

Seogchan Kang

List of Publications by Year in descending order

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103
papers

10,558
citations

47409

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42259

96
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104
docs citations

104
times ranked

9609
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#	ARTICLE	IF	CITATIONS
1	Multi-Pronged Investigation of Volatile Compound-Mediated Interactions of <i>Fusarium oxysporum</i> with Plants, Fungi, and Bacteria. <i>Methods in Molecular Biology</i> , 2022, 2391, 109-127.	0.4	1
2	Time-Lapse Imaging of Root Pathogenesis and Fungal Proliferation Without Physically Disrupting Roots. <i>Methods in Molecular Biology</i> , 2022, 2391, 153-170.	0.4	0
3	A rice gene encoding glycosyl hydrolase plays contrasting roles in immunity depending on the type of pathogens. <i>Molecular Plant Pathology</i> , 2022, 23, 400-416.	2.0	12
4	<i>Phytophthora</i> spp. Associated with Appalachian Oak Forests and Waterways in Pennsylvania, with <i>P. abietivora</i> as a Pathogen of Five Native Woody Plant Species. <i>Plant Disease</i> , 2022, 106, 1143-1156.	0.7	8
5	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
6	Genomics and Informatics, Conjoined Tools Vital for Understanding and Protecting Plant Health. <i>Phytopathology</i> , 2022, 112, 981-995.	1.1	2
7	FUSARIUM-ID v.3.0: An Updated, Downloadable Resource for <i>Fusarium</i> Species Identification. <i>Plant Disease</i> , 2022, 106, 1610-1616.	0.7	27
8	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	1.1	107
9	Harnessing Chemical Ecology for Environment-Friendly Crop Protection. <i>Phytopathology</i> , 2021, 111, 1697-1710.	1.1	11
10	Evaluation of multi-color genetically encoded Ca ²⁺ indicators in filamentous fungi. <i>Fungal Genetics and Biology</i> , 2021, 149, 103540.	0.9	2
11	First Report of <i>Aloe vera</i> Rust Caused by <i>Uromyces aloes</i> in an Ornamental Nursery in the United States. <i>Plant Disease</i> , 2021, 105, 3739.	0.7	0
12	Optimization of <i>Agrobacterium tumefaciens</i> -Mediated Transformation of <i>Xylaria grammica</i> EL000614, an Endolichenic Fungus Producing Grammicin. <i>Mycobiology</i> , 2021, 49, 491-497.	0.6	1
13	First report of <i>Fusarium equiseti</i> causing wilt on lentils (<i>Lens culinaris</i> Medik.) in Pakistan. <i>Journal of Plant Pathology</i> , 2020, 102, 571-571.	0.6	1
14	Two nuclear effectors of the rice blast fungus modulate host immunity via transcriptional reprogramming. <i>Nature Communications</i> , 2020, 11, 5845.	5.8	75
15	<i>Phytophthora</i> Diversity in Pennsylvania Nurseries and Greenhouses Inferred from Clinical Samples Collected over Four Decades. <i>Microorganisms</i> , 2020, 8, 1056.	1.6	19
16	Molecular changes associated with spontaneous phenotypic variation of <i>Paenibacillus polymyxa</i> , a commonly used biocontrol agent, and temperature-dependent control of variation. <i>Scientific Reports</i> , 2020, 10, 16586.	1.6	8
17	Metabolomics, an Essential Tool in Exploring and Harnessing Microbial Chemical Ecology. <i>Phytobiomes Journal</i> , 2020, 4, 195-210.	1.4	16
18	Molecular Mechanism Underlying Mechanical Wounding-Induced Flavonoid Accumulation in <i>Dalbergia odorifera</i> T. Chen, an Endangered Tree That Produces Chinese Rosewood. <i>Genes</i> , 2020, 11, 478.	1.0	17

