Nancy P Keller

List of Publications by Year
in descending order

228 papers	26,702 citations	8732 75 h-index	7136 153 g-index
246 all docs	246 docs citations	246 times ranked	17230 citing authors

#	Article	IF	Citations
1	One Juliet and four Romeos: VeA and its methyltransferases. Frontiers in Microbiology, 2015, 6, 1.	1.5	1,444
2	Fungal secondary metabolism â€” from biochemistry to genomics. Nature Reviews Microbiology, 2005, 3, 937-947.	13.6	1,425
3	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	13.7	1,272
4	Pathogenesis of<i>Aspergillus fumigatus</i>in Invasive Aspergillosis. Clinical Microbiology Reviews, 2009, 22, 447-465.	5.7	885
5	LaeA, a Regulator of Secondary Metabolism in Aspergillus spp. Eukaryotic Cell, 2004, 3, 527-535.	3.4	869
6	Relationship between Secondary Metabolism and Fungal Development. Microbiology and Molecular Biology Reviews, 2002, 66, 447-459.	2.9	865
7	VelB/VeA/LaeA Complex Coordinates Light Signal with Fungal Development and Secondary Metabolism. Science, 2008, 320, 1504-1506.	6.0	843
8	Fungal secondary metabolism: regulation, function and drug discovery. Nature Reviews Microbiology, 2019, 17, 167-180.	13.6	804
9	Minimum Information about a Biosynthetic Gene cluster. Nature Chemical Biology, 2015, 11, 625-631.	3.9	715
10	Metabolic Pathway Gene Clusters in Filamentous Fungi. Fungal Genetics and Biology, 1997, 21, 17-29.	0.9	563
11	<i>Aspergillus flavus</i>. Annual Review of Phytopathology, 2011, 49, 107-133.	3.5	521
12	Regulation of Secondary Metabolism in Filamentous Fungi. Annual Review of Phytopathology, 2005, 43, 437-458.	3.5	454
13	Histone Deacetylase Activity Regulates Chemical Diversity in <i>Aspergillus</i>. Eukaryotic Cell, 2007, 6, 1656-1664.	3.4	403
14	Genetic Involvement of a cAMP-Dependent Protein Kinase in a G Protein Signaling Pathway Regulating Morphological and Chemical Transitions in <i>Aspergillus nidulans</i>. Genetics, 2001, 157, 591-600.	1.2	398
15	Chromatin-level regulation of biosynthetic gene clusters. Nature Chemical Biology, 2009, 5, 462-464.	3.9	358
16	Transcriptional Regulation of Chemical Diversity in Aspergillus fumigatus by LaeA. PLoS Pathogens, 2007, 3, e50.	2.1	326
17	LaeA, a Regulator of Morphogenetic Fungal Virulence Factors. Eukaryotic Cell, 2005, 4, 1574-1582.	3.4	298
18	A Gene Cluster Containing Two Fungal Polyketide Synthases Encodes the Biosynthetic Pathway for a Polyketide, Asperfuranone, in <i>Aspergillus nidulans</i>. Journal of the American Chemical Society, 2009, 131, 2965-2970.	6.6	292

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19	Heterochromatic marks are associated with the repression of secondary metabolism clusters in Aspergillus nidulans. Molecular Microbiology, 2010, 76, 1376-1386.	1.2	292
20	Oxylipins as developmental and hostâ€"fungal communication signals. Trends in Microbiology, 2007, 15, 109-118.	3.5	289
21	veA Is Required for Toxin and Sclerotial Production in Aspergillus parasiticus. Applied and Environmental Microbiology, 2004, 70, 4733-4739.	1.4	249
22	Conservation of structure and function of the aflatoxin regulatory geneaflR fromAspergillus nidulans andA. flavus. Current Genetics, 1996, 29, 549-555.	0.8	236
23	FfVel1 and FfLae1, components of a <i>velvet</i>â€like complex in <i>Fusarium fujikuroi</i>, affect differentiation, secondary metabolism and virulence. Molecular Microbiology, 2010, 77, 972-994.	1.2	234
24	Secondary metabolism in fungi: does chromosomal location matter?. Current Opinion in Microbiology, 2010, 13, 431-436.	2.3	232
25	Growing a circular economy with fungal biotechnology: a white paper. Fungal Biology and Biotechnology, 2020, 7, 5.	2.5	228
