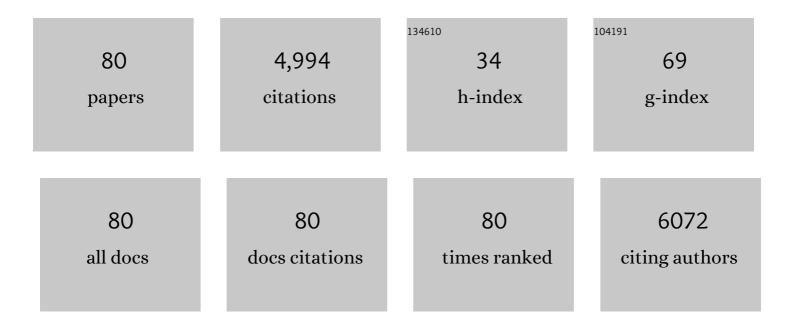
Wusirika Ramakrishna

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transposons: Unexpected players in cancer. Gene, 2022, 808, 145975.	1.0	15
2	Bacillus sp. and arbuscular mycorrhizal fungi consortia enhance wheat nutrient and yield in the second-year field trial: Superior performance in comparison with chemical fertilizers. Journal of Applied Microbiology, 2022, 132, 2203-2219.	1.4	12
3	<i>Bacillus subtilis</i> impact on plant growth, soil health and environment: Dr. Jekyll and Mr. Hyde. Journal of Applied Microbiology, 2022, 132, 3543-3562.	1.4	69
4	Wheat grain proteomic and protein–metabolite interactions analyses provide insights into plant growth promoting bacteria–arbuscular mycorrhizal fungi–wheat interactions. Plant Cell Reports, 2022, 41, 1417-1437.	2.8	9
5	Pseudomonas citronellolis alleviates arsenic toxicity and maintains cellular homeostasis in chickpea (Cicer arietinum L.). Plant Physiology and Biochemistry, 2022, 184, 26-39.	2.8	5
6	<i>Bacillus subtilis</i> CP4, isolated from native soil in combination with arbuscular mycorrhizal fungi promotes biofortification, yield and metabolite production in wheat under field conditions. Journal of Applied Microbiology, 2021, 131, 339-359.	1.4	28
7	Anticancer Activities of Plant Secondary Metabolites: Rice Callus Suspension Culture as a New Paradigm. Rice Science, 2021, 28, 13-30.	1.7	22
8	Co-occurrence and patterns of phosphate solubilizing, salt and metal tolerant and antibiotic-resistant bacteria in diverse soils. 3 Biotech, 2021, 11, 356.	1.1	4
9	Plant Growth Promoting Rhizobacteria, Arbuscular Mycorrhizal Fungi and Their Synergistic Interactions to Counteract the Negative Effects of Saline Soil on Agriculture: Key Macromolecules and Mechanisms. Microorganisms, 2021, 9, 1491.	1.6	46
10	Application of CRISPR–Cas9 in plant–plant growth-promoting rhizobacteria interactions for next Green Revolution. 3 Biotech, 2021, 11, 492.	1.1	3
11	Anti-inflammatory Effects of Northern Highbush Blueberry Extract on an <i>In Vitro</i> Inflammatory Bowel Disease Model. Nutrition and Cancer, 2020, 72, 1178-1190.	0.9	5
12	Brown gold of marginal soil: Plant growth promoting bacteria to overcome plant abiotic stress for agriculture, biofuels and carbon sequestration. Science of the Total Environment, 2020, 711, 135062.	3.9	55
13	Bacteria from native soil in combination with arbuscular mycorrhizal fungi augment wheat yield and biofortification. Plant Physiology and Biochemistry, 2020, 150, 222-233.	2.8	55
14	Pseudomonas citronellolis; a multi-metal resistant and potential plant growth promoter against arsenic (V) stress in chickpea. Plant Physiology and Biochemistry, 2019, 142, 179-192.	2.8	33
15	Plant growth promoting bacteria in agriculture: Two sides of a coin. Applied Soil Ecology, 2019, 138, 10-18.	2.1	174
16	Nutrient enhancement of chickpea grown with plant growth promoting bacteria in local soil of Bathinda, Northwestern India. Physiology and Molecular Biology of Plants, 2019, 25, 1251-1259.	1.4	24
17	Anti-inflammatory and immune-modulating effects of rice callus suspension culture (RCSC) and bioactive fractions in an in vitro inflammatory bowel disease model. Phytomedicine, 2019, 57, 364-376.	2.3	5
18	Comparative metabolic profiling of vetiver (Chrysopogon zizanioides) and maize (Zea mays) under lead stress. Chemosphere, 2018, 193, 903-911.	4.2	41

