

Trevor C Charles

List of Publications by Year in descending order

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122
papers

7,890
citations

87723

38
h-index

56606

83
g-index

135
all docs

135
docs citations

135
times ranked

9653
citing authors

#	ARTICLE	IF	CITATIONS
1	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
2	Microbiome definition re-visited: old concepts and new challenges. <i>Microbiome</i> , 2020, 8, 103.	4.9	903
3	Amelioration of high salinity stress damage by plant growth-promoting bacterial endophytes that contain ACC deaminase. <i>Plant Physiology and Biochemistry</i> , 2014, 80, 160-167.	2.8	442
4	Isolation and characterization of new plant growth-promoting bacterial endophytes. <i>Applied Soil Ecology</i> , 2012, 61, 217-224.	2.1	299
5	An ACC Deaminase Minus Mutant of <i>Enterobacter cloacae</i> UW4 No Longer Promotes Root Elongation. <i>Current Microbiology</i> , 2000, 41, 101-105.	1.0	205
6	A chromosomally encoded two-component sensory transduction system is required for virulence of <i>Agrobacterium tumefaciens</i> . <i>Journal of Bacteriology</i> , 1993, 175, 6614-6625.	1.0	185
7	Expression of an Exogenous 1-Aminocyclopropane-1-Carboxylate Deaminase Gene in <i>Sinorhizobium meliloti</i> Increases Its Ability To Nodulate Alfalfa. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5891-5897.	1.4	172
8	1-Aminocyclopropane-1-Carboxylate (ACC) Deaminase Genes in Rhizobia from Southern Saskatchewan. <i>Microbial Ecology</i> , 2009, 57, 423-436.	1.4	170
9	The role of PHB metabolism in the symbiosis of rhizobia with legumes. <i>Applied Microbiology and Biotechnology</i> , 2006, 71, 377-386.	1.7	156
10	A novel bacteriocin, thuricin 17, produced by plant growth promoting rhizobacteria strain <i>Bacillus thuringiensis</i> NEB17: isolation and classification. <i>Journal of Applied Microbiology</i> , 2006, 100, 545-554.	1.4	138
11	Analysis of C4-dicarboxylate transport genes in <i>Rhizobium meliloti</i> . <i>Molecular Microbiology</i> , 1989, 3, 813-823.	1.2	137
12	A bioinformatics approach to the determination of genes involved in endophytic behavior in <i>Burkholderia</i> spp.. <i>Journal of Theoretical Biology</i> , 2014, 343, 193-198.	0.8	124
13	Delay of flower senescence by bacterial endophytes expressing 1-aminocyclopropane-1-carboxylate deaminase. <i>Journal of Applied Microbiology</i> , 2012, 113, 1139-1144.	1.4	123
14	Current and future resources for functional metagenomics. <i>Frontiers in Microbiology</i> , 2015, 6, 1196.	1.5	120
15	Multisubstrate Isotope Labeling and Metagenomic Analysis of Active Soil Bacterial Communities. <i>MBio</i> , 2014, 5, e01157-14.	1.8	109
16	Elucidation of gibberellin biosynthesis in bacteria reveals convergent evolution. <i>Nature Chemical Biology</i> , 2017, 13, 69-74.	3.9	103
17	A global pH sensor: <i>Agrobacterium</i> sensor protein ChvG regulates acid-inducible genes on its two chromosomes and Ti plasmid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12369-12374.	3.3	102
18	The class IId bacteriocin thuricin-17 increases plant growth. <i>Planta</i> , 2009, 229, 747-755.	1.6	87

