, Schulz D, Kämmer P, Großmann P, Wolf T, Schäuble S, Panagiotou G, Brunke S, Hube B (2022) From environmental adaptation to host survival: Attributes that mediate pathogenicity of *Candida auris*. *Virulence* 13(1), 191-214.

Alonso-Roman R, Last A, Mirhakkak MH, Sprague JL, Möller L, Großmann P, Graf K, Gratz R, Mogavero S, Vylkova S, Panagiotou G, Schäuble S, Hube B, Gresnigt MS (2022) *Lactobacillus rhamnosus* colonisation antagonizes *Candida albicans* by forcing metabolic adaptations that compromise pathogenicity. *Nat Commun* 13(1), 3192.

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.

Jia W, Panagiotou G (2022) Recent advances in diabetes and microbiota. *Sci Bull* 67(17), 1720-1723. (Review)

Jurgens SD, Eisenhauer N, Buscot F, Chatzinotas A, Chaudhari NM, Heintz-Buschart A, Kallies R, Küsel K, Litchman E, Macdonald CA, Müller S, Reuben RC, Nunes da Rocha U, Panagiotou G, Rillig MC, Singh BK (2022) Potential of microbiome-based solutions for agrifood systems. *Nature Food* 3(8), 557-560. (Review)

Leung H, Long X, Ni Y, Qian L, Nychas E, Siliceo SL, Pohl D, Hanhineva K, Liu Y, Xu A, Nielsen HB, Belda E, Clément K, Loomba R, Li H, Jia W, Panagiotou G (2022) Risk assessment with gut microbiome and metabolite markers in NAFLD development. *Sci Transl Med* 14(648), eabk0855.

Russell TJ, De Silva EK, Crowley VM, Shaw-Saliba K, Dube N, Josling G, Pasaje CFA, Kouskoumvekaki I, Panagiotou G, Niles JC, Jacobs-Lorena M, Denise Okafor C, Gamo FJ, Llinás M<sup>#</sup> (2022) Inhibitors of ApiAP2 protein DNA binding exhibit multistage activity against *Plasmodium* parasites. *PLOS Pathog* 18(10), e1010887.

Tappe B, Lauruschkat C, Strobel L, Kurzai O, Rebhan S, Kraus S, Lauruschkat C, Garcia JP, Bussemer L, Possler L, Held M, Huenniger K, Kniemeyer O, Schäuble S, Brakhage AA, Panagiotou G, White L, Einsele H, Löffler J, Wurster S (2022) COVID-19 patients share common, corticosteroid-independent features of impaired host immunity to pathogenic molds. *Front Immunol* 13, 954985.

Zoran T, Seelbinder B, White PL, Price JS, Kraus S, Kurzai O, Linde J, Häder A, Loeffler C, Grigoleit GU, Einsele H, Panagiotou G, Loeffler J, Schäuble S (2022) Molecular profiling reveals characteristic and decisive signatures in patients after allogeneic stem cell transplantation suffering from invasive pulmonary aspergillosis. *J Fungi (Basel)* 8(2), 171.

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.

Boysen JM, Saeed N, Wolf T, Panagiotou G, Hillmann F (2021) The peroxiredoxin asp f3 acts as redox sensor in *Aspergillus fumigatus*. *Genes* 12(5), 668.

Kang K, Imamovic L, Misiakou M, Sørensen MB, Heshiki Y, Ni Y, Zheng T, Li J, Ellabaan MMH, Colomer-Lluch M, Rode AA, Bytzer P, Panagiotou G#, Sommer MOA (corresponding author#) (2021) Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. *Gut Microbes* 13(1), 1-19.

Lauruschkat CD, Etter S, Schnack E, Ebel F, Schäuble S, Page L, Rümens D, Dragan M, Schlegel N, Panagiotou G, Kniemeyer O, Brakhage AA, Einsele H, Wurster S, Loeffler J (2021) Chronic occupational mold exposure drives expansion of *Aspergillus*-reactive type 1 and type 2 T-helper cell responses. *J Fungi* 7(9), 698.

Li Z, Geffers R, Jain G, Klawonn F, Kökpınar Ö, Nimtze M, Schmidt-Heck W, Rinas U (2021) Transcriptional network analysis identifies key elements governing the recombinant protein production provoked reprogramming of carbon and energy metabolism in *Escherichia coli* BL21 (DE3) *Engineering Reports* , e12393.

Loos D\*, Zhang L, Beemelmans C, Kurzai O, Panagiotou G# (2021) DANIEL: A user-friendly web server for fungal ITS amplicon sequencing data. *Front Microbiol* 12, 720513.

Marfil-Sanchez A\*, Seelbinder B\*, Ni Y, Varga J, Berta J, Hollosi V, Dome B, Megyesfalvi Z, Dulka E, Galffy G, Weiss GJ, Panagiotou G#, Zoltan Lohinai Z# (2021) Gut microbiome functionality might be associated with exercise tolerance and recurrence of resected early-stage lung cancer patients. *PLOS One* 16(11), e0259898.

Marfil-Sánchez A\*, Zhang L\*, Alonso-Pernas P, Mirhakkak M, Mueller M, Seelbinder B, Ni Y, Santhanam R, Busch A, Beemelmans C, Ermolaeva M, Bauer M#, Panagiotou G# (2021) An integrative understanding of the large metabolic shifts induced by antibiotics in critical illness. *Gut Microbes* 13(1), 1993598.

Mazumdar T, Teh BS, Murali A, Schmidt-Heck W, Schlenker Y, Vogel H, Boland W (2021) Transcriptomics reveal the survival strategies of *Enterococcus mundtii* in the gut of *Spodoptera littoralis*. *J Chem Ecol* 47(2), 227-241.

Mirhakkak M, Schäuble S, Klassert T, Brunke S, Brandt P, Loos D, Uribe R, de Oliveira Lino FS, Ni Y, Vylkova S, Slevogt H, Hube B, Weiss G, Sommer M, Panagiotou G# (2021) Metabolic modeling predicts specific gut bacteria as key determinants for *Candida albicans* colonization levels. *ISME J* 15(5), 1257-1270.

Ni Y\*, Lohinai Z\*, Heshiki Y, Dome B, Moldvay J, Dulka E, Galffy G, Berta J, Weiss GJ, Sommer MOA, Panagiotou G# (2021) Distinct composition and metabolic functions of human gut microbiota are associated with cachexia in lung cancer patients. *ISME J* 15(11), 3207-3220.

Nong W, Qu Z, Barton-Owen T, Wong YPA, Yin Yip H, Lee HT, Narayana S, Baril T, Swale T, Cao J, Chan TF, Kwan HS, Ming NS, Panagiotou G, Qian PY, Qiu JW, Yip KY, Ismail N, Pati S, John A, Tobe ST, Bendena WG, Cheung SG, Hayward A, Hui JHL (2021) Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. *Commun Biol* 4(1), 83.

Patumcharoenpol P, Nakphaichit M, Panagiotou G, Senavongse A, Suratannon N, Vongsangnak W (2021) MetGEMs toolbox: Metagenome-scale models as integrative toolbox for uncovering metabolic functions and routes of human gut microbiome. *PLOS Comput Biol* 17(1), e1008487.

Zhang J, Ni Y, Qian L, Fang Q, Zheng T, Zhang M, Gao Q, Zhang Y, Ni J, Hou X, Bao Y, Kovatcheva-Datchary P, Xu A, Li H, Panagiotou G<sup>#</sup>, Jia W (2021) Decreased abundance of *Akkermansia muciniphila* leads to the impairment of insulin secretion and glucose homeostasis in lean type 2 diabetes. *Adv Sci (Weinh)* 8(16), e2100536.

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.

Blango MG, Pschibul A, Riviaccio F, Krüger T, Rafiq M, Jia L, Zheng T, Goldmann M, Voltersen V, Li J, Panagiotou G, Kniemeyer O, Brakhage AA (2020) Dynamic surface proteomes of allergenic fungal conidia. *J Proteome Res* 19(5), 2092-2104.

Cakir T, Uddin R, Panagiotou G, Durmuş S (2020) Novel approaches for systems biology of metabolism-oriented pathogen-human interactions: A mini-review *Front Cell Infect Microbiol* 10, 52. (Review)

Campos G, Schmidt-Heck W<sup>\*</sup>, De Smedt J, Widera A, Ghallab A, Pütter L, González D, Edlund K, Cadenas C, Marchan R, Guthke R, Verfaillie C, Hetz C, Sachinidis A, Braeuning A, Schwarz M, Weiß TS, Banhart BK, Hoek J, Vadigepalli R, Willy J, Stevens JL, Hay DC, Hengstler JG, Godoy P (2020) Inflammation-associated suppression of metabolic gene networks in acute and chronic liver disease. *Arch Toxicol* 94(1), 205-217.

Dissanayake TK, Schäuble S, Mirhakkak MH, Wu WL, Ng CK, Yip C-Y, García-López A, Wolf T, Yeung ML, Chan KH, Yuen KY, Panagiotou G, To KKW (2020) Comparative transcriptomic analysis of rhinovirus and influenza virus infection. *Front Microbiol* 11(1580), 1-13.

Gill H, Leung GMK, Yim R, Lee P, Pang HH, Ip HW, Leung RYY, Li J, Panagiotou G, Ma ESK, Kwong YL (2020) Myeloproliferative neoplasms treated with hydroxyurea, pegylated interferon alpha-2A or ruxolitinib: Clinicohematologic responses, quality-of-life changes and safety in the real-world setting. *Hematology* 25(1), 247-257.