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19	Evolution of the Genes Encoding Effector Candidates Within Multiple Pathotypes of <i>Magnaporthe oryzae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2575.	1.5	31
20	Secreted metabolite-mediated interactions between rhizosphere bacteria and <i>Trichoderma</i> biocontrol agents. <i>PLoS ONE</i> , 2019, 14, e0227228.	1.1	22
21	Disruption and Overexpression of the Gene Encoding ACC (1-Aminocyclopropane-1-Carboxylic Acid) Deaminase in Soil-Borne Fungal Pathogen <i>Verticillium dahliae</i> Revealed the Role of ACC as a Potential Regulator of Virulence and Plant Defense. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 639-653.	1.4	28
22	A Plate-based Assay for Studying How Fungal Volatile Compounds (VCs) Affect Plant Growth and Development and the Identification of VCs via SPME-GC-MS. <i>Bio-protocol</i> , 2019, 9, e3166.	0.2	3
23	Do volatile compounds produced by <i>Fusarium oxysporum</i> and <i>Verticillium dahliae</i> affect stress tolerance in plants?. <i>Mycology</i> , 2018, 9, 166-175.	2.0	31
24	Roles of three <i>Fusarium graminearum</i> membrane Ca ²⁺ channels in the formation of Ca ²⁺ signatures, growth, development, pathogenicity and mycotoxin production. <i>Fungal Genetics and Biology</i> , 2018, 111, 30-46.	0.9	24
25	Volatile Compound-Mediated Recognition and Inhibition Between <i>Trichoderma</i> Biocontrol Agents and <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2614.	1.5	85
26	Volatile Compounds Emitted by Diverse <i>Verticillium</i> Species Enhance Plant Growth by Manipulating Auxin Signaling. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1021-1031.	1.4	36
27	The U.S. Culture Collection Network Responding to the Requirements of the Nagoya Protocol on Access and Benefit Sharing. <i>MBio</i> , 2017, 8, .	1.8	30
28	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
29	Stop and smell the fungi: Fungal volatile metabolites are overlooked signals involved in fungal interaction with plants. <i>Fungal Biology Reviews</i> , 2016, 30, 134-144.	1.9	70
30	Development of a transformation system for <i>Hirsutella</i> spp. and visualization of the mode of nematode infection by GFP-labeled <i>H. minnesotensis</i> . <i>Scientific Reports</i> , 2015, 5, 10477.	1.6	9
31	<i>Fusarium Oxysporum</i> Volatiles Enhance Plant Growth Via Affecting Auxin Transport and Signaling. <i>Frontiers in Microbiology</i> , 2015, 6, 1248.	1.5	96
32	DNA sequence-based identification of <i>Fusarium</i> : Current status and future directions. <i>Phytoparasitica</i> , 2015, 43, 583-595.	0.6	275
33	Roles of three <i>Fusarium oxysporum</i> calcium ion (Ca ²⁺) channels in generating Ca ²⁺ signatures and controlling growth. <i>Fungal Genetics and Biology</i> , 2015, 82, 145-157.	0.9	19
34	The United States Culture Collection Network (USCCN): Enhancing Microbial Genomics Research through Living Microbe Culture Collections. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5671-5674.	1.4	33
35	Plant Pathology 2.0. <i>Molecular Plant Pathology</i> , 2014, 15, 315-318.	2.0	4
36	<i>Fusarium oxysporum</i> . , 2014, , 99-119.		9