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19	Preformed dimeric state of the sensor protein VirA is involved in plant–Agrobacterium signal transduction.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 9939-9943.	3.3	77
20	Cellobiose dehydrogenase is essential for wood invasion and nonessential for kraft pulp delignification by <i>Trametes versicolor</i> . Enzyme and Microbial Technology, 2001, 29, 478-489.	1.6	74
21	Genetic map of <i>Rhizobium meliloti</i> megaplasmid pRmeSU47b. Journal of Bacteriology, 1990, 172, 2469-2476.	1.0	67
22	ACC deaminase from plant growth-promoting bacteria affects crown gall development. Canadian Journal of Microbiology, 2007, 53, 1291-1299.	0.8	67
23	Co-inoculation dose and root zone temperature for plant growth promoting rhizobacteria on soybean [<i>Glycine max</i> (L.) Merr] grown in soil-less media. Soil Biology and Biochemistry, 2002, 34, 1953-1957.	4.2	62
24	Isolation of Poly-3-Hydroxybutyrate Metabolism Genes from Complex Microbial Communities by Phenotypic Complementation of Bacterial Mutants. Applied and Environmental Microbiology, 2006, 72, 384-391.	1.4	60
25	Roles of poly-3-hydroxybutyrate (PHB) and glycogen in symbiosis of <i>Sinorhizobium meliloti</i> with <i>Medicago sp.</i> . Microbiology (United Kingdom), 2007, 153, 388-398.	0.7	57
26	Null mutations in <i>Sinorhizobium meliloti</i> <i>exoS</i> and <i>chvI</i> demonstrate the importance of this two-component regulatory system for symbiosis. Molecular Microbiology, 2009, 74, 1223-1237.	1.2	56
27	Low temperature tolerant <i>Bradyrhizobium japonicum</i> strains allowing improved nodulation and nitrogen fixation of soybean in a short season (cool spring) area. European Journal of Agronomy, 2003, 19, 205-213.	1.9	53
28	Two-Component Sensory Transduction Systems in Phytobacteria. Annual Review of Phytopathology, 1992, 30, 463-484.	3.5	51
29	Identification and characterization of new LuxR/LuxI-type quorum sensing systems from metagenomic libraries. Environmental Microbiology, 2010, 12, 105-117.	1.8	51
30	Megaplasmid and Chromosomal Loci for the PHB Degradation Pathway in <i>Rhizobium</i> (<i>Sinorhizobium</i>) <i>meliloti</i> . Genetics, 1997, 146, 1211-1220.	1.2	51
31	Cloning and sequencing of a gene encoding cellobiose dehydrogenase from <i>Trametes versicolor</i> . Gene, 1998, 210, 211-219.	1.0	49
32	Functional metagenomics reveals novel β -galactosidases not predictable from gene sequences. PLoS ONE, 2017, 12, e0172545.	1.1	48
33	Requirement for the Enzymes Acetoacetyl Coenzyme A Synthetase and Poly-3-Hydroxybutyrate (PHB) Synthase for Growth of <i>Sinorhizobium meliloti</i> on PHB Cycle Intermediates. Journal of Bacteriology, 2000, 182, 2113-2118.	1.0	45
34	Synthesis and Physical Properties of Polyhydroxyalkanoate Polymers with Different Monomer Compositions by Recombinant <i>Pseudomonas putida</i> LS46 Expressing a Novel PHA SYNTHASE (PhaC116) Enzyme. Applied Sciences (Switzerland), 2017, 7, 242.	1.3	44
35	Heterologous complementation of the exopolysaccharide synthesis and carbon utilization phenotypes of <i>Sinorhizobium meliloti</i> Rm1021 polyhydroxyalkanoate synthesis mutants. FEMS Microbiology Letters, 2004, 239, 277-283.	0.7	43
36	Versatile broad-host-range cosmids for construction of high quality metagenomic libraries. Journal of Microbiological Methods, 2014, 99, 27-34.	0.7	42