26	Sequence-specific binding by Aspergillus nidulans AflR, a C6 zinc cluster protein regulating mycotoxin biosynthesis. Molecular Microbiology, 1998, 28, 1355-1365.	1.2	222
27	Translating biosynthetic gene clusters into fungal armor and weaponry. Nature Chemical Biology, 2015, 11, 671-677.	3.9	207
28	GliZ, a Transcriptional Regulator of Gliotoxin Biosynthesis, Contributes to Aspergillus fumigatus Virulence. Infection and Immunity, 2006, 74, 6761-6768.	1.0	203
29	Requirement of LaeA for secondary metabolism and sclerotial production in Aspergillus flavus. Fungal Genetics and Biology, 2008, 45, 1422-1429.	0.9	201
30	Secondary metabolic gene cluster silencing in Aspergillus nidulans. Molecular Microbiology, 2006, 61, 1636-1645.	1.2	200
31	Molecular mechanisms of Aspergillus flavus secondary metabolism and development. Fungal Genetics and Biology, 2014, 66, 11-18.	0.9	195
32	pH Regulation of Sterigmatocystin and Aflatoxin Biosynthesis in Aspergillus spp.. Phytopathology, 1997, 87, 643-648.	1.1	193
33	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. PLoS Biology, 2017, 15, e2003583.	2.6	187
34	Prototype of an intertwined secondary-metabolite supercluster. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17065-17070.	3.3	174
35	The Lipid Body Protein, PpoA, Coordinates Sexual and Asexual Sporulation in Aspergillus nidulans. Journal of Biological Chemistry, 2004, 279, 11344-11353.	1.6	171
36	Beyond aflatoxin: four distinct expression patterns and functional roles associated with <i>Aspergillus flavus</i> secondary metabolism gene clusters. Molecular Plant Pathology, 2010, 11, 213-226.	2.0	168

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37	Strategies for mining fungal natural products. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 301-313.	1.4	168
38	Three putative oxylipin biosynthetic genes integrate sexual and asexual development in Aspergillus nidulans. Microbiology (United Kingdom), 2005, 151, 1809-1821.	0.7	163
39	HdaA, a class 2 histone deacetylase of Aspergillus fumigatus, affects germination and secondary metabolite production. Fungal Genetics and Biology, 2009, 46, 782-790.	0.9	159
40	Characterization of the <i>Aspergillus nidulans</i> Monodictyphenone Gene Cluster. Applied and Environmental Microbiology, 2010, 76, 2067-2074.	1.4	159
41	Suspended microfluidics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10111-10116.	3.3	156
42	Distinct Roles for VeA and LaeA in Development and Pathogenesis of<i>Aspergillus flavus</i>. Eukaryotic Cell, 2009, 8, 1051-1060.	3.4	154
43	A scalable platform to identify fungal secondary metabolites and their gene clusters. Nature Chemical Biology, 2017, 13, 895-901.	3.9	154
44	Transcriptional regulatory elements in fungal secondary metabolism. Journal of Microbiology, 2011, 49, 329-339.	1.3	150
45	Oxylipins act as determinants of natural product biosynthesis and seed colonization in Aspergillus nidulans. Molecular Microbiology, 2006, 59, 882-892.	1.2	144
46	Mitochondrial Î²-oxidation in Aspergillus nidulans. Molecular Microbiology, 2004, 54, 1173-1185.	1.2	128
47	Pka, Ras and RGS Protein Interactions Regulate Activity of AflR, a Zn(II)2Cys6 Transcription Factor in <i>Aspergillus nidulans</i>. Genetics, 2003, 165, 1095-1104.	1.2	128
48	On top of biosynthetic gene clusters: How epigenetic machinery influences secondary metabolism in fungi. Biotechnology Advances, 2019, 37, 107345.	6.0	122
49	Molecular genetic analysis of the orsellinic acid/F9775 genecluster of Aspergillus nidulans. Molecular BioSystems, 2010, 6, 587-593.	2.9	118
50	Toward Awakening Cryptic Secondary Metabolite Gene Clusters in Filamentous Fungi. Methods in Enzymology, 2012, 517, 303-324.	0.4	116
