

Regine Kahmann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1331275/publications.pdf>

Version: 2024-02-01

107
papers

16,453
citations

16451

64
h-index

30087

103
g-index

114
all docs

114
docs citations

114
times ranked

10564
citing authors

#	ARTICLE	IF	CITATIONS
1	The Top 10 fungal pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2012, 13, 414-430.	4.2	3,270
2	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101.	27.8	1,113
3	Fungal Effectors and Plant Susceptibility. <i>Annual Review of Plant Biology</i> , 2015, 66, 513-545.	18.7	1,006
4	Metabolic priming by a secreted fungal effector. <i>Nature</i> , 2011, 478, 395-398.	27.8	509
5	The b alleles of <i>U. maydis</i> , whose combinations program pathogenic development, code for polypeptides containing a homeodomain-related motif. <i>Cell</i> , 1990, 60, 295-306.	28.9	429
6	The a mating type locus of <i>U. maydis</i> specifies cell signaling components. <i>Cell</i> , 1992, 68, 441-450.	28.9	398
7	A two-component regulatory system for self/non-self recognition in <i>Ustilago maydis</i> . <i>Cell</i> , 1992, 68, 647-657.	28.9	367
8	Reprogramming a maize plant: transcriptional and metabolic changes induced by the fungal biotroph <i>Ustilago maydis</i> . <i>Plant Journal</i> , 2008, 56, 181-195.	5.7	328
9	<i>Ustilago maydis</i> as a Pathogen. <i>Annual Review of Phytopathology</i> , 2009, 47, 423-445.	7.8	314
10	Pathogenicity Determinants in Smut Fungi Revealed by Genome Comparison. <i>Science</i> , 2010, 330, 1546-1548.	12.6	301
11	Identification of genes in the bW/bE regulatory cascade in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2001, 42, 1047-1063.	2.5	286
12	Pep1, a Secreted Effector Protein of <i>Ustilago maydis</i> , Is Required for Successful Invasion of Plant Cells. <i>PLoS Pathogens</i> , 2009, 5, e1000290.	4.7	285
13	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. <i>MBio</i> , 2020, 11, .	4.1	275
14	Multiallelic recognition: Nonself-dependent dimerization of the bE and bW homeodomain proteins in <i>ustilago maydis</i> . <i>Cell</i> , 1995, 81, 73-83.	28.9	268
15	An <i>Ustilago maydis</i> Gene Involved in H ₂ O ₂ Detoxification Is Required for Virulence. <i>Plant Cell</i> , 2007, 19, 2293-2309.	6.6	234
16	A secreted <i>Ustilago maydis</i> effector promotes virulence by targeting anthocyanin biosynthesis in maize. <i>ELife</i> , 2014, 3, e01355.	6.0	217
17	The MAP kinase Kpp2 regulates mating and pathogenic development in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 1999, 34, 1007-1017.	2.5	209
18	Genome editing in <i>Ustilago maydis</i> using the CRISPR-Cas system. <i>Fungal Genetics and Biology</i> , 2016, 89, 3-9.	2.1	192

#	ARTICLE	IF	CITATIONS
19	Ustilago maydis effectors and their impact on virulence. Nature Reviews Microbiology, 2017, 15, 409-421.	28.6	188
20	The Biotrophic Development of <i>Ustilago maydis</i> Studied by RNA-Seq Analysis. Plant Cell, 2018, 30, 300-323.	6.6	186
21	Tagging pathogenicity genes in <i>Ustilago maydis</i> by restriction enzyme-mediated integration (REMI). Molecular Genetics and Genomics, 1995, 248, 547-52.	2.4	182
22	Indoleacetic acid (IAA) biosynthesis in the smut fungus <i>Ustilago maydis</i> and its relevance for increased IAA levels in infected tissue and host tumour formation. Molecular Plant Pathology, 2008, 9, 339-355.	4.2	162
23	The secretome of the maize pathogen <i>Ustilago maydis</i> . Fungal Genetics and Biology, 2008, 45, S63-S70.	2.1	162
24	Genome Comparison of Barley and Maize Smut Fungi Reveals Targeted Loss of RNA Silencing Components and Species-Specific Presence of Transposable Elements. Plant Cell, 2012, 24, 1733-1745.	6.6	159
25	A Ferroxidation/Permeation Iron Uptake System Is Required for Virulence in <i>Ustilago maydis</i> . Plant Cell, 2006, 18, 3332-3345.	6.6	154
26	Regulation of mating and pathogenic development in <i>Ustilago maydis</i> . Current Opinion in Microbiology, 2004, 7, 666-672.	5.1	142
27	Mating and Pathogenic Development of the Smut Fungus <i>Ustilago maydis</i> Are Regulated by One Mitogen-Activated Protein Kinase Cascade. Eukaryotic Cell, 2003, 2, 1187-1199.	3.4	138
28	<i>Ustilago maydis</i> : how its biology relates to pathogenic development. New Phytologist, 2004, 164, 31-42.	7.3	138
29	Two linked genes encoding a secreted effector and a membrane protein are essential for <i>Ustilago maydis</i> -induced tumour formation. Molecular Microbiology, 2011, 81, 751-766.	2.5	138
30	Manipulation of Phytohormone Pathways by Effectors of Filamentous Plant Pathogens. Frontiers in Plant Science, 2019, 10, 822.	3.6	135
31	Fungal model systems and the elucidation of pathogenicity determinants. Fungal Genetics and Biology, 2014, 70, 42-67.	2.1	133
32	A homologue of the transcriptional repressor Ssn6p antagonizes cAMP signalling in <i>Ustilago maydis</i> . Molecular Microbiology, 2001, 40, 719-730.	2.5	130
33	A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. Genome Biology and Evolution, 2016, 8, 681-704.	2.5	125
34	Environmental Signals Controlling Sexual Development of the Corn Smut Fungus <i>Ustilago maydis</i> through the Transcriptional Regulator Prf1. Plant Cell, 1999, 11, 1293-1305.	6.6	120
35	Physical and chemical plant-derived signals induce differentiation in <i>Ustilago maydis</i> . Molecular Microbiology, 2009, 71, 895-911.	2.5	120
36	Sho1 and Msb2-Related Proteins Regulate Appressorium Development in the Smut Fungus <i>Ustilago maydis</i> . Plant Cell, 2010, 22, 2085-2101.	6.6	120

