

Jaeyoung Choi

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

4,140
citations

346980

22
h-index

182931

54
g-index

56
all docs

56
docs citations

56
times ranked

6047
citing authors

#	ARTICLE	IF	CITATIONS
1	Alternative splicing diversifies the transcriptome and proteome of the rice blast fungus during host infection. <i>RNA Biology</i> , 2022, 19, 373-386.	1.5	12
2	Genetic Diversity and Association Analysis for Carotenoid Content among Sprouts of Cowpea (<i>Vigna</i>) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	1.8	8
3	Genomics and Informatics, Conjoined Tools Vital for Understanding and Protecting Plant Health. <i>Phytopathology</i> , 2022, 112, 981-995.	1.1	2
4	A comparative genomic analysis of lichen-forming fungi reveals new insights into fungal lifestyles. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
5	Anti- <i>Staphylococcal</i> activity of a cyclic lipopeptide, C ₁₅ - <i>bacillomycin D</i> , produced by <i>Bacillus velezensis</i> NST6. <i>Journal of Applied Microbiology</i> , 2021, 131, 93-104.	1.4	11
6	Complete genome sequence of <i>Bacillus velezensis</i> NST6 and comparison with the species belonging to operational group B. <i>amyloliquefaciens</i> . <i>Genomics</i> , 2021, 113, 380-386.	1.3	11
7	Fucoxanthin biosynthesis has a positive correlation with the specific growth rate in the culture of microalga <i>Phaeodactylum tricornutum</i> . <i>Journal of Applied Phycology</i> , 2021, 33, 1473-1485.	1.5	17
8	Diversity, population structure, and linkage disequilibrium among cowpea accessions. <i>Plant Genome</i> , 2021, 14, e20113.	1.6	11
9	Genome Analysis of <i>Streptomycesnojiriensis</i> JCM 3382 and Distribution of Gene Clusters for Three Antibiotics and an Azasugar across the Genus <i>Streptomyces</i> . <i>Microorganisms</i> , 2021, 9, 1802.	1.6	5
10	Two nuclear effectors of the rice blast fungus modulate host immunity via transcriptional reprogramming. <i>Nature Communications</i> , 2020, 11, 5845.	5.8	75
11	Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. <i>Mycobiology</i> , 2020, 48, 373-382.	0.6	9
12	Genome-wide functional analysis of phosphatases in the pathogenic fungus <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2020, 11, 4212.	5.8	22
13	Fusion of Spectroscopy and Cobalt Electrochemistry Data for Estimating Phosphate Concentration in Hydroponic Solution. <i>Sensors</i> , 2019, 19, 2596.	2.1	14
14	Genomic Insights into the Rice Blast Fungus through Estimation of Gene Emergence Time in Phylogenetic Context. <i>Mycobiology</i> , 2018, 46, 361-369.	0.6	3
15	Global DNA Methylation in the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> and Genome-Wide Changes in DNA Methylation Accompanied with Sectorization. <i>Frontiers in Plant Science</i> , 2018, 9, 103.	1.7	20
16	Comparative analysis of genome sequences of the conifer tree pathogen, <i>Heterobasidion annosum</i> s.s .. <i>Genomics Data</i> , 2017, 14, 106-113.	1.3	10
17	Kingdom-Wide Analysis of Fungal Small Secreted Proteins (SSPs) Reveals their Potential Role in Host Association. <i>Frontiers in Plant Science</i> , 2016, 7, 186.	1.7	165
18	Systematic functional analysis of kinases in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2016, 7, 12766.	5.8	112

