

# Sun Tae Kim

## List of Publications by Year in descending order

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122  
papers

4,205  
citations

101543

36  
h-index

133252

59  
g-index

123  
all docs

123  
docs citations

123  
times ranked

4943  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic analysis of pathogen-responsive proteins from rice leaves induced by rice blast fungus, <i>Magnaporthe grisea</i> . <i>Proteomics</i> , 2004, 4, 3569-3578.	2.2	210
2	Overexpression of <i>PYL5</i> in rice enhances drought tolerance, inhibits growth, and modulates gene expression. <i>Journal of Experimental Botany</i> , 2014, 65, 453-464.	4.8	204
3	Plantacyanin Plays a Role in Reproduction in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 138, 778-789.	4.8	183
4	Proteomic analysis of differentially expressed proteins induced by rice blast fungus and elicitor in suspension-cultured rice cells. <i>Proteomics</i> , 2003, 3, 2368-2378.	2.2	166
5	Two-dimensional electrophoretic analysis of rice proteins by polyethylene glycol fractionation for protein arrays. <i>Electrophoresis</i> , 2001, 22, 2103-2109.	2.4	163
6	Mlo, a Modulator of Plant Defense and Cell Death, Is a Novel Calmodulin-binding Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 19304-19314.	3.4	130
7	Ethylene: A Master Regulator of Salinity Stress Tolerance in Plants. <i>Biomolecules</i> , 2020, 10, 959.	4.0	125
8	In-depth insight into in vivo apoplastic secretome of rice- <i>Magnaporthe oryzae</i> interaction. <i>Journal of Proteomics</i> , 2013, 78, 58-71.	2.4	104
9	The rice pathogen-related protein 10 (JlOsPR10) is induced by abiotic and biotic stresses and exhibits ribonuclease activity. <i>Plant Cell Reports</i> , 2008, 27, 593-603.	5.6	96
10	Overexpression of a Pathogenesis-Related Protein 10 Enhances Biotic and Abiotic Stress Tolerance in Rice. <i>Plant Pathology Journal</i> , 2016, 32, 552-562.	1.7	85
11	Overexpression of rice isoflavone reductase-like gene ( <i>OsIRL</i> ) confers tolerance to reactive oxygen species. <i>Physiologia Plantarum</i> , 2010, 138, 1-9.	5.2	72
12	Analysis of embryonic proteome modulation by GA and ABA from germinating rice seeds. <i>Proteomics</i> , 2008, 8, 3577-3587.	2.2	70
13	The RNase Activity of Rice Probenazole-Induced Protein1 (PBZ1) Plays a Key Role in Cell Death in Plants. <i>Molecules and Cells</i> , 2011, 31, 25-32.	2.6	70
14	In vitro and in vivo anticancer effects of <i>Lithospermum erythrorhizon</i> extract on B16F10 murine melanoma. <i>Journal of Ethnopharmacology</i> , 2012, 144, 335-345.	4.1	70
15	Rice proteomics: A model system for crop improvement and food security. <i>Proteomics</i> , 2014, 14, 593-610.	2.2	68
16	Developing Rice Embryo Proteomics Reveals Essential Role for Embryonic Proteins in Regulation of Seed Germination. <i>Journal of Proteome Research</i> , 2009, 8, 3598-3605.	3.7	66
17	Secretome analysis of differentially induced proteins in rice suspension-cultured cells triggered by rice blast fungus and elicitor. <i>Proteomics</i> , 2009, 9, 1302-1313.	2.2	65
18	Proteomics survey of Solanaceae family: Current status and challenges ahead. <i>Journal of Proteomics</i> , 2017, 169, 41-57.	2.4	65