Gill H, Yim R, Pang HH, Lee P, Chan TSY, Hwang YY, Leung GMK, Ip HW, Leung RYY, Yip SF, Kho B, Lee HKK, Mak V, Chan CC, Lau JSM, Lau CK, Lin SY, Wong RSM, Li W, Ma ESK, Li J, Panagiotou G, Sim JPY, Lie AKW, Kwong YL (2020) Clofarabine, cytarabine, and mitoxantrone in refractory/relapsed acute myeloid leukemia: High response rates and effective bridge to allogeneic hematopoietic stem cell transplantation. *Cancer Med* 9(10), 3371-3382.

Haange SB, Jehmlich N, Krügel U, Hintschich C, Wehrmann D, Hankir M, Seyfried F, Froment J, Hübschmann T, Müller S, Wissenbach DK, Kang K, Buettner C, Panagiotou G, Noll M, Rolle-Kampczyk U, Fenske W, von Bergen M (2020) Gastric bypass surgery in a rat model alters the community structure and functional composition of the intestinal microbiota independently of

weight loss. *Microbiome* 8(1), 13.

Heshiki Y, Vazquez-Urbe R, Li J, Ni Y, Quainoo S, Imamovic L, Li J, Sørensen M, Chow BKC, Weiss GJ, Xu A, Sommer MOA, Panagiotou G (2020) Predictable modulation of cancer treatment outcomes by the gut microbiota. *Microbiome* 8(1), 28.

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.

Khaliq W, Großmann P, Neugebauer S, Kleyman A, Domizi R, Calcinaro S, Brealey D, Gräler M, Kiehintopf M, Schäuble S, Singer M, Panagiotou G\*\*, Bauer M\*\* (corresponding authors\*\*) (2020) Lipid metabolic signatures deviate in sepsis survivors compared to non-survivors. *Comput Struct Biotechnol J* 18, 3678-3691.

Liu Y, Wang Y, Ni Y, Cheung CKY, Lam KSL, Wang Y, Xia Z, Ye D, Guo J, Tse MA, Panagiotou G\*\*, Xu A\*\* (corresponding authors\*\*) (2020) Gut microbiome fermentation determines the efficacy of exercise for diabetes prevention. *Cell Metab* 31(1), 77-91.

Machata S, Müller MM, Lehmann R, Sieber P, Panagiotou G, Carvalho A, Cunha C, Lagrou K, Maertens J, Slevogt H, Jacobsen ID (2020) Proteome analysis of bronchoalveolar lavage fluids reveals host and fungal proteins highly expressed during invasive pulmonary aspergillosis in mice and humans. *Virulence* 11(1), 1337-1351.

Merk R, Heßelbach K, Osipova A, Popadić D, Schmidt-Heck W, Kim GJ, Günther S, Piñeres A G, Merfort I, Humar M (2020) Particulate matter (PM2.5) from biomass combustion induces an anti-oxidative response and cancer drug resistance in human bronchial epithelial BEAS-2B cells. *Int J Environ Res Public Health* 17(21), 8193.

Nie X, Chen J, Ma X, Ni Y, Shen Y, Yu H, Panagiotou G\*\*, Bao Y\*\* (corresponding authors\*\*) (2020) A metagenome-wide association study of gut microbiome and visceral fat accumulation. *Comput Struct Biotechnol J* 18, 2596-2609.

Reimann L, Schwäble AN, Fricke AL, Mühlhäuser WWD, Leber Y, Lohanadan K, Puchinger MG, Schäuble S, Faessler E, Wiese H, Reichenbach C, Knapp B, Peikert CD, Drepper F, Hahn U, Kreutz C, van der Ven PFM, Radziwill G, Djinić-Carugo K, Fürst DO, Warscheid B (2020) Phosphoproteomics identifies dual-site phosphorylation in an extended basophilic motif regulating FILIP1-mediated degradation of filamin-C. *Commun Biol* 3(1), 253.

Seelbinder B, Chen J, Brunke S, Vazquez-Urbe R, Santhanam R, Meyer AC, de Oliveira Lino FS, Chan KF, Loos D, Imamovic L, Tsang CC, Lam RP, Sridhar S, Kang K, Hube B, Woo PCY, Sommer MOA, Panagiotou G (2020) Antibiotics create a shift from mutualism to competition in human gut communities with a longer-lasting impact on fungi than bacteria. *Microbiome* 8(1), 133.

Seelbinder B, Wallstabe J, Marischen L, Weiss E, Wurster S, Page L, Löffler C, Bussemer L, Schmitt AN, Wolf T, Linde J, Cicin-Sain L, Becker J, Kalinke U, Vogel J, Panagiotou G, Einsele H, Westermann AJ, Schauble S, Loeffler J (2020) Triple RNA-seq reveals synergy in a human virus-fungus co-infection model. *Cell Reports* 33(7), 108389.

Shopova IA, Belyaev I, Dasari P, Jahreis S, Stroe MC, Cseresnyés Z, Zimmermann AK, Medyukhina A, Svensson C-M, Krüger T, Szeifert V, Nietzsche S, Conrad T, Blango MG, Kniemeyer O, von Lilienfeld-Toal M, Zipfel PF, Ligeti E, Figge MT, Brakhage AA (2020) Human

neutrophils produce antifungal extracellular vesicles against *Aspergillus fumigatus*. *mBio* 11(2), e00596-20.

Tomasovic A, Brand T, Schanbacher C, Kramer S, Hümmert MW, Godoy P, Schmidt-Heck W, Nordbeck P, Ludwig J, Homann S, Wiegner A, Shaykhutdinov T, Kratz C, Knüchel R, Müller-Hermelink HK, Rosenwald A, Frey N, Eichler J, Dobrev D, El-Armouche A, Hengstler JG, Müller OJ, Hinrichs K, Cuello F, Zerneck A, Lorenz K (2020) Interference with ERK-dimerization at the nucleocytoplasmic interface targets pathological ERK1/2 signaling without cardiotoxic side-effects. *Nat Commun* 11(1), 1733.

Barber AE\*, Weber M, Kaerger K, Linde J, Götz 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.

Chen J\*, McIlroy SE, Archana A, Baker DM, Panagiotou G\*\* (2019) A pollution gradient contributes to the taxonomic, functional, and resistome diversity of microbial communities in marine sediments. *Microbiome* 7(1), 104.

Fabian A, Stegner S, Miarka L, Zimmermann J, Lenk L, Rahn S, Buttlar J, Viol F, Knaack H, Esser D, Schäuble S, Großmann P, Marinos G, Häslér R, Mikulits W, Saur D, Kaleta C, Schäfer H, Sebens S (2019) Metastasis of pancreatic cancer: An uninfamed liver micromilieu controls cell growth and cancer stem cell properties by oxidative phosphorylation in pancreatic ductal epithelial cells. *Cancer Lett* 453, 95-106.

Heberle AM, Razquin Navas P, Langelaar-Makkinje M, Kasack K, Sadik A, Faessler E, Hahn U, Marx-Stoelting P, Opitz CA, Sers C, Heiland I, Schäuble S, Thedieck K (2019) The PI3K and MAPK/p38 pathways control stress granule assembly in a hierarchical manner. *Life Sci Alliance* 2(2), e201800257.

Kang K, Bergdahl B, Machado D, Dato L, Han TL, Li J, Villas-Boas S, Herrgård MJ, Förster J, Panagiotou G (2019) Linking genetic, metabolic and phenotypic diversity among *S. cerevisiae* strains using multi-omics associations *Gigascience* 8(4), giz015.

Kaur S, Rawal P, Siddiqui H, Rohilla S, Sharma S, Tripathi DM, Baweja S, Hassan M, Vlaic S, Guthke R, Thomas M, Dayoub R, Bihari C, Sarin SK, Weiss TS (2019) Increased expression of RUNX1 in liver correlates with NASH activity score in patients with non-alcoholic Steatohepatitis (NASH). *Cells* 8(10), 1277.

Li J, Rettedal EA, van der Helm E, Ellabaan M, Panagiotou G\*\*, Sommer MOA\*\* (corresponding authors\*\*) (2019) Antibiotic treatment drives the diversification of the human gut resistome. *Genom Proteom Bioinf* 17(1), 39-51.

Marbach-Breitrück E, Matz-Soja M, Abraham U, Schmidt-Heck W, Sales S, Rennert C, Kern M, Aleithe S, Spormann L, Thiel C, Gerlini R, Arnold K, Klötting N, Guthke R, Rozman D, Teperino R, Shevchenko A, Kramer A, Gebhardt R (2019) Tick-Tock Hedgehog-Mutual crosstalk with liver circadian clock promotes liver steatosis. *J Hepatol* 70(6), 1192-1202.

Wang Y, Tatham MH, Schmidt-Heck W, Swann C, Singh-Dolt K, Meseguer-Ripolles J, Lucendo-Villarin B, Kunath T, Rudd TR, Smith AJH, Hengstler JG, Godoy P, Hay RT, Hay DC (2019) Multiomics analyses of HNF4 $\alpha$  protein domain function during human pluripotent stem cell differentiation. *iScience* 16, 206-217.

Zhang L, Ouyang Y, Li H, Shen L, Ni Y, Fang Q, Wu G, Qian L, Xiao Y, Zhang J, Yin P, Panagiotou G, Xu G, Ye J, Jia W (2019) Metabolic phenotypes and the gut microbiota in response to dietary resistant starch type 2 in normal-weight subjects: a randomized crossover trial. *Sci Rep* 9(1), 4736.

