

Jaeyoung Choi

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

4,140
citations

304743

22
h-index

161849

54
g-index

56
all docs

56
docs citations

56
times ranked

5462
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. <i>Nature Genetics</i> , 2014, 46, 270-278.	21.4	867
2	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	21.4	840
3	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.	3.6	165
4	FTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. <i>Bioinformatics</i> , 2008, 24, 1024-1025.	4.1	162
5	Fungal Secretome Database: Integrated platform for annotation of fungal secretomes. <i>BMC Genomics</i> , 2010, 11, 105.	2.8	160
6	Systematic functional profiling of transcription factor networks in <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2015, 6, 6757.	12.8	155
7	Systematic and searchable classification of cytochrome P450 proteins encoded by fungal and oomycete genomes. <i>BMC Genomics</i> , 2012, 13, 525.	2.8	150
8	Insights on the Evolution of Mycoparasitism from the Genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 465-480.	2.5	150
9	Fungal cytochrome P450 database. <i>BMC Genomics</i> , 2008, 9, 402.	2.8	134
10	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.	3.3	115
11	Systematic functional analysis of kinases in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2016, 7, 12766.	12.8	112
12	Secret lifestyles of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2014, 4, 5135.	3.3	104
13	CFGP: a web-based, comparative fungal genomics platform. <i>Nucleic Acids Research</i> , 2007, 36, D562-D571.	14.5	76
14	Two nuclear effectors of the rice blast fungus modulate host immunity via transcriptional reprogramming. <i>Nature Communications</i> , 2020, 11, 5845.	12.8	75
15	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.	2.8	72
16	fPoxDB: fungal peroxidase database for comparative genomics. <i>BMC Microbiology</i> , 2014, 14, 117.	3.3	72
17	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.	3.3	71
18	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.	14.5	63

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19	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.	4.7	61
20	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.	14.5	51
21	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , 2014, 30, 343-354.	1.7	40
22	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.	2.9	38
23	funRNA: a fungi-centered genomics platform for genes encoding key components of RNAi. <i>BMC Genomics</i> , 2014, 15, S14.	2.8	25
24	Draft Genome Sequence of Lichen-Forming Fungus <i>Cladonia metacorallifera</i> Strain KoLRI002260. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
25	Genome-wide functional analysis of phosphatases in the pathogenic fungus <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2020, 11, 4212.	12.8	22
26	Draft Genome Sequence of <i>Umbilicaria muehlenbergii</i> KoLRI000956, a Lichen-Forming Fungus Amenable to Genetic Manipulation. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
27	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.	3.6	20
28	Draft Genome Sequence of <i>Cladonia macilenta</i> KoLRI003786, a Lichen-Forming Fungus Producing Biruloquinone. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
29	SNUGB: a versatile genome browser supporting comparative and functional fungal genomics. <i>BMC Genomics</i> , 2008, 9, 586.	2.8	17
30	IMGD: an integrated platform supporting comparative genomics and phylogenetics of insect mitochondrial genomes. <i>BMC Genomics</i> , 2009, 10, 148.	2.8	17
31	Fucoxanthin biosynthesis has a positive correlation with the specific growth rate in the culture of microalga <i>Phaeodactylum tricorutum</i> . <i>Journal of Applied Phycology</i> , 2021, 33, 1473-1485.	2.8	17
32	<i>Phytophthora</i> Database 2.0: Update and Future Direction. <i>Phytopathology</i> , 2013, 103, 1204-1208.	2.2	16
33	Draft Genome Sequence of Lichen-Forming Fungus <i>Caloplaca flavorubescens</i> Strain KoLRI002931. <i>Genome Announcements</i> , 2013, 1, .	0.8	16
34	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.	2.5	16
35	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.	2.5	14
36	Fusion of Spectroscopy and Cobalt Electrochemistry Data for Estimating Phosphate Concentration in Hydroponic Solution. <i>Sensors</i> , 2019, 19, 2596.	3.8	14

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37	dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav052-bav052.	3.0	13
38	Potential roles of laccases on virulence of <i>Heterobasidion annosum</i> s.s.. <i>Microbial Pathogenesis</i> , 2015, 81, 16-21.	2.9	12
39	Alternative splicing diversifies the transcriptome and proteome of the rice blast fungus during host infection. <i>RNA Biology</i> , 2022, 19, 373-386.	3.1	12
40	Anti- <i>Staphylococcal</i> activity of a cyclic lipopeptide, C ₁₅ bacillomycin D, produced by <i>Bacillus velezensis</i> NST6. <i>Journal of Applied Microbiology</i> , 2021, 131, 93-104.	3.1	11
41	Complete genome sequence of <i>Bacillus velezensis</i> NST6 and comparison with the species belonging to operational group <i>B. amyloliquefaciens</i> . <i>Genomics</i> , 2021, 113, 380-386.	2.9	11
42	Diversity, population structure, and linkage disequilibrium among cowpea accessions. <i>Plant Genome</i> , 2021, 14, e20113.	2.8	11
43	Draft Genome Sequence of <i>Endocarpon pusillum</i> Strain KoLRILF000583. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
44	dbCRY: a Web-based comparative and evolutionary genomics platform for blue-light receptors. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau037.	3.0	10
45	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
46	Eukaryotic DNA/K Database: A Comprehensive Phylogenomic Analysis Platform for the DNAJ/K Family. <i>Genomics and Informatics</i> , 2013, 11, 52.	0.8	10
47	Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. <i>Mycobiology</i> , 2020, 48, 373-382.	1.7	9
48	Genetic Diversity and Association Analysis for Carotenoid Content among Sprouts of Cowpea (<i>Vigna</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	4.9	8
49	A comparative genomic analysis of lichen-forming fungi reveals new insights into fungal lifestyles. <i>Scientific Reports</i> , 2022, 12, .	3.3	6
50	Genome Analysis of <i>Streptomyces nojiriensis</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.	3.6	5
51	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.	1.7	4
52	Genomic Insights into the Rice Blast Fungus through Estimation of Gene Emergence Time in Phylogenetic Context. <i>Mycobiology</i> , 2018, 46, 361-369.	1.7	3
53	Genomics and Informatics, Conjoined Tools Vital for Understanding and Protecting Plant Health. <i>Phytopathology</i> , 2022, 112, 981-995.	2.2	2
54	In Silico Sequence Analysis Reveals New Characteristics of Fungal NADPH Oxidase Genes. <i>Mycobiology</i> , 2014, 42, 241-248.	1.7	1