Trevor C Charles

List of Publications by Year in Descending Order

123 papers	5,310 citations	36 h-index	71 g-index
134 ext. papers	6,706 ext. citations	5.2 avg, IF	5.56 L-index

#	Paper	IF	Citations
123	Driving factors influencing the rhizobacteriome community structure of plants adapted to multiple climatic stressors in edaphic savannas. *Science of the Total Environment*, **2021**, 769, 145214	10.2	6
122	Development of Microbiome Biobanks - Challenges and Opportunities. *Trends in Microbiology*, **2021**, 29, 89-92	12.4	12
121	Impacts on International Research Collaborations from DSI/ABS Uncertainty. *Trends in Biotechnology*, **2021**, 39, 430-433	15.1	
120	Genome Sequence of Brevundimonas sp., an Arsenic Resistant Soil Bacterium. *Diversity*, **2021**, 13, 344	2.5	4
119	Sequence polarity between the promoter and the adjacent gene modulates promoter activity. *Plasmid*, **2021**, 117, 102598	3.3	0
118	Metagenome-Assembled Genome Sequences of Five Strains from the (Prairie Vole) Fecal Microbiome. *Microbiology Resource Announcements*, **2020**, 9,	1.3	2
117	Time Series Resolution of the Fish Necrobiome Reveals a Decomposer Succession Involving Toxigenic Bacterial Pathogens. *MSystems*, **2020**, 5,	7.6	5
116	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida. *PLoS ONE*, **2020**, 15, e0218302	3.7	9
115	Isolation and Identification of Endophytic Bacteria from Mycorrhizal Tissues of Terrestrial Orchids from Southern Chile. *Diversity*, **2020**, 12, 55	2.5	12
114	Microbiome definition re-visited: old concepts and new challenges. *Microbiome*, **2020**, 8, 103	16.6	271
113	Unraveling a Tangled Skein: Evolutionary Analysis of the Bacterial Gibberellin Biosynthetic Operon. *MSphere*, **2020**, 5,	5	4
112	Fungal and Bacterial Microbiome Associated with the Rhizosphere of Native Plants from the Atacama Desert. *Microorganisms*, **2020**, 8,	4.9	18
111	Slr4, a newly identified S-layer protein from marine Gammaproteobacteria, is a major biofilm matrix component. *Molecular Microbiology*, **2020**, 114, 979-990	4.1	1
110	Dynamics of microbial populations and diversity in NAPL contaminated peat soil under varying water table conditions. *Environmental Research*, **2020**, 191, 110167	7.9	8
109	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida **2020**, 15, e0218302		
108	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida **2020**, 15, e0218302		
107	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida **2020**, 15, e0218302		

106	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida **2020**, 15, e0218302		
105	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida **2020**, 15, e0218302		
104	Lactic acid containing polymers produced in engineered Sinorhizobium meliloti and Pseudomonas putida **2020**, 15, e0218302		
103	Enhanced Arsenic Tolerance in Inoculated with Arsenic-Resistant and Plant Growth Promoter Microorganisms from a Heavy Metal-Polluted Soil. *Microorganisms*, **2019**, 7,	4.9	17
102	Designer Sinorhizobium meliloti strains and multi-functional vectors enable direct inter-kingdom DNA transfer. *PLoS ONE*, **2019**, 14, e0206781	3.7	12
101	Does a carbonatite deposit influence its surrounding ecosystem?. *Facets*, **2019**, 4, 389-406	2.3	2
100	An engineered GFP fluorescent bacterial biosensor for detecting and quantifying silver and copper ions. *BioMetals*, **2019**, 32, 265-272	3.4	6
99	Developing a System for Function-Based Screening of DNA from the Human Gut Microbiome. *MSystems*, **2018**, 3,	7.6	4
98	Methods for the Isolation of Genes Encoding Novel PHA Metabolism Enzymes from Complex Microbial Communities. *Methods in Molecular Biology*, **2017**, 1539, 237-248	1.4	1
97	A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, **2017**, 551, 457-463	50.4	1076
96	Endophytic Phytohormones and Their Role in Plant Growth Promotion **2017**, 89-105		18
95	Metagenomic Cosmid Libraries Suitable for Functional Screening in Proteobacteria **2017**, 1-11		1
94	Synthesis and Physical Properties of Polyhydroxyalkanoate Polymers with Different Monomer Compositions by Recombinant Pseudomonas putida LS46 Expressing a Novel PHA SYNTHASE (PhaC116) Enzyme. *Applied Sciences (Switzerland)*, **2017**, 7, 242	2.6	35
93	The Completed PacBio Single-Molecule Real-Time Sequence of Strain OB3b Reveals the Presence of a Third Large Plasmid. *Genome Announcements*, **2017**, 5,		3
92	Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella. *Nature Communications*, **2017**, 8, 521	17.4	27
91	Transcriptome Analysis of Polyhydroxybutyrate Cycle Mutants Reveals Discrete Loci Connecting Nitrogen Utilization and Carbon Storage in. *MSystems*, **2017**, 2,	7.6	10
90	Elucidation of gibberellin biosynthesis in bacteria reveals convergent evolution. *Nature Chemical Biology*, **2017**, 13, 69-74	11.7	68
89	Functional metagenomics reveals novel β-galactosidases not predictable from gene sequences. *PLoS ONE*, **2017**, 12, e0172545	3.7	29