Zheng T, Li J, Ni Y, Kang K, Misiakou MA, Imamovic L, Chow BKC, Rode AA, Bytzer P, Sommer M, Panagiotou G\*\* (2019) Mining, analyzing, and integrating viral signals from metagenomic data. *Microbiome* 7(1), 42.

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.

Aramillo Irizar P, Schäuble S, Esser D, Groth M, Frahm C, Priebe S, Baumgart M, Hartmann N, Marthandan S, Menzel U, Müller J, Schmidt S, Ast V, Caliebe A, König R, Krawczak M, Ristow M, Schuster S, Cellerino A, Diekmann S, Englert C, Hemmerich P, Sühnel J, Guthke R, Witte OW, Platzer M, Ruppin E, Kaleta C (2018) Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. *Nat Commun* 9(1), 327.

Baumeister T, Ueberschaar N, Schmidt-Heck W, Mohr JF, Deicke M, Wichard T, Guthke R, Pohnert G (2018) DeltaMS: A tool to track isotopologues in GC- and LC-MS data. *Metabolomics* 14(4), 41.

Conrad T\*, Kniemeyer O, Henkel SG, Krüger T, Mattern DJ, Valiante V, Guthke R, Jacobsen ID, Brakhage AA, Vlais 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.

Fischer J, Müller SY, Netzker T, Jäger N, Gacek-Matthews A, Scherlach K, Stroe MC, García-Altare M, Pezzini F, Schoeler H, Reichelt M, Gershenzon, Krespach MK, Shelest E, Schroeckh V, Valiante V, Heinzl T, Hertweck C, Strauss J, Brakhage AA (2018) Chromatin mapping identifies BasR, a key regulator of bacteria-triggered production of fungal secondary metabolites. *eLife* 7, e40969.

Gill H, Ip HW, Yim R, Tang WF, Pang HH, Lee P, Leung GMK, Li J, Tang K, So JCC, Leung RYY, Li J, Panagiotou G, Lam CCK, Kwong YL (2018) Next-generation sequencing with a 54-gene panel identified unique mutational profile and prognostic markers in Chinese patients with myelofibrosis. *Ann Hematol* 98(4), 869-879.

Godoy P, Schmidt-Heck W, Hellwig B, Nell P, Feuerborn D, Rahnenführer J, Kattler K, Walter J, Blüthgen N, Hengstler JG (2018) Assessment of stem cell differentiation based on genome-wide expression profiles. *Philos Trans R Soc Lond B Biol Sci* 373(1750), 20170221. (Review)

Imamovic L, Misiakou MA, van der Helm E, Panagiotou G, Muniesa M, Sommer MOA (2018) Complete genome sequence of *Escherichia coli* strain WG5. *Genome Announc* 6(2), e01403-17.

Kang K, Ni Y, Li J, Imamovic L, Sarkar C, Kobler MD, Heshiki Y, Zheng T, Kumari S, Wong JCY, Archana A, Wong CWM, Dingle C, Denizen S, Baker DM, Sommer MOA, Webster CJ, Panagiotou G\*\* (2018) The environmental exposures and inner- and intercity traffic flows of the metro system may contribute to the human skin microbiome and resistome. *Cell Reports* 24(5), 1190-1202.

- Lau SKP, Teng JLL, Chiu TH, Chan E, Tsang AKL, Panagiotou G, Zhai SL, Woo PCY (2018) Differential microbial communities of omnivorous and herbivorous cattle in Southern China. *Comput Struct Biotechnol J* 16, 54-60.
- Lehmann R, Müller MM, Klassert TE, Driesch D, Stock M, Conrad T, Moore C, Schier U, Guthke R, Slevogt H (2018) Differential regulation of the transcriptomic and secretomic landscape of sensor and effector functions of human airway epithelial cells. *Mucosal Immunol* 11(3), 627-642.
- Popadić D, Heßelbach K, Richter-Brockmann S, Kim GJ, Flemming S, Schmidt-Heck W, Häupl T, Bonin M, Dornhof R, Achten C, Günther S, Humar M, Merfort I (2018) Gene expression profiling of human bronchial epithelial cells exposed to fine particulate matter (PM(2.5)) from biomass combustion. *Toxicol Appl Pharmacol* 347, 10-22.
- Ravichandran M, Priebe S, Grigolon G, Rozarov L, Groth M, Laube B, Guthke R, Platzer M, Zarse K, Ristow M (2018) Impairing L-threonine catabolism promotes healthspan through proteotoxic methylglyoxal. *Cell Metabolism* 27(4), 914-925.e5..
- Rennert C, Vlais S, Marbach-Breitrück E, Thiel C, Sales S, Shevchenko A, Gebhardt R, Matz-Soja M (2018) The diurnal timing of starvation differently impacts murine hepatic gene expression and lipid metabolism – A systems biology analysis using self-organizing maps. *Front Physiol* 9, 1180.
- Schaarschmidt B, Vlais S, Medyukhina A, Neugebauer S, Nietzsche S, Gonnert FA, Rödel J, Singer M, Kiehntopf M, Figge MT, Jacobsen ID, Bauer M, Press AT (2018) Molecular signatures of liver dysfunction are distinct in fungal and bacterial infections in mice. *Theranostics* 8(14), 3766-3780.
- Schmidt H, Vlais S, Krüger T, Schmidt F, Balkenhohl J, Dandekar T, Guthke R, Kniemeyer O, Heinekamp T, Brakhage AA (2018) Proteomics of *Aspergillus fumigatus* conidia-containing phagolysosomes identifies processes governing immune evasion. *Mol Cell Proteomics* 17(6), 1084-1096.
- Scholz SS, Schmidt-Heck W, Guthke R, Furch ACU, Reichelt M, Gershenzon J, Oelmüller R (2018) *Verticillium dahliae*-Arabidopsis interaction causes changes in gene expression profiles and jasmonate levels on different time scales. *Front Microbiol* 9, 217.
- Sieber P, Platzer M, Schuster S (2018) The definition of open reading frame revisited. *Trends Genet* 34(3), 167-170.
- 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.
- Tauber JP, Gallegos-Monterrosa R, Kovacs AT, Shelest E, Hoffmeister D (2018) Dissimilar pigment regulation in *Serpula lacrymans* and *Paxillus involutus* during interkingdom interactions. *Microbiology* 164(1), 65-77.
- Vlais S, Conrad T, Tokarski-Schnelle C, Gustafsson M, Dahmen U, Guthke R, Schuster S (2018) ModuleDiscoverer: Identification of regulatory modules in protein-protein interaction networks. *Sci Rep* 8(1), 433.
- Weber M, Schaer J, Walther G, Kaerger K, Steinmann J, Rath PM, Spiess B, Buchheidt D, Hamprecht A, Kurzai O (2018) FunResDB-A web resource for genotypic susceptibility testing of



*Aspergillus fumigatus*. *Med Mycol* 56(1), 117-120.

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)

Blin K, Wolf T, Chevrette M, Lu X, Schwalen C, Kautsar S, Suarez Duran, H, de los Santos E, Kim HU, Nave M, Dickschat J, Mitchell D, Shelest E, Breitling R, Takano E, Lee SY, Weber T, Medema M (2017) antiSMASH 4.0 — Improvements in Chemistry Prediction and Gene Cluster Boundary Identification. *Nucleic Acids Res* 45(W1), W36-W41.

Christ B, Dahmen U, Herrmann KH, König M, Reichenbach JR, Ricken T, Schleicher J, Ole Schwen L, Vlaic S, Waschinsky N (2017) Computational Modeling in Liver Surgery. *Front Physiol* 8, 906. (Review)

de Vries RP, Riley R, Wiebenga A, Aguilar-Osorio G, Amillis S, Uchima CA, Anderluh G, Asadollahi M, Askin M, Barry K, Battaglia E, Bayram Ö, Benocci T, Braus-Stromeyer SA, Caldana C, Cánovas D, Cerqueira GC, Chen F, Chen W, Choi C, Clum A, Dos Santos RA, Damásio AR, Diallinas G, Emri T, Fekete E, Flipphi M, Freyberg S, Gallo A, Gournas C, Habgood R, Hainaut M, Harispe ML, Henrissat B, Hildén KS, Hope R, Hossain A, Karabika E, Karaffa L, Karányi Z, Kraševc N, Kuo A, Kusch H, LaButti K, Lagendijk EL, Lapidus A, Lévassieur A, Lindquist E, Lipzen A, Logrieco AF, MacCabe A, Mäkelä MR, Malavazi I, Melin P, Meyer V, Mielnichuk N, Miskei M, Molnár ÁP, Mulé G, Ngan CY, Orejas M, Orosz E, Ouedraogo JP, Overkamp KM, Park HS, Perrone G, Piumi F, Punt PJ, Ram AF, Ramón A, Rauscher S, Record E, Riaño-Pachón DM, Robert V, Röhrig J, Ruller R, Salamov A, Salih NS, Samson RA, Sándor E, Sanguinetti M, Schütze T, Sepčić K, Shelest E, Sherlock G, Sophianopoulou V, Squina FM, Sun H, Susca A, Todd RB, Tsang A, Unkles SE, van de Wiele N, van Rossen-Uffink D, Oliveira JV, Vesth TC, Visser J, Yu JH, Zhou M, Andersen MR, Archer DB, Baker SE, Benoit I, Brakhage AA, Braus GH, Fischer R, Frisvad JC, Goldman GH, Houburaken J, Oakley B, Pócsi I, Scazzocchio C, Seiboth B, vanKuyk PA, Wortman J, Dyer PS, Grigoriev IV (2017) Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus *Aspergillus*. *Genome Biol* 18(1), 28.