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37	The <i>chvH</i> Locus of <i>Agrobacterium</i> Encodes a Homologue of an Elongation Factor Involved in Protein Synthesis. <i>Journal of Bacteriology</i> , 2001, 183, 36-45.	1.0	40
38	<i>Sinorhizobium meliloti</i> 1021 Loss-of-Function Deletion Mutation in <i>chvI</i> and Its Phenotypic Characteristics. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 153-160.	1.4	40
39	Enhanced Arsenic Tolerance in <i>Triticum aestivum</i> Inoculated with Arsenic-Resistant and Plant Growth Promoter Microorganisms from a Heavy Metal-Polluted Soil. <i>Microorganisms</i> , 2019, 7, 348.	1.6	40
40	<i>ndvF</i> , a novel locus located on megaplasmid pRmeSU47b (pEXO) of <i>Rhizobium meliloti</i> , is required for normal nodule development. <i>Journal of Bacteriology</i> , 1991, 173, 3981-3992.	1.0	39
41	Inhibition of the expression of <i>Bradyrhizobium japonicum</i> nod genes at low temperatures. <i>Soil Biology and Biochemistry</i> , 1996, 28, 1579-1583.	4.2	39
42	Influence of the Poly-3-Hydroxybutyrate (PHB) Granule-Associated Proteins (PhaP1 and PhaP2) on PHB Accumulation and Symbiotic Nitrogen Fixation in <i>Sinorhizobium meliloti</i> Rm1021. <i>Journal of Bacteriology</i> , 2007, 189, 9050-9056.	1.0	39
43	Endophytic Phytohormones and Their Role in Plant Growth Promotion. , 2017, , 89-105.		39
44	Fungal and Bacterial Microbiome Associated with the Rhizosphere of Native Plants from the Atacama Desert. <i>Microorganisms</i> , 2020, 8, 209.	1.6	39
45	Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella. <i>Nature Communications</i> , 2017, 8, 521.	5.8	35
46	ACC deaminase activity in avirulent <i>Agrobacterium tumefaciens</i> D3. <i>Canadian Journal of Microbiology</i> , 2011, 57, 278-286.	0.8	34
47	NodMutDB: a database for genes and mutants involved in symbiosis. <i>Bioinformatics</i> , 2005, 21, 2927-2929.	1.8	32
48	Nonlinear electrophoresis for purification of soil DNA for metagenomics. <i>Journal of Microbiological Methods</i> , 2012, 88, 35-40.	0.7	32
49	Ti Plasmid and Chromosomally Encoded Two-Component Systems Important in Plant Cell Transformation by <i>Agrobacterium</i> Species. , 0, , 367-385.		32
50	Harvesting of novel polyhydroxyalkanoate (PHA) synthase encoding genes from a soil metagenome library using phenotypic screening. <i>FEMS Microbiology Letters</i> , 2011, 321, 150-156.	0.7	31
51	Development of Microbiome Biobanks – Challenges and Opportunities. <i>Trends in Microbiology</i> , 2021, 29, 89-92.	3.5	31
52	ACC deaminase increases the <i>Agrobacterium tumefaciens</i> -mediated transformation frequency of commercial canola cultivars. <i>FEMS Microbiology Letters</i> , 2010, 307, 185-190.	0.7	30
53	Comparison of the symbiotic and competition phenotypes of <i>Sinorhizobium meliloti</i> PHB synthesis and degradation pathway mutants. <i>Canadian Journal of Microbiology</i> , 2005, 51, 599-604.	0.8	29
54	Discrete Regions of the Sensor Protein VirA Determine the Strain-Specific Ability of <i>Agrobacterium</i> to Agroinfect Maize. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 221-227.	1.4	27

