

Publications

Atanasoff-Kardjaleff AK, Berger H, Steinert K, Janevska S, Ponts N, Humpf HU, Kalinina S, Studt-Reinhold L (2024) Incorporation of the histone variant H2A.Z counteracts gene silencing mediated by H3K27 trimethylation in *Fusarium fujikuroi*. *Epigenetics Chromatin* 17(1), 7.

Jojić K*, Gherlone F*, Cseresnyés Z, Bissell AU, Hoefgen S, Hoffmann S, Huang Y, Janevska S, Figge MT, Valiante V (2024) The spatial organization of sphingofungin biosynthesis in *Aspergillus fumigatus* and its cross-interaction with sphingolipid metabolism. *mBio* 15(3), e0019524.

Talbi N*, Blekemolen MC*, Janevska S, Zendler DP, van Tilbeurgh H, Fudal I, Takken FLW (2024) Facilitation of symplastic effector protein mobility by paired effectors is conserved in different classes of fungal pathogens. *Mol Plant Microbe Interact* 37(3), 304-314.

Bissell AU, Rautschek J, Hoefgen S, Raguz L, Mattern DJ, Saeed N, Janevska S, Jojić K, Huang Y, Kufs JE, Herboeck B, Guo H, Hillmann F, Beemelmans C, Valiante V (2022) Biosynthesis of the sphingolipid inhibitors sphingofungins in filamentous fungi requires aminomalonnate as a metabolic precursor. *ACS Chem Biol* 17(2), 386-394.

Janevska S, Ferling I, Jojić K, Rautschek J, Hoefgen S, Proctor RH, Hillmann F, Valiante V (2020) Self-protection against the sphingolipid biosynthesis inhibitor fumonisin B1 is conferred by a *FUM* cluster-encoded ceramide synthase. *mBio* 11(3), e00455-20.

Burkhardt I, Ye Z, Janevska S, Tudzynski B, Dickschat JS (2019) Biochemical and mechanistic characterization of the fungal reverse *N*-1-dimethylallyltryptophan synthase DMATS1Ff. *ACS Chem Biol* 14(12), 2922-2931.

Manfiolli AO, Siqueira FS, Dos Reis TF, Van Dijck P, Schrevens S, Hoefgen S, Föge M, Straßburger M, de Assis LJ, Heinekamp T, Rocha MC, Janevska S, Brakhage AA, Malavazi I, Goldman GH, Valiante V (2019) Mitogen-activated protein kinase cross-talk interaction modulates the production of melanins in *Aspergillus fumigatus*. *mBio* 10(2), e00215-19.

Janevska S, Baumann L, Sieber CMK, Münsterkötter M, Ulrich J, Kämper J, Güldener U, Tudzynski B (2018) Elucidation of the two H3K36me3 histone methyltransferases Set2 and Ash1 in *Fusarium fujikuroi* unravels their different chromosomal targets and a major impact of Ash1 on genome stability. *Genetics* 208(1), 153-171.

Janevska S, Güldener U, Sulyok M, Tudzynski B, Studt L (2018) Set1 and Kdm5 are antagonists for H3K4 methylation and regulators of the major conidiation-specific transcription factor gene *ABA1* in *Fusarium fujikuroi*. *Environ Microbiol* 20(9), 3343-3362.

Janevska S, Tudzynski B (2018) Secondary metabolism in *Fusarium fujikuroi*: strategies to unravel the function of biosynthetic pathways. *Appl Microbiol Biotechnol* 102(2), 615-630. (Review)

Niehaus EM, Rindermann L, Janevska S, Münsterkötter M, Güldener U, Tudzynski B (2018) Analysis of the global regulator Lae1 uncovers a connection between Lae1 and the histone acetyltransferase HAT1 in *Fusarium fujikuroi*. *Appl Microbiol Biotechnol* 102(1), 279-295.

Arndt B, Janevska S, Schmid R, Hübner F, Tudzynski B, Humpf HU (2017) A fungal *N*-dimethylallyltryptophan metabolite from *Fusarium fujikuroi*. *ChemBioChem* 18(10), 899-904.

Janevska S, Arndt B, Baumann L, Apken LH, Mauriz Marques LM, Humpf HU, Tudzynski B (2017) Establishment of the inducible Tet-on system for the activation of the silent trichosetin gene cluster in *Fusarium fujikuroi*. *Toxins (Basel)* 9(4), 126.

Niehaus EM^{*}, Kim HK^{*}, Münsterkötter M^{*}, Janevska S^{*}, Arndt B, Kalinina SA, Houterman PM, Ahn IP, Alberti I, Tonti S, Kim DW, Sieber CMK, Humpf HU, Yun SH, Güldener U, Tudzynski B (2017) Comparative genomics of geographically distant *Fusarium fujikuroi* isolates revealed two distinct pathotypes correlating with secondary metabolite profiles. *PLoS Pathog* 13(10), e1006670.

Janevska S, Arndt B, Niehaus EM, Burkhardt I, Rösler SM, Brock NL, Humpf HU, Dickschat JS, Tudzynski B (2016) Gibepyrone biosynthesis in the rice pathogen *Fusarium fujikuroi* is facilitated by a small polyketide synthase gene cluster. *J Biol Chem* 291(53), 27403-27420.

Studt L, Janevska S, Arndt B, Boedi S, Sulyok M, Humpf HU, Tudzynski B, Strauss J (2016) Lack of the COMPASS component Ccl1 reduces H3K4 trimethylation levels and affects transcription of secondary metabolite genes in two plant-pathogenic *Fusarium* species. *Front Microbiol* 7, 2144.

Studt L^{*}, Janevska S^{*}, Niehaus EM, Burkhardt I, Arndt B, Sieber CM, Humpf HU, Dickschat JS, Tudzynski B (2016) Two separate key enzymes and two pathway-specific transcription factors are involved in fusaric acid biosynthesis in *Fusarium fujikuroi*. *Environ Microbiol* 18(3), 936-956.

Michielse CB^{*}, Studt L^{*}, Janevska S, Sieber CM, Arndt B, Espino JJ, Humpf HU, Güldener U, Tudzynski B (2015) The global regulator FfSge1 is required for expression of secondary metabolite gene clusters but not for pathogenicity in *Fusarium fujikuroi*. *Environ Microbiol* 17(8), 2690-2708.

Niehaus EM^{*}, Janevska S^{*}, von Bargen KW^{*}, Sieber CM, Harrer H, Humpf HU, Tudzynski B (2014) Apicidin F: characterization and genetic manipulation of a new secondary metabolite gene cluster in the rice pathogen *Fusarium fujikuroi*. *PLoS One* 9(7), e103336.

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