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.

Heshiki Y, Dissanayake T, Zheng T, Kang K, Yueqiong N, Xu Z, Sarkar C, Woo PCY, Chow BKC, Baker D, Yan A, Webster CJ, Panagiotou G<sup>\*\*</sup>, Li J<sup>\*\*</sup> (2017) Toward a Metagenomic Understanding on the Bacterial Composition and Resistome in Hong Kong Banknotes. *Front Microbiol* 8, 632.

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.

Mattern DJ, Valiante V, Horn F, Petzke L, Brakhage AA (2017) Rewiring of the Austinoid Biosynthetic Pathway in Filamentous Fungi. *ACS Chem Biol* 12(12), 2927-2933.

Müller MM, Lehmann R, Klassert TE, Reifenstein S, Conrad T, Moore C, Kuhn A, Behnert A, Guthke R, Driesch D, Slevogt H (2017) Global analysis of glycoproteins identifies markers of endotoxin tolerant monocytes and GPR84 as a modulator of TNF $\alpha$  expression. *Sci Rep* 7(1), 838.

Ni Y, Jensen K, Kouskoumvekaki I<sup>\*\*</sup>, Panagiotou G<sup>\*\*</sup> (2017) NutriChem 2.0: exploring the effect of plant-based foods on human health and drug efficacy. *Database* (2017),

Ni Y, Wong VHY, Tai WCS, Li J, Wong WY, Lee MML, Fong FLY, El-Nezami H<sup>\*\*</sup>, Panagiotou G<sup>\*\*</sup> (2017) A metagenomic study of the preventive effect of *Lactobacillus rhamnosus* GG on intestinal polyp formation in ApcMin/+ mice. *J Appl Microbiol* 122(3), 770-784.

Rennert C, Eplinius F, Hofmann U, Johanning J, Rolfs F, Schmidt-Heck W, Guthke R, Gebhardt R, Ricken AM, Matz-Soja M (2017) Conditional loss of hepatocellular Hedgehog signaling in female mice leads to the persistence of hepatic steroidogenesis, androgenization and infertility. *Arch Toxicol* 91(11), 3677-3687.

Schleicher J, Dahmen U, Guthke R, Schuster S (2017) Zonation of hepatic fat accumulation: insights from mathematical modelling of nutrient gradients and fatty acid uptake. *J R Soc Interface* 14(133), pii: 20170443.

Schmidt-Heck W, Wönne EC, Hiller T, Menzel U, Koczan D, Damm G, Seehofer D, Knöspel F, Freyer N, Guthke R, Dooley S, Zeilinger K (2017) Global transcriptional response of human liver cells to ethanol stress of different strength reveals hormetic behavior. *Alcohol Clin Exp Res* 41(5), 883-894.

Shelest E (2017) Transcription Factors in Fungi: TFome Dynamics, Three Major Families, and Dual-Specificity TFs. *Front Genet* 8, 53.

Valiante V, Mattern DJ, Schüffler A, Horn F, Walther G, Scherlach K, Petzke L, Dickhaut J, Guthke R, Hertweck C, Nett M, Thines E, Brakhage AA (2017) Discovery of an Extended Austinoid Biosynthetic Pathway in *Aspergillus calidoustus*. *ACS Chem Biol* 12(5), 1227-1234.

Zheng T, Ni Y, Li J, Chow BKC, Panagiotou G<sup>\*\*</sup> (2017) Designing Dietary Recommendations Using System Level Interactomics Analysis and Network-Based Inference. *Front Physiol* 8, 753.

Baumgart M, Priebe S, Groth M, Hartmann N, Menzel U, Pandolfini L, Ristow M, Englert C, Guthke R, Platzer M, Cellerino A (2016) Longitudinal transcriptional analysis of vertebrate aging identifies mitochondrial complex I as a small molecule-sensitive modifier of lifespan. *Cell Systems* 2(2), 122-132.

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- $\kappa$ B mediated stress response in the intestinal epithelial cell line C2BB<sub>e</sub>1. *Cellular Microbiology* 18(7), 889-904.

Corrochano LM, Kuo A, Marcet-Houben M, Polaino S, Salamov A, Villalobos-Escobedo JM, Grimwood J, Álvarez MI, Avalos J, Bauer D, Benito EP, Benoit I, Burger G, Camino LP, Cánovas D, Cerdá-Olmedo E, Cheng JF, Domínguez A, Eliáš M, Eslava AP, Glaser F, Gutiérrez G, Heitman J, Henrissat B, Iturriaga EA, Lang BF, Lavín JL, Lee SC, Li W, Lindquist E, López-García S, Luque EM, Marcos AT, Martin J, McCluskey K, Medina HR, Miralles-Durán A, Miyazaki A, Muñoz-Torres E, Oguiza JA, Ohm RA, Olmedo M, Orejas M, Ortiz-Castellanos L, Pisabarro AG, Rodríguez-Romero J, Ruiz-Herrera J, Ruiz-Vázquez R, Sanz C, Schackwitz W, Shahriari M, Shelest E, Silva-Franco F, Soanes D, Syed K, Tagua VG, Talbot NJ, Thon MR, Tice H, de Vries RP, Wiebenga A, Yadav JS, Braun EL, Baker SE, Garre V, Schmutz J, Horwitz BA, Torres-Martínez S, Idnurm A, Herrera-Estrella A, Gabaldón T, Grigoriev IV (2016) Expansion of signal transduction pathways in fungi by extensive genome duplication *Current Biology* 26(12),

1577-1584.

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.

Durmus S, Cakir T, Guthke R (2016) Computational systems biology of pathogen-host interactions *Front. Microbiol.* 7, 21. (Review)

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.

Godoy P, Widera A, Schmidt-Heck W, Campos G, Meyer C, Cadenas C, Reif R, Stöber R, Hammad S, Pütter L, Gianmoena K, Marchan R, Ghallab A, Edlund K, Nüssler A, Thasler WE, Damm G, Seehofer D, Weiss TS, Dirsch O, Dahmen U, Gebhardt R, Chaudhari U, Meganathan K, Sachinidis A, Kelm J, Hofmann U, Zahedi RP, Guthke R, Blüthgen N, Dooley S, Hengstler JG (2016) Gene network activity in cultivated primary hepatocytes is highly similar to diseased mammalian liver tissue. *Arch Toxicol* 90(10), 2513-2529.

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.

Kröber A, Scherlach K, Hortschansky P, Shelest E, Staib P, Kniemeyer O, Brakhage AA (2016)

HapX Mediates Iron Homeostasis in the Pathogenic Dermatophyte *Arthroderma benhamiae* but Is Dispensable for Virulence. *PLOS ONE* 11(3), e0150701.

Kroll K, Shekhova E, Mattern DJ, Thywissen A, Jacobsen ID, Strassburger M, Heinekamp T, Shelest E, Brakhage AA, Kniemeyer O (2016) The hypoxia-induced dehydrogenase HorA is required for coenzyme Q10 biosynthesis, azole sensitivity and virulence of *Aspergillus fumigatus* *Mol Microbiol* 101(1), 92-108.

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.

Marthandan S, Baumgart M, Priebe S, Groth M, Schaer J, Kaether C, Guthke R, Cellerino A, Platzer M, Diekmann S, Hemmerich P (2016) Conserved Senescence Associated Genes and Pathways in Primary Human Fibroblasts Detected by RNA-Seq. *PLOS ONE* 11(5), e0154531.

Matz-Soja M, Rennert C, Schönefeld K, Aleithe S, Boettger J, Schmidt-Heck W, Weiss TS, Hovhannisyanyan A, Zellmer S, Klötting N, Schulz A, Kratzsch J, Guthke R, Gebhardt R (2016) Hedgehog signaling is a potent regulator of liver lipid metabolism and reveals a GLI-code associated with steatosis *eLife* 5, e13308.

Rischer M, Klassen J, Wolf T, Guo H, Shelest E, Clardy J, Beemelmans C (2016) Draft Genome Sequence of *Shewanella* sp. P1-14-1, a Bacterial Inducer of Settlement and Morphogenesis in Larvae of the Marine Hydroid Hydractinia Echinata *Genome Announc* 4(1), e00003-16.

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

Shelest E, Wingender E (2016) Systems biology of transcription regulation *Front. Genet.* 7, 124. (Review)

Tauber JP, Schroeckh V, Shelest E, Brakhage AA, Hoffmeister D (2016) Bacteria induce pigment formation in the basidiomycete *Serpula lacrymans*. *Environ Microbiol* 18, 5218-5227.

Teutschbein J, Simon S, Lothar J, Springer J, Hortschansky P, Morton CO, Löffler J, Einsele H, Conneally E, Rogers TR, Guthke R, Brakhage AA, Kniemeyer O (2016) Proteomic profiling of serological responses to *Aspergillus fumigatus* antigens in patients with invasive aspergillosis. *J Proteome Res* 15(5), 1580-1591.