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19	Proteome analysis of rice blast fungus ( <i>Magnaporthe grisea</i> ) proteome during appressorium formation. <i>Proteomics</i> , 2004, 4, 3579-3587.	2.2	63
20	Comparative Secretome Investigation of <i>Magnaporthe oryzae</i> Proteins Responsive to Nitrogen Starvation. <i>Journal of Proteome Research</i> , 2011, 10, 3136-3148.	3.7	62
21	Depletion of abundant plant RuBisCO protein using the protamine sulfate precipitation method. <i>Proteomics</i> , 2013, 13, 2176-2179.	2.2	61
22	<i>Magnaporthe oryzae</i> -Secreted Protein MSP1 Induces Cell Death and Elicits Defense Responses in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 299-312.	2.6	61
23	In-depth proteomic analysis of Glycine max seeds during controlled deterioration treatment reveals a shift in seed metabolism. <i>Journal of Proteomics</i> , 2017, 169, 125-135.	2.4	61
24	Proteomic analysis of the secretome of rice calli. <i>Physiologia Plantarum</i> , 2009, 135, 331-341.	5.2	60
25	Proteomics Analysis of Rice Lesion Mimic Mutant ( <i>spl1</i> ) Reveals Tightly Localized Probenazole-Induced Protein (PBZ1) in Cells Undergoing Programmed Cell Death. <i>Journal of Proteome Research</i> , 2008, 7, 1750-1760.	3.7	55
26	Abnormal Chloroplast Development and Growth Inhibition in Rice Thioredoxin $m$ Knock-Down Plants. <i>Plant Physiology</i> , 2008, 148, 808-817.	4.8	55
27	Proteomics of weakly bound cell wall proteins in rice calli. <i>Journal of Plant Physiology</i> , 2009, 166, 675-685.	3.5	49
28	Rice C2-Domain Proteins Are Induced and Translocated to the Plasma Membrane in Response to a Fungal Elicitor. <i>Biochemistry</i> , 2003, 42, 11625-11633.	2.5	47
29	Exogenous Free Ubiquitin Enhances Lily Pollen Tube Adhesion to an in Vitro Stylar Matrix and May Facilitate Endocytosis of SCA. <i>Plant Physiology</i> , 2006, 142, 1397-1411.	4.8	46
30	Expression of BrD1, a Plant Defensin from Brassica rapa, Confers Resistance against Brown Planthopper ( <i>Nilaparvata lugens</i> ) in Transgenic Rices. <i>Molecules and Cells</i> , 2009, 28, 131-138.	2.6	45
31	Proteomics of rice and <i>Cochliobolus miyabeanus</i> fungal interaction: Insight into proteins at intracellular and extracellular spaces. <i>Proteomics</i> , 2014, 14, 2307-2318.	2.2	45
32	Major Quantitative Trait Loci and Putative Candidate Genes for Powdery Mildew Resistance and Fruit-Related Traits Revealed by an Intraspecific Genetic Map for Watermelon ( <i>Citrullus lanatus</i> var.) <i>Tj ETQq0 0 0 r25 /Overlook 10 Tf 5</i>	2.5	44
33	Proteomics of Rice– <i>Magnaporthe oryzae</i> Interaction: What Have We Learned So Far?. <i>Frontiers in Plant Science</i> , 2019, 10, 1383.	3.6	42
34	Common bean proteomics: Present status and future strategies. <i>Journal of Proteomics</i> , 2017, 169, 239-248.	2.4	41
35	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
36	Secretome analysis of the rice bacterium <i>Xanthomonas oryzae</i> ( <i>Xoo</i> ) using in vitro and in planta systems. <i>Proteomics</i> , 2013, 13, 1901-1912.	2.2	38