#	ARTICLE	IF	CITATIONS
37	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013, 4, e00572-12.	4.1	118
38	An unusual MAP kinase is required for efficient penetration of the plant surface by <i>Ustilago maydis</i> . <i>EMBO Journal</i> , 2003, 22, 2199-2210.	7.8	116
39	PKA and MAPK phosphorylation of Prf1 allows promoter discrimination in <i>Ustilago maydis</i> . <i>EMBO Journal</i> , 2003, 22, 5817-5826.	7.8	114
40	Genetic regulation of mating and dimorphism in <i>Ustilago maydis</i> . <i>Canadian Journal of Botany</i> , 1995, 73, 320-325.	1.1	111
41	CRISPR-Cas9 genome editing approaches in filamentous fungi and oomycetes. <i>Fungal Genetics and Biology</i> , 2019, 130, 43-53.	2.1	111
42	Arbuscular cell invasion coincides with extracellular vesicles and membrane tubules. <i>Nature Plants</i> , 2019, 5, 204-211.	9.3	107
43	Establishment of compatibility in the <i>Ustilago maydis</i> /maize pathosystem. <i>Journal of Plant Physiology</i> , 2008, 165, 29-40.	3.5	106
44	The <i>Ustilago maydis</i> repetitive effector Rsp3 blocks the antifungal activity of mannose-binding maize proteins. <i>Nature Communications</i> , 2018, 9, 1711.	12.8	102
45	Characterization of the Largest Effector Gene Cluster of <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2014, 10, e1003866.	4.7	100
46	<i>Ustilago maydis</i> Mating Hyphae Orient Their Growth toward Pheromone Sources. <i>Fungal Genetics and Biology</i> , 1996, 20, 299-312.	2.1	98
47	<i>Ustilago maydis</i> Infection Strongly Alters Organic Nitrogen Allocation in Maize and Stimulates Productivity of Systemic Source Leaves. <i>Plant Physiology</i> , 2009, 152, 293-308.	4.8	98
48	Mating Type Loci of <i>Sporisorium reilianum</i> : Novel Pattern with Three a and Multiple b Specificities. <i>Eukaryotic Cell</i> , 2005, 4, 1317-1327.	3.4	97
49	<i>Ustilago maydis</i> : Dissecting the Molecular Interface between Pathogen and Plant. <i>PLoS Pathogens</i> , 2012, 8, e1002955.	4.7	95
50	The use of FLP-mediated recombination for the functional analysis of an effector gene family in the biotrophic smut fungus <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2010, 187, 957-968.	7.3	93
51	Plant Surface Cues Prime <i>Ustilago maydis</i> for Biotrophic Development. <i>PLoS Pathogens</i> , 2014, 10, e1004272.	4.7	91
52	A split motor domain in a cytoplasmic dynein. <i>EMBO Journal</i> , 2001, 20, 5091-5100.	7.8	89
53	Degradation of the plant defence hormone salicylic acid by the biotrophic fungus <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2013, 89, 179-188.	2.5	88
54	In Vitro Translocation Experiments with RxLR-Reporter Fusion Proteins of Avr1b from <i>Phytophthora sojae</i> and AVR3a from <i>Phytophthora infestans</i> Fail to Demonstrate Specific Autonomous Uptake in Plant and Animal Cells. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 528-536.	2.6	87