88	Engineering of Escherichia coli for direct and modulated biosynthesis of poly(3-hydroxybutyrate-co-3-hydroxyvalerate) copolymer using unrelated carbon sources. *Scientific Reports*, **2016**, 6, 36470	4.9	18
87	Novel polyhydroxyalkanoate copolymers produced in Pseudomonas putida by metagenomic polyhydroxyalkanoate synthases. *Applied Microbiology and Biotechnology*, **2016**, 100, 7611-27	5.7	12
86	An analysis of the validity and utility of the proximon proposition. *Functional and Integrative Genomics*, **2016**, 16, 215-20	3.8	2
85	Genome-engineered Sinorhizobium meliloti for the production of poly(lactic-co-3-hydroxybutyric) acid copolymer. *Canadian Journal of Microbiology*, **2016**, 62, 130-8	3.2	10
84	Metagenomic Approaches to Identify Novel Organisms from the Soil Environment in a Classroom Setting. *Journal of Microbiology and Biology Education*, **2016**, 17, 423-429	1.3	2
83	Strong spurious transcription likely contributes to DNA insert bias in typical metagenomic clone libraries. *Microbiome*, **2015**, 3, 22	16.6	14
82	Current and future resources for functional metagenomics. *Frontiers in Microbiology*, **2015**, 6, 1196	5.7	81
81	A bioinformatics approach to the determination of genes involved in endophytic behavior in Burkholderia spp. *Journal of Theoretical Biology*, **2014**, 343, 193-8	2.3	97
80	Amelioration of high salinity stress damage by plant growth-promoting bacterial endophytes that contain ACC deaminase. *Plant Physiology and Biochemistry*, **2014**, 80, 160-7	5.4	336
79	Versatile broad-host-range cosmids for construction of high quality metagenomic libraries. *Journal of Microbiological Methods*, **2014**, 99, 27-34	2.8	37
78	Evaluation of a pooled strategy for high-throughput sequencing of cosmid clones from metagenomic libraries. *PLoS ONE*, **2014**, 9, e98968	3.7	12
77	Multisubstrate isotope labeling and metagenomic analysis of active soil bacterial communities. *MBio*, **2014**, 5, e01157-14	7.8	89
76	MetaProx: the database of metagenomic proximons. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014,	5	6
75	Members of the Sinorhizobium meliloti ChvI regulon identified by a DNA binding screen. *BMC Microbiology*, **2013**, 13, 132	4.5	11
74	Meeting report: 1st international functional metagenomics workshop may 7-8, 2012, st. Jacobs, ontario, Canada. *Standards in Genomic Sciences*, **2013**, 8, 106-11		2
73	Delay of flower senescence by bacterial endophytes expressing 1-aminocyclopropane-1-carboxylate deaminase. *Journal of Applied Microbiology*, **2012**, 113, 1139-44	4.7	102
72	Nonlinear electrophoresis for purification of soil DNA for metagenomics. *Journal of Microbiological Methods*, **2012**, 88, 35-40	2.8	28
71	Isolation and characterization of new plant growth-promoting bacterial endophytes. *Applied Soil Ecology*, **2012**, 61, 217-224	5	218