Valiante V, Baldin C, Hortschansky P, Jain R, Thywißen A, Straßburger M, Shelest E, Heinekamp T, Brakhage AA (2016) The *Aspergillus fumigatus* conidial melanin production is regulated by the bifunctional bHLH DevR and MADS-box RlmA transcription factors. *Mol Microbiol* 102(2), 321-335.

Voigt K, Wolf T, Ochsenreiter K, Nagy G, Kaerger K, Shelest E, Papp T (2016) 15 Genetic and metabolic aspects of primary and secondary metabolism of the Zygomycetes In: Hoffmeister D. (eds) *Biochemistry and Molecular Biology* (ed.) *The Mycota* Vol. III: 3rd edition. III, pp. 361-385. Springer Verlag, Berlin, Heidelberg, New York. (Review)

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.

Böttger J, Arnold K, Thiel C, Rennert C, Aleithe S, Hofmann U, Vlaic S, Sales S, Shevchenko A, Matz-Soja M (2015) RNAi in murine hepatocytes: the agony of choice--a study of the influence of lipid-based transfection reagents on hepatocyte metabolism. *Arch Toxicol* 89(9), 1579-1588.

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.

Cameron K, Tan R, Schmidt-Heck W, Campos G, Lyall MJ, Wang Y, Lucendo-Villarin B, Szkolnicka D, Bates N, Kimber SJ, Hengstler JG, Godoy P, Forbes SJ, Hay DC (2015) Recombinant Laminins Drive the Differentiation and Self-Organization of hESC-Derived Hepatocytes. *Stem Cell Reports* ,

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.

Durmus S, Cakir T, Ozgur A, Guthke R (2015) A review on Computational Systems Biology of Pathogen-Host Interactions *Front Microbiol* 6, 235.

Feuer R, Vlaic S, Arlt J, Sawodny O, Dahmen U, Zanger UM, Thomas M (2015) LEMming: A Linear Error Model to Normalize Parallel Quantitative Real-Time PCR (qPCR) Data as an Alternative to Reference Gene Based Methods. *PLoS One* 10(9), e0135852.

Godoy P, Schmidt-Heck W, Natarajan K, Lucendo-Villarin B, Szkolnicka D, Asplund A, Bjorquist P, Widera A, Stoeber R, Campos G, Hammad S, Sachinidis A, Damm G, Weiss TS, Nussler A, Synnergren J, Edlund K, Küppers-Munther B, Hay D, Hengstler JG (2015) Gene networks and transcription factor motifs defining the differentiation of stem cells into hepatocyte-like cells. *J Hepatol* [Epub ahead of print]

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, Üzümlü 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.

Klassen JL, Rischer M, Wolf T, Guo H, Shelest E, Clardy J, Beemelmans C (2015) Genome Sequences of Three *Pseudoalteromonas* Strains P1-8, P1-11 and P1-30 Isolated from the Marine Hydroid *Hydractinia echinata* *Genome Announc*. 3(6), e01380-15.

Klassen JL, Wolf T, Rischer M, Guo H, Shelest E, Clardy J, Beemelmans C (2015) Draft Genome Sequences of Six *Pseudoalteromonas* sp. Strains P1-7a, P1-9, P1-13-1a, P1-16-1b, P1-25 and P1-26, which Induce Larval Settlement and Metamorphosis in *Hydractinia echinata* *Genome Announc*. 3(6), e01477-15.

Kramer M, Quickert S, Sponholz C, Menzel U, Paxian M, Huse K, Platzer M, Bauer M, Claus RA (2015) Alternative splicing of SMPD1 in human sepsis *PLoS One* ,

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.

Macheleidt J, Scherlach K, Neuwirth T, Schmidt-Heck W, Straßburger M, Spraker J, Baccile JA, Schroeder FC, Keller NP, Hertweck C, Heinekamp T, Brakhage AA (2015) Transcriptome analysis of cAMP-dependent protein kinase A regulated genes reveals the production of the novel natural compound fumipyrrole by *Aspergillus fumigatus* *Mol Microbiol* 96(1), 148-162.

Mansfeld J, Urban N, Priebe S, Groth M, Frahm C, Hartmann N, Gebauer J, Ravichandran M, Dommaschk A, Schmeisser S, Kuhlowl D, Monajembashi S, Bremer-Streck S, Hemmerich P, Kiehntopf M, Zamboni N, Englert C, Guthke R, Kaleta C, Platzer M, Sühnel J, Witte O, Zarse K, Ristow M (2015) Branched-Chain Amino Acid Catabolism is a Conserved Genetic Regulator of Physiological Aging *Nature Communications* 6, 10043.

Marthandan S, Priebe S, Groth M, Guthke R, Platzer M, Hemmerich P, Diekmann S (2015) Hormetic effect of rotenone in primary human fibroblasts. *Immunity & Ageing* 12, 11.

Marthandan S\*, Priebe S\*, Baumgart M, Groth M, Cellerino A, Guthke R, Platzer P, Hemmerich P and Diekmann S (2015) Similarities in gene expression profiles during in vitro aging of primary human embryonic lung and foreskin fibroblasts *BioMed Research International* 2015, ID 731938.

Prauß MTE, Schäuble S, Guthke R, Schuster S (2015) Computing the various pathways of penicillin synthesis and their molar yields. *Biotechnology and Bioengineering* 113(1), 173-181.

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.

Reichwald K, Petzold A, Koch P, Downie BR, Hartmann N, Pietsch S, Baumgart M, Chalopin D, Felder M, Bens M, Sahm A, Szafranski K, Taudien S, Groth M, Arisi I, Weise A, Bhatt SS, Sharma V, Kraus JM, Schmid F, Priebe S, Liehr T, Görlach M, Than ME, Hiller M, Kestler HA, Volff JN, Scharl M, Cellerino A, Englert C, Platzer M (2015) Insights into Sex Chromosome Evolution and Aging from the Genome of a Short-Lived Fish. *Cell* 163(6), 1527-1538.

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)

Schmidt-Heck W+, Matz-Soja M+, Aleithe S, Guthke R, Gebhardt R (2015) Fuzzy modeling reveals a dynamic self-sustaining network of the GLI transcription factors controlling important metabolic regulators in adult mouse hepatocytes *Molecular BioSystems* 11(8), 2190-2197.

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.

Shelest E, Heimerl N, Fichtner M, Sasso S (2015) Multimodular type I polyketide synthases in algae evolve by module duplications and displacement of AT domains in trans *BMC genomics* 16(1), 1015.

Sponholz C, Kramer M, Schöneweck F, Menzel U, Inanloo Rahatloo K, Giamarellos-Bourboulis EJ, Papavassileiou V, Lymberopoulou K, Pavlaki M, Koutelidakis I, Perdios I, Scherag A, Bauer M, Platzer M, Huse K (2015) Polymorphisms of cystathionine beta-synthase gene are associated with susceptibility to sepsis. *Eur J Hum Genet* [Epub ahead of print]

Valiante V, Monteiro MC, Martín J, Altwasser R, El Aouad N, González I, Kniemeyer O, Mellado E, Palomo S, de Pedro N, Pérez-Victoria I, Tormo JR, Vicente F, Reyes F, Genilloud O, Brakhage AA (2015) Hitting the caspofungin salvage pathway of human-pathogenic fungi with the novel lasso peptide humidimycin (MDN-0010). *Antimicrob Agents Chemother* 59(9), 5145-5153.

Vettorazzi S, Bode C, Dejager L, Frappart L, Shelest E, Klauen C, Tasdogan A, Reichardt HM, Libert C, Schneider M, Weih F, Uhlenhaut H, David J-P, Gräler M, Kleiman A, Tuckermann JP (2015) Glucocorticoids limit acute lung inflammation in concert with inflammatory stimuli by induction of SphK1 *Nature Communications* 6, 7796.

Vlaic S, Altwasser R, Kupfer P, Nilsson CL, Emmett M, Meyer-Baese A, Guthke R (2015) Inference of Predictive Phospho-Regulatory Networks from LC-MS/MS Phosphoproteomics Data In: INSTICC, Portugal (eds.) Communications in Computer and Information Science BIOINFOMATICS 2016 - 7th Int. Conf. Bioinformatics Models, Methods and Algorithms, Rome, Italy, 02/21/2016-02/23/2016, Springer.

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),

Wolf T, Shelest V, Nath N, Shelest E (2015) CASSIS and SMIPS: Promoter-based prediction of secondary metabolite gene clusters in eukaryotic genomes *Bioinformatics* 32(8), 1138-1143.

Baumgart M, Groth M, Priebe S, Savino A, Testa G, Dix A, Ripa R, Spallotta F, Gaetano C, Ori M, Terzibasi Tozzini E, Guthke R, Platzer M, Cellerino A (2014) RNA-seq of the aging brain in the short-lived fish *N. furzeri* - conserved pathways and novel genes associated with neurogenesis. *Aging Cell* 13(6), 965-974.

Bohnert M, Nützmann HW, Schroeckh V, Horn F, Dahse HM, Brakhage AA, Hoffmeister D (2014) Cytotoxic and antifungal activities of melleolide antibiotics follow dissimilar structure-activity relationships. *Phytochemistry* 105, 101-108.

Campos G, Schmidt-Heck W, Ghallab A, Rochlitz K, Pütter L, Medinas DB, Hetz C, Widera A, Cadenas C, Begher-Tibbe B, Reif R, Günther G, Sachinidis A, Hengstler JG, Godoy P (2014) The transcription factor CHOP, a central component of the transcriptional regulatory network induced upon CCl4 intoxication in mouse liver, is not a critical mediator of hepatotoxicity. *Arch Toxicol* 88(6), 1267-1280.

