

Heenam Kim

List of Publications by Year in descending order

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papers

5,151
citations

201674

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docs citations

45
times ranked

5831
citing authors

#	ARTICLE	IF	CITATIONS
1	Do an Altered Gut Microbiota and an Associated Leaky Gut Affect COVID-19 Severity?. <i>MBio</i> , 2021, 12, .	4.1	62
2	Non-catalytic-Region Mutations Conferring Transition of Class A β -Lactamases Into ESBLs. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 598998.	3.5	0
3	Mutations in ArgS Arginine-tRNA Synthetase Confer Additional Antibiotic Tolerance Protection to Extended-Spectrum- β -Lactamase-Producing <i>Burkholderia thailandensis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	1
4	Mutations in MetG (methionyl-tRNA synthetase) and TrmD [tRNA (guanine-N1)-methyltransferase] conferring meropenem tolerance in <i>Burkholderia thailandensis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 332-338.	3.0	7
5	Antibiotic Scars Left on the Gut Microbiota from the Stringent Response. <i>Trends in Microbiology</i> , 2018, 26, 735-737.	7.7	6
6	High adaptability of the omega loop underlies the substrate-spectrum-extension evolution of a class A β -lactamase, PenL. <i>Scientific Reports</i> , 2016, 6, 36527.	3.3	15
7	<i>Faecalibacterium prausnitzii</i> subspecies "level dysbiosis in the human gut microbiome underlying atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 852-860.	2.9	292
8	Cell Wall Recycling-Linked Coregulation of AmpC and PenB β -Lactamases through <i>ampD</i> Mutations in <i>Burkholderia cenocepacia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7602-7610.	3.2	24
9	The Tandem Repeats Enabling Reversible Switching between the Two Phases of β -Lactamase Substrate Spectrum. <i>PLoS Genetics</i> , 2014, 10, e1004640.	3.5	11
10	Deletion Mutations Conferring Substrate Spectrum Extension in the Class A β -Lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6265-6269.	3.2	11
11	Development of a random genomic DNA microarray for the detection and identification of <i>Listeria monocytogenes</i> in milk. <i>International Journal of Food Microbiology</i> , 2013, 161, 134-141.	4.7	41
12	Substrate Spectrum Extension of PenA in <i>Burkholderia thailandensis</i> with a Single Amino Acid Deletion, Glu168del. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4005-4008.	3.2	15
13	Twelve Positions in a β -Lactamase That Can Expand Its Substrate Spectrum with a Single Amino Acid Substitution. <i>PLoS ONE</i> , 2012, 7, e37585.	2.5	36
14	Our Genome and Our other Genome: Understanding humans as Symbionts with Microbes. <i>Journal of Bacteriology and Virology</i> , 2012, 42, 101.	0.1	1
15	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
16	The Early Stage of Bacterial Genome-Reductive Evolution in the Host. <i>PLoS Pathogens</i> , 2010, 6, e1000922.	4.7	98
17	Investigation of plasma-functionalized multiwalled carbon nanotube film and its application of DNA sensor for <i>Legionella pneumophila</i> detection. <i>Talanta</i> , 2010, 82, 904-911.	5.5	19
18	Simple Sequence Repeat (SSR)-Based Gene Diversity in <i>Burkholderia pseudomallei</i> and <i>Burkholderia mallei</i> . <i>Molecules and Cells</i> , 2009, 27, 237-241.	2.6	8

