Kenneth C Ehrlich

List of Publications by Year
in descending order

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84 papers	4,774 citations	81900 39 h-index	102487 66 g-index
91 all docs	91 docs citations	91 times ranked	3532 citing authors

#	Article	IF	Citations
1	Clustered Pathway Genes in Aflatoxin Biosynthesis. Applied and Environmental Microbiology, 2004, 70, 1253-1262.	3.1	713
2	Aflatoxin Biosynthesis Cluster Gene cypA Is Required for G Aflatoxin Formation. Applied and Environmental Microbiology, 2004, 70, 6518-6524.	3.1	169
3	An isolate of Aspergillus flavus used to reduce aflatoxin contamination in cottonseed has a defective polyketide synthase gene. Applied Microbiology and Biotechnology, 2004, 65, 473-478.	3.6	148
4	Digestion of highly modified bacteriophage DNA by restriction endonucleases. Nucleic Acids Research, 1982, 10, 1579-1591.	14.5	125
5	Toxins of Filamentous Fungi. , 2002, 81, 167-206.		124
6	CpG methylation inhibits binding of several sequence-specific DNA-binding proteins from pea, wheat, soybean and cauliflower. Plant Molecular Biology, 1991, 17, 111-123.	3.9	118
7	Aflatoxin-producing Aspergillus species from Thailand. International Journal of Food Microbiology, 2007, 114, 153-159.	4.7	117
8	Protein synthesis inhibition by 8-oxo-12,13-epoxytrichothecenes. Biochimica Et Biophysica Acta - General Subjects, 1987, 923, 206-213.	2.4	110
9	Sequence comparison of aflR from different Aspergillus species provides evidence for variability in regulation of aflatoxin production. Fungal Genetics and Biology, 2003, 38, 63-74.	2.1	109
10	NsdC and NsdD Affect Aspergillus flavus Morphogenesis and Aflatoxin Production. Eukaryotic Cell, 2012, 11, 1104-1111.	3.4	109
11	Non-aflatoxigenic Aspergillus flavus to prevent aflatoxin contamination in crops: advantages and limitations. Frontiers in Microbiology, 2014, 5, 50.	3.5	109
12	Cyclopiazonic Acid Biosynthesis of Aspergillus flavus and Aspergillus oryzae. Toxins, 2009, 1, 74-99.	3.4	105
13	Aflatoxigenicity in Aspergillus: molecular genetics, phylogenetic relationships and evolutionary implications. Mycopathologia, 2006, 162, 167-177.	3.1	97
14	Characterization of the Critical Amino Acids of an Aspergillus parasiticus Cytochrome P-450 Monooxygenase Encoded by ordA That Is Involved in the Biosynthesis of Aflatoxins B ₁ , G ₁ , B ₂ , and G ₂. Applied and Environmental Microbiology, 1998, 64, 4834-4841.	3.1	91
15	Induction of the Soybean Phytoalexins Coumestrol and Glyceollin byAspergillus. Journal of Agricultural and Food Chemistry, 2000, 48, 2167-2172.	5.2	88
16	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
17	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
18	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

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19	What does genetic diversity of Aspergillus flavus tell us about Aspergillus oryzae?. International Journal of Food Microbiology, 2010, 138, 189-199.	4.7	75
20	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
21	Functional characterization of a veA-dependent polyketide synthase gene in Aspergillus flavus necessary for the synthesis of asparasone, a sclerotium-specific pigment. Fungal Genetics and Biology, 2014, 64, 25-35.	2.1	67
22	An Aspergillus flavus secondary metabolic gene cluster containing a hybrid PKSâ€“NRPS is necessary for synthesis of the 2-pyridones, leporins. Fungal Genetics and Biology, 2015, 81, 88-97.	2.1	67
23	The Aflatoxin Biosynthesis Cluster Gene, aflX , Encodes an Oxidoreductase Involved in Conversion of Versicolorin A to Demethylsterigmatocystin. Applied and Environmental Microbiology, 2006, 72, 1096-1101.	3.1	63
24	Aflatoxin Biosynthesis Is a Novel Source of Reactive Oxygen Speciesâ€”A Potential Redox Signal to Initiate Resistance to Oxidative Stress?. Toxins, 2015, 7, 1411-1430.	3.4	63
25	Characterization of the promoter for the gene encoding the aflatoxin biosynthetic pathway regulatory protein AFLR. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1999, 1444, 412-417.	2.4	61
26	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
27	Association of 5-hydroxymethylation and 5-methylation of DNA cytosine with tissue-specific gene expression. Epigenetics, 2017, 12, 123-138.	2.7	61
28	Binding sites in mammalian genes and viral gene regulatory regions recognized by methylated DNA-binding protein. Nucleic Acids Research, 1990, 18, 6253-6260.	14.5	60
29	Aflatoxin biosynthesis. Revista Iberoamericana De Micologia, 2002, 19, 191-200.	0.9	60
30	Fragmentation of an aflatoxinâ€like gene cluster in a forest pathogen. New Phytologist, 2013, 198, 525-535.	7.3	55
31	Characterization of the Aspergillus parasiticus niaD and niiA gene cluster. Current Genetics, 1996, 30, 68-75.	1.7	54
32	Predicted Roles of the Uncharacterized Clustered Genes in Aflatoxin Biosynthesis. Toxins, 2009, 1, 37-58.	3.4	54
33	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
34	Alteration of Different Domains in AFLR Affects Aflatoxin Pathway Metabolism inAspergillus parasiticusTransformants. Fungal Genetics and Biology, 1998, 23, 279-287.	2.1	50
35	Analysis of single nucleotide polymorphisms in three genes shows evidence for genetic isolation of certain Aspergillus flavus vegetative compatibility groups. FEMS Microbiology Letters, 2007, 268, 231-236.	1.8	48
36	Starter unit specificity directs genome mining of polyketide synthase pathways in fungi. Bioorganic Chemistry, 2008, 36, 16-22.	4.1	48

