Perng-Kuang Chang

List of Publications by Year
in descending order

55 papers	3,275 citations	186265 28 h-index	155660 55 g-index
57 all docs	57 docs citations	57 times ranked	2154 citing authors

#	Article	IF	Citations
1	Clustered Pathway Genes in Aflatoxin Biosynthesis. Applied and Environmental Microbiology, 2004, 70, 1253-1262.	3.1	713
2	Sequence breakpoints in the aflatoxin biosynthesis gene cluster and flanking regions in nonaflatoxigenic Aspergillus flavus isolates. Fungal Genetics and Biology, 2005, 42, 914-923.	2.1	219
3	Aflatoxin Biosynthesis Cluster Gene cypA Is Required for G Aflatoxin Formation. Applied and Environmental Microbiology, 2004, 70, 6518-6524.	3.1	169
4	The Aspergillus parasiticus protein AFLJ interacts with the aflatoxin pathway-specific regulator AFLR. Molecular Genetics and Genomics, 2003, 268, 711-719.	2.1	148
5	Clustered genes involved in cyclopiazonic acid production are next to the aflatoxin biosynthesis gene cluster in Aspergillus flavus. Fungal Genetics and Biology, 2009, 46, 176-182.	2.1	125
6	Development and refinement of a high-efficiency gene-targeting system for Aspergillus flavus. Journal of Microbiological Methods, 2010, 81, 240-246.	1.6	109
7	Cyclopiazonic Acid Biosynthesis of Aspergillus flavus and Aspergillus oryzae. Toxins, 2009, 1, 74-99.	3.4	105
8	Loss of msnA, a Putative Stress Regulatory Gene, in Aspergillus parasiticus and Aspergillus flavus Increased Production of Conidia, Aflatoxins and Kojic Acid. Toxins, 2011, 3, 82-104.	3.4	88
9	Association of aflatoxin biosynthesis and sclerotial development in Aspergillus parasiticus. Mycopathologia, 2002, 153, 41-48.	3.1	84
10	Cladal relatedness among Aspergillus oryzae isolates and Aspergillus flavus S and L morphotype isolates. International Journal of Food Microbiology, 2006, 108, 172-177.	4.7	84
11	Deletion of the Aspergillus flavus Orthologue of A. nidulans fluG Reduces Conidiation and Promotes Production of Sclerotia but Does Not Abolish Aflatoxin Biosynthesis. Applied and Environmental Microbiology, 2012, 78, 7557-7563.	3.1	79
12	Effects of laeA deletion on Aspergillus flavus conidial development and hydrophobicity may contribute to loss of aflatoxin production. Fungal Biology, 2012, 116, 298-307.	2.5	76
13	What does genetic diversity of Aspergillus flavus tell us about Aspergillus oryzae?. International Journal of Food Microbiology, 2010, 138, 189-199.	4.7	75
14	aflT, a MFS transporter-encoding gene located in the aflatoxin gene cluster, does not have a significant role in aflatoxin secretion. Fungal Genetics and Biology, 2004, 41, 911-920.	2.1	74
15	Aspergillus flavus VelB acts distinctly from VeA in conidiation and may coordinate with FluG to modulate sclerotial production. Fungal Genetics and Biology, 2013, 58-59, 71-79.	2.1	72
16	Suppression of Aflatoxin Biosynthesis in Aspergillus flavus by 2-Phenylethanol Is Associated with Stimulated Growth and Decreased Degradation of Branched-Chain Amino Acids. Toxins, 2015, 7, 3887-3902.	3.4	69
17	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.	1.8	61
18	Genome-wide analysis of the Zn(II)2Cys6 zinc cluster-encoding gene family in Aspergillus flavus. Applied Microbiology and Biotechnology, 2013, 97, 4289-4300.	3.6	61

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19	Lack of interaction between AFLR and AFLJ contributes to nonaflatoxigenicity of Aspergillus sojae. Journal of Biotechnology, 2004, 107, 245-253.	3.8	59
20	Identification of genetic defects in the atoxigenic biocontrol strain Aspergillus flavus K49 reveals the presence of a competitive recombinant group in field populations. International Journal of Food Microbiology, 2012, 154, 192-196.	4.7	54
21	Pre-termination in aflR of Aspergillus sojae inhibits aflatoxin biosynthesis. Applied Microbiology and Biotechnology, 2001, 55, 585-589.	3.6	53
22	Repressor-AFLR interaction modulates aflatoxin biosynthesis in Aspergillus parasiticus. Mycopathologia, 1999, 147, 105-112.	3.1	49
23	Biosynthesis of conidial and sclerotial pigments in Aspergillus species. Applied Microbiology and Biotechnology, 2020, 104, 2277-2286.	3.6	47
24	adhA in Aspergillus parasiticus Is Involved in Conversion of 5â€²-Hydroxyaverantin to Averufin. Applied and Environmental Microbiology, 2000, 66, 4715-4719.	3.1	40
25	Understanding nonaflatoxigenicity of Aspergillus sojae: a windfall of aflatoxin biosynthesis research. Applied Microbiology and Biotechnology, 2007, 76, 977-984.	3.6	38
26	A highly efficient gene-targeting system for Aspergillus parasiticus. Letters in Applied Microbiology, 2008, 46, 587-592.	2.2	36
27	Genes differentially expressed by Aspergillus flavus strains after loss of aflatoxin production by serial transfers. Applied Microbiology and Biotechnology, 2007, 77, 917-925.	3.6	34
28	Nonaflatoxigenic Aspergillus flavus TX9-8 competitively prevents aflatoxin accumulation by A. flavus isolates of large and small sclerotial morphotypes. International Journal of Food Microbiology, 2007, 114, 275-279.	4.7	32
29	Characterization of a partial duplication of the aflatoxin gene cluster in Aspergillus parasiticus ATCC 56775. Applied Microbiology and Biotechnology, 2002, 58, 632-636.	3.6	31
30	Are the Genes nadA and norB Involved in Formation of Aflatoxin G1?. International Journal of Molecular Sciences, 2008, 9, 1717-1729.	4.1	28
31	The Aspergillus parasiticus estA-Encoded Esterase Converts Versiconal Hemiacetal Acetate to Versiconal and Versiconol Acetate to Versiconol in Aflatoxin Biosynthesis. Applied and Environmental Microbiology, 2004, 70, 3593-3599.	3.1	27
32	Aspergillus flavus GPI-anchored protein-encoding ecm33 has a role in growth, development, aflatoxin biosynthesis, and maize infection. Applied Microbiology and Biotechnology, 2018, 102, 5209-5220.	3.6	27
33	Comparison of aflatoxin production of Aspergillus flavus at different temperatures and media: Proteome analysis based on TMT. International Journal of Food Microbiology, 2019, 310, 108313.	4.7	25
34	Monitoring Metabolite Production of Aflatoxin Biosynthesis by Orbitrap Fusion Mass Spectrometry and a D-Optimal Mixture Design Method. Analytical Chemistry, 2018, 90, 14331-14338.	6.5	24
35	Aspergillus flavus aswA , a gene homolog of Aspergillus nidulans oefC , regulates sclerotial development and biosynthesis of sclerotium-associated secondary metabolites. Fungal Genetics and Biology, 2017, 104, 29-37.	2.1	23
36	Characterization of aflatoxigenic and non-aflatoxigenic Aspergillus flavus isolates from pistachio. Mycotoxin Research, 2012, 28, 67-75.	2.3	20