70	Site-specific bacterial chromosome engineering: ΦC31 integrase mediated cassette exchange (IMCE). *Journal of Visualized Experiments*, **2012**,	1.6	9
69	The fluorescence theatre: a cost-effective device using theatre gels for fluorescent protein and dye screening. *Canadian Journal of Microbiology*, **2011**, 57, 339-42	3.2	3
68	ACC deaminase activity in avirulent Agrobacterium tumefaciens D3. *Canadian Journal of Microbiology*, **2011**, 57, 278-86	3.2	33
67	Open resource metagenomics: a model for sharing metagenomic libraries. *Standards in Genomic Sciences*, **2011**, 5, 203-10		16
66	Harvesting of novel polyhydroxyalkanaote (PHA) synthase encoding genes from a soil metagenome library using phenotypic screening. *FEMS Microbiology Letters*, **2011**, 321, 150-6	2.9	29
65	ACC deaminase increases the Agrobacterium tumefaciens-mediated transformation frequency of commercial canola cultivars. *FEMS Microbiology Letters*, **2010**, 307, 185-90	2.9	17
64	Identification and characterization of new LuxR/LuxI-type quorum sensing systems from metagenomic libraries. *Environmental Microbiology*, **2010**, 12, 105-17	5.2	46
63	Methods for the isolation of genes encoding novel PHB cycle enzymes from complex microbial communities. *Methods in Molecular Biology*, **2010**, 668, 235-46	1.4	4
62	Sinorhizobium meliloti 1021 loss-of-function deletion mutation in chvI and its phenotypic characteristics. *Molecular Plant-Microbe Interactions*, **2010**, 23, 153-60	3.6	28
61	Identification and characterization of the intracellular poly-3-hydroxybutyrate depolymerase enzyme PhaZ of Sinorhizobium meliloti. *BMC Microbiology*, **2010**, 10, 92	4.5	12
60	Evaluation of Bacterial Community Structure and Its Influence on Sulfide Oxidation in a Bio-Leaching Environment. *Geomicrobiology Journal*, **2009**, 26, 44-54	2.5	2
59	The class IId bacteriocin thuricin-17 increases plant growth. *Planta*, **2009**, 229, 747-55	4.7	66
58	1-aminocyclopropane-1-carboxylate (ACC) deaminase genes in rhizobia from southern Saskatchewan. *Microbial Ecology*, **2009**, 57, 423-36	4.4	143
57	Null mutations in Sinorhizobium meliloti exoS and chvI demonstrate the importance of this two-component regulatory system for symbiosis. *Molecular Microbiology*, **2009**, 74, 1223-37	4.1	41
56	Mutational analysis of the Sinorhizobium meliloti short-chain dehydrogenase/reductase family reveals substantial contribution to symbiosis and catabolic diversity. *Molecular Plant-Microbe Interactions*, **2008**, 21, 979-87	3.6	23
55	Influence of the poly-3-hydroxybutyrate (PHB) granule-associated proteins (PhaP1 and PhaP2) on PHB accumulation and symbiotic nitrogen fixation in Sinorhizobium meliloti Rm1021. *Journal of Bacteriology*, **2007**, 189, 9050-6	3.5	36
54	Presence of a novel 16S-23S rRNA gene intergenic spacer insert in Bradyrhizobium canariense strains. *FEMS Microbiology Letters*, **2007**, 269, 207-12	2.9	7
53	Roles of poly-3-hydroxybutyrate (PHB) and glycogen in symbiosis of Sinorhizobium meliloti with Medicago sp. *Microbiology (United Kingdom)*, **2007**, 153, 388-398	2.9	50