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19	Metabolomics, biomass and lignocellulosic total sugars analysis in foxtail millet (Setaria italica) inoculated with different combinations of plant growth promoting bacteria and mycorrhiza. Communications in Plant Sciences, 2018, 8, .	0.1	13
20	Proteomics provides insights into biological pathways altered by plant growth promoting bacteria and arbuscular mycorrhiza in sorghum grown in marginal soil. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 243-251.	1.1	24
21	Plant Tolerance to Combined Stress: An Overview. , 2017, , 83-90.		2
22	Mycorrhiza and heavy metal resistant bacteria enhance growth, nutrient uptake and alter metabolic profile of sorghum grown in marginal soil. Chemosphere, 2016, 157, 33-41.	4.2	56
23	Rice callus suspension culture inhibits growth of cell lines of multiple cancer types and induces apoptosis in lung cancer cell line. BMC Complementary and Alternative Medicine, 2016, 16, 427.	3.7	11
24	Prohibitin as the Molecular Binding Switch in the Retinal Pigment Epithelium. Protein Journal, 2016, 35, 1-16.	0.7	22
25	Identification of Biochemical Pathways Associated with Lead Tolerance and Detoxification in <i>Chrysopogon zizanioides</i> L. Nash (Vetiver) by Metabolic Profiling. Environmental Science & Technology, 2016, 50, 2530-2537.	4.6	62
26	Differential regulation of genes by retrotransposons in rice promoters. Plant Molecular Biology, 2015, 87, 603-613.	2.0	8
27	Mycorrhiza and PGPB modulate maize biomass, nutrient uptake and metabolic pathways in maize grown in mining-impacted soil. Plant Physiology and Biochemistry, 2015, 97, 390-399.	2.8	48
28	Sorghum as a Biological Model for Studying the Effect of Microbial Interactions on Growth and Metabolic Activity in Miningâ€Impacted Soil. FASEB Journal, 2015, 29, LB206.	0.2	0
29	Machine Learning Approaches Distinguish Multiple Stress Conditions using Stress-Responsive Genes and Identify Candidate Genes for Broad Resistance in Rice. Plant Physiology, 2014, 164, 481-495.	2.3	129
30	Integrated Metabolomic and Proteomic Approaches Dissect the Effect of Metal-Resistant Bacteria on Maize Biomass and Copper Uptake. Environmental Science & Technology, 2014, 48, 1184-1193.	4.6	69
31	Major cis-regulatory elements for rice bidirectional promoter activity reside in the 5′-untranslated regions. Gene, 2013, 526, 400-410.	1.0	10
32	Genes and Co-Expression Modules Common to Drought and Bacterial Stress Responses in Arabidopsis and Rice. PLoS ONE, 2013, 8, e77261.	1.1	103
33	Mutational, proteomic and metabolomic analysis of a plant growth promoting copper-resistant <i>Pseudomonas</i> spp FEMS Microbiology Letters, 2012, 335, 140-148.	0.7	15
34	Retrotransposon insertions in rice gene pairs associated with reduced conservation of gene pairs in grass genomes. Genomics, 2012, 99, 308-314.	1.3	4
35	Anticancer Activity of Rice Callus Suspension Culture. Phytotherapy Research, 2012, 26, 1075-1081.	2.8	12
36	A Novel Non-wounding Transient Expression Assay for Cereals Mediated by Agrobacterium tumefaciens. Plant Molecular Biology Reporter, 2012, 30, 36-45.	1.0	8

Wusirika Ramakrishna

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37	Bioinformatic Analysis of Epigenetic and MicroRNA Mediated Regulation of Drought Responsive Genes in Rice. PLoS ONE, 2012, 7, e49331.	1.1	41
38	Polymorphisms and evolutionary history of retrotransposon insertions in rice promoters. Genome, 2011, 54, 629-638.	0.9	8
39	Effect of multiple metal resistant bacteria from contaminated lake sediments on metal accumulation and plant growth. Journal of Hazardous Materials, 2011, 189, 531-539.	6.5	141
40	Detection of Genetic Variability using Random Amplified Polymorphic DNA Markers in Some Accessions of Moringa oleifera Lam. from Northern Nigeria. International Journal of Botany, 2011, 7, 237-242.	0.2	13
41	Conservation, Rearrangement, and Deletion of Gene Pairs During the Evolution of Four Grass Genomes. DNA Research, 2010, 17, 343-352.	1.5	9
42	Genome-wide comparative analysis of putative bidirectional promoters from rice, Arabidopsis and Populus. Gene, 2009, 429, 65-73.	1.0	45
43	Analysis of genes associated with retrotransposons in the rice genome. Genetica, 2008, 134, 297-310.	0.5	20
44	Retrotransposon insertion polymorphisms in six rice genes and their evolutionary history. Gene, 2008, 412, 50-58.	1.0	16
45	Comparative Analysis of Divergent and Convergent Gene Pairs and Their Expression Patterns in Rice, Arabidopsis, and <i>Populus</i> Â Â Â. Plant Physiology, 2008, 147, 1763-1773.	2.3	52
46	Differential Expansion and Expression of α- and β-Tubulin Gene Families in Populus Â. Plant Physiology, 2007, 145, 961-973.	2.3	88
47	Identification of stress-responsive genes in an indica rice (Oryza sativa L.) using ESTs generated from drought-stressed seedlings. Journal of Experimental Botany, 2007, 58, 253-265.	2.4	127
48	Fine mapping of the Pc locus of Sorghum bicolor, a gene controlling the reaction to a fungal pathogen and its host-selective toxin. Theoretical and Applied Genetics, 2007, 114, 961-970.	1.8	28
49	Gene Loss and Movement in the Maize Genome. Genome Research, 2004, 14, 1924-1931.	2.4	186
50	Close Split of Sorghum and Maize Genome Progenitors. Genome Research, 2004, 14, 1916-1923.	2.4	443
51	Consistent over-estimation of gene number in complex plant genomes. Current Opinion in Plant Biology, 2004, 7, 732-736.	3.5	176
52	On the Tetraploid Origin of the Maize Genome. Comparative and Functional Genomics, 2004, 5, 281-284.	2.0	61
53	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization. Science, 2004, 303, 1640-1644.	6.0	999
54	A Novel Small Heat Shock Protein Gene, vis1, Contributes to Pectin Depolymerization and Juice Viscosity in Tomato Fruit. Plant Physiology, 2003, 131, 725-735.	2.3	63