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37	Transcriptomic profiles of Aspergillus flavus CA42, a strain that produces small sclerotia, by decanal treatment and after recovery. Fungal Genetics and Biology, 2014, 68, 39-47.	2.1	20
38	Cyclopiazonic acid biosynthesis byAspergillus flavus. Toxin Reviews, 2011, 30, 79-89.	3.4	17
39	Identification of a copper-transporting ATPase involved in biosynthesis of A. flavus conidial pigment. Applied Microbiology and Biotechnology, 2019, 103, 4889-4897.	3.6	17
40	Deletion of the Delta12-oleic acid desaturase gene of a nonaflatoxigenic Aspergillus parasiticus field isolate affects conidiation and sclerotial development. Journal of Applied Microbiology, 2004, 97, 1178-1184.	3.1	15
41	Genomeâ€wide nucleotide variation distinguishesAspergillus flavusfromAspergillus oryzaeand helps to reveal origins of atoxigenicA. flavusbiocontrol strains. Journal of Applied Microbiology, 2019, 127, 1511-1520.	3.1	15
42	Transcriptional Regulation of Aflatoxin Biosynthesis and Conidiation in Aspergillus flavus by Wickerhamomyces anomalus WRL-076 for Reduction of Aflatoxin Contamination. Toxins, 2019, 11, 81.	3.4	15
43	Two New Aspergillus flavus Reference Genomes Reveal a Large Insertion Potentially Contributing to Isolate Stress Tolerance and Aflatoxin Production. G3: Genes, Genomes, Genetics, 2020, 10, 3515-3531.	1.8	15
44	Development of an Enzyme-Linked Immunosorbent Assay Method Specific for the Detection of G-Group Aflatoxins. Toxins, 2016, 8, 5.	3.4	14
45	New Insights of Transcriptional Regulator AflR in Aspergillus flavus Physiology. Microbiology Spectrum, 2022, 10, e0079121.	3.0	14
46	Molasses supplementation promotes conidiation but suppresses aflatoxin production by small sclerotial Aspergillus flavus. Letters in Applied Microbiology, 2007, 44, 131-137.	2.2	11
47	High sequence variations in the region containing genes encoding a cellular morphogenesis protein and the repressor of sexual development help to reveal origins of Aspergillus oryzae. International Journal of Food Microbiology, 2015, 200, 66-71.	4.7	11
48	Deciphering the origin ofAspergillus flavusNRRL21882, the active biocontrol agent of Aflaâ€Guard^{Â®}. Letters in Applied Microbiology, 2021, 72, 509-516.	2.2	11
49	Identification of AflR Binding Sites in the Genome of Aspergillus flavus by ChIP-Seq. Journal of Fungi (Basel, Switzerland), 2020, 6, 52.	3.5	9
50	Genetic Variability ofAspergillus flavusIsolates from a Mississippi Corn Field. Scientific World Journal, The, 2014, 2014, 1-8.	2.1	8
51	Aspergillus flavus La3279, a component strain of the Aflasafeâ„¢ biocontrol product, contains a partial aflatoxin biosynthesis gene cluster followed by a genomic region highly variable among A. flavus isolates. International Journal of Food Microbiology, 2022, 366, 109559.	4.7	7
52	The Aspergillus flavus fluP-associated metabolite promotes sclerotial production. Fungal Biology, 2016, 120, 1258-1268.	2.5	5
53	Authentication of Aspergillus parasiticus strains in the genome database of the National Center for Biotechnology Information. BMC Research Notes, 2021, 14, 111.	1.4	5
54	Genome Sequence of an Aspergillus flavus CA14 Strain That Is Widely Used in Gene Function Studies. Microbiology Resource Announcements, 2019, 8, .	0.6	4

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55	Prevalence of NRRL21882-like (Afla-GuardÂ®) Aspergillus flavus on sesame seeds grown in research fields in the Mississippi Delta. Biocontrol Science and Technology, 2020, 30, 1090-1099.	1.3	4