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37	Successful <i>Agrobacterium</i> mediated transformation of <i>Thielaviopsis basicola</i> by optimizing multiple conditions. <i>Fungal Biology</i> , 2014, 118, 675-682.	1.1	5
38	Roles of Forkhead-box Transcription Factors in Controlling Development, Pathogenicity, and Stress Response in <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , 2014, 30, 136-150.	0.7	23
39	<i>Phytophthora</i> Database 2.0: Update and Future Direction. <i>Phytopathology</i> , 2013, 103, 1204-1208.	1.1	16
40	Phylogenetic analyses of RPB1 and RPB2 support a middle Cretaceous origin for a clade comprising all agriculturally and medically important fusaria. <i>Fungal Genetics and Biology</i> , 2013, 52, 20-31.	0.9	366
41	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. <i>Phytopathology</i> , 2013, 103, 400-408.	1.1	219
42	Sniffing on Microbes: Diverse Roles of Microbial Volatile Organic Compounds in Plant Health. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 835-843.	1.4	269
43	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
44	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
45	<i>Agrobacterium tumefaciens</i> -Mediated Transformation of the Lichen Fungus, <i>Umbilicaria muehlenbergii</i> . <i>PLoS ONE</i> , 2013, 8, e83896.	1.1	42
46	Quantitative and Microscopic Assessment of Compatible and Incompatible Interactions between Chickpea Cultivars and <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> Races. <i>PLoS ONE</i> , 2013, 8, e61360.	1.1	49
47	The G protein β^2 subunit controls virulence and multiple growth- and development-related traits in <i>Verticillium dahliae</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 271-283.	0.9	82
48	Expression of the Cameleon calcium biosensor in fungi reveals distinct Ca ²⁺ signatures associated with polarized growth, development, and pathogenesis. <i>Fungal Genetics and Biology</i> , 2012, 49, 589-601.	0.9	48
49	Systematic and searchable classification of cytochrome P450 proteins encoded by fungal and oomycete genomes. <i>BMC Genomics</i> , 2012, 13, 525.	1.2	150
50	Phylogenetic diversity of insecticolous fusaria inferred from multilocus DNA sequence data and their molecular identification via FUSARIUM-ID and <i>Fusarium</i> MLST. <i>Mycologia</i> , 2012, 104, 427-445.	0.8	164
51	Real-time PCR Detection of <i>Rhodococcus fascians</i> and Discovery of New Plants Associated with <i>R. fascians</i> in Pennsylvania. <i>Plant Health Progress</i> , 2012, 13, .	0.8	12
52	Atomic Force Microscopy: A Tool for Studying Biophysical Surface Properties Underpinning Fungal Interactions with Plants and Substrates. <i>Methods in Molecular Biology</i> , 2012, 835, 151-164.	0.4	3
53	Loss of cAMP-Dependent Protein Kinase A Affects Multiple Traits Important for Root Pathogenesis by <i>Fusarium oxysporum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 719-732.	1.4	44
54	<i>VdSNF1</i> , the Sucrose Nonfermenting Protein Kinase Gene of <i>Verticillium dahliae</i> , Is Required for Virulence and Expression of Genes Involved in Cell-Wall Degradation. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 129-142.	1.4	111

