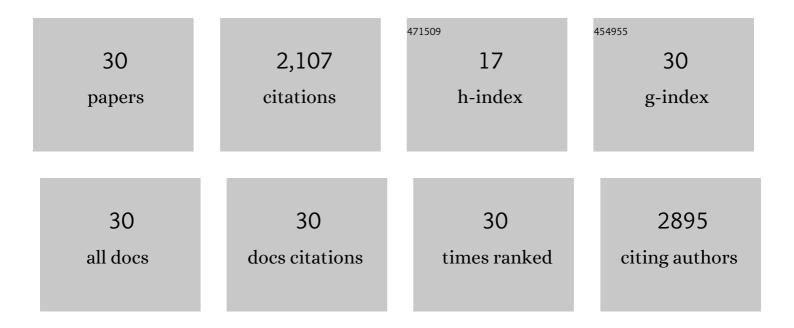
Ze-Chun Yuan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Evaluating the biocontrol potential of Canadian strain Bacillus velezensis 1B-23 via its surfactin production at various pHs and temperatures. BMC Biotechnology, 2021, 21, 31.	3.3	11
2	Surfactin-producing Bacillus velezensis 1B-23 and Bacillus sp. 1D-12 protect tomato against bacterial canker caused by Clavibacter michiganensis subsp. michiganensis. Journal of Plant Pathology, 2020, 102, 451-458.	1.2	12
3	Isolation and characterization of Burkholderia cenocepacia CR318, a phosphate solubilizing bacterium promoting corn growth. Microbiological Research, 2020, 233, 126395.	5.3	50
4	Characterization and genomic analysis of a diesel-degrading bacterium, Acinetobacter calcoaceticus CA16, isolated from Canadian soil. BMC Biotechnology, 2020, 20, 39.	3.3	20
5	Isolation and characterization of novel bacterial strains for integrated solar-bioelectrokinetic of soil contaminated with heavy petroleum hydrocarbons. Chemosphere, 2019, 237, 124514.	8.2	12
6	RNA polymerase II-independent recruitment of SPT6L at transcription start sites in Arabidopsis. Nucleic Acids Research, 2019, 47, 6714-6725.	14.5	24
7	Bacteria in Cancer Therapeutics: A Framework for Effective Therapeutic Bacterial Screening and Identification. Journal of Cancer, 2019, 10, 1781-1793.	2.5	15
8	Genomeâ€wide occupancy of histone H3K27 methyltransferases <scp>CURLY LEAF</scp> and <scp>SWINGER</scp> in <i>Arabidopsis</i> seedlings. Plant Direct, 2019, 3, e00100.	1.9	70
9	Characterization and complete genome analysis of the surfactin-producing, plant-protecting bacterium Bacillus velezensis 9D-6. BMC Microbiology, 2019, 19, 5.	3.3	62
10	<i>Clavibacter michiganensis</i> ssp. <i>michiganensis</i> : bacterial canker of tomato, molecular interactions and disease management. Molecular Plant Pathology, 2018, 19, 2036-2050.	4.2	81
11	Solar power enhancement of electrokinetic bioremediation of phenanthrene by <i>Mycobacterium pallens</i> . Bioremediation Journal, 2017, 21, 53-70.	2.0	7
12	Complete Genome Sequence of Burkholderia cenocepacia CR318, a Phosphate-Solubilizing Bacterium Isolated from Corn Root. Genome Announcements, 2017, 5, .	0.8	4
13	Cytosolic acetyl-CoA promotes histone acetylation predominantly at H3K27 in Arabidopsis. Nature Plants, 2017, 3, 814-824.	9.3	85
14	A Hydroponic Co-cultivation System for Simultaneous and Systematic Analysis of Plant/Microbe Molecular Interactions and Signaling. Journal of Visualized Experiments, 2017, , .	0.3	1
15	MsmiR156 affects global gene expression and promotes root regenerative capacity and nitrogen fixation activity in alfalfa. Transgenic Research, 2017, 26, 541-557.	2.4	28
16	Complete Genome Sequence of Acinetobacter calcoaceticus CA16, a Bacterium Capable of Degrading Diesel and Lignin. Genome Announcements, 2017, 5, .	0.8	8
17	Current knowledge and perspectives of Paenibacillus: a review. Microbial Cell Factories, 2016, 15, 203.	4.0	638
18	Isolation, identification and characterization of Paenibacillus polymyxa CR1 with potentials for biopesticide, biofertilization, biomass degradation and biofuel production. BMC Microbiology, 2016, 16, 244.	3.3	128

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19	Complete Genome Sequence of <i>Arthrobacter</i> sp. Strain LS16, Isolated from Agricultural Soils with Potential for Applications in Bioremediation and Bioproducts. Genome Announcements, 2016, 4, .	0.8	9
20	Agrobacterium tumefaciens responses to plant-derived signaling molecules. Frontiers in Plant Science, 2014, 5, 322.	3.6	108
21	Complete Genome Sequence of Paenibacillus polymyxa CR1, a Plant Growth-Promoting Bacterium Isolated from the Corn Rhizosphere Exhibiting Potential for Biocontrol, Biomass Degradation, and Biofuel Production. Genome Announcements, 2014, 2, .	0.8	22
22	Comparative and genetic analysis of the four sequenced Paenibacillus polymyxa genomes reveals a diverse metabolism and conservation of genes relevant to plant-growth promotion and competitiveness. BMC Genomics, 2014, 15, 851.	2.8	72
23	Development and validation of an rDNA operon based primer walking strategy applicable to de novo bacterial genome finishing. Frontiers in Microbiology, 2014, 5, 769.	3.5	5
24	A Really Useful Pathogen, Agrobacterium tumefaciens. Plant Cell, 2012, 24, tpc.112.tt1012.	6.6	8
25	Comparative transcriptome analysis of <i>Agrobacterium tumefaciens</i> in response to plant signal salicylic acid, indole-3-acetic acid and γ-amino butyric acid reveals signalling cross-talk and <i>Agrobacterium</i> -plant co-evolution. Cellular Microbiology, 2008, 10, 2339-2354.	2.1	102
26	Transcriptome Profiling and Functional Analysis of <i>Agrobacterium tumefaciens</i> Reveals a General Conserved Response to Acidic Conditions (pH 5.5) and a Complex Acid-Mediated Signaling Involved in <i>Agrobacterium</i> -Plant Interactions. Journal of Bacteriology, 2008, 190, 494-507.	2.2	109
27	The plant signal salicylic acid shuts down expression of the <i>vir</i> regulon and activates quormone-quenching genes in <i>Agrobacterium</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11790-11795.	7.1	152
28	Genome prediction of PhoB regulated promoters in Sinorhizobium meliloti and twelve proteobacteria. Nucleic Acids Research, 2006, 34, 2686-2697.	14.5	122
29	Regulation and Properties of PstSCAB, a High-Affinity, High-Velocity Phosphate Transport System of <i>Sinorhizobium meliloti</i> . Journal of Bacteriology, 2006, 188, 1089-1102.	2.2	100
30	Phosphate limitation induces catalase expression inSinorhizobium meliloti,Pseudomonas aeruginosaandAgrobacterium tumefaciens. Molecular Microbiology, 2005, 58, 877-894.	2.5	42