#	ARTICLE	IF	CITATIONS
55	Comparative analyses of secreted proteins in plant pathogenic smut fungi and related basidiomycetes. <i>Fungal Genetics and Biology</i> , 2018, 112, 21-30.	2.1	86
56	Characterization of a <i>Ustilago maydis</i> Gene Specifically Induced during the Biotrophic Phase: Evidence for Negative as Well as Positive Regulation. <i>Molecular and Cellular Biology</i> , 2000, 20, 329-339.	2.3	85
57	The induction of sexual development and virulence in the smut fungus <i>Ustilago maydis</i> depends on Crk1, a novel MAPK protein. <i>Genes and Development</i> , 2004, 18, 3117-3130.	5.9	76
58	Filament-Specific Expression of a Cellulase Gene in the Dimorphic Fungus <i>Ustilago maydis</i> . <i>Biological Chemistry Hoppe-Seyler</i> , 1995, 376, 617-626.	1.4	75
59	How filamentous plant pathogen effectors are translocated to host cells. <i>Current Opinion in Plant Biology</i> , 2017, 38, 19-24.	7.1	75
60	Two Potential Indole-3-Acetaldehyde Dehydrogenases in the Phytopathogenic Fungus <i>Ustilago maydis</i> . <i>FEBS Journal</i> , 1996, 242, 648-656.	0.2	74
61	A maize-specifically expressed gene cluster in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2002, 43, 75-93.	2.5	71
62	Endoplasmic Reticulum Glucosidase II Is Required for Pathogenicity of <i>Ustilago maydis</i> [W]. <i>Plant Cell</i> , 2005, 17, 3532-3543.	6.6	71
63	Systemic virus-induced gene silencing allows functional characterization of maize genes during biotrophic interaction with <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2011, 189, 471-483.	7.3	71
64	A protein with similarity to the human retinoblastoma binding protein 2 acts specifically as a repressor for genes regulated by the b mating type locus in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2000, 38, 154-166.	2.5	66
65	The WOPR Protein Ros1 Is a Master Regulator of Sporogenesis and Late Effector Gene Expression in the Maize Pathogen <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005697.	4.7	65
66	Activation of the cAMP Pathway in <i>Ustilago maydis</i> Reduces Fungal Proliferation and Teliospore Formation in Plant Tumors. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 1034-1040.	2.6	63
67	Identification of a target gene for the bE-bW homeodomain protein complex in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2000, 37, 54-66.	2.5	61
68	Repellents have functionally replaced hydrophobins in mediating attachment to a hydrophobic surface and in formation of hydrophobic aerial hyphae in <i>Ustilago maydis</i> . <i>Microbiology (United Kingdom)</i> , 2010, 154, 1050-1059.	1.9	51
69	Microbial effectors target multiple steps in the salicylic acid production and signaling pathway. <i>Frontiers in Plant Science</i> , 2015, 6, 349.	3.6	58
70	The histone deacetylase Hda1 from <i>Ustilago maydis</i> is essential for teliospore development. <i>Molecular Microbiology</i> , 2002, 46, 1169-1182.	2.5	54
71	Pheromone-regulated target genes respond differentially to MAPK phosphorylation of transcription factor Prf1. <i>Molecular Microbiology</i> , 2008, 69, 1041-1053.	2.5	50
72	A complete toolset for the study of <i>Ustilago bromivora</i> and <i>Brachypodium</i> sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016, 5, .	6.0	49

