

Publications

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.

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.

Rennert C, Vlaic 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, Vlaic S, Medyukhina A, Neugebauer S, Nietzsche S, Gonnert FA, Rödel J, Singer M, Kiehnkopf 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, Vlaic 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.

Vlaic 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.

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)

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.

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.

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.

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.

Kupfer P, Huber R, Weber M, Vlaic 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.

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 BIOCOMP'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. BIOCOMP'13, BIOCOMP'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.

Kupfer P, Vlaic S, Huber R, Kinne 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.

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.

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.

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.

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