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55	Mutational Analysis of the Sinorhizobium meliloti Short-Chain Dehydrogenase/Reductase Family Reveals Substantial Contribution to Symbiosis and Catabolic Diversity. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 979-987.	1.4	27
56	Isolation and Identification of Endophytic Bacteria from Mycorrhizal Tissues of Terrestrial Orchids from Southern Chile. <i>Diversity</i> , 2020, 12, 55.	0.7	26
57	Identification of an Acetoacetyl Coenzyme A Synthetase-Dependent Pathway for Utilization of l-(+)-3-Hydroxybutyrate in Sinorhizobium meliloti. <i>Journal of Bacteriology</i> , 2002, 184, 1571-1577.	1.0	25
58	Strong spurious transcription likely contributes to DNA insert bias in typical metagenomic clone libraries. <i>Microbiome</i> , 2015, 3, 22.	4.9	25
59	Methylmalonyl-CoA mutase encoding gene of Sinorhizobium meliloti. <i>Gene</i> , 1999, 226, 121-127.	1.0	24
60	The effect of temperature and genistein concentration on lipo-chitooligosaccharide (LCO) production by wild-type and mutant strains of Bradyrhizobium japonicum. <i>Soil Biology and Biochemistry</i> , 2002, 34, 1175-1180.	4.2	24
61	Engineering of Escherichia coli for direct and modulated biosynthesis of poly(3-hydroxybutyrate-co-3-hydroxyvalerate) copolymer using unrelated carbon sources. <i>Scientific Reports</i> , 2016, 6, 36470.	1.6	24
62	Genetic transformation of Trametes versicolor to phleomycin resistance with the dominant selectable marker shble. <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 201-204.	1.7	23
63	Application of crossover-PCR-mediated deletion-insertion mutagenesis to analysis of the bdhA-xdhA2-xdhB2 mixed-function operon of Sinorhizobium meliloti. <i>Archives of Microbiology</i> , 2003, 179, 301-304.	1.0	22
64	Designer Sinorhizobium meliloti strains and multi-functional vectors enable direct inter-kingdom DNA transfer. <i>PLoS ONE</i> , 2019, 14, e0206781.	1.1	21
65	Bradyrhizobium japonicum mutants allowing improved nodulation and nitrogen fixation of field-grown soybean in a short season area. <i>Journal of Agricultural Science</i> , 2002, 138, 293-300.	0.6	20
66	Open resource metagenomics: a model for sharing metagenomic libraries. <i>Standards in Genomic Sciences</i> , 2011, 5, 203-210.	1.5	20
67	Transcriptome Analysis of Polyhydroxybutyrate Cycle Mutants Reveals Discrete Loci Connecting Nitrogen Utilization and Carbon Storage in Sinorhizobium meliloti. <i>MSystems</i> , 2017, 2, .	1.7	19
68	Lactose utilization and enzymes encoded by megaplasmids in Rhizobium meliloti SU47: implications for population studies. <i>Journal of General Microbiology</i> , 1990, 136, 2497-2502.	2.3	18
69	Effect of experimental contamination with the explosive hexahydro-1,3,5-trinitro-1,3,5-triazine on soil bacterial communities. <i>FEMS Microbiology Ecology</i> , 2003, 43, 255-262.	1.3	18
70	Evaluation of a Pooled Strategy for High-Throughput Sequencing of Cosmid Clones from Metagenomic Libraries. <i>PLoS ONE</i> , 2014, 9, e98968.	1.1	18
71	Sinorhizobium meliloti strain 1021bioSandbdhAgene transcriptions are both affected by biotin available in defined medium. <i>FEMS Microbiology Letters</i> , 2000, 182, 41-44.	0.7	17
72	Novel polyhydroxyalkanoate copolymers produced in Pseudomonas putida by metagenomic polyhydroxyalkanoate synthases. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7611-7627.	1.7	17

