

Kenneth C Ehrlich

List of Publications by Year in descending order

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4,774
citations

81900

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91
docs citations

91
times ranked

3532
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	4.1	5
2	Epigenetics of Mitochondria-Associated Genes in Striated Muscle. Epigenomes, 2022, 6, 1.	1.8	3
3	Epigenetics and expression of key genes associated with cardiac fibrosis: <i>NLRP3</i> , <i>MMP2</i> , <i>MMP9</i> , <i>CCN2/CTGF</i> and <i>AGT</i> . Epigenomics, 2021, 13, 219-234.	2.1	16
4	Epigenetics of Muscle- and Brain-Specific Expression of KLHL Family Genes. International Journal of Molecular Sciences, 2020, 21, 8394.	4.1	14
5	Epigenetics of Skeletal Muscle-Associated Genes in the ASB, LRRC, TMEM, and OSBPL Gene Families. Epigenomes, 2020, 4, 1.	1.8	23
6	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene <i>TBX15</i> . Epigenetics, 2020, 15, 728-749.	2.7	11
7	Tissue-specific epigenetics of atherosclerosis-related <i>ANGPT</i> and <i>ANGPTL</i> genes. Epigenomics, 2019, 11, 169-186.	2.1	30
8	Data showing atherosclerosis-associated differentially methylated regions are often at enhancers. Data in Brief, 2019, 23, 103812.	1.0	9
9	Atherosclerosis-associated differentially methylated regions can reflect the disease phenotype and are often at enhancers. Atherosclerosis, 2019, 280, 183-191.	0.8	29
10	Developmentally linked human DNA hypermethylation is associated with down-modulation, repression, and upregulation of transcription. Epigenetics, 2018, 13, 275-289.	2.7	31
11	Association of 5-hydroxymethylation and 5-methylation of DNA cytosine with tissue-specific gene expression. Epigenetics, 2017, 12, 123-138.	2.7	61
12	The <i>Aspergillus flavus</i> fluP-associated metabolite promotes sclerotial production. Fungal Biology, 2016, 120, 1258-1268.	2.5	5
13	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
14	Regulation of the aflatoxin-like toxin dothistromin by AflJ. Fungal Biology, 2015, 119, 503-508.	2.5	4
15	An <i>Aspergillus flavus</i> secondary metabolic gene cluster containing a hybrid PKS-NRPS is necessary for synthesis of the 2-pyridones, leporins. Fungal Genetics and Biology, 2015, 81, 88-97.	2.1	67
16	Aflatoxin Biosynthesis Is a Novel Source of Reactive Oxygen Species—A Potential Redox Signal to Initiate Resistance to Oxidative Stress?. Toxins, 2015, 7, 1411-1430.	3.4	63
17	Use of UHPLC high-resolution Orbitrap mass spectrometry to investigate the genes involved in the production of secondary metabolites in <i>Aspergillus flavus</i> . Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2015, 32, 1656-1673.	2.3	18
18	Comparison of Expression of Secondary Metabolite Biosynthesis Cluster Genes in <i>Aspergillus flavus</i> , <i>A. parasiticus</i> , and <i>A. oryzae</i> . Toxins, 2014, 6, 1916-1928.	3.4	45