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55	Cyber infrastructure for Fusarium: three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. <i>Nucleic Acids Research</i> , 2011, 39, D640-D646.	6.5	63
56	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	2.1	477
57	<i>Pseudomonas</i> sp. LSW25R, antagonistic to plant pathogens, promoted plant growth, and reduced blossom-end rot of tomato fruits in a hydroponic system. <i>European Journal of Plant Pathology</i> , 2010, 126, 1-11.	0.8	31
58	Fungal Secretome Database: Integrated platform for annotation of fungal secretomes. <i>BMC Genomics</i> , 2010, 11, 105.	1.2	160
59	Enhanced defense responses of tomato plants against late blight pathogen <i>Phytophthora infestans</i> by pre-inoculation with rhizobacteria. <i>Crop Protection</i> , 2010, 29, 1406-1412.	1.0	17
60	Functional characterization and manipulation of the apicidin biosynthetic pathway in <i>Fusarium semitectum</i> . <i>Molecular Microbiology</i> , 2010, 76, 456-466.	1.2	54
61	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
62	Multilocus phylogenetics show high levels of endemic fusaria inhabiting Sardinian soils (Tyrrhenian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	34
63	Translocation of <i>Magnaporthe oryzae</i> Effectors into Rice Cells and Their Subsequent Cell-to-Cell Movement. <i>Plant Cell</i> , 2010, 22, 1388-1403.	3.1	426
64	Internet-Accessible DNA Sequence Database for Identifying Fusaria from Human and Animal Infections. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3708-3718.	1.8	446
65	Roles of the catalytic subunit of cAMP-dependent protein kinase A in virulence and development of the soilborne plant pathogen <i>Verticillium dahliae</i> . <i>Fungal Genetics and Biology</i> , 2010, 47, 406-415.	0.9	100
66	The Promise and Pitfalls of Sequence-Based Identification of Plant-Pathogenic Fungi and Oomycetes. <i>Phytopathology</i> , 2010, 100, 732-737.	1.1	72
67	Rice Blast Fungus (<i>Magnaporthe oryzae</i>) Infects Arabidopsis via a Mechanism Distinct from That Required for the Infection of Rice. <i>Plant Physiology</i> , 2009, 149, 474-486.	2.3	63
68	The ER Chaperone LHS1 Is Involved in Asexual Development and Rice Infection by the Blast Fungus <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2009, 21, 681-695.	3.1	126
69	IMGD: an integrated platform supporting comparative genomics and phylogenetics of insect mitochondrial genomes. <i>BMC Genomics</i> , 2009, 10, 148.	1.2	17
70	Infection Biology of <i>Moniliophthora perniciosa</i> on <i>Theobroma cacao</i> and Alternate Solanaceous Hosts. <i>Tropical Plant Biology</i> , 2009, 2, 149-160.	1.0	30
71	A two-locus DNA sequence database for typing plant and human pathogens within the <i>Fusarium oxysporum</i> species complex. <i>Fungal Genetics and Biology</i> , 2009, 46, 936-948.	0.9	275
72	Ratios of Cells With and Without Virulence Genes in <i>Rhodococcus fascians</i> Populations Correlate with Degrees of Symptom Development. <i>Plant Disease</i> , 2009, 93, 499-506.	0.7	21

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73	Fungal cytochrome P450 database. BMC Genomics, 2008, 9, 402.	1.2	134
74	SNUGB: a versatile genome browser supporting comparative and functional fungal genomics. BMC Genomics, 2008, 9, 586.	1.2	17
75	Phytophthora quercetorum sp. nov., a novel species isolated from eastern and north-central USA oak forest soils. Mycological Research, 2008, 112, 906-916.	2.5	24
76	A multi-locus phylogeny for Phytophthora utilizing markers derived from complete genome sequences. Fungal Genetics and Biology, 2008, 45, 266-277.	0.9	417
77	Microsclerotia development in Verticillium dahliae: Regulation and differential expression of the hydrophobin gene VDH1. Fungal Genetics and Biology, 2008, 45, 1525-1532.	0.9	56
78	TTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. Bioinformatics, 2008, 24, 1024-1025.	1.8	162
79	<i>Phytophthora</i> Database: A Forensic Database Supporting the Identification and Monitoring of <i>Phytophthora</i>. Plant Disease, 2008, 92, 966-972.	0.7	64
80	Genome Organization and Evolution of the <i>AVR-Pita</i> Avirulence Gene Family in the <i>Magnaporthe grisea</i> Species Complex. Molecular Plant-Microbe Interactions, 2008, 21, 658-670.	1.4	127
81	CFGP: a web-based, comparative fungal genomics platform. Nucleic Acids Research, 2007, 36, D562-D571.	6.5	76
82	In vivo time-lapse documentation using confocal and multi-photon microscopy reveals the mechanisms of invasion into the Arabidopsis root vascular system by Fusarium oxysporum. Fungal Genetics and Biology, 2007, 44, 1011-1023.	0.9	81
83	Genome-wide functional analysis of pathogenicity genes in the rice blast fungus. Nature Genetics, 2007, 39, 561-565.	9.4	205
84	Genome-wide analysis of T-DNA integration into the chromosomes of <i>Magnaporthe oryzae</i>. Molecular Microbiology, 2007, 66, 371-382.	1.2	90
85	Genome-wide analysis of T-DNA integration into the chromosomes of Magnaporthe oryzae. Molecular Microbiology, 2007, 66, 826-826.	1.2	4
86	Filamentous Fungi (Magnaporthe grisea and Fusarium oxysporum). , 2006, 344, 403-420.		55
87	Plant Pathogen Culture Collections: It Takes a Village to Preserve These Resources Vital to the Advancement of Agricultural Security and Plant Pathology. Phytopathology, 2006, 96, 920-925.	1.1	26
88	Mutations in VMK1, a mitogen-activated protein kinase gene, affect microsclerotia formation and pathogenicity in Verticillium dahliae. Current Genetics, 2005, 48, 109-116.	0.8	103
89	Rice Defense Mechanisms Against Cochliobolus miyabeanus and Magnaporthe grisea Are Distinct. Phytopathology, 2005, 95, 1248-1255.	1.1	63
90	A dual selection based, targeted gene replacement tool for Magnaporthe grisea and Fusarium oxysporum. Fungal Genetics and Biology, 2005, 42, 483-492.	0.9	129