Grinberg M, Stöber RM, Edlund K, Rempel E, Godoy P, Reif R, Widera A, Madjar K, Schmidt-Heck W, Marchan R, Sachinidis A, Spitkovsky D, Hescheler J, Carmo H, Arbo MD, van de Water B, Wink S, Vinken M, Rogiers V, Escher S, Hardy B, Mitic D, Myatt G, Waldmann T, Mardinoglu A, Damm G, Seehofer D, Nüssler A, Weiss TS, Oberemm A, Lampen A, Schaap MM, Luijten M, van Steeg H, Thasler WE, Kleinjans JC, Stierum RH, Leist M, Rahnenführer J, Hengstler JG (2014) Toxicogenomics directory of chemically exposed human hepatocytes. *Arch Toxicol* 88(12), 2261-2287.

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, Rittweger M, Taubert J, Lysenko A, Rawlings C, Guthke R (2014) Interactive exploration of integrated biological datasets using context-sensitive workflows *Front Genet* 5, 21.

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.

Horn F, Valiante V, Guthke R, Brakhage AA (2014) Data-driven systems biology of fungal infections. In: Sullivan D, Moran GP (eds.) *Human pathogenic Fungi: Molecular biology and pathogenic mechanisms* Caister Academic Press, Norfolk, UK. ISBN: 978-1-908230-44.

Kroll K, Pächt V, Hillmann F, Vaknin Y, Schmidt-Heck W, Roth M, Jacobsen ID, Osherov N, Brakhage AA, Kniemeyer O (2014) Identification of hypoxia-inducible target genes of *Aspergillus fumigatus* by transcriptome analysis reveals cellular respiration as important contributor to hypoxic survival. *Eukaryot Cell* 13(9), 1241-1253.

Kupfer P, Huber R, Weber M, Vlais S, Häupl T, Koczan D, Guthke R, Kinne RW (2014) Novel application of multi-stimuli network inference to synovial fibroblasts of rheumatoid arthritis patients. *BMC Med Genomics* 7(1), 40-40.

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.

Manchanda H, Seidel N, Krumbholz A, Sauerbrei A, Schmidtke M, Guthke R (2014) Within-host influenza dynamics: a small-scale mathematical modeling approach. *Biosystems* 118, 51-59.

Marthandan S, Priebe S, Hemmerich P, Klement K, Diekmann S (2014) Long-term quiescent fibroblast cells transit into senescence. *PLOS ONE* 9(12), e115597.

Matz-Soja M, Aleithe S, Marbach E, Böttger J, Arnold K, Schmidt-Heck W, Kratzsch J, Gebhardt R (2014) Hepatic hedgehog signaling contributes to the regulation of IGF-I and IGFBP serum levels *Cell Communication and Signaling* 12, 11.

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.

Sasso S, Shelest E, Hoffmeister D (2014) Comments on the distribution and phylogeny of type I polyketide synthases and nonribosomal peptide synthetases in eukaryotes. *Proc Natl Acad Sci U S A* 111, E3946.

Schleicher J, Guthke R, Dahmen U, Dirsch O, Holzhuetter HG, Schuster S (2014) A theoretical study of lipid accumulation in the liver-implications for nonalcoholic fatty liver disease. *Biochim Biophys Acta* 1841(1), 62-69.

Schliess F, Hoehme S, Henkel S, Ghallab A, Driesch D, Böttger J, Guthke R, Pfaff M, Hengstler J, Gebhardt R, Häussinger D, Drasdo D, Zellmer S (2014) Integrated metabolic spatial-temporal model for prediction of ammonia detoxification during liver damage and regeneration *Hepatology* 60(6), 2040-2051.

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.

Shelest E, Voigt K (2014) Genomics to study basal lineage fungal biology: phylogenomics suggest a common origin In: Alistair J.B. Brown (ed.) *The Mycota XIII, Fungal Genomics* 2. edition. 13, pp. 31-60. Springer, Berlin, Heidelberg.

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.

Weimer S, Priebs J, Kuhlow D, Groth M, Priebe S, Mansfeld J, Merry TL, Dubuis S, Laube S, Pfeiffer AF, Schulz TJ, Guthke R, Platzer M, Zamboni N, Zarse K, Ristow M (2014) D-Glucosamine Supplementation Extends Lifespan of Nematodes and Aging Mice *Nature Communications* 5, 3563.

Woetzel D, Huber R, Kupfer P, Pohlers D, Pfaff M, Driesch D, Häupl T, Koczan D, Stiehl P, Guthke R, Kinne RW (2014) Identification of rheumatoid arthritis and osteoarthritis patients by transcriptome-based rule set generation. *Arthritis Res Ther* 16(2), R84.

Zaehle C, Gressler M, Shelest E, Geib E, Hertweck C, Brock M (2014) Terrein Biosynthesis in *Aspergillus terreus* and Its Impact on Phytotoxicity. *Chem Biol* 21(6), 719-731.

Zhang X, Müller S, Möller M, Huse K, Taudien S, Book M, Stuber F, Platzer M, Groth M (2014) 8p23 beta-defensin copy number determination by single-locus pseudogene-based paralog ratio tests risk bias due to low-frequency sequence variations. *BMC Genomics* 15, 64-64.

Altwasser R, Guthke R, Vlaic S, Emmett MR, Conrad CA, Meyer-Baese A (2013) Model order reduction of deterministic and stochastic gene regulatory networks. In: Hamid R. Arabnia, Quoc-Nam Tran (eds.) *Proceedings of the International Conference on Bioinformatics and Computational Biology BIOCAMP'13 13th Int. Conf. Bioinformatics and Computational Biology, Las Vegas/USA, 09/16/2012-09/19/2012*, pp. 487-496. CSREA Press, USA. ISBN: 1-60132-234-8.

Altwasser R, Guthke R, Vlaic S, Emmett MR, Conrad CA, Meyer-Baese A (2013) Almost sure stability of stochastic gene regulatory networks with mode-dependent interval delays. In: *Proc. BIOCAMP'13, BIOCAMP'12, Proc. 13th Int. Conf. Bioinformatics and Computational Biology, Las Vegas/USA, 09/16/2012-09/19/2012*, pp. 468-477. CSREA Press, Las Vegas, USA. ISBN: 1-60132-234-8.

Gurovic VMS, Müller S, Domin N, Seccareccia I, Nietzsche S, Martin K, Nett M (2013) *Micromonospora schwarzwaldensis* sp. nov., a producer of telomycin, isolated from soil. *Int J Syst Evol Microbiol* 63(Pt 10), 3812-3817.

König CC, Scherlach K, Schroeckh V, Horn F, Nietzsche S, Brakhage AA, Hertweck C (2013) Bacterium induces cryptic meroterpenoid pathway in the pathogenic fungus *Aspergillus fumigatus*. *Chembiochem* 14(8), 938-942.

Kramer M, Sponholz C, Slaba M, Wissuwa B, Claus RA, Menzel U, Huse K, Platzer M, Bauer M

(2013) Alternative 5' untranslated regions are involved in expression regulation of human heme oxygenase-1. *PLoS One* 8(10), e77224-e77224.

Kupfer P, Vlais S, Huber R, Kinnne RW, Guthke R (2013) Different stimuli for inference of gene regulatory network in rheumatoid arthritis In: Pedro Fernandes, Jordi Solé-Casals, Ana Fred and Hugo Gamboa (eds.) Bioinformatics 2013 - 4th Int. Conf. on Bioinformatics Models, Methods and Algorithms International Conference on Bioinformatics Models, Methods and Algorithms, Barcelona /Spain, 02/11/2013-02/14/2013, pp. 282-287.SCITEPRESS – Science and Technology Publications, Lissabon /Portugal. ISBN: 978-989-8565358.

Martin R, Albrecht-Eckardt D, Brunke S, Hube B, Hünninger K, Kurzai O (2013) A core filamentation response network in *Candida albicans* is restricted to eight genes. *PLoS One* 8(3), e58613.

Otzen C, Müller S, Jacobsen ID, Brock M (2013) Phylogenetic and phenotypic characterisation of the 3-ketoacyl-CoA thiolase gene family from the opportunistic human pathogenic fungus *Candida albicans*. *FEMS Yeast Res* 13(6), 553-564.

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.

Petzold A, Reichwald K, Groth M, Taudien S, Hartmann N, Priebe S, Shagin D, Englert C, Platzer M (2013) The transcript catalogue of the short-lived fish *Nothobranchius furzeri* provides insights into age-dependent changes of mRNA levels. *BMC Genomics* 14, 185-185.

Priebe S, Menzel U (2013) Assignment of orthologous genes by utilization of multiple databases: the orthology package in R In: Pedro Fernandes, Jordi Solé-Casals, Ana Fred and Hugo Gamboa (eds.) Bioinformatics 2013 - 4th Int. Conf. on Bioinformatics Models, Methods and Algorithms 1. International Conference on Bioinformatics Models, Methods and Algorithms, Barcelona /Spain, 02/11/2013-02/14/2013, pp. 105-110.SCITEPRESS – Science and Technology Publications, Lissabon /Portugal. ISBN: 978-989-8565358.

Priebe S, Menzel U, Zarse K, Groth M, Platzer M, Ristow M, Guthke R (2013) Extension of life span by impaired glucose metabolism in *Caenorhabditis elegans* is accompanied by structural rearrangements of the transcriptomic network. *PLoS One* 8(10), e77776.