51	Overexpression of the <i><scp>A</scp>spergillus nidulans</i> histone 4 acetyltransferase <scp>EsaA</scp> increases activation of secondary metabolite production. Molecular Microbiology, 2012, 86, 314-330.	1.2	116
52	Fundamental Contribution of Î²-Oxidation to Polyketide Mycotoxin Production In Planta. Molecular Plant-Microbe Interactions, 2005, 18, 783-793.	1.4	115
53	Aspergillus Cyclooxygenase-Like Enzymes Are Associated with Prostaglandin Production and Virulence. Infection and Immunity, 2005, 73, 4548-4559.	1.0	112
54	A Nonribosomal Peptide Synthetase-Derived Iron(III) Complex from the Pathogenic Fungus <i>Aspergillus fumigatus</i>. Journal of the American Chemical Society, 2013, 135, 2064-2067.	6.6	111

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55	Functional Analyses of <i>Trichoderma reesei</i> LAE1 Reveal Conserved and Contrasting Roles of This Regulator. G3: Genes, Genomes, Genetics, 2013, 3, 369-378.	0.8	109
56	Characterization of Aspergillus fumigatus Isolates from Air and Surfaces of the International Space Station. MSphere, 2016, 1, .	1.3	108
57	<i>Ralstonia solanacearum</i> lipopeptide induces chlamydospore development in fungi and facilitates bacterial entry into fungal tissues. ISME Journal, 2016, 10, 2317-2330.	4.4	108
58	Macrophages inhibit Aspergillus fumigatus germination and neutrophil-mediated fungal killing. PLoS Pathogens, 2018, 14, e1007229.	2.1	106
59	Resistance Gene-Guided Genome Mining: Serial Promoter Exchanges in <i>Aspergillus nidulans</i> Reveal the Biosynthetic Pathway for Fellutamide B, a Proteasome Inhibitor. ACS Chemical Biology, 2016, 11, 2275-2284.	1.6	105
60	Mycotoxins in Conversation With Bacteria and Fungi. Frontiers in Microbiology, 2019, 10, 403.	1.5	103
61	Homologous NRPSâ€like Gene Clusters Mediate Redundant Smallâ€Molecule Biosynthesis in <i>Aspergillus flavus</i>. Angewandte Chemie - International Edition, 2013, 52, 1590-1594.	7.2	101
62	Accurate prediction of the Aspergillus nidulans terrequinone gene cluster boundaries using the transcriptional regulator LaeA. Fungal Genetics and Biology, 2007, 44, 1134-1145.	0.9	99
63	The Antioxidant Gallic Acid Inhibits Aflatoxin Formation in Aspergillus flavus by Modulating Transcription Factors FarB and CreA. Toxins, 2018, 10, 270.	1.5	96
64	Aspergillus fumigatus Copper Export Machinery and Reactive Oxygen Intermediate Defense Counter Host Copper-Mediated Oxidative Antimicrobial Offense. Cell Reports, 2017, 19, 1008-1021.	2.9	95
65	Aspergillus Oxylipin Signaling and Quorum Sensing Pathways Depend on G Protein-Coupled Receptors. Toxins, 2012, 4, 695-717.	1.5	94
66	An interpreted atlas of biosynthetic gene clusters from 1,000 fungal genomes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	94
67	An <i>Aspergillus nidulans</i> bZIP response pathway hardwired for defensive secondary metabolism operates through <i>aflR</i>. Molecular Microbiology, 2012, 83, 1024-1034.	1.2	93
68	LaeA regulation of secondary metabolism modulates virulence in <i>Penicillium expansum</i> and is mediated by sucrose. Molecular Plant Pathology, 2017, 18, 1150-1163.	2.0	93
69	Large-Scale Metabolomics Reveals a Complex Response of <i>Aspergillus nidulans</i> to Epigenetic Perturbation. ACS Chemical Biology, 2015, 10, 1535-1541.	1.6	90
70	bZIP transcription factors affecting secondary metabolism, sexual development and stress responses in Aspergillus nidulans. Microbiology (United Kingdom), 2013, 159, 77-88.	0.7	89
71	Identification of Dioxygenases Required for Aspergillus Development. Journal of Biological Chemistry, 2007, 282, 34707-34718.	1.6	88
72	Secondary metabolite arsenal of an opportunistic pathogenic fungus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20160023.	1.8	88