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55	Genomic Colinearity as a Tool for Plant Gene Isolation. , 2003, 236, 109-122.		8
56	Structural Analysis of the Maize Rp1 Complex Reveals Numerous Sites and Unexpected Mechanisms of Local Rearrangement. Plant Cell, 2002, 14, 3213-3223.	3.1	72
57	Exceptional haplotype variation in maize. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9093-9095.	3.3	17
58	Comparative Sequence Analysis of the Sorghum RphRegion and the Maize Rp1 Resistance Gene Complex. Plant Physiology, 2002, 130, 1728-1738.	2.3	42
59	Novel genes are enriched in normalized cDNA libraries from drought-stressed seedlings of rice (Oryza) Tj ETQq1 1	0,784314	rgBT /Overl
60	Frequent Genic Rearrangements in Two Regions of Grass Genomes Identified by Comparative Sequence Analysis. Comparative and Functional Genomics, 2002, 3, 165-166.	2.0	5
61	Cereal genes similar to Snf2 define a new subfamily that includes human and mouse genes. Molecular Genetics and Genomics, 2002, 268, 488-499.	1.0	17
62	Genomic sequencing reveals gene content, genomic organization, and recombination relationships in barley. Functional and Integrative Genomics, 2002, 2, 51-59.	1.4	65
63	Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5Am. Functional and Integrative Genomics, 2002, 2, 70-80.	1.4	153
64	Numerous small rearrangements of gene content, order and orientation differentiate grass genomes. Plant Molecular Biology, 2002, 48, 821-827.	2.0	105
65	The Regulatory Regions Required for <i>B</i> ′ Paramutation and Expression Are Located Far Upstream of the Maize <i>b1</i> Transcribed Sequences. Genetics, 2002, 162, 917-930.	1.2	116
66	Different Types and Rates of Genome Evolution Detected by Comparative Sequence Analysis of Orthologous Segments From Four Cereal Genomes. Genetics, 2002, 162, 1389-1400.	1.2	132
67	Potential of (GATA)n microsatellites from rice for inter- and intra-specific variability studies. BMC Evolutionary Biology, 2001, 1, 7.	3.2	15
68	Comparative Sequence Analysis of Colinear Barley and Rice Bacterial Artificial Chromosomes. Plant Physiology, 2001, 125, 1342-1353.	2.3	204
69	Sequence variations at a complex microsatellite locus in rice and its conservation in cereals. Theoretical and Applied Genetics, 2000, 101, 1291-1298.	1.8	24
70	Phylogenetic classification and molecular evolution of knotted1 homeobox genes. Theoretical and Applied Genetics, 1999, 99, 203-209.	1.8	4
71	Microsatellite (GATA)n reveals sex-specific differences in Papaya. Theoretical and Applied Genetics, 1999, 99, 1047-1052.	1.8	85
72	Differential Methylation of Microsatellite and Minisatellite Loci in Rice. Cereal Research Communications, 1999, 27, 365-371.	0.8	0

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73	Expansion of a (GA) dinucleotide at a microsatellite locus associated with domestication in rice. Biochemical Genetics, 1998, 36, 323-327.	0.8	15
74	Identification of minor DNA variations in rice somaclonal variants. Plant Cell Reports, 1998, 18, 55-58.	2.8	24
75	Evolutionary and polymorphic organization of the knotted1 homeobox in cereals. Theoretical and Applied Genetics, 1998, 97, 135-140.	1.8	7
76	DNA fingerprinting of Indian isolates of Xanthomonas oryzae pv. oryzae. Theoretical and Applied Genetics, 1997, 95, 103-111.	1.8	10
77	DNA fingerprinting to detect genetic variation in rice using hypervariable DNA sequences. Theoretical and Applied Genetics, 1995, 90, 1000-1006.	1.8	29
78	DNA fingerprinting detects genetic variability in the pearl millet downy mildew pathogen (Sclerospora) Tj ETQq0	0 0 rgBT /0	Overlock 10 1

79	(CAC)5 detects DNA fingerprints and sequences homologous to gene transcripts in rice. Biochemical Genetics, 1994, 32, 1-8.	0.8	24

80 Comparative Genomics. , 0, , 144-154.