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73	Members of the <i>Sinorhizobium meliloti</i> ChvI regulon identified by a DNA binding screen. <i>BMC Microbiology</i> , 2013, 13, 132.	1.3	16
74	Lactic acid containing polymers produced in engineered <i>Sinorhizobium meliloti</i> and <i>Pseudomonas putida</i> . <i>PLoS ONE</i> , 2020, 15, e0218302.	1.1	16
75	Dynamics of microbial populations and diversity in NAPL contaminated peat soil under varying water table conditions. <i>Environmental Research</i> , 2020, 191, 110167.	3.7	15
76	Purification and characterization of homodimeric methylmalonyl-CoA mutase from <i>Sinorhizobium meliloti</i> . <i>Archives of Microbiology</i> , 2003, 180, 151-154.	1.0	14
77	Effects of Nitrogen and Phosphorus Limitation on the Activated Sludge Biomass in a Kraft Mill Biotreatment System. <i>Water Environment Research</i> , 2006, 78, 2303-2310.	1.3	14
78	Identification and characterization of the intracellular poly-3-hydroxybutyrate depolymerase enzyme PhaZ of <i>Sinorhizobium meliloti</i> . <i>BMC Microbiology</i> , 2010, 10, 92.	1.3	14
79	Time Series Resolution of the Fish Necrobiome Reveals a Decomposer Succession Involving Toxigenic Bacterial Pathogens. <i>MSystems</i> , 2020, 5, .	1.7	14
80	Driving factors influencing the rhizobacteriome community structure of plants adapted to multiple climatic stressors in edaphic savannas. <i>Science of the Total Environment</i> , 2021, 769, 145214.	3.9	14
81	The <i>ntrA</i> gene of <i>Agrobacterium tumefaciens</i> : identification, cloning, and phenotype of a site-directed mutant. <i>Journal of Bacteriology</i> , 1992, 174, 2720-2723.	1.0	13
82	Genome-engineered <i>Sinorhizobium meliloti</i> for the production of poly(lactic-co-3-hydroxybutyric) acid copolymer. <i>Canadian Journal of Microbiology</i> , 2016, 62, 130-138.	0.8	13
83	Metagenomic Approaches to Identify Novel Organisms from the Soil Environment in a Classroom Setting. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 423-429.	0.5	12
84	An engineered GFP fluorescent bacterial biosensor for detecting and quantifying silver and copper ions. <i>BioMetals</i> , 2019, 32, 265-272.	1.8	12
85	Low Temperature-Tolerant <i>Bradyrhizobium japonicum</i> Strains Allowing Improved Soybean Yield in Short-Season Areas. <i>Agronomy Journal</i> , 2002, 94, 870-875.	0.9	10
86	Characterization of <i>fbdhA</i> , encoding the enzyme d-3-hydroxybutyrate dehydrogenase, from <i>Sinorhizobium</i> sp. strain NGR234. <i>FEMS Microbiology Letters</i> , 2005, 242, 87-94.	0.7	9
87	Site-specific Bacterial Chromosome Engineering: Î C31 Integrase Mediated Cassette Exchange (IMCE). <i>Journal of Visualized Experiments</i> , 2012, , .	0.2	9
88	Developing a <i>Bacteroides</i> System for Function-Based Screening of DNA from the Human Gut Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	9
89	Genome Sequence of <i>Brevundimonas</i> sp., an Arsenic Resistant Soil Bacterium. <i>Diversity</i> , 2021, 13, 344.	0.7	9
90	<i>Bradyrhizobium japonicum</i> Mutants with Enhanced Sensitivity to Genistein Resulting in Altered <i>nod</i> Gene Regulation. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 1404-1410.	1.4	8