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73	A call to arms: Mustering secondary metabolites for success and survival of an opportunistic pathogen. PLoS Pathogens, 2019, 15, e1007606.	2.1	88
74	Microbial metabolomics in open microscale platforms. Nature Communications, 2016, 7, 10610.	5.8	86
75	Identification of Cryptic Products of the Gliotoxin Gene Cluster Using NMR-Based Comparative Metabolomics and a Model for Gliotoxin Biosynthesis. Journal of the American Chemical Society, 2011, 133, 9678-9681.	6.6	85
76	Oxygenase Coordination Is Required for Morphological Transition and the Hostâ€“Fungus Interaction of<i>Aspergillus flavus</i>. Molecular Plant-Microbe Interactions, 2009, 22, 882-894.	1.4	84
77	Genome-Based Cluster Deletion Reveals an Endocrocin Biosynthetic Pathway in Aspergillus fumigatus. Applied and Environmental Microbiology, 2012, 78, 4117-4125.	1.4	83
78	Distinct Innate Immune Phagocyte Responses to Aspergillus fumigatus Conidia and Hyphae in Zebrafish Larvae. Eukaryotic Cell, 2014, 13, 1266-1277.	3.4	82
79	Suppressor Mutagenesis Identifies a Velvet Complex Remediator of Aspergillus nidulans Secondary Metabolism. Eukaryotic Cell, 2010, 9, 1816-1824.	3.4	79
80	Plant-like biosynthesis of isoquinoline alkaloids in Aspergillus fumigatus. Nature Chemical Biology, 2016, 12, 419-424.	3.9	79
81	Microbial volatile communication in human organotypic lung models. Nature Communications, 2017, 8, 1770.	5.8	78
82	The epigenetic reader SntB regulates secondary metabolism, development and global histone modifications in Aspergillus flavus. Fungal Genetics and Biology, 2018, 120, 9-18.	0.9	77
83	Secondary Metabolism and Development Is Mediated by LlmF Control of VeA Subcellular Localization in Aspergillus nidulans. PLoS Genetics, 2013, 9, e1003193.	1.5	76
84	Fungal artificial chromosomes for mining of the fungal secondary metabolome. BMC Genomics, 2015, 16, 343.	1.2	76
85	A peanut seed lipoxygenase responsive to Aspergillus colonization. Plant Molecular Biology, 2000, 42, 689-701.	2.0	73
86	Unraveling polyketide synthesis in members of the genus Aspergillus. Applied Microbiology and Biotechnology, 2010, 86, 1719-1736.	1.7	73
87	Low-Volume Toolbox for the Discovery of Immunosuppressive Fungal Secondary Metabolites. PLoS Pathogens, 2013, 9, e1003289.	2.1	73
88	Conserved Responses in a War of Small Molecules between a Plant-Pathogenic Bacterium and Fungi. MBio, 2018, 9, .	1.8	73
89	RcoA has pleiotropic effects on Aspergillus nidulans cellular development. Molecular Microbiology, 2001, 39, 1482-1493.	1.2	72
90	H3K9 Methylation Regulates Growth and Development in <i>Aspergillus fumigatus</i>. Eukaryotic Cell, 2008, 7, 2052-2060.	3.4	71

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91	Global Survey of Canonical Aspergillus flavus G Protein-Coupled Receptors. MBio, 2014, 5, e01501-14.	1.8	71
92	Production of cross-kingdom oxylipins by pathogenic fungi: An update on their role in development and pathogenicity. Journal of Microbiology, 2016, 54, 254-264.	1.3	71
93	Secondary metabolism in <i>Penicillium expansum</i>: Emphasis on recent advances in patulin research. Critical Reviews in Food Science and Nutrition, 2018, 58, 2082-2098.	5.4	71
94	<i>Penicillium expansum:</i> biology, omics, and management tools for a global postharvest pathogen causing blue mould of pome fruit. Molecular Plant Pathology, 2020, 21, 1391-1404.	2.0	71
95	Regulation of aflatoxin synthesis by FadA/cAMP/protein kinase A signaling in Aspergillus parasiticus. Mycopathologia, 2004, 158, 219-232.	1.3	70
96	Redox Metabolites Signal Polymicrobial Biofilm Development via the NapA Oxidative Stress Cascade in Aspergillus. Current Biology, 2015, 25, 29-37.	1.8	70