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37	HypC, the Anthrone Oxidase Involved in Aflatoxin Biosynthesis. Applied and Environmental Microbiology, 2010, 76, 3374-3377.	3.1	47
38	Comparison of Expression of Secondary Metabolite Biosynthesis Cluster Genes in Aspergillus flavus, A. parasiticus, and A. oryzae. Toxins, 2014, 6, 1916-1928.	3.4	45
39	Methylated DNA-binding protein is present in various mammalian cell types. Nucleic Acids Research, 1988, 16, 8029-8044.	14.5	43
40	Effect of site-specific DNA methylation and mutagenesis on recognition by methylated DNA-binding protein from human placenta. Nucleic Acids Research, 1986, 14, 8387-8397.	14.5	42
41	An Aflatoxin Biosynthesis Cluster Gene Encodes a Novel Oxidase Required for Conversion of Versicolorin A to Sterigmatocystin. Applied and Environmental Microbiology, 2005, 71, 8963-8965.	3.1	42
42	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
43	Synthetic Strategy of Nonreducing Iterative Polyketide Synthases and the Origin of the Classical â€œStarterâ€•Unit Effectâ€• ChemBioChem, 2008, 9, 1019-1023.	2.6	40
44	DNA cytosine methylation and hydroxymethylation at the borders. Epigenomics, 2014, 6, 563-566.	2.1	38
45	Effect of DNA methylation on the binding of vertebrate and plant proteins to DNA. , 1993, 64, 145-168.		38
46	Related sites in human and herpesvirus DNA recognized by methylated DNA-binding protein from human placenta. Nucleic Acids Research, 1989, 17, 1459-1474.	14.5	37
47	Use of Pyrosequencing to Quantify Incidence of a Specific Aspergillus flavus Strain Within Complex Fungal Communities Associated with Commercial Cotton Crops. Phytopathology, 2008, 98, 282-288.	2.2	36
48	Three MDBP sites in the immediate-early enhancer-promoter region of human cytomegalovirus. Virology, 1991, 182, 865-869.	2.4	35
49	Developmentally linked human DNA hypermethylation is associated with down-modulation, repression, and upregulation of transcription. Epigenetics, 2018, 13, 275-289.	2.7	31
50	DNA fromAspergillus flavuscontains 5-methylcytosine. FEMS Microbiology Letters, 2001, 205, 151-155.	1.8	30
51	Dothistromin genes at multiple separate loci are regulated by AflR. Fungal Genetics and Biology, 2013, 51, 12-20.	2.1	30
52	Tissue-specific epigenetics of atherosclerosis-related ANGPT and ANGPTL genes. Epigenomics, 2019, 11, 169-186.	2.1	30
53	A broad bean cDNA clone encoding a DNA-binding protein resembling mammalian CREB in its sequence specificity and DNA methylation sensitivity. Gene, 1992, 117, 169-178.	2.2	29
54	Atherosclerosis-associated differentially methylated regions can reflect the disease phenotype and are often at enhancers. Atherosclerosis, 2019, 280, 183-191.	0.8	29