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91	FUSARIUM-ID v. 1.0: A DNA Sequence Database for Identifying Fusarium. <i>European Journal of Plant Pathology</i> , 2004, 110, 473-479.	0.8	860
92	Cloning and targeted disruption, via <i>Agrobacterium tumefaciens</i> -mediated transformation, of a trypsin protease gene from the vascular wilt fungus <i>Verticillium dahliae</i> . <i>Current Genetics</i> , 2004, 45, 104-110.	0.8	82
93	Molecular and Genetic Basis of Plant-Fungal Pathogen Interactions. <i>Applied Mycology and Biotechnology</i> , 2004, 4, 59-97.	0.3	1
94	In Vivo Microscopy of Vascular Wilt Disease in <i>Arabidopsis thaliana</i> . <i>Microscopy and Microanalysis</i> , 2004, 10, 216-217.	0.2	0
95	Loss of function of the <i>Fusarium oxysporum</i> SNF1 gene reduces virulence on cabbage and <i>Arabidopsis</i> . <i>Current Genetics</i> , 2003, 44, 49-57.	0.8	140
96	Evolution and Organization of a Highly Dynamic, Subtelomeric Helicase Gene Family in the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Genetics</i> , 2002, 162, 103-112.	1.2	45
97	Organization and Distribution Pattern of MGLR-3, a Novel Retrotransposon in the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Fungal Genetics and Biology</i> , 2001, 32, 11-19.	0.9	34
98	Gain of Virulence Caused by Insertion of a Pot3 Transposon in a <i>Magnaporthe grisea</i> Avirulence Gene. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 671-674.	1.4	191
99	Identification of the First Fungal Annexin: Analysis of Annexin Gene Duplications and Implications for Eukaryotic Evolution. <i>Journal of Molecular Evolution</i> , 1998, 47, 531-543.	0.8	61
100	Expressed Sequences from Conidial, Mycelial, and Sexual Stages of <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 1997, 21, 348-363.	0.9	151
101	Sequence of the met-10+ locus of <i>Neurospora crassa</i> : homology to a sequence of unknown function in <i>Saccharomyces cerevisiae</i> chromosome 8. <i>Gene</i> , 1995, 162, 111-115.	1.0	3
102	The <i>PWL</i> Host Specificity Gene Family in the Blast Fungus <i>Magnaporthe grisea</i> . <i>Molecular Plant-Microbe Interactions</i> , 1995, 8, 939.	1.4	266
103	Functional domains of the transcriptional activator NUC-1 in <i>Neurospora crassa</i> . <i>Gene</i> , 1993, 130, 259-264.	1.0	13