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37	A Multi-Omics Analysis of <i>Glycine max</i> Leaves Reveals Alteration in Flavonoid and Isoflavonoid Metabolism Upon Ethylene and Abscisic Acid Treatment. <i>Proteomics</i> , 2018, 18, e1700366.	2.2	38
38	Proteomic analysis of reactive oxygen species (ROS)-related proteins in rice roots. <i>Plant Cell Reports</i> , 2008, 27, 363-375.	5.6	34
39	Two SCA (Stigma/Style Cysteine-rich Adhesin) Isoforms Show Structural Differences That Correlate with Their Levels of in Vitro Pollen Tube Adhesion Activity. <i>Journal of Biological Chemistry</i> , 2007, 282, 33845-33858.	3.4	33
40	Comparative investigation of seed coats of brown-versus yellow-colored soybean seeds using an integrated proteomics and metabolomics approach. <i>Proteomics</i> , 2015, 15, 1706-1716.	2.2	32
41	Seed coat color and seed weight contribute differential responses of targeted metabolites in soybean seeds. <i>Food Chemistry</i> , 2017, 214, 248-258.	8.2	32
42	A proteomic insight into the MSP1 and flg22 induced signaling in <i>Oryza sativa</i> leaves. <i>Journal of Proteomics</i> , 2019, 196, 120-130.	2.4	31
43	<i>GORI</i> , encoding the WD40 domain protein, is required for pollen tube germination and elongation in rice. <i>Plant Journal</i> , 2021, 105, 1645-1664.	5.7	31
44	Coupling of gel-based 2-DE and 1-DE shotgun proteomics approaches to dig deep into the leaf senescence proteome of <i>Glycine max</i> . <i>Journal of Proteomics</i> , 2016, 148, 65-74.	2.4	30
45	Identification of Msp1-Induced Signaling Components in Rice Leaves by Integrated Proteomic and Phosphoproteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4135.	4.1	30
46	Analysis of dynamic protein carbonylation in rice embryo during germination through AP-SWATH. <i>Proteomics</i> , 2016, 16, 989-1000.	2.2	29
47	A comparative proteomics survey of proteins responsive to phosphorous starvation in roots of hydroponically-grown rice seedlings. <i>Journal of the Korean Society for Applied Biological Chemistry</i> , 2011, 54, 667-677.	0.9	28
48	Comprehensive identification of LMW-GS genes and their protein products in a common wheat variety. <i>Functional and Integrative Genomics</i> , 2016, 16, 269-279.	3.5	27
49	An insight into the tomato spotted wilt virus (TSWV), tomato and thrips interaction. <i>Plant Biotechnology Reports</i> , 2018, 12, 157-163.	1.5	26
50	CAFRI-Rice: CRISPR applicable functional redundancy inspector to accelerate functional genomics in rice. <i>Plant Journal</i> , 2020, 104, 532-545.	5.7	26
51	Proteomics and Metabolomics Studies on the Biotic Stress Responses of Rice: an Update. <i>Rice</i> , 2021, 14, 30.	4.0	26
52	Altered Gene Expression and Intracellular Changes of the Viable But Nonculturable State in <i>Ralstonia solanacearum</i> by Copper Treatment. <i>Plant Pathology Journal</i> , 2013, 29, 374-385.	1.7	26
53	A rice isoflavone reductase-like gene, OsIRL, is induced by rice blast fungal elicitor. <i>Molecules and Cells</i> , 2003, 16, 224-31.	2.6	26
54	Expression of a salt-induced protein (SALT) in suspension-cultured cells and leaves of rice following exposure to fungal elicitor and phytohormones. <i>Plant Cell Reports</i> , 2004, 23, 256-262.	5.6	25