52	ACC deaminase from plant growth-promoting bacteria affects crown gall development. *Canadian Journal of Microbiology*, **2007**, 53, 1291-9	3.2	57
51	The role of PHB metabolism in the symbiosis of rhizobia with legumes. *Applied Microbiology and Biotechnology*, **2006**, 71, 377-86	5.7	115
50	Isolation of poly-3-hydroxybutyrate metabolism genes from complex microbial communities by phenotypic complementation of bacterial mutants. *Applied and Environmental Microbiology*, **2006**, 72, 384-91	4.8	57
49	Effects of nitrogen and phosphorus limitation on the activated sludge biomass in a kraft mill biotreatment system. *Water Environment Research*, **2006**, 78, 2303-10	2.8	12
48	A novel bacteriocin, thuricin 17, produced by plant growth promoting rhizobacteria strain Bacillus thuringiensis NEB17: isolation and classification. *Journal of Applied Microbiology*, **2006**, 100, 545-54	4.7	107
47	Comparison of the symbiotic and competition phenotypes of Sinorhizobium meliloti PHB synthesis and degradation pathway mutants. *Canadian Journal of Microbiology*, **2005**, 51, 599-604	3.2	27
46	Characterization of bdhA, encoding the enzyme D-3-hydroxybutyrate dehydrogenase, from Sinorhizobium sp. strain NGR234. *FEMS Microbiology Letters*, **2005**, 242, 87-94	2.9	8
45	NodMutDB: a database for genes and mutants involved in symbiosis. *Bioinformatics*, **2005**, 21, 2927-9	7.2	20
44	Functional Analysis of Genes of Unknown Functions in Sinorhizobium meliloti 1021 **2005**, 115-118		
43	Functional Genomic Analysis of the SDR Family in Sinorhizobium meliloti **2005**, 129-130		
42	Further Investigation of the Roles of Poly-3-Hydroxybutyrate (PHB) and Glycogen in Sinorhizobium mellioti-Medicago SP. Symbiosis **2005**, 311-312		
41	Expression of an exogenous 1-aminocyclopropane-1-carboxylate deaminase gene in Sinorhizobium meliloti increases its ability to nodulate alfalfa. *Applied and Environmental Microbiology*, **2004**, 70, 5891-7	4.8	154
40	Heterologous complementation of the exopolysaccharide synthesis and carbon utilization phenotypes of Sinorhizobium meliloti Rm1021 polyhydroxyalkanoate synthesis mutants. *FEMS Microbiology Letters*, **2004**, 239, 277-83	2.9	37
39	Growth and nodulation competitiveness of poly(3-hydroxybutyrate) metabolism mutants of Sinorhizobium meliloti and effects of exogenous biotin. *Chinese Journal of Agricultural Biotechnology*, **2004**, 1, 93-98		
38	Application of crossover-PCR-mediated deletion-insertion mutagenesis to analysis of the bdhA-xdhA2-xdhB2 mixed-function operon of Sinorhizobium meliloti. *Archives of Microbiology*, **2003**, 179, 301-4	3	21
37	Purification and characterization of homodimeric methylmalonyl-CoA mutase from Sinorhizobium meliloti. *Archives of Microbiology*, **2003**, 180, 151-4	3	13
36	Low temperature tolerant Bradyrhizobium japonicum strains allowing improved nodulation and nitrogen fixation of soybean in a short season (cool spring) area. *European Journal of Agronomy*, **2003**, 19, 205-213	5	42
35	Effect of experimental contamination with the explosive hexahydro-1,3,5-trinitro-1,3,5-triazine on soil bacterial communities. *FEMS Microbiology Ecology*, **2003**, 43, 255-62	4.3	15