97	Harnessing diverse transcriptional regulators for natural product discovery in fungi. Natural Product Reports, 2020, 37, 6-16.	5.2	70
98	Polyketide Production of Pestaloficiols and Macrodiolide Ficiolides Revealed by Manipulations of Epigenetic Regulators in an Endophytic Fungus. Organic Letters, 2016, 18, 1832-1835.	2.4	68
99	Aspergillus nidulans Mutants Defective in stc Gene Cluster Regulation. Genetics, 1999, 153, 715-720.	1.2	68
100	A Novel Automethylation Reaction in the Aspergillus nidulans LaeA Protein Generates S-Methylmethionine. Journal of Biological Chemistry, 2013, 288, 14032-14045.	1.6	66
101	Fungal attack and host defence pathways unveiled in nearâ€avirulent interactions of <i>Penicillium expansum creA </i>mutants on apples. Molecular Plant Pathology, 2018, 19, 2635-2650.	2.0	66
102	A Visual Pattern of Mycotoxin Production in Maize Kernels byAspergillusspp.. Phytopathology, 1994, 84, 483.	1.1	66
103	Increased conidiation associated with progression along the sterigmatocystin biosynthetic pathway. Mycologia, 2004, 96, 1190-1198.	0.8	65
104	Lipo-chitooligosaccharides as regulatory signals of fungal growth and development. Nature Communications, 2020, 11, 3897.	5.8	65
105	Loss of CclA, required for histone 3 lysine 4 methylation, decreases growth but increases secondary metabolite production in<i>Aspergillus fumigatus</i>. PeerJ, 2013, 1, e4.	0.9	63
106	Characterization of the Aspergillus parasiticus Î”12-desaturase gene: a role for lipid metabolism in the Aspergillusâ€“seed interaction. Microbiology (United Kingdom), 2004, 150, 2881-2888.	0.7	61
107	Spatial and temporal control of fungal natural product synthesis. Natural Product Reports, 2014, 31, 1277-1286.	5.2	61
108	Redundant synthesis of a conidial polyketide by two distinct secondary metabolite clusters in <scp><i>A</i></scp><i>spergillus fumigatus</i>. Environmental Microbiology, 2016, 18, 246-259.	1.8	61

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109	<i>Aspergillus fumigatus</i> LaeA-Mediated Phagocytosis Is Associated with a Decreased Hydrophobin Layer. Infection and Immunity, 2010, 78, 823-829.	1.0	60
110	The Aspergillus fumigatus Damage Resistance Protein Family Coordinately Regulates Ergosterol Biosynthesis and Azole Susceptibility. MBio, 2016, 7, e01919-15.	1.8	60
111	Perturbations in small molecule synthesis uncovers an iron-responsive secondary metabolite network in Aspergillus fumigatus. Frontiers in Microbiology, 2014, 5, 530.	1.5	59
112	Metabolomics and genomics in natural products research: complementary tools for targeting new chemical entities. Natural Product Reports, 2021, 38, 2041-2065.	5.2	59
113	Co-ordination between BrlA regulation and secretion of the oxidoreductase FmqD directs selective accumulation of fumiquinazoline C to conidial tissues in<i>A</i><i>spergillus fumigatus</i>. Cellular Microbiology, 2014, 16, 1267-1283.	1.1	58
114	An LaeA- and BrlA-Dependent Cellular Network Governs Tissue-Specific Secondary Metabolism in the Human Pathogen Aspergillus fumigatus. MSphere, 2018, 3, .	1.3	58
115	Involvement of transposon-like elements in penicillin gene cluster regulation. Fungal Genetics and Biology, 2010, 47, 423-432.	0.9	57
116	Heterogeneity Confounds Establishment of â€œaâ€•Model Microbial Strain. MBio, 2017, 8, .	1.8	57
117	New Aspercryptins, Lipopeptide Natural Products, Revealed by HDAC Inhibition in <i>Aspergillus nidulans</i>. ACS Chemical Biology, 2016, 11, 2117-2123.	1.6	56
118	A Volatile Relationship: Profiling an Inter-Kingdom Dialogue Between two Plant Pathogens, Ralstonia Solanacearum and Aspergillus Flavus. Journal of Chemical Ecology, 2014, 40, 502-513.	0.9	55
119	Bacterialâ€“fungal interactions revealed by genome-wide analysis of bacterial mutant fitness. Nature Microbiology, 2021, 6, 87-102.	5.9	49