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55	Protamine sulfate precipitation method depletes abundant plant seed-storage proteins: A case study on legume plants. <i>Proteomics</i> , 2015, 15, 1760-1764.	2.2	25
56	Label-free quantitative secretome analysis of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> highlights the involvement of a novel cysteine protease in its pathogenicity. <i>Journal of Proteomics</i> , 2017, 169, 202-214.	2.4	25
57	Label-free quantitative proteomic analysis of <i>Panax ginseng</i> leaves upon exposure to heat stress. <i>Journal of Ginseng Research</i> , 2019, 43, 143-153.	5.7	24
58	TGFamâ€Finder : a novel solution for targetâ€gene family annotation in plants. <i>New Phytologist</i> , 2020, 227, 1568-1581.	7.3	23
59	Isolation of TC/AG Repeat Microsatellite Sequences for Fingerprinting Rice Blast Fungus and Their Possible Horizontal Transfer to Plant Species. <i>Molecules and Cells</i> , 2000, 10, 127-134.	2.6	22
60	Biotic Stress-Responsive Rice Proteome: An Overview. <i>Journal of Plant Biology</i> , 2011, 54, 219-226.	2.1	22
61	Comparative Biochemical and Proteomic Analyses of Soybean Seed Cultivars Differing in Protein and Oil Content. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 7134-7142.	5.2	22
62	Metabolic Profiling-Based Evaluation of the Fermentative Behavior of <i>Aspergillus oryzae</i> and <i>Bacillus subtilis</i> for Soybean Residues Treated at Different Temperatures. <i>Foods</i> , 2020, 9, 117.	4.3	22
63	Secreted Alpha-N-Arabinofuranosidase B Protein Is Required for the Full Virulence of <i>Magnaporthe oryzae</i> and Triggers Host Defences. <i>PLoS ONE</i> , 2016, 11, e0165149.	2.5	21
64	Concepts and strategies of soybean seed proteomics using the shotgun proteomics approach. <i>Expert Review of Proteomics</i> , 2019, 16, 795-804.	3.0	21
65	Phytochemistry of ginsenosides: Recent advancements and emerging roles. <i>Critical Reviews in Food Science and Nutrition</i> , 2023, 63, 613-640.	10.3	21
66	In-Depth Investigation of Low-Abundance Proteins in Matured and Filling Stages Seeds of <i>Glycine max</i> Employing a Combination of Protamine Sulfate Precipitation and TMT-Based Quantitative Proteomic Analysis. <i>Cells</i> , 2020, 9, 1517.	4.1	19
67	Comprehensive analysis of the expression of twenty-seven beta-1, 3-glucanase genes in rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.6	19
68	Abundant storage protein depletion from tuber proteins using ethanol precipitation method: Suitability to proteomics study. <i>Proteomics</i> , 2015, 15, 1765-1769.	2.2	17
69	Progress Toward Rice Seed OMICS in Low-Level Gamma Radiation Environment in Iitate Village, Fukushima. <i>Journal of Heredity</i> , 2018, 109, 206-211.	2.4	17
70	OsMTD2â€mediated reactive oxygen species (ROS) balance is essential for intact pollenâ€tube elongation in rice. <i>Plant Journal</i> , 2021, 107, 1131-1147.	5.7	17
71	Proteome Analysis of Disease Resistance against <i>Ralstonia solanacearum</i> in Potato Cultivar CT206-10. <i>Plant Pathology Journal</i> , 2016, 32, 25-32.	1.7	17
72	High-throughput proteome analysis reveals changes of primary metabolism and energy production under artificial aging treatment in <i>Glycine max</i> seeds. <i>Applied Biological Chemistry</i> , 2016, 59, 841-853.	1.9	16