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19	DNA cytosine methylation and hydroxymethylation at the borders. <i>Epigenomics</i> , 2014, 6, 563-566.	2.1	38
20	Functional characterization of a veA-dependent polyketide synthase gene in <i>Aspergillus flavus</i> necessary for the synthesis of asparasone, a sclerotium-specific pigment. <i>Fungal Genetics and Biology</i> , 2014, 64, 25-35.	2.1	67
21	Identification of novel metabolites from <i>Aspergillus flavus</i> by high resolution and multiple stage mass spectrometry. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2014, 31, 111-120.	2.3	24
22	Transcriptomic profiles of <i>Aspergillus flavus</i> CA42, a strain that produces small sclerotia, by decanal treatment and after recovery. <i>Fungal Genetics and Biology</i> , 2014, 68, 39-47.	2.1	20
23	Non-aflatoxigenic <i>Aspergillus flavus</i> to prevent aflatoxin contamination in crops: advantages and limitations. <i>Frontiers in Microbiology</i> , 2014, 5, 50.	3.5	109
24	Dothistromin genes at multiple separate loci are regulated by AflR. <i>Fungal Genetics and Biology</i> , 2013, 51, 12-20.	2.1	30
25	<i>Aspergillus flavus</i> VelB acts distinctly from VeA in conidiation and may coordinate with FluG to modulate sclerotial production. <i>Fungal Genetics and Biology</i> , 2013, 58-59, 71-79.	2.1	72
26	Genome-wide analysis of the Zn(II)2Cys6 zinc cluster-encoding gene family in <i>Aspergillus flavus</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4289-4300.	3.6	61
27	Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. <i>New Phytologist</i> , 2013, 198, 525-535.	7.3	55
28	Association with AflR in Endosomes Reveals New Functions for AflJ in Aflatoxin Biosynthesis. <i>Toxins</i> , 2012, 4, 1582-1600.	3.4	25
29	Deletion of the <i>Aspergillus flavus</i> Orthologue of <i>A. nidulans</i> fluG Reduces Conidiation and Promotes Production of Sclerotia but Does Not Abolish Aflatoxin Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7557-7563.	3.1	79
30	NsdC and NsdD Affect <i>Aspergillus flavus</i> Morphogenesis and Aflatoxin Production. <i>Eukaryotic Cell</i> , 2012, 11, 1104-1111.	3.4	109
31	Effects of laeA deletion on <i>Aspergillus flavus</i> conidial development and hydrophobicity may contribute to loss of aflatoxin production. <i>Fungal Biology</i> , 2012, 116, 298-307.	2.5	76
32	Functional and phylogenetic analysis of the <i>Aspergillus ochraceoroseus</i> aflQ (ordA) gene ortholog. <i>Mycologia</i> , 2012, 104, 857-864.	1.9	9
33	Identification of genetic defects in the atoxigenic biocontrol strain <i>Aspergillus flavus</i> K49 reveals the presence of a competitive recombinant group in field populations. <i>International Journal of Food Microbiology</i> , 2012, 154, 192-196.	4.7	54
34	Conversion of 11-hydroxy-O-methylsterigmatocystin to aflatoxin G1 in <i>Aspergillus parasiticus</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 635-650.	3.6	18
35	Expression Profiling of Non-Aflatoxigenic <i>Aspergillus parasiticus</i> Mutants Obtained by 5-Azacytosine Treatment or Serial Mycelial Transfer. <i>Toxins</i> , 2011, 3, 932-948.	3.4	28
36	What does genetic diversity of <i>Aspergillus flavus</i> tell us about <i>Aspergillus oryzae</i> ?. <i>International Journal of Food Microbiology</i> , 2010, 138, 189-199.	4.7	75