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91	Presence of a novel 16S-23S rRNA gene intergenic spacer insert in Bradyrhizobium canariense strains. FEMS Microbiology Letters, 2007, 269, 207-212.	0.7	7
92	MetaProx: the database of metagenomic proximons. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	7
93	Unraveling a Tangled Skein: Evolutionary Analysis of the Bacterial Gibberellin Biosynthetic Operon. MSphere, 2020, 5, .	1.3	7
94	Low Temperature-Tolerant Strains Allowing Improved Soybean Yield in Short-Season Areas. Agronomy Journal, 2002, 94, 870.	0.9	7
95	Metagenome-Assembled Genome Sequences of Five Strains from the <i>Microtus ochrogaster</i> (Prairie Vole) Fecal Microbiome. Microbiology Resource Announcements, 2020, 9, .	0.3	5
96	Bradyrhizobium japonicum Mutants Allowing Improved Soybean Yield in Short Season Areas with Cool Spring Soil Temperatures. Crop Science, 2002, 42, 1186-1190.	0.8	4
97	Methods for the Isolation of Genes Encoding Novel PHB Cycle Enzymes from Complex Microbial Communities. Methods in Molecular Biology, 2010, 668, 235-246.	0.4	4
98	The Fluorescence Theatre: a cost-effective device using theatre gels for fluorescent protein and dye screening. Canadian Journal of Microbiology, 2011, 57, 339-342.	0.8	4
99	The Completed PacBio Single-Molecule Real-Time Sequence of Methylophilus trichosporium Strain OB3b Reveals the Presence of a Third Large Plasmid. Genome Announcements, 2017, 5, .	0.8	4
100	Slr4, a newly identified σ -layer protein from marine Gammaproteobacteria, is a major biofilm matrix component. Molecular Microbiology, 2020, 114, 979-990.	1.2	4
101	Evaluation of Bacterial Community Structure and Its Influence on Sulfide Oxidation in a Bio-Leaching Environment. Geomicrobiology Journal, 2009, 26, 44-54.	1.0	2
102	Meeting Report: 1st International Functional Metagenomics Workshop May 7-8, 2012, St. Jacobs, Ontario, Canada.. Standards in Genomic Sciences, 2013, 8, 106-111.	1.5	2
103	An analysis of the validity and utility of the proximon proposition. Functional and Integrative Genomics, 2016, 16, 215-220.	1.4	2
104	Metagenomic Cosmid Libraries Suitable for Functional Screening in Proteobacteria. , 2017, , 1-11.		2
105	Does a carbonatite deposit influence its surrounding ecosystem?. Facets, 2019, 4, 389-406.	1.1	2
106	Methods for the Isolation of Genes Encoding Novel PHA Metabolism Enzymes from Complex Microbial Communities. Methods in Molecular Biology, 2017, 1539, 237-248.	0.4	1
107	Sequence polarity between the promoter and the adjacent gene modulates promoter activity. Plasmid, 2021, 117, 102598.	0.4	1
108	Sinorhizobium meliloti strain 1021 bioS and bdhA gene transcriptions are both affected by biotin available in defined medium. , 0, .		1

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109	Growth and nodulation competitiveness of poly(3-hydroxybutyrate) metabolism mutants of <i>Sinorhizobium meliloti</i> and effects of exogenous biotin. <i>Chinese Journal of Agricultural Biotechnology</i> , 2004, 1, 93-98.	0.1	0
110	Impacts on International Research Collaborations from DSI/ABS Uncertainty. <i>Trends in Biotechnology</i> , 2021, 39, 430-433.	4.9	0
111	<i>Open Resource Metagenomics.</i> , 2013, , 1-3.		0
112	<i>Stable Isotope Probing and Metagenomics.</i> , 0, , 97-114.		0
113	<i>Open Resource Metagenomics.</i> , 2015, , 573-575.		0
114	Functional Analysis of Genes of Unknown Functions in <i>Sinorhizobium meliloti</i> 1021. , 2005, , 115-118.		0
115	Functional Genomic Analysis of the SDR Family in <i>Sinorhizobium meliloti</i> . , 2005, , 129-130.		0
116	Further Investigation of the Roles of Poly-3-Hydroxybutyrate (PHB) and Glycogen in <i>Sinorhizobium meliloti</i> - <i>Medicago SP.</i> <i>Symbiosis.</i> , 2005, , 311-312.		0
117	Title is missing!. , 2020, 15, e0218302.		0
118	Title is missing!. , 2020, 15, e0218302.		0
119	Title is missing!. , 2020, 15, e0218302.		0
120	Title is missing!. , 2020, 15, e0218302.		0
121	Title is missing!. , 2020, 15, e0218302.		0
122	Title is missing!. , 2020, 15, e0218302.		0