#	ARTICLE	IF	CITATIONS
73	Identification of O-mannosylated Virulence Factors in <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002563.	4.7	48
74	Positively Selected Effector Genes and Their Contribution to Virulence in the Smut Fungus <i>Sporisorium reilianum</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 629-645.	2.5	48
75	A kiwellin disarms the metabolic activity of a secreted fungal virulence factor. <i>Nature</i> , 2019, 565, 650-653.	27.8	48
76	Improved expression of single-chain antibodies in <i>Ustilago maydis</i> . <i>Journal of Biotechnology</i> , 2014, 191, 165-175.	3.8	45
77	The High-Mobility-Group Domain Transcription Factor Rop1 Is a Direct Regulator of <i>prf1</i> in <i>Ustilago maydis</i> . <i>Eukaryotic Cell</i> , 2005, 4, 379-391.	3.4	44
78	Neofunctionalization of the secreted Tin2 effector in the fungal pathogen <i>Ustilago maydis</i> . <i>Nature Microbiology</i> , 2019, 4, 251-257.	13.3	43
79	The GÎ ² -Subunit-Encoding Gene <i>bpp1</i> Controls Cyclic-AMP Signaling in <i>Ustilago maydis</i> . <i>Eukaryotic Cell</i> , 2004, 3, 806-814.	3.4	42
80	The dual specificity phosphatase Rok1 negatively regulates mating and pathogenicity in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2009, 73, 73-88.	2.5	35
81	Virulence function of the <i>Ustilago maydis</i> sterol carrier protein 2. <i>New Phytologist</i> , 2018, 220, 553-566.	7.3	33
82	A conserved co-chaperone is required for virulence in fungal plant pathogens. <i>New Phytologist</i> , 2016, 209, 1135-1148.	7.3	31
83	A cell surface-exposed protein complex with an essential virulence function in <i>Ustilago maydis</i> . <i>Nature Microbiology</i> , 2021, 6, 722-730.	13.3	31
84	Cell wall-associated effectors of plant-colonizing fungi. <i>Mycologia</i> , 2021, 113, 247-260.	1.9	28
85	Hap2 regulates the pheromone response transcription factor <i>prf1</i> in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2009, 72, 683-698.	2.5	27
86	Chitosan and Chitin Deacetylase Activity Are Necessary for Development and Virulence of <i>Ustilago maydis</i> . <i>MBio</i> , 2021, 12, .	4.1	27
87	A sevenâ€WD40 protein related to human RACK1 regulates mating and virulence in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2011, 81, 1484-1498.	2.5	26
88	Common motifs in the response of cereal primary metabolism to fungal pathogens are not based on similar transcriptional reprogramming. <i>Frontiers in Plant Science</i> , 2011, 2, 39.	3.6	25
89	An assay for entry of secreted fungal effectors into plant cells. <i>New Phytologist</i> , 2017, 213, 956-964.	7.3	25
90	Three regulators of <i>G</i> protein signaling differentially affect mating, morphology and virulence in the smut fungus <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2017, 105, 901-921.	2.5	23

#	ARTICLE	IF	CITATIONS
91	The Top 10 fungal pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2012, , no-no.	4.2	22
92	Experimental approaches to investigate effector translocation into host cells in the <i>Ustilago maydis</i> /maize pathosystem. <i>European Journal of Cell Biology</i> , 2015, 94, 349-358.	3.6	20
93	The functionally conserved effector Sta1 is a fungal cell wall protein required for virulence in <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2020, 227, 185-199.	7.3	20
94	A small <i>Ustilago maydis</i> effector acts as a novel adhesin for hyphal aggregation in plant tumors. <i>New Phytologist</i> , 2021, 231, 416-431.	7.3	16
95	The AGC Ser/Thr kinase Aga1 is essential for appressorium formation and maintenance of the actin cytoskeleton in the smut fungus <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2010, 78, 1484-1499.	2.5	15
96	Creating novel specificities in a fungal nonself recognition system by single step homologous recombination events. <i>New Phytologist</i> , 2020, 228, 1001-1010.	7.3	13
97	Population Genomics of the Maize Pathogen <i>Ustilago maydis</i> : Demographic History and Role of Virulence Clusters in Adaptation. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	11
98	Mating in the Smut Fungi: From a to b to the Downstream Cascades. , 0, , 377-387.		10
99	The two paralogous kiwellin proteins KWL1 and KWL1-b from maize are structurally related and have overlapping functions in plant defense. <i>Journal of Biological Chemistry</i> , 2020, 295, 7816-7825.	3.4	9
100	Nuclear status and leaf tumor formation in the <i>Ustilago maydis</i> "maize pathosystem. <i>New Phytologist</i> , 2021, 231, 399-415.	7.3	6
101	The insertion of a mitochondrial selfish element into the nuclear genome and its consequences. <i>Ecology and Evolution</i> , 2020, 10, 11117-11132.	1.9	4
102	Single and Multiplexed Gene Editing in <i>Ustilago maydis</i> Using CRISPR-Cas9. <i>Bio-protocol</i> , 2018, 8, e2928.	0.4	4
103	Repeat-containing effectors of filamentous pathogens and symbionts. <i>Current Opinion in Microbiology</i> , 2018, 46, 123-130.	5.1	3
104	The power of discussion: Support for women at the fungal Gordon Research Conference. <i>Fungal Genetics and Biology</i> , 2018, 121, 65-67.	2.1	2
105	Lebenswissenschaften im Umbruch. <i>BioSpektrum</i> , 2015, 21, 135-135.	0.0	0
106	The Biotrophic Phase of <i>Ustilago maydis</i> : Novel Determinants for Compatibility. , 2008, , 173-182.		0
107	My Personal Journey from the Fascination for Phages to a Tumor-Inducing Fungal Pathogen of Corn. <i>Annual Review of Microbiology</i> , 2022, 76, .	7.3	0