

Natalie Abrams

List of Publications by Year in descending order

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36
papers

7,967
citations

201674

27
h-index

330143

37
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37
all docs

37
docs citations

37
times ranked

9331
citing authors

#	ARTICLE	IF	CITATIONS
1	The COG database: new developments in phylogenetic classification of proteins from complete genomes. <i>Nucleic Acids Research</i> , 2001, 29, 22-28.	14.5	1,733
2	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272
3	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , 2005, 438, 1157-1161.	27.8	1,128
4	SMURF: Genomic mapping of fungal secondary metabolite clusters. <i>Fungal Genetics and Biology</i> , 2010, 47, 736-741.	2.1	698
5	CDD: a curated Entrez database of conserved domain alignments. <i>Nucleic Acids Research</i> , 2003, 31, 383-387.	14.5	673
6	Genome sequencing and analysis of the filamentous fungus <i>Penicillium chrysogenum</i> . <i>Nature Biotechnology</i> , 2008, 26, 1161-1168.	17.5	427
7	Sodium Ion Cycle in Bacterial Pathogens: Evidence from Cross-Genome Comparisons. <i>Microbiology and Molecular Biology Reviews</i> , 2001, 65, 353-370.	6.6	206
8	Beyond aflatoxin: four distinct expression patterns and functional roles associated with <i>Aspergillus flavus</i> secondary metabolism gene clusters. <i>Molecular Plant Pathology</i> , 2010, 11, 213-226.	4.2	168
9	Systematic and searchable classification of cytochrome P450 proteins encoded by fungal and oomycete genomes. <i>BMC Genomics</i> , 2012, 13, 525.	2.8	150
10	Mobile elements and mitochondrial genome expansion in the soil fungus and potato pathogen <i>Rhizoctonia solani</i> AG-3. <i>FEMS Microbiology Letters</i> , 2014, 352, 165-173.	1.8	143
11	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2003, 31, 474-477.	14.5	137
12	Tight control of mycotoxin biosynthesis gene expression in <i>Aspergillus flavus</i> by temperature as revealed by RNA-Seq. <i>FEMS Microbiology Letters</i> , 2011, 322, 145-149.	1.8	115
13	Continuing Evolution of <i>Burkholderia mallei</i> Through Genome Reduction and Large-Scale Rearrangements. <i>Genome Biology and Evolution</i> , 2010, 2, 102-116.	2.5	106
14	Potential of <i>Aspergillus flavus</i> genomics for applications in biotechnology. <i>Trends in Biotechnology</i> , 2009, 27, 151-157.	9.3	96
15	Genome Sequence of <i>Aspergillus flavus</i> NRRL 3357, a Strain That Causes Aflatoxin Contamination of Food and Feed. <i>Genome Announcements</i> , 2015, 3, .	0.8	96
16	What can comparative genomics tell us about species concepts in the genus <i>Aspergillus</i> ?. <i>Studies in Mycology</i> , 2007, 59, 11-17.	7.2	83
17	Inactivation of <i>Pasteurella</i> (<i>Mannheimia</i>) <i>haemolytica</i> Leukotoxin Causes Partial Attenuation of Virulence in a Calf Challenge Model. <i>Infection and Immunity</i> , 2000, 68, 3916-3922.	2.2	74
18	Gene Expression Profiling and Identification of Resistance Genes to <i>Aspergillus flavus</i> Infection in Peanut through EST and Microarray Strategies. <i>Toxins</i> , 2011, 3, 737-753.	3.4	67

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19	Evidence for genetic differentiation and variable recombination rates among Dutch populations of the opportunistic human pathogen <i>Aspergillus fumigatus</i> . <i>Molecular Ecology</i> , 2012, 21, 57-70.	3.9	65
20	The histone variant H2A.X is a regulator of the epithelialâ€mesenchymal transition. <i>Nature Communications</i> , 2016, 7, 10711.	12.8	62
21	Development stage-specific proteomic profiling uncovers small, lineage specific proteins most abundant in the <i>Aspergillus Fumigatus</i> conidial proteome. <i>Proteome Science</i> , 2012, 10, 30.	1.7	56
22	Genetic Analysis Using an Isogenic Mating Pair of <i>Aspergillus fumigatus</i> Identifies Azole Resistance Genes and Lack of MAT Locusâ€™s Role in Virulence. <i>PLoS Pathogens</i> , 2015, 11, e1004834.	4.7	52
23	Draft Genome Sequence of the Plant-Pathogenic Soil Fungus <i>Rhizoctonia solani</i> Anastomosis Group 3 Strain Rhs1AP. <i>Genome Announcements</i> , 2014, 2, .	0.8	49
24	Clonality Despite Sex: The Evolution of Host-Associated Sexual Neighborhoods in the Pathogenic Fungus <i>Penicillium marneffei</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002851.	4.7	44
25	Carbohydrateâ€active enzymes revealed in <i>Coptotermes formosanus</i> (Isoptera: Rhinotermitidae) transcriptome. <i>Insect Molecular Biology</i> , 2012, 21, 235-245.	2.0	43
26	Whole genome comparison of the <i>A. fumigatus</i> family. <i>Medical Mycology</i> , 2006, 44, 3-7.	0.7	42
27	Hydrolysis of filterâ€paper cellulose to glucose by two recombinant endogenous glycosyl hydrolases of <i>Coptotermes formosanus</i> . <i>Insect Science</i> , 2010, 17, 245-252.	3.0	36
28	Large-Scale Transcriptional Response to Hypoxia in <i>Aspergillus fumigatus</i> Observed Using RNAseq Identifies a Novel Hypoxia Regulated ncRNA. <i>Mycopathologia</i> , 2014, 178, 331-339.	3.1	29
29	Genome Sequence of the AIDS-Associated Pathogen <i>Penicillium marneffei</i> (ATCC18224) and Its Near Taxonomic Relative <i>Talaromyces stipitatus</i> (ATCC10500). <i>Genome Announcements</i> , 2015, 3, .	0.8	29
30	Plasmids for heterologous expression in <i>Pasteurella haemolytica</i> . <i>Gene</i> , 1997, 186, 207-211.	2.2	24
31	Identification of the Genomic Insertion Site of Pmel-1 TCR Î± and Î² Transgenes by Next-Generation Sequencing. <i>PLoS ONE</i> , 2014, 9, e96650.	2.5	24
32	Phylogenomic Analysis of the <i>Giardia intestinalis</i> Transcarboxylase Reveals Multiple Instances of Domain Fusion and Fission in the Evolution of Biotin-Dependent Enzymes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 172-189.	1.0	15
33	Triallelic SNP-mediated genotyping of regenerated protoplasts of the heterokaryotic fungus <i>Rhizoctonia solani</i> . <i>Journal of Biotechnology</i> , 2012, 158, 144-150.	3.8	8
34	Evolution of Eukaryotic Gene Repertoire and Gene Structure: Discovering the Unexpected Dynamics of Genome Evolution. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 293-302.	1.1	6
35	<i>Escherichia coli</i> strain for thermoinducible T7 RNA polymerase-driven expression. <i>Gene</i> , 1996, 177, 267-268.	2.2	4
36	Metabolic Regulation of Inflammation and Its Resolution: Current Status, Clinical Needs, Challenges, and Opportunities. <i>Journal of Immunology</i> , 2021, 207, 2625-2630.	0.8	2