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37	Absence of the aflatoxin biosynthesis gene, norA, allows accumulation of deoxyaflatoxin B1 in <i>Aspergillus flavus</i> cultures. <i>FEMS Microbiology Letters</i> , 2010, 305, 65-70.	1.8	13
38	HypC, the Anthrone Oxidase Involved in Aflatoxin Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3374-3377.	3.1	47
39	Predicted Roles of the Uncharacterized Clustered Genes in Aflatoxin Biosynthesis. <i>Toxins</i> , 2009, 1, 37-58.	3.4	54
40	Cyclopiazonic Acid Biosynthesis of <i>Aspergillus flavus</i> and <i>Aspergillus oryzae</i> . <i>Toxins</i> , 2009, 1, 74-99.	3.4	105
41	Aflatoxin-like Gene Clusters and How They Evolved. , 2009, , 65-75.		5
42	Acyl Carrier Protein Phosphopantetheinyltransferase Partnerships in Fungal Fatty Acid Synthases. <i>ChemBioChem</i> , 2008, 9, 1559-1563.	2.6	22
43	Synthetic Strategy of Nonreducing Iterative Polyketide Synthases and the Origin of the Classical Starter Unit Effect. <i>ChemBioChem</i> , 2008, 9, 1019-1023.	2.6	40
44	Starter unit specificity directs genome mining of polyketide synthase pathways in fungi. <i>Bioorganic Chemistry</i> , 2008, 36, 16-22.	4.1	48
45	Use of Pyrosequencing to Quantify Incidence of a Specific <i>Aspergillus flavus</i> Strain Within Complex Fungal Communities Associated with Commercial Cotton Crops. <i>Phytopathology</i> , 2008, 98, 282-288.	2.2	36
46	Are the Genes nadA and norB Involved in Formation of Aflatoxin G1?. <i>International Journal of Molecular Sciences</i> , 2008, 9, 1717-1729.	4.1	28
47	Polyketide Biosynthesis in Fungi. <i>ACS Symposium Series</i> , 2007, , 68-80.	0.5	1
48	Analysis of single nucleotide polymorphisms in three genes shows evidence for genetic isolation of certain <i>Aspergillus flavus</i> vegetative compatibility groups. <i>FEMS Microbiology Letters</i> , 2007, 268, 231-236.	1.8	48
49	Aflatoxin-producing <i>Aspergillus</i> species from Thailand. <i>International Journal of Food Microbiology</i> , 2007, 114, 153-159.	4.7	117
50	Aflatoxigenicity in <i>Aspergillus</i> : molecular genetics, phylogenetic relationships and evolutionary implications. <i>Mycopathologia</i> , 2006, 162, 167-177.	3.1	97
51	Cladal relatedness among <i>Aspergillus oryzae</i> isolates and <i>Aspergillus flavus</i> S and L morphotype isolates. <i>International Journal of Food Microbiology</i> , 2006, 108, 172-177.	4.7	84
52	The Aflatoxin Biosynthesis Cluster Gene, aflX , Encodes an Oxidoreductase Involved in Conversion of Versicolorin A to Demethylsterigmatocystin. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1096-1101.	3.1	63
53	Divergent regulation of aflatoxin production at acidic pH by two <i>Aspergillus</i> strains. <i>Mycopathologia</i> , 2005, 159, 579-581.	3.1	28
54	An Aflatoxin Biosynthesis Cluster Gene Encodes a Novel Oxidase Required for Conversion of Versicolorin A to Sterigmatocystin. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8963-8965.	3.1	42