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19	Systematic characterization of the peroxidase gene family provides new insights into fungal pathogenicity in <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2015, 5, 11831.	1.6	71
20	dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav052-bav052.	1.4	13
21	Insights on the Evolution of Mycoparasitism from the Genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 465-480.	1.1	150
22	Genome-wide profiling of DNA methylation provides insights into epigenetic regulation of fungal development in a plant pathogenic fungus, <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2015, 5, 8567.	1.6	115
23	Potential roles of laccases on virulence of <i>Heterobasidion annosum</i> s.s.. <i>Microbial Pathogenesis</i> , 2015, 81, 16-21.	1.3	12
24	Systematic functional profiling of transcription factor networks in <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2015, 6, 6757.	5.8	155
25	Regulation of Cellular Diacylglycerol through Lipid Phosphate Phosphatases Is Required for Pathogenesis of the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2014, 9, e100726.	1.1	14
26	In Silico Sequence Analysis Reveals New Characteristics of Fungal NADPH Oxidase Genes. <i>Mycobiology</i> , 2014, 42, 241-248.	0.6	1
27	funRNA: a fungi-centered genomics platform for genes encoding key components of RNAi. <i>BMC Genomics</i> , 2014, 15, S14.	1.2	25
28	Draft Genome Sequence of <i>Umbilicaria muehlenbergii</i> KoLRILF000956, a Lichen-Forming Fungus Amenable to Genetic Manipulation. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
29	Draft Genome Sequence of <i>Endocarpon pusillum</i> Strain KoLRILF000583. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
30	Draft Genome Sequence of Lichen-Forming Fungus <i>Cladonia metacorallifera</i> Strain KoLRI002260. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
31	dbCRY: a Web-based comparative and evolutionary genomics platform for blue-light receptors. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau037.	1.4	10
32	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014, 46, 270-278.	9.4	867
33	fPoxDB: fungal peroxidase database for comparative genomics. <i>BMC Microbiology</i> , 2014, 14, 117.	1.3	72
34	Secret lifestyles of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2014, 4, 5135.	1.6	104
35	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , 2014, 30, 343-354.	0.7	40
36	Analysis of in planta Expressed Orphan Genes in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , 2014, 30, 367-374.	0.7	4

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37	<i>Phytophthora</i> Database 2.0: Update and Future Direction. <i>Phytopathology</i> , 2013, 103, 1204-1208.	1.1	16
38	Fungal plant cell wall-degrading enzyme database: a platform for comparative and evolutionary genomics in fungi and Oomycetes. <i>BMC Genomics</i> , 2013, 14, S7.	1.2	72
39	Genome-scale analysis of ABC transporter genes and characterization of the ABCC type transporter genes in <i>Magnaporthe oryzae</i> . <i>Genomics</i> , 2013, 101, 354-361.	1.3	38
40	Draft Genome Sequence of Lichen-Forming Fungus <i>Caloplaca flavorubescens</i> Strain KoLRI002931. <i>Genome Announcements</i> , 2013, 1, .	0.8	16
41	Draft Genome Sequence of <i>Cladonia macilenta</i> KoLRI003786, a Lichen-Forming Fungus Producing Biruloquinone. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
42	Global Expression Profiling of Transcription Factor Genes Provides New Insights into Pathogenicity and Stress Responses in the Rice Blast Fungus. <i>PLoS Pathogens</i> , 2013, 9, e1003350.	2.1	61
43	CFGP 2.0: a versatile web-based platform for supporting comparative and evolutionary genomics of fungi and Oomycetes. <i>Nucleic Acids Research</i> , 2013, 41, D714-D719.	6.5	51
44	Experimental Evolution Reveals Genome-Wide Spectrum and Dynamics of Mutations in the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2013, 8, e65416.	1.1	16
45	Eukaryotic DNAJ/K Database: A Comprehensive Phylogenomic Analysis Platform for the DNAJ/K Family. <i>Genomics and Informatics</i> , 2013, 11, 52.	0.4	10
46	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	9.4	840
47	Systematic and searchable classification of cytochrome P450 proteins encoded by fungal and oomycete genomes. <i>BMC Genomics</i> , 2012, 13, 525.	1.2	150
48	Cyber infrastructure for <i>Fusarium</i> : three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. <i>Nucleic Acids Research</i> , 2011, 39, D640-D646.	6.5	63
49	Fungal Secretome Database: Integrated platform for annotation of fungal secretomes. <i>BMC Genomics</i> , 2010, 11, 105.	1.2	160
50	IMGD: an integrated platform supporting comparative genomics and phylogenetics of insect mitochondrial genomes. <i>BMC Genomics</i> , 2009, 10, 148.	1.2	17
51	Fungal cytochrome P450 database. <i>BMC Genomics</i> , 2008, 9, 402.	1.2	134
52	SNUGB: a versatile genome browser supporting comparative and functional fungal genomics. <i>BMC Genomics</i> , 2008, 9, 586.	1.2	17
53	FTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. <i>Bioinformatics</i> , 2008, 24, 1024-1025.	1.8	162
54	CFGP: a web-based, comparative fungal genomics platform. <i>Nucleic Acids Research</i> , 2007, 36, D562-D571.	6.5	76