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73	A secreted chitinase-like protein (<sc>OsCLP</sc>) supports root growth through calcium signaling in <i>Oryza sativa</i>. <i>Physiologia Plantarum</i> , 2017, 161, 273-284.	5.2	16
74	Characterization of a newly identified rice chitinase-like protein (OsCLP) homologous to xylanase inhibitor. <i>BMC Biotechnology</i> , 2013, 13, 4.	3.3	15
75	Ginseng ( <i>Panax sp.</i> ) proteomics: an update. <i>Applied Biological Chemistry</i> , 2017, 60, 311-320.	1.9	15
76	Integrated Proteomics and Metabolomics Analysis Highlights Correlative Metabolite-Protein Networks in Soybean Seeds Subjected to Warm-Water Soaking. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8057-8067.	5.2	15
77	A TMT-Based Quantitative Proteome Analysis to Elucidate the TSWV Induced Signaling Cascade in Susceptible and Resistant Cultivars of <i>Solanum lycopersicum</i> . <i>Plants</i> , 2020, 9, 290.	3.5	15
78	Physiological and proteomic analysis of young rice leaves grown under nitrogen-starvation conditions. <i>Plant Biotechnology Reports</i> , 2011, 5, 309-315.	1.5	13
79	Sound wave affects the expression of ethylene biosynthesis-related genes through control of transcription factors RIN and HB-1. <i>Plant Biotechnology Reports</i> , 2016, 10, 437-445.	1.5	13
80	Prefractionation of protein samples for proteome analysis by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. <i>Molecules and Cells</i> , 2003, 16, 316-22.	2.6	13
81	Global Transcriptome Profiling of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> under in planta Growth and in vitro Culture Conditions. <i>Plant Pathology Journal</i> , 2017, 33, 458-466.	1.7	12
82	Comparative phosphoproteome analysis upon ethylene and abscisic acid treatment in <i>Glycine max</i> leaves. <i>Plant Physiology and Biochemistry</i> , 2018, 130, 173-180.	5.8	12
83	Overexpression of rice NAC transcription factor OsNAC58 on increased resistance to bacterial leaf blight. <i>Journal of Plant Biotechnology</i> , 2017, 44, 149-155.	0.4	12
84	Comparative proteome profiling of susceptible and resistant rice cultivars identified an arginase involved in rice defense against <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 171, 105-114.	5.8	12
85	Comparative proteomic analysis of host responses to <i>Plasmodiophora brassicae</i> infection in susceptible and resistant <i>Brassica oleracea</i> . <i>Plant Biotechnology Reports</i> , 2020, 14, 263-274.	1.5	11
86	Proteomics Analysis of Early Salt-Responsive Proteins in Ginseng ( <i>Panax ginseng</i> C. A. Meyer) Leaves. <i>Korean Journal of Medicinal Crop Science</i> , 2014, 22, 398-404.	0.4	11
87	Proteomics in Plant Defense Response. , 0, , 585-604.		10
88	Redox properties of a thioredoxin-like <i>Arabidopsis</i> protein, AtTDX. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 2213-2221.	2.3	10
89	Protein profiles secreted from phylloplane of rice leaves free from cytosolic proteins: Application to study rice-Magnaporthe <i>Oryzae</i> interactions. <i>Physiological and Molecular Plant Pathology</i> , 2014, 88, 28-35.	2.5	10
90	Label-free quantitative proteome data associated with MSP1 and flg22 induced signaling in rice leaves. <i>Data in Brief</i> , 2018, 20, 204-209.	1.0	10

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91	A New SNP in Rice Gene Encoding Pyruvate Phosphate Dikinase (PPDK) Associated with Floury Endosperm. <i>Genes</i> , 2020, 11, 465.	2.4	10
92	Proteomic analysis of Korean ginseng ( <i>Panax ginseng</i> C. A. Meyer) following exposure to salt stress. <i>Journal of Plant Biotechnology</i> , 2008, 35, 185-193.	0.4	10
93	Proteasome Inhibitors Affect Appressorium Formation and Pathogenicity of the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , 2011, 27, 225-231.	1.7	10
94	Transcriptomic Analysis of <i>Oryza sativa</i> Leaves Reveals Key Changes in Response to <i>Magnaporthe oryzae</i> MSP1. <i>Plant Pathology Journal</i> , 2018, 34, 257-268.	1.7	9
95	Transcriptome Analysis of ABA/JA-Dual Responsive Genes in Rice Shoot and Root. <i>Current Genomics</i> , 2017, 19, 4-11.	1.6	8
96	Physiological and proteomic analysis of plant growth enhancement by the rhizobacteria <i>Bacillus</i> sp. JS. <i>Genes and Genomics</i> , 2018, 40, 129-136.	1.4	8
97	Label-free quantitative proteomic analysis determines changes in amino acid and carbohydrate metabolism in three cultivars of Jerusalem artichoke tubers. <i>Plant Biotechnology Reports</i> , 2019, 13, 111-122.	1.5	8
98	Depletion of RuBisCO Protein Using the Protamine Sulfate Precipitation Method. <i>Methods in Molecular Biology</i> , 2015, 1295, 225-233.	0.9	8
99	Optimization of Protein Isolation and Label-Free Quantitative Proteomic Analysis in Four Different Tissues of Korean Ginseng. <i>Plants</i> , 2021, 10, 1409.	3.5	7
100	Crop proteomics: Practical method for high resolution of two-dimensional electrophoresis. <i>Journal of Plant Biotechnology</i> , 2012, 39, 81-92.	0.4	7
101	Rice Proteomic Analysis: Sample Preparation for Protein Identification. <i>Methods in Molecular Biology</i> , 2013, 956, 151-184.	0.9	6
102	Analysis of Grinding Kinetics and Flow Behavior of Adzuki Bean ( <i>Vigna angularis</i> L. var. <i>seoulensis</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.9	6
103	An Integrated Approach for the Efficient Extraction and Solubilization of Rice Microsomal Membrane Proteins for High-Throughput Proteomics. <i>Frontiers in Plant Science</i> , 2021, 12, 723369.	3.6	6
104	Differential Proteome and Secretome Analysis During Rice-Pathogen Interaction. <i>Methods in Molecular Biology</i> , 2014, 1072, 563-572.	0.9	6
105	Effect of Phytohormones and Chemical Inhibitors on Pathogenesis-related Genes Identified by Differential Hybridization in Rice Suspension Culture Cells. <i>Plant Pathology Journal</i> , 2010, 26, 386-393.	1.7	5
106	Unravelling the <i>Helianthus tuberosus</i> L. (Jerusalem Artichoke, Kiku-lmo) Tuber Proteome by Label-Free Quantitative Proteomics. <i>Molecules</i> , 2022, 27, 1111.	3.8	5
107	Molecular and functional characterization of a PEX14 cDNA from rice. <i>Plant Science</i> , 2004, 166, 123-130.	3.6	4
108	Proteome data associated with the leaf senescence in <i>Glycine max</i> . <i>Data in Brief</i> , 2016, 9, 90-95.	1.0	4