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55	An isolate of <i>Aspergillus flavus</i> used to reduce aflatoxin contamination in cottonseed has a defective polyketide synthase gene. <i>Applied Microbiology and Biotechnology</i> , 2004, 65, 473-478.	3.6	148
56	Clustered Pathway Genes in Aflatoxin Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1253-1262.	3.1	713
57	Aflatoxin Biosynthesis Cluster Gene <i>cypA</i> Is Required for G Aflatoxin Formation. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6518-6524.	3.1	169
58	Sequence comparison of <i>aflR</i> from different <i>Aspergillus</i> species provides evidence for variability in regulation of aflatoxin production. <i>Fungal Genetics and Biology</i> , 2003, 38, 63-74.	2.1	109
59	Toxins of Filamentous Fungi. , 2002, 81, 167-206.		124
60	Promoter elements in the aflatoxin pathway polyketide synthase gene. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002, 1576, 171-175.	2.4	24
61	Molecular and functional characterization of a second copy of the aflatoxin regulatory gene, <i>aflR-2</i> , from <i>Aspergillus parasiticus</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002, 1576, 316-323.	2.4	25
62	Aflatoxin biosynthesis. <i>Revista Iberoamericana De Micologia</i> , 2002, 19, 191-200.	0.9	60
63	DNA from <i>Aspergillus flavus</i> contains 5-methylcytosine. <i>FEMS Microbiology Letters</i> , 2001, 205, 151-155.	1.8	30
64	Promoter elements involved in the expression of the <i>Aspergillus parasiticus</i> aflatoxin biosynthesis pathway gene <i>avnA</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2000, 1491, 7-12.	2.4	16
65	<i>adhA</i> in <i>Aspergillus parasiticus</i> Is Involved in Conversion of 5-Hydroxyaverantin to Averufin. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4715-4719.	3.1	40
66	Induction of the Soybean Phytoalexins Coumestrol and Glyceollin by <i>Aspergillus</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2000, 48, 2167-2172.	5.2	88
67	Characterization of the promoter for the gene encoding the aflatoxin biosynthetic pathway regulatory protein AFLR. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999, 1444, 412-417.	2.4	61
68	Alteration of Different Domains in AFLR Affects Aflatoxin Pathway Metabolism in <i>Aspergillus parasiticus</i> Transformants. <i>Fungal Genetics and Biology</i> , 1998, 23, 279-287.	2.1	50
69	Characterization of the Critical Amino Acids of an <i>Aspergillus parasiticus</i> Cytochrome P-450 Monooxygenase Encoded by <i>ordA</i> That Is Involved in the Biosynthesis of Aflatoxins B ₁ , G ₁ , B ₂ , and G ₂ . <i>Applied and Environmental Microbiology</i> , 1998, 64, 4834-4841.	3.1	91
70	Characterization of the <i>Aspergillus parasiticus</i> <i>niaD</i> and <i>niaA</i> gene cluster. <i>Current Genetics</i> , 1996, 30, 68-75.	1.7	54
71	Characterization of DBPm, a plant protein that binds to DNA containing 5-methylcytosine. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1993, 1172, 108-116.	2.4	22
72	Effect of DNA methylation on the binding of vertebrate and plant proteins to DNA. , 1993, 64, 145-168.		38

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73	A broad bean cDNA clone encoding a DNA-binding protein resembling mammalian CREB in its sequence specificity and DNA methylation sensitivity. <i>Gene</i> , 1992, 117, 169-178.	2.2	29
74	Three MDBP sites in the immediate-early enhancer-promoter region of human cytomegalovirus. <i>Virology</i> , 1991, 182, 865-869.	2.4	35
75	CpG methylation inhibits binding of several sequence-specific DNA-binding proteins from pea, wheat, soybean and cauliflower. <i>Plant Molecular Biology</i> , 1991, 17, 111-123.	3.9	118
76	Binding sites in mammalian genes and viral gene regulatory regions recognized by methylated DNA-binding protein. <i>Nucleic Acids Research</i> , 1990, 18, 6253-6260.	14.5	60
77	How different DNA sequences are recognized by a DNA-binding protein: effects of partial proteolysis. <i>Nucleic Acids Research</i> , 1989, 17, 8611-8629.	14.5	19
78	Related sites in human and herpesvirus DNA recognized by methylated DNA-binding protein from human placenta. <i>Nucleic Acids Research</i> , 1989, 17, 1459-1474.	14.5	37
79	Preparation of the <i>Fusarium</i> toxin, nivalenol, by oxidation of the putative biosynthetic precursor, 7-deoxynivalenol. <i>Mycopathologia</i> , 1989, 107, 111-114.	3.1	3
80	Methylated DNA-binding protein is present in various mammalian cell types. <i>Nucleic Acids Research</i> , 1988, 16, 8029-8044.	14.5	43
81	Protein synthesis inhibition by 8-oxo-12,13-epoxytrichothecenes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1987, 923, 206-213.	2.4	110
82	Effect of site-specific DNA methylation and mutagenesis on recognition by methylated DNA-binding protein from human placenta. <i>Nucleic Acids Research</i> , 1986, 14, 8387-8397.	14.5	42
83	Mycotoxins in Grain Dust: Method for Analysis of Aflatoxins, Ochratoxin A, Zearalenone, Vomitoxin, and Secalonic Acid D. <i>Journal of the Association of Official Analytical Chemists</i> , 1984, 67, 963-967.	0.2	5
84	Digestion of highly modified bacteriophage DNA by restriction endonucleases. <i>Nucleic Acids Research</i> , 1982, 10, 1579-1591.	14.5	125