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55	Divergent regulation of aflatoxin production at acidic pH by two Aspergillus strains. Mycopathologia, 2005, 159, 579-581.	3.1	28
56	Are the Genes nadA and norB Involved in Formation of Aflatoxin G1?. International Journal of Molecular Sciences, 2008, 9, 1717-1729.	4.1	28
57	Expression Profiling of Non-Aflatoxigenic Aspergillus parasiticus Mutants Obtained by 5-Azacytosine Treatment or Serial Mycelial Transfer. Toxins, 2011, 3, 932-948.	3.4	28
58	Molecular and functional characterization of a second copy of the aflatoxin regulatory gene, aflR-2, from Aspergillus parasiticus. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1576, 316-323.	2.4	25
59	Association with AflR in Endosomes Reveals New Functions for AflJ in Aflatoxin Biosynthesis. Toxins, 2012, 4, 1582-1600.	3.4	25
60	Promoter elements in the aflatoxin pathway polyketide synthase gene. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1576, 171-175.	2.4	24
61	Identification of novel metabolites fromAspergillus flavusby high resolution and multiple stage mass spectrometry. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2014, 31, 111-120.	2.3	24
62	Epigenetics of Skeletal Muscle-Associated Genes in the ASB, LRRC, TMEM, and OSBPL Gene Families. Epigenomes, 2020, 4, 1.	1.8	23
63	Characterization of DBPm, a plant protein that binds to DNA containing 5-methylcytosine. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1993, 1172, 108-116.	2.4	22
64	Acylâ€Carrier Proteinâ€“Phosphopantetheinyltransferase Partnerships in Fungal Fatty Acid Synthases. ChemBioChem, 2008, 9, 1559-1563.	2.6	22
65	DNA Hypomethylation in Intragenic and Intergenic Enhancer Chromatin of Muscle-Specific Genes Usually Correlates with their Expression. Yale Journal of Biology and Medicine, 2016, 89, 441-455.	0.2	22
66	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
67	How different DNA sequences are recognized by a DNA-binding protein: effects of partial proteolysis. Nucleic Acids Research, 1989, 17, 8611-8629.	14.5	19
68	Conversion of 11-hydroxy-O-methylsterigmatocystin to aflatoxin G1 in Aspergillus parasiticus. Applied Microbiology and Biotechnology, 2011, 90, 635-650.	3.6	18
69	Use of UHPLC high-resolution Orbitrap mass spectrometry to investigate the genes involved in the production of secondary metabolites inAspergillus flavus. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2015, 32, 1656-1673.	2.3	18
70	Promoter elements involved in the expression of the Aspergillus parasiticus aflatoxin biosynthesis pathway gene avnA. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2000, 1491, 7-12.	2.4	16
71	Epigenetics and expression of key genes associated with cardiac fibrosis:NLRP3, MMP2, MMP9, CCN2/CTGFandAGT. Epigenomics, 2021, 13, 219-234.	2.1	16
72	Epigenetics of Muscle- and Brain-Specific Expression of KLHL Family Genes. International Journal of Molecular Sciences, 2020, 21, 8394.	4.1	14

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73	Absence of the aflatoxin biosynthesis gene, norA, allows accumulation of deoxyaflatoxin B1 in Aspergillus flavus cultures. FEMS Microbiology Letters, 2010, 305, 65-70.	1.8	13
74	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene TBX15. Epigenetics, 2020, 15, 728-749.	2.7	11
75	Functional and phylogenetic analysis of the Aspergillus ochraceoroseus aflQ (ordA) gene ortholog. Mycologia, 2012, 104, 857-864.	1.9	9
76	Data showing atherosclerosis-associated differentially methylated regions are often at enhancers. Data in Brief, 2019, 23, 103812.	1.0	9
77	Mycotoxins in Grain Dust: Method for Analysis of Aflatoxins, Ochratoxin A, Zearalenone,Vomitoxin, and Secalonic Acid D. Journal of the Association of Official Analytical Chemists, 1984, 67, 963-967.	0.2	5
78	The Aspergillus flavus fluP-associated metabolite promotes sclerotial production. Fungal Biology, 2016, 120, 1258-1268.	2.5	5
79	Aflatoxin-like Gene Clusters and How They Evolved. , 2009, , 65-75.		5
80	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	4.1	5
81	Regulation of the aflatoxin-like toxin dothistromin by AflJ. Fungal Biology, 2015, 119, 503-508.	2.5	4
82	Preparation of theFusarium toxin, nivalenol, by oxidation of the putative biosynthetic precursor, 7-deoxynivalenol. Mycopathologia, 1989, 107, 111-114.	3.1	3
83	Epigenetics of Mitochondria-Associated Genes in Striated Muscle. Epigenomes, 2022, 6, 1.	1.8	3
84	Polyketide Biosynthesis in Fungi. ACS Symposium Series, 2007, , 68-80.	0.5	1