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19	Crystal structure of a PduO-type ATP:cobalamin adenosyltransferase from <i>Burkholderia thailandensis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1066-1070.	2.6	5
20	SreA-mediated iron regulation in <i>Aspergillus fumigatus</i> . <i>Molecular Microbiology</i> , 2008, 70, 27-43.	2.5	233
21	Microarray data mining using landmark gene-guided clustering. <i>BMC Bioinformatics</i> , 2008, 9, 92.	2.6	20
22	Opine-Based <i>Agrobacterium</i> Competitiveness: Dual Expression Control of the Agrocinopine Catabolism (<i>acc</i>) Operon by Agrocinopines and Phosphate Levels. <i>Journal of Bacteriology</i> , 2008, 190, 3700-3711.	2.2	18
23	<i>Aspergillus flavus</i> genomics as a tool for studying the mechanism of aflatoxin formation. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2008, 25, 1152-1157.	2.3	38
24	Sub-Telomere Directed Gene Expression during Initiation of Invasive Aspergillosis. <i>PLoS Pathogens</i> , 2008, 4, e1000154.	4.7	228
25	Impaired Ribosome Biogenesis Disrupts the Integration between Morphogenesis and Nuclear Duplication during the Germination of <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2008, 7, 575-583.	3.4	11
26	Transcriptional Regulation of Chemical Diversity in <i>Aspergillus fumigatus</i> by LaeA. <i>PLoS Pathogens</i> , 2007, 3, e50.	4.7	326
27	Aflatoxin formation and gene expression in response to carbon source media shift in <i>Aspergillus parasiticus</i> . <i>Food Additives and Contaminants</i> , 2007, 24, 1051-1060.	2.0	30
28	Type VI secretion is a major virulence determinant in <i>Burkholderia mallei</i> . <i>Molecular Microbiology</i> , 2007, 64, 1466-1485.	2.5	293
29	Genome sequence alterations detected upon passage of <i>Burkholderia mallei</i> ATCC 23344 in culture and in mammalian hosts. <i>BMC Genomics</i> , 2006, 7, 228.	2.8	27
30	Development of a polymerase chain reaction assay for the specific identification of <i>Burkholderia mallei</i> and differentiation from <i>Burkholderia pseudomallei</i> and other closely related <i>Burkholderiaceae</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2006, 55, 37-45.	1.8	32
31	The aflatoxin pathway regulator AfIR induces gene transcription inside and outside of the aflatoxin biosynthetic cluster. <i>FEMS Microbiology Letters</i> , 2006, 255, 275-279.	1.8	148
32	Transcriptome analysis of <i>Aspergillus fumigatus</i> exposed to voriconazole. <i>Current Genetics</i> , 2006, 50, 32-44.	1.7	152
33	Genomic patterns of pathogen evolution revealed by comparison of <i>Burkholderia pseudomallei</i> , the causative agent of melioidosis, to avirulent <i>Burkholderia thailandensis</i> . <i>BMC Microbiology</i> , 2006, 6, 46.	3.3	158
34	Evolution of sensory complexity recorded in a myxobacterial genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15200-15205.	7.1	424
35	Genome-wide expression analysis of iron regulation in <i>Burkholderia pseudomallei</i> and <i>Burkholderia mallei</i> using DNA microarrays. <i>FEMS Microbiology Letters</i> , 2005, 252, 327-335.	1.8	51
36	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272

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37	Bacterial genome adaptation to niches: Divergence of the potential virulence genes in three Burkholderia species of different survival strategies. BMC Genomics, 2005, 6, 174.	2.8	142
38	The Aspergillus fumigatus StuA Protein Governs the Up-Regulation of a Discrete Transcriptional Program during the Acquisition of Developmental Competence. Molecular Biology of the Cell, 2005, 16, 5866-5879.	2.1	114
39	What the Aspergillus genomes have told us. Medical Mycology, 2005, 43, 3-5.	0.7	31
40	Contribution of Gene Loss to the Pathogenic Evolution of Burkholderia pseudomallei and Burkholderia mallei. Infection and Immunity, 2004, 72, 4172-4187.	2.2	112
41	Transcriptional divergence of the duplicated oxidative stress-responsive genes in the Arabidopsis genome. Plant Journal, 2004, 41, 212-220.	5.7	48
42	Structural flexibility in the Burkholderia mallei genome. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14246-14251.	7.1	366
43	Gene Expression Analyses of Arabidopsis Chromosome 2 Using a Genomic DNA Amplicon Microarray. Genome Research, 2003, 13, 327-340.	5.5	29
44	Opine Catabolic Loci from Agrobacterium Plasmids Confer Chemotaxis to Their Cognate Substrates. Molecular Plant-Microbe Interactions, 1998, 11, 131-143.	2.6	35
45	Characterization of the acc operon from the nopaline-type Ti plasmid pTiC58, which encodes utilization of agrocinopines A and B and susceptibility to agrocin 84. Journal of Bacteriology, 1997, 179, 7559-7572.	2.2	55