Schmeisser K, Mansfeld J, Kuhlow D, Weimer S, Priebe S, Heiland I, Birringer M, Groth M, Segref A, Kanfi Y, Price NL, Schmeisser S, Schuster S, Pfeiffer AF, Guthke R, Platzer M, Hoppe T, Cohen HY, Zarse K, Sinclair DA, Ristow M (2013) Role of sirtuins in lifespan regulation is linked to methylation of nicotinamide. *Nat Chem Biol* 9(11), 693-700.

Schmeisser S, Priebe S, Groth M, Monajembashi S, Hemmerich P, Guthke R, Platzer M, Ristow M (2013) Neuronal ROS signaling rather than AMPK/sirtuin-mediated energy sensing links dietary restriction to lifespan extension. *Mol Metab* 2(2), 92-9102.

Schmeisser S, Schmeisser K, Weimer S, Groth M, Priebe S, Fazius E, Kuhlow D, Pick D, Einax JW, Guthke R, Platzer M, Zarse K, Ristow M (2013) Mitochondrial hormesis links low-dose arsenite exposure to lifespan extension. *Aging Cell* 12(3), 508-517.

Ullmann-Zeunert L, Stanton MA, Wielsch N, Bartram S, Hummert C, Svatoš A, Baldwin IT, Groten K (2013) Quantification of growth-defense trade-offs in a common currency: nitrogen required for

phenolamide biosynthesis is not derived from ribulose-1,5-bisphosphate carboxylase/oxygenase turnover. *Plant J* 75(3), 417-429.

Vlaic S, Hoffmann B, Kupfer P, Weber M, Dräger A (2013) GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. *Bioinformatics* 29(17), 2216-2217.

Weber M, Henkel SG, Vlaic S, Guthke R, van Zoelen EJ, Driesch D (2013) Inference of dynamical gene-regulatory networks based on time-resolved multi-stimuli multi-experiment data applying NetGenerator V2.0. *BMC Syst Biol* 7, 1.

Weber M, Sotoca AM, Kupfer P, Guthke R, van Zoelen EJ (2013) Dynamic modelling of microRNA regulation during mesenchymal stem cell differentiation. *BMC Syst Biol* 7, 124.

Wolf T, Shelest V, Shelest E (2013) Motif-based method for genome-wide prediction of eukaryotic gene clusters In: A. Petrosino, L. Maddalena, P. Pala (eds.) Lecture Notes in Computer Science (LNCS) 2nd International Workshop on Pattern Recognition in Proteomics, Structural Biology and Bioinformatics, Naples, Italien, 09/09/2013-09/10/2013, 8158, pp. 389-398. Springer-Verlag, Berlin, Heidelberg.

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

Baumgart M, Groth M, Priebe S, Appelt J, Guthke R, Platzer M, Cellerino A (2012) Age-dependent regulation of tumor-related microRNAs in the brain of the annual fish *Nothobranchius furzeri*. *Mech Ageing Dev* 133(5), 226-233.

Druzhinina IS, Shelest E, Kubicek CP (2012) Novel traits of Trichoderma predicted through the analysis of its secretome. *FEMS Microbiol Lett* 337(1), 1-9.

Erdmann S, Freihorst D, Raudaskoski M, Schmidt-Heck W, Jung EM, Senftleben D, Kothe E (2012) Transcriptome and functional analysis of mating in the basidiomycete Schizophyllum commune. *Eukaryot Cell* 11(5), 571-589.

Fazius F, Shelest E, Gebhardt P, Brock M (2012) The fungal  $\alpha$ -aminoadipate pathway for lysine biosynthesis requires two enzymes of the aconitase family for the isomerization of homocitrate to homoisocitrate. *Mol Microbiol* 86(6), 1508-1530.

Fuellen G, Dengjel J, Hoeflich A, Hoeijemakers J, Kestler HA, Kowald A, Priebe S, Rebholz-Schuhmann D, Schmeck B, Schmitz U, Stolzing A, Sühnel J, Wuttke D, Vera J (2012) Systems biology and bioinformatics in aging research: a workshop report. *Rejuvenation Res* 15(6), 631-641.

Gerke J, Bayram O, Feussner K, Landesfeind M, Shelest E, Feussner I, Braus GH (2012) Breaking the silence: protein stabilization uncovers silenced biosynthetic gene clusters in the fungus *Aspergillus nidulans*. *Appl Environ Microbiol* 78(23), 8234-8244.

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

Hecker M, Goertsches RH, Fatum C, Koczan D, Thiesen HJ, Guthke R, Zettl UK (2012) Network analysis of transcriptional regulation in response to intramuscular interferon- $\beta$ -1a multiple sclerosis

treatment. *Pharmacogenomics J* 12(4), 360.

Horn F, Heinekamp T, Kniemeyer O, Pollmächer J, Valiante V, Brakhage AA (2012) Systems biology of fungal infection. *Front Microbiol* 3, 108.

Kastner S, Müller S, Natesan L, König GM, Guthke R, Nett M (2012) 4-Hydroxyphenylglycine biosynthesis in *Herpetosiphon aurantiacus*: a case of gene duplication and catalytic divergence. *Arch Microbiol* 194(6), 557-566.

Kremling A, Goehler A, Jahreis K, Nees M, Auerbach B, Schmidt-Heck W, Kökpinar O, Geffers R, Rinas U, Bettenbrock K (2012) Analysis and Design of Stimulus Response Curves of *E. coli*. *Metabolites* 2(4), 844-871.

Kupfer P, Guthke R, Pohlers D, Huber R, Koczan D, Kinne RW (2012) Batch correction of microarray data substantially improves the identification of genes differentially expressed in rheumatoid arthritis and osteoarthritis. *BMC Med Genomics* 5, 23.

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.

Martinez DA, Oliver BG, Gräser Y, Goldberg JM, Li W, Martinez-Rossi NM, Monod M, Shelest E, Barton RC, Birch E, Brakhage AA, Chen Z, Gurr SJ, Heiman D, Heitman J, Kostl I, Rossi A, Saif S, Samalova M, Saunders CW, Shea T, Summerbell RC, Xu J, Young S, Zeng Q, Birren BW, Cuomo CA, White TC (2012) Comparative genome analysis of *Trichophyton rubrum* and related dermatophytes reveals candidate genes involved in infection. *MBio* 3(5), e00259.

Müller S, Baldin C, Groth M, Guthke R, Kniemeyer O, Brakhage AA, Valiante V (2012) Comparison of transcriptome technologies in the pathogenic fungus *Aspergillus fumigatus* reveals novel insights into the genome and MpkA dependent gene expression. *BMC Genomics* 13, 519.

Rauchfuss F, Lambeck S, Claus RA, Ullmann J, Schulz T, Weber M, Katenkamp K, Guthke R, Bauer M, Settmacher U (2012) Sustained liver regeneration after portal vein embolization - a human molecular pilot study. *Dig Liver Dis* 44(8), 681-688.

Simon S, Guthke R, Kamradt T, Frey O (2012) Multivariate analysis of flow cytometric data using decision trees. *Front Microbiol* 3, 114.

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.

Wartenberg D, Vödisch M, Kniemeyer O, Albrecht-Eckardt D, Scherlach K, Winkler R, Weide M, Brakhage AA (2012) Proteome analysis of the farnesol-induced stress response in *Aspergillus nidulans* - The role of a putative dehydrin. *J Proteomics* 75(13), 4038-4049.

Werner S, Schroeter A, Schimek C, Vlaic S, Wöstemeyer J, Schuster S (2012) Model of the

synthesis of trisporic acid in Mucorales showing bistability. *IET Syst Biol* 6(6), 207-214.

Zarse K, Schmeisser S, Groth M, Priebe S, Beuster G, Kuhlow D, Guthke R, Platzer M, Kahn CR, Ristow M (2012) Impaired insulin/IGF1 signaling extends life span by promoting mitochondrial L-proline catabolism to induce a transient ROS signal. *Cell Metab* 15(4), 451-465.

Albrecht D, Kniemeyer O, Mech F, Gunzer M, Brakhage A, Guthke R (2011) On the way toward systems biology of *Aspergillus fumigatus* infection. *Int J Med Microbiol* 301(5), 453-459.

Burmester A, Shelest E, Glöckner G, Heddergott C, Schindler S, Staib P, Heidel A, Felder M, Petzold A, Szafranski K, Feuermann M, Pedruzzi I, Priebe S, Groth M, Winkler R, Li W, Kniemeyer O, Schroeckh V, Hertweck C, Hube B, White TC, Platzer M, Guthke R, Heitman J, Wöstemeyer J, Zipfel PF, Monod M, Brakhage AA (2011) Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. *Genome Biol* 12(1), R7.

Fazius E, Shelest V, Shelest E (2011) SiTaR: a novel tool for transcription factor binding site prediction. *Bioinformatics* 27(20), 2806-2811.

Göhler AK, Kökpinar Ö, Schmidt-Heck W, Geffers R, Guthke R, Rinas U, Schuster S, Jahreis K, Kaleta C (2011) More than just a metabolic regulator - elucidation and validation of new targets of PdhR in *Escherichia coli*. *BMC Syst Biol* 5, 197.

Kaleta C, de Figueiredo LF, Werner S, Guthke R, Ristow M, Schuster S (2011) In silico evidence for gluconeogenesis from fatty acids in humans. *PLOS Comput Biol* 7(7), e1002116.

