Heenam Kim

List of Publications by Year
in descending order

45 papers	5,151 citations	201674 27 h-index	243625 44 g-index
45 all docs	45 docs citations	45 times ranked	5831 citing authors

#	Article	IF	Citations
1	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	27.8	1,272
2	Evolution of sensory complexity recorded in a myxobacterial genome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15200-15205.	7.1	424
3	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
4	Transcriptional Regulation of Chemical Diversity in Aspergillus fumigatus by LaeA. PLoS Pathogens, 2007, 3, e50.	4.7	326
5	Type VI secretion is a major virulence determinant inBurkholderia mallei. Molecular Microbiology, 2007, 64, 1466-1485.	2.5	293
6	Faecalibacterium prausnitzii subspeciesâ€“level dysbiosis in the human gut microbiome underlying atopic dermatitis. Journal of Allergy and Clinical Immunology, 2016, 137, 852-860.	2.9	292
7	SreAâ€mediated iron regulation in Aspergillus fumigatus. Molecular Microbiology, 2008, 70, 27-43.	2.5	233
8	Sub-Telomere Directed Gene Expression during Initiation of Invasive Aspergillosis. PLoS Pathogens, 2008, 4, e1000154.	4.7	228
9	Genomic patterns of pathogen evolution revealed by comparison of Burkholderia pseudomallei, the causative agent of melioidosis, to avirulent Burkholderia thailandensis. BMC Microbiology, 2006, 6, 46.	3.3	158
10	Transcriptome analysis of Aspergillus fumigatus exposed to voriconazole. Current Genetics, 2006, 50, 32-44.	1.7	152
11	The aflatoxin pathway regulator AflR induces gene transcription inside and outside of the aflatoxin biosynthetic cluster. FEMS Microbiology Letters, 2006, 255, 275-279.	1.8	148
12	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
13	TheAspergillus fumigatusStuA 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
14	Contribution of Gene Loss to the Pathogenic Evolution of Burkholderia pseudomallei and Burkholderia mallei. Infection and Immunity, 2004, 72, 4172-4187.	2.2	112
15	Continuing Evolution of Burkholderia mallei Through Genome Reduction and Large-Scale Rearrangements. Genome Biology and Evolution, 2010, 2, 102-116.	2.5	106
16	The Early Stage of Bacterial Genome-Reductive Evolution in the Host. PLoS Pathogens, 2010, 6, e1000922.	4.7	98
17	Do an Altered Gut Microbiota and an Associated Leaky Gut Affect COVID-19 Severity?. MBio, 2021, 12, .	4.1	62
18	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