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109	Phosphoproteome data from abscisic acid and ethylene treated Glycine max leaves. Data in Brief, 2018, 20, 516-520.	1.0	4
110	A TMT-based quantitative proteomic analysis provides insights into the protein changes in the seeds of high- and low- protein content soybean cultivars. Journal of Plant Biotechnology, 2020, 47, 209-217.	0.4	4
111	Overexpression of ADP-glucose pyrophosphorylase (IbAGPaseS) affects expression of carbohydrate regulated genes in sweet potato [Ipomoea batatas (L.) Lam. cv. Yulmi]. Genes and Genomics, 2015, 37, 595-605.	1.4	3
112	Gel-based and gel-free proteome data associated with controlled deterioration treatment of Glycine max seeds. Data in Brief, 2017, 15, 449-453.	1.0	3
113	A modified transient gene expression protocol for subcellular protein localization analysis in rice. Plant Biotechnology Reports, 2020, 14, 131-138.	1.5	3
114	Gene Expression Profiling in Rice Infected with Rice Blast Fungus using SAGE. Plant Pathology Journal, 2008, 24, 384-391.	1.7	3
115	An IbEF1 from sweet potato promotes flowering in transgenic tobacco. Genes and Genomics, 2011, 33, 335-341.	1.4	2
116	Development of a Simple and Reproducible Method for Removal of Contaminants from Ginseng Protein Samples Prior to Proteomics Analysis. Journal of Life Science, 2015, 25, 826-832.	0.2	1
117	A Protocol for the Plasma Membrane Proteome Analysis of Rice Leaves. Methods in Molecular Biology, 2020, 2139, 107-115.	0.9	1
118	Application of mass-spectrometry compatible photocleavable surfactant for next-generation proteomics using rice leaves. Journal of Plant Biotechnology, 2021, 48, 165-172.	0.4	0
119	Proteomics of plant-fungal pathogen interaction: an overview. Journal of Plant Biotechnology, 2014, 41, 1-9.	0.4	0
120	Optimization of in vitro lily culture system with different treatments of taurine. Journal of Plant Biotechnology, 2017, 44, 484-489.	0.4	0
121	Unraveling the Molecular Mechanism of Magnaporthe oryzae Induced Signaling Cascade in Rice. , 2020, , 363-377.		0
122	Proteomics as a tool to understand the biology of agricultural crops. , 2022, , 107-122.		0