120	LaeA, a global regulator ofAspergillustoxins. Medical Mycology, 2006, 44, 83-85.	0.3	47
121	Revitalization of a Forward Genetic Screen Identifies Three New Regulators of Fungal Secondary Metabolism in the Genus <i>Aspergillus</i>. MBio, 2017, 8, .	1.8	47
122	The Zebrafish as a Model Host for Invasive Fungal Infections. Journal of Fungi (Basel, Switzerland), 2018, 4, 136.	1.5	47
123	Club Cell TRPV4 Serves as a Damage Sensor Driving Lung Allergic Inflammation. Cell Host and Microbe, 2020, 27, 614-628.e6.	5.1	47
124	Rac2 Functions in Both Neutrophils and Macrophages To Mediate Motility and Host Defense in Larval Zebrafish. Journal of Immunology, 2016, 197, 4780-4790.	0.4	46
125	Deletion of a global regulator LaeB leads to the discovery of novel polyketides in Aspergillus nidulans. Organic and Biomolecular Chemistry, 2018, 16, 4973-4976.	1.5	46
126	In the fungus where it happens: History and future propelling Aspergillus nidulans as the archetype of natural products research. Fungal Genetics and Biology, 2020, 144, 103477.	0.9	46

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127	The bZIP Protein MeaB Mediates Virulence Attributes in Aspergillus flavus. PLoS ONE, 2013, 8, e74030.	1.1	44
128	Fungal Isocyanide Synthases and Xanthocillin Biosynthesis in Aspergillus fumigatus. MBio, 2018, 9, .	1.8	44
129	A Multifaceted Role of Tryptophan Metabolism and Indoleamine 2,3-Dioxygenase Activity in Aspergillus fumigatusâ€"Host Interactions. Frontiers in Immunology, 2017, 8, 1996.	2.2	44
130	FleA Expression in Aspergillus fumigatus Is Recognized by Fucosylated Structures on Mucins and Macrophages to Prevent Lung Infection. PLoS Pathogens, 2016, 12, e1005555.	2.1	44
131	Defects in Conidiophore Development and Conidium-Macrophage Interactions in a Dioxygenase Mutant of Aspergillus fumigatus. Infection and Immunity, 2008, 76, 3214-3220.	1.0	43
132	The HosA Histone Deacetylase Regulates Aflatoxin Biosynthesis Through Direct Regulation of Aflatoxin Cluster Genes. Molecular Plant-Microbe Interactions, 2019, 32, 1210-1228.	1.4	42
133	A cryptic pigment biosynthetic pathway uncovered by heterologous expression is essential for conidial development in <i>Pestalotiopsis fici</i>. Molecular Microbiology, 2017, 105, 469-483.	1.2	39
134	A Cellular Fusion Cascade Regulated by LaeA Is Required for Sclerotial Development in Aspergillus flavus. Frontiers in Microbiology, 2017, 8, 1925.	1.5	39
135	RsmA Regulates Aspergillus fumigatus Gliotoxin Cluster Metabolites Including Cyclo(L-Phe-L-Ser), a Potential New Diagnostic Marker for Invasive Aspergillosis. PLoS ONE, 2013, 8, e62591.	1.1	38
136	NRPS-Derived Isoquinolines and Lipopetides Mediate Antagonism between Plant Pathogenic Fungi and Bacteria. ACS Chemical Biology, 2018, 13, 171-179.	1.6	38
137	<scp>VeA</scp> and <scp>MvlA</scp> repression of the cryptic orsellinic acid gene cluster in <i><scp>A</scp>spergillus nidulans</i> involves histone 3 acetylation. Molecular Microbiology, 2013, 89, 963-974.	1.2	37
138	Transcriptome analysis of cyclic <scp>AMP</scp>â€dependent protein kinase <scp>A</scp>â€"regulated genes reveals the production of the novel natural compound fumipyrrole by <scp><i>A</i></scp><i>spergillus fumigatus</i>. Molecular Microbiology, 2015, 96, 148-162.	1.2	37
139	A possible role for fumagillin in cellular damage during host infection by <i>Aspergillus fumigatus</i>. Virulence, 2018, 9, 1548-1561.	1.8	37
140	Fungal oxylipins direct programmed developmental switches in filamentous fungi. Nature Communications, 2020, 11, 5158.	5.8	37
141	Apple Intrinsic Factors Modulating the Global Regulator, LaeA, the Patulin Gene Cluster and Patulin Accumulation During Fruit Colonization by Penicillium expansum. Frontiers in Plant Science, 2018, 9, 1094.	1.7	35