#	Article	IF	Citations
19	Genome-wide expression analysis of iron regulation inBurkholderia pseudomalleiandBurkholderia malleiusing DNA microarrays. FEMS Microbiology Letters, 2005, 252, 327-335.	1.8	51
20	Transcriptional divergence of the duplicated oxidative stress-responsive genes in the Arabidopsis genome. Plant Journal, 2004, 41, 212-220.	5.7	48
21	Development of a random genomic DNA microarray for the detection and identification of Listeria monocytogenes in milk. International Journal of Food Microbiology, 2013, 161, 134-141.	4.7	41
22	Aspergillus flavusgenomics as a tool for studying the mechanism of aflatoxin formation. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2008, 25, 1152-1157.	2.3	38
23	Twelve Positions in a Î²-Lactamase That Can Expand Its Substrate Spectrum with a Single Amino Acid Substitution. PLoS ONE, 2012, 7, e37585.	2.5	36
24	Opine Catabolic Loci from Agrobacterium Plasmids Confer Chemotaxis to Their Cognate Substrates. Molecular Plant-Microbe Interactions, 1998, 11, 131-143.	2.6	35
25	Development of a polymerase chain reaction assay for the specific identification of Burkholderia mallei and differentiation from Burkholderia pseudomallei and other closely related Burkholderiaceae. Diagnostic Microbiology and Infectious Disease, 2006, 55, 37-45.	1.8	32
26	What theAspergillusgenomes have told us. Medical Mycology, 2005, 43, 3-5.	0.7	31
27	Aflatoxin formation and gene expression in response to carbon source media shift inAspergillus parasiticus. Food Additives and Contaminants, 2007, 24, 1051-1060.	2.0	30
28	Gene Expression Analyses of Arabidopsis Chromosome 2 Using a Genomic DNA Amplicon Microarray. Genome Research, 2003, 13, 327-340.	5.5	29
29	Genome sequence alterations detected upon passage of Burkholderia mallei ATCC 23344 in culture and in mammalian hosts. BMC Genomics, 2006, 7, 228.	2.8	27
30	Cell Wall Recycling-Linked Coregulation of AmpC and PenB Î²-Lactamases through ampD Mutations in Burkholderia cenocepacia. Antimicrobial Agents and Chemotherapy, 2015, 59, 7602-7610.	3.2	24
31	Microarray data mining using landmark gene-guided clustering. BMC Bioinformatics, 2008, 9, 92.	2.6	20
32	Investigation of plasma-functionalized multiwalled carbon nanotube film and its application of DNA sensor for Legionella pneumophila detection. Talanta, 2010, 82, 904-911.	5.5	19
33	Opine-BasedAgrobacteriumCompetitiveness: Dual Expression Control of the Agrocinopine Catabolism (acc) Operon by Agrocinopines and Phosphate Levels. Journal of Bacteriology, 2008, 190, 3700-3711.	2.2	18
34	Substrate Spectrum Extension of PenA in Burkholderia thailandensis with a Single Amino Acid Deletion, Glu168del. Antimicrobial Agents and Chemotherapy, 2012, 56, 4005-4008.	3.2	15
35	High adaptability of the omega loop underlies the substrate-spectrum-extension evolution of a class A Î²-lactamase, PenL. Scientific Reports, 2016, 6, 36527.	3.3	15
36	Impaired Ribosome Biogenesis Disrupts the Integration between Morphogenesis and Nuclear Duplication during the Germination of Aspergillus fumigatus. Eukaryotic Cell, 2008, 7, 575-583.	3.4	11

#	Article	IF	Citations
37	The Tandem Repeats Enabling Reversible Switching between the Two Phases of Î²-Lactamase Substrate Spectrum. PLoS Genetics, 2014, 10, e1004640.	3.5	11
38	Deletion Mutations Conferring Substrate Spectrum Extension in the Class A Î²-Lactamase. Antimicrobial Agents and Chemotherapy, 2014, 58, 6265-6269.	3.2	11
39	Simple Sequence Repeat (SSR)-Based Gene Diversity in Burkholderia pseudomallei and Burkholderia mallei. Molecules and Cells, 2009, 27, 237-241.	2.6	8
40	Mutations in MetG (methionyl-tRNA synthetase) and TrmD [tRNA (guanine-N1)-methyltransferase] conferring meropenem tolerance in Burkholderia thailandensis. Journal of Antimicrobial Chemotherapy, 2018, 73, 332-338.	3.0	7
41	Antibiotic Scars Left on the Gut Microbiota from the Stringent Response. Trends in Microbiology, 2018, 26, 735-737.	7.7	6
42	Crystal structure of a PduOâ€type ATP:cobalamin adenosyltransferase from Burkholderia thailandensis. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1066-1070.	2.6	5
43	Our Genome and Our other Genome: Understanding humans as Symbionts with Microbes. Journal of Bacteriology and Virology, 2012, 42, 101.	0.1	1
44	Mutations in ArgS Arginine-tRNA Synthetase Confer Additional Antibiotic Tolerance Protection to Extended-Spectrum-Î²-Lactamase-Producing Burkholderia thailandensis. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	1
45	Non-catalytic-Region Mutations Conferring Transition of Class A Î²-Lactamases Into ESBLs. Frontiers in Molecular Biosciences, 2020, 7, 598998.	3.5	0