Keller J, Ringseis R, Priebe S, Guthke R, Kluge H, Eder K (2011) Effect of L-carnitine on the hepatic transcript profile in piglets as animal model. *Nutr Metab (Lond)* 8, 76.

Keller J, Ringseis R, Priebe S, Guthke R, Kluge H, Eder K (2011) Dietary L-carnitine alters gene expression in skeletal muscle of piglets. *Mol Nutr Food Res* 55(3), 419-429.

Mech F<sup>\*</sup>, Thywissen A<sup>\*</sup>, Guthke R, Brakhage AA, Figge MT (2011) Automated image analysis of the host-pathogen interaction between phagocytes and *Aspergillus fumigatus*. *PLOS ONE* 6(5), e19591, <sup>\*</sup>authors contributed equally.

Müller S, Fleck CB, Wilson D, Hummert C, Hube B, Brock M (2011) Gene acquisition, duplication and metabolic specification: the evolution of fungal methylisocitrate lyases. *Environ Microbiol* 13(6), 1534-1548.

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.

Wessely F, Bartl M, Guthke R, Li P, Schuster S, Kaleta C (2011) Optimal regulatory strategies for metabolic pathways in *Escherichia coli* depending on protein costs. *Mol Syst Biol* 7, 515.

Albrecht D, Guthke R, Brakhage AA, Kniemeyer O (2010) Integrative analysis of the heat shock response in *Aspergillus fumigatus*. *BMC Genomics* 11, 32.

Albrecht D, Kniemeyer O, Brakhage AA, Guthke R (2010) Missing values in gel-based proteomics. *Proteomics* 10(6), 1202-1211.

Bergmann S, Funk AN, Scherlach K, Schroeckh V, Shelest E, Horn U, Hertweck C, Brakhage AA

- (2010) Activation of a silent fungal polyketide biosynthesis pathway through regulatory cross talk with a cryptic nonribosomal peptide synthetase gene cluster. *Appl Environ Microbiol* 76(24), 8143-8149.
- El-Kased RF, Koy C, Lorenz P, Drynda S, Guthke R, Qian Z, Koczan D, Li Y, Kekow J, Thiesen HJ, Glocker MO (2010) Mass spectrometric and peptide chip epitope analysis on the RA33 autoantigen with sera from rheumatoid arthritis patients. *Eur J Mass Spectrom (Chichester, Eng)* 16(3), 443-451.
- Hummert S, Hummert C, Schröter A, Hube B, Schuster S (2010) Game theoretical modelling of survival strategies of *Candida albicans* inside macrophages. *J Theor Biol* 264(2), 312-318.
- Kaleta C, Göhler A, Schuster S, Jahreis K, Guthke R, Nikolajewa S (2010) Integrative inference of gene-regulatory networks in *Escherichia coli* using information theoretic concepts and sequence analysis. *BMC Syst Biol* 4, 116.
- 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.
- Shelest V, Albrecht D, Shelest E (2010) DistanceScan: a tool for promoter modeling. *Bioinformatics* 26(11), 1460-1462.
- Teutschbein J, Albrecht D, Pötsch M, Guthke R, Aimanianda V, Clavaud C, Latgé JP, Brakhage AA, Kniemeyer O (2010) Proteome profiling and functional classification of intracellular proteins from conidia of the human-pathogenic mold *Aspergillus fumigatus*. *J Proteome Res* 9(7), 3427-3442.
- Zellmer S, Schmidt-Heck W, Godoy P, Weng H, Meyer C, Lehmann T, Sparna T, Schormann W, Hammad S, Kreutz C, Timmer J, von Weizsäcker F, Thürmann PA, Merfort I, Guthke R, Dooley S, Hengstler JG, Gebhardt R (2010) Transcription factors ETF, E2F, and SP-1 are involved in cytokine-independent proliferation of murine hepatocytes. *Hepatology* 52(6), 2127-2136.
- Acikgöz A, Karim N, Giri S, Schmidt-Heck W, Bader A (2009) Two compartment model of diazepam biotransformation in an organotypical culture of primary human hepatocytes. *Toxicol Appl Pharmacol* 234(2), 179-191.
- Hecker M, Goertsches RH, Engelmann R, Thiesen HJ, Guthke R (2009) Integrative modeling of transcriptional regulation in response to antirheumatic therapy. *BMC Bioinformatics* 10, 262.
- Hecker M, Lambeck S, Toepfer S, van Someren E, Guthke R (2009) Gene regulatory network inference: data integration in dynamic models-a review. *Biosystems* 96(1), 86-8103. (Review)
- Kienbaum M, Koy C, Montgomery HV, Drynda S, Lorenz P, Illges H, Tanaka K, Kekow J, Guthke R, Thiesen HJ, Glocker MO (2009) MS characterization of apheresis samples from rheumatoid arthritis patients for the improvement of immunoadsorption therapy - a pilot study. *Proteomics Clin Appl* 3(7), 797-809.
- Linde J, Olsson B, Lubovac Z (2009) Network Properties for Ranking Predicted miRNA Targets in Breast Cancer. *Adv Bioinformatics* , 182689-182689.
- Schroeckh V, Scherlach K, Nützmänn HW, Shelest E, Schmidt-Heck W, Schuemann J, Martin K, Hertweck C, Brakhage AA (2009) Intimate bacterial-fungal interaction triggers biosynthesis of

archetypal polyketides in *Aspergillus nidulans*. *Proc Natl Acad Sci U S A* 106(34), 14558-14563.

Vödisch M, Albrecht D, Lessing F, Schmidt AD, Winkler R, Guthke R, Brakhage AA, Kniemeyer O (2009) Two-dimensional proteome reference maps for the human pathogenic filamentous fungus *Aspergillus fumigatus*. *Proteomics* 9(5), 1407-1415.

Wollbold J, Huber R, Pohlers D, Koczan D, Guthke R, Kinne RW, Gausmann U (2009) Adapted Boolean network models for extracellular matrix formation. *BMC Syst Biol* 3, 77.

Zellmer S, Sickinger S, Schmidt-Heck W, Guthke R, Gebhardt R (2009) Heterogeneous expression of suppressor of cytokine signalling 2 (SOCS-2) in liver tissue. *J Anat* 215(2), 176-183.

Dürschmid K, Reischer H, Schmidt-Heck W, Hrebicek T, Guthke R, Rizzi A, Bayer K (2008) Monitoring of transcriptome and proteome profiles to investigate the cellular response of *E. coli* towards recombinant protein expression under defined chemostat conditions. *J Biotechnol* 135(1), 34-44.

Glahn F, Schmidt-Heck W, Zellmer S, Guthke R, Wiese J, Golka K, Hergenröder R, Degen GH, Lehmann T, Hermes M, Schormann W, Brulport M, Bauer A, Bedawy E, Gebhardt R, Hengstler JG, Foth H (2008) Cadmium, cobalt and lead cause stress response, cell cycle deregulation and increased steroid as well as xenobiotic metabolism in primary normal human bronchial epithelial cells which is coordinated by at least nine transcription factors. *Arch Toxicol* 82(8), 513-524.

Huber R, Hummert C, Gausmann U, Pohlers D, Koczan D, Guthke R, Kinne RW (2008) Identification of intra-group, inter-individual, and gene-specific variances in mRNA expression profiles in the rheumatoid arthritis synovial membrane. *Arthritis Res Ther* 10(4), R98.

Koczan D, Drynda S, Hecker M, Drynda A, Guthke R, Kekow J, Thiesen HJ (2008) Molecular discrimination of responders and nonresponders to anti-TNF alpha therapy in rheumatoid arthritis by etanercept. *Arthritis Res Ther* 10(3), R50.

Shelest E (2008) Transcription factors in fungi. *FEMS Microbiol Lett* 286(2), 145-151.

Guthke R, Kniemeyer O, Albrecht D, Brakhage AA, Moeller U (2007) Discovery of gene regulatory networks in *Aspergillus fumigatus*. *Lect Notes Bioinf* 4366,

Otero JM, Panagiotou G, Olsson L (2007) Fueling industrial biotechnology growth with bioethanol. *Adv Biochem Eng Biotechnol* 108, 1-40.

Glocker MO, Guthke R, Kekow J, Thiesen HJ (2006) Rheumatoid arthritis, a complex multifactorial disease: on the way toward individualized medicine. *Med Res Rev* 26(1), 63-87.

Müller U, Ernst G, Melle C, Guthke R, von Eggeling F (2006) Convergence of the proteomic pattern in cancer. *Bioinformatics* 22(11), 1293-1296.

Guthke R, Möller U, Hoffmann M, Thies F, Töpfer S (2005) Dynamic network reconstruction from gene expression data applied to immune response during bacterial infection. *Bioinformatics* 21(8), 1626-1634.

Klenk M, Koczan D, Guthke R, Nakata M, Thiesen HJ, Podbielski A, Kreikemeyer B (2005) Global epithelial cell transcriptional responses reveal *Streptococcus pyogenes* Fas regulator activity

association with bacterial aggressiveness. *Cell Microbiol* 7(9), 1237-1250.

Koczan D, Guthke R, Thiesen HJ, Ibrahim SM, Kundt G, Krentz H, Gross G, Kunz M (2005) Gene expression profiling of peripheral blood mononuclear leukocytes from psoriasis patients identifies new immune regulatory molecules. *Eur J Dermatol* 15(4), 251-257.

\*equal contribution #corresponding author