142	New Insight Into Pathogenicity and Secondary Metabolism of the Plant Pathogen Penicillium expansum Through Deletion of the Epigenetic Reader SntB. Frontiers in Microbiology, 2020, 11, 610.	1.5	35
143	Anaerobic gut fungi are an untapped reservoir of natural products. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
144	Microevolution in the pansecondary metabolome of <i>Aspergillus flavus</i> and its potential macroevolutionary implications for filamentous fungi. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34

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145	Increased Conidiation Associated with Progression along the Sterigmatocystin Biosynthetic Pathway. Mycologia, 2004, 96, 1190.	0.8	33
146	The bZIP transcription factor PfZipA regulates secondary metabolism and oxidative stress response in the plant endophytic fungus Pestalotiopsis fici. Fungal Genetics and Biology, 2015, 81, 221-228.	0.9	32
147	Contributions of Spore Secondary Metabolites to UV-C Protection and Virulence Vary in Different Aspergillus fumigatus Strains. MBio, 2020, 11, .	1.8	32
148	Diversity of Secondary Metabolism in Aspergillus nidulans Clinical Isolates. MSphere, 2020, 5, .	1.3	32
149	Functional Characterization of Clinical Isolates of the Opportunistic Fungal Pathogen Aspergillus nidulans. MSphere, 2020, 5, .	1.3	32
150	NosA, a transcription factor important in Aspergillus fumigatus stress and developmental response, rescues the germination defect of a laeA deletion. Fungal Genetics and Biology, 2012, 49, 857-865.	0.9	31
151	Spatial regulation of a common precursor from two distinct genes generates metabolite diversity. Chemical Science, 2015, 6, 5913-5921.	3.7	31
152	Diketopiperazine Formation in Fungi Requires Dedicated Cyclization and Thiolation Domains. Angewandte Chemie - International Edition, 2019, 58, 14589-14593.	7.2	31
153	Unearthing fungal chemodiversity and prospects for drug discovery. Current Opinion in Microbiology, 2019, 51, 22-29.	2.3	31
154	Chemical signals driving <scp>bacterialâ€“fungal</scp> interactions. Environmental Microbiology, 2021, 23, 1334-1347.	1.8	31
155	Dual-purpose isocyanides produced by <i>Aspergillus fumigatus</i> contribute to cellular copper sufficiency and exhibit antimicrobial activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	31
156	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. ACS Chemical Biology, 2018, 13, 1142-1147.	1.6	30
157	Depsipeptide Aspergillicins Revealed by Chromatin Reader Protein Deletion. ACS Chemical Biology, 2019, 14, 1121-1128.	1.6	30
158	Copper Utilization, Regulation, and Acquisition by Aspergillus fumigatus. International Journal of Molecular Sciences, 2019, 20, 1980.	1.8	30
159	Letâ€™s Get Physical: Bacterial-Fungal Interactions and Their Consequences in Agriculture and Health. Journal of Fungi (Basel, Switzerland), 2020, 6, 243.	1.5	30
160	Two Î”9-stearic acid desaturases are required for Aspergillus nidulans growth and development. Fungal Genetics and Biology, 2004, 41, 501-509.	0.9	29
161	Telomere position effect is regulated by heterochromatin-associated proteins and NkuA in Aspergillus nidulans. Microbiology (United Kingdom), 2010, 156, 3522-3531.	0.7	29
162	CoIN: co-inducible nitrate expression system for secondary metabolites in Aspergillus nidulans. Fungal Biology and Biotechnology, 2018, 5, 6.	2.5	29

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164	Blockage of methylcitrate cycle inhibits polyketide production in Aspergillus nidulans. Molecular Microbiology, 2004, 52, 541-550.	1.2	28
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