34	Low Temperature‐Tolerant Bradyrhizobium japonicum Strains Allowing Improved Soybean Yield in Short-Season Areas. *Agronomy Journal*, **2002**, 94, 870-875	2.2	7
33	Identification of an acetoacetyl coenzyme A synthetase-dependent pathway for utilization of L-(+)-3-hydroxybutyrate in Sinorhizobium meliloti. *Journal of Bacteriology*, **2002**, 184, 1571-7	3.5	23
32	A global pH sensor: Agrobacterium sensor protein ChvG regulates acid-inducible genes on its two chromosomes and Ti plasmid. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 12369-74	11.5	90
31	Bradyrhizobium japonicum mutants allowing improved nodulation and nitrogen fixation of field-grown soybean in a short season area. *Journal of Agricultural Science*, **2002**, 138, 293-300	1	15
30	The effect of temperature and genistein concentration on lipo-chitooligosaccharide (LCO) production by wild-type and mutant strains of Bradyrhizobium japonicum. *Soil Biology and Biochemistry*, **2002**, 34, 1175-1180	7.5	24
29	Co-inoculation dose and root zone temperature for plant growth promoting rhizobacteria on soybean [Glycine max (L.) Merr] grown in soil-less media. *Soil Biology and Biochemistry*, **2002**, 34, 1953-1957	7.5	49
28	Bradyrhizobium japonicum Mutants Allowing Improved Soybean Yield in Short Season Areas with Cool Spring Soil Temperatures. *Crop Science*, **2002**, 42, 1186-1190	2.4	3
27	Low Temperature‐Tolerant Bradyrhizobium japonicum Strains Allowing Improved Soybean Yield in Short-Season Areas. *Agronomy Journal*, **2002**, 94, 870	2.2	5
26	Genetic transformation of Trametes versicolor to phleomycin resistance with the dominant selectable marker shble. *Applied Microbiology and Biotechnology*, **2001**, 56, 201-4	5.7	22
25	Cellobiose dehydrogenase is essential for wood invasion and nonessential for kraft pulp delignification by Trametes versicolor. *Enzyme and Microbial Technology*, **2001**, 29, 478-489	3.8	61
24	The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis. *Journal of Bacteriology*, **2001**, 183, 36-45	3.5	36
23	Bradyrhizobium japonicum mutants with enhanced sensitivity to genistein resulting in altered nod gene regulation. *Molecular Plant-Microbe Interactions*, **2001**, 14, 1404-10	3.6	7
22	Sinorhizobium meliloti strain 1021 bioS and bdhA gene transcriptions are both affected by biotin available in defined medium. *FEMS Microbiology Letters*, **2000**, 182, 41-4	2.9	14
21	An ACC deaminase minus mutant of Enterobacter cloacae UW4 no longer promotes root elongation. *Current Microbiology*, **2000**, 41, 101-5	2.4	184
20	Requirement for the enzymes acetoacetyl coenzyme A synthetase and poly-3-hydroxybutyrate (PHB) synthase for growth of Sinorhizobium meliloti on PHB cycle intermediates. *Journal of Bacteriology*, **2000**, 182, 2113-8	3.5	39
19	Methylmalonyl-CoA mutase encoding gene of Sinorhizobium meliloti. *Gene*, **1999**, 226, 121-7	3.8	22
18	Cloning and sequencing of a gene encoding cellobiose dehydrogenase from Trametes versicolor. *Gene*, **1998**, 210, 211-9	3.8	45
17	Discrete regions of the sensor protein virA determine the strain-specific ability of Agrobacterium to agroinfect maize. *Molecular Plant-Microbe Interactions*, **1997**, 10, 221-7	3.6	24

16	Megaplasmid and chromosomal loci for the PHB degradation pathway in Rhizobium (Sinorhizobium) meliloti. *Genetics*, **1997**, 146, 1211-20	4	46
15	Inhibition of the expression of Bradyrhizobium japonicum nod genes at low temperatures. *Soil Biology and Biochemistry*, **1996**, 28, 1579-1583	7.5	34
14	A chromosomally encoded two-component sensory transduction system is required for virulence of Agrobacterium tumefaciens. *Journal of Bacteriology*, **1993**, 175, 6614-25	3.5	156
13	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, 9939-43	11.5	65
12	Two-component sensory transduction systems in phytobacteria. *Annual Review of Phytopathology*, **1992**, 30, 463-84	10.8	47
11	The ntrA gene of Agrobacterium tumefaciens: identification, cloning, and phenotype of a site-directed mutant. *Journal of Bacteriology*, **1992**, 174, 2720-3	3.5	12
10	ndvF, a novel locus located on megaplasmid pRmeSU47b (pEXO) of Rhizobium meliloti, is required for normal nodule development. *Journal of Bacteriology*, **1991**, 173, 3981-92	3.5	32
9	Genetic map of Rhizobium meliloti megaplasmid pRmeSU47b. *Journal of Bacteriology*, **1990**, 172, 2469-76	3.5	57
8	Lactose utilization and enzymes encoded by megaplasmids in Rhizobium meliloti SU47: implications for population studies. *Journal of General Microbiology*, **1990**, 136, 2497-2502		17
7	Analysis of C4-dicarboxylate transport genes in Rhizobium meliloti. *Molecular Microbiology*, **1989**, 3, 813-23	4.2	123
6	Ti Plasmid and Chromosomally Encoded Two-Component Systems Important in Plant Cell Transformation by Agrobacterium Species367-385		30
5	Lactic Acid Containing Polymers Produced in EngineeredSinorhizobium melilotiandPseudomonas putida		1
4	Sinorhizobium meliloti strain 1021 bioS and bdhA gene transcriptions are both affected by biotin available in defined medium		1
3	Development of a GFP Fluorescent Bacterial Biosensor for the Detection and Quantification of Silver and Copper Ions		1
2	Stable Isotope Probing and Metagenomics97-114		
1	Alcov: Estimating Variant of Concern Abundance from SARS-CoV-2 Wastewater Sequencing Data		2