

# Wayne G Reeve

## List of Publications by Year in descending order

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72  
papers

1,317  
citations

430874

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78  
docs citations

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times ranked

1353  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microvirga lupini sp. nov., Microvirga lotononidis sp. nov. and Microvirga zambiensis sp. nov. are alphaproteobacterial root-nodule bacteria that specifically nodulate and fix nitrogen with geographically and taxonomically separate legume hosts. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2579-2588.	1.7	174
2	Constructs for insertional mutagenesis, transcriptional signal localization and gene regulation studies in root nodule and other bacteria. Microbiology (United Kingdom), 1999, 145, 1307-1316.	1.8	114
3	Complete genome sequence of the Medicago microsymbiont Ensifer (Sinorhizobium) medicae strain WSM419. Standards in Genomic Sciences, 2010, 2, 77-86.	1.5	100
4	ActP controls copper homeostasis in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> and <i>Sinorhizobium meliloti</i> preventing low pH-induced copper toxicity. Molecular Microbiology, 2002, 43, 981-991.	2.5	91
5	Symbiotic <i>Burkholderia</i> Species Show Diverse Arrangements of <i>nif</i> and <i>nod</i> Genes and Lack Typical High-Affinity Cytochrome <i>cbb3</i> Oxidase Genes. Molecular Plant-Microbe Interactions, 2016, 29, 609-619.	2.6	62
6	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2304, an effective microsymbiont of the South American clover <i>Trifolium polymorphum</i> . Standards in Genomic Sciences, 2010, 2, 66-76.	1.5	60
7	A Genomic Encyclopedia of the Root Nodule Bacteria: assessing genetic diversity through a systematic biogeographic survey. Standards in Genomic Sciences, 2015, 10, 14.	1.5	55
8	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers. Standards in Genomic Sciences, 2010, 2, 347-356.	1.5	53
9	The transcriptional regulator gene <i>phrR</i> in <i>Sinorhizobium meliloti</i> WSM419 is regulated by low pH and other stresses. Microbiology (United Kingdom), 1998, 144, 3335-3342.	1.8	49
10	Nodule morphology, symbiotic specificity and association with unusual rhizobia are distinguishing features of the genus <i>Listia</i> within the southern African crotalarioid clade <i>Lotononis</i> s.l.. Annals of Botany, 2013, 112, 1-15.	2.9	47
11	Ribosomal protein biomarkers provide root nodule bacterial identification by MALDI-TOF MS. Applied Microbiology and Biotechnology, 2015, 99, 5547-5562.	3.6	47
12	The <i>Sinorhizobium medicae</i> WSM419 <i>lpiA</i> gene is transcriptionally activated by <i>FsrR</i> and required to enhance survival in lethal acid conditions. Microbiology (United Kingdom), 2006, 152, 3049-3059.	1.8	42
13	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. Scientific Reports, 2015, 5, 16825.	3.3	33
14	Genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1689, the microsymbiont of the one flowered clover <i>Trifolium uniflorum</i> . Standards in Genomic Sciences, 2013, 9, 527-539.	1.5	27
15	Root nodule bacteria isolated from South African <i>Lotononis bainesii</i> , <i>L. listii</i> and <i>L. solitudinis</i> are species of <i>Methylobacterium</i> that are unable to utilize methanol. Archives of Microbiology, 2009, 191, 311-318.	2.2	24
16	Genome sequence of the Lotus spp. microsymbiont <i>Mesorhizobium loti</i> strain R7A. Standards in Genomic Sciences, 2014, 9, 6.	1.5	22
17	Probing for pH-Regulated Proteins in <i>Sinorhizobium medicae</i> Using Proteomic Analysis. Journal of Molecular Microbiology and Biotechnology, 2004, 7, 140-147.	1.0	19
18	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> Strain CC1192, an Efficient Nitrogen-Fixing Microsymbiont of <i>Cicer arietinum</i> . Genome Announcements, 2016, 4, .	0.8	19

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19	Novel heavy metal resistance gene clusters are present in the genome of <i>Cupriavidus neocaledonicus</i> STM 6070, a new species of <i>Mimosa pudica</i> microsymbiont isolated from heavy-metal-rich mining site soil. <i>BMC Genomics</i> , 2020, 21, 214.	2.8	18
20	Complete genome sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> type strain (WSM1271T). <i>Standards in Genomic Sciences</i> , 2013, 9, 462-472.	1.5	17
21	Genome sequence of <i>Ensifer meliloti</i> strain WSM1022; a highly effective microsymbiont of the model legume <i>Medicago truncatula</i> A17. <i>Standards in Genomic Sciences</i> , 2013, 9, 315-324.	1.5	13
22	<i>Sinorhizobium medicae</i> genes whose regulation involves the ActS and/or ActR signal transduction proteins. <i>FEMS Microbiology Letters</i> , 2004, 236, 21-31.	1.8	13
23	Complete genome sequence of <i>Mesorhizobium opportunistum</i> type strain WSM2075T. <i>Standards in Genomic Sciences</i> , 2013, 9, 294-303.	1.5	12
24	Genome sequence of <i>Ensifer</i> sp. TW10; a <i>Tephrosia wallichii</i> (Biyani) microsymbiont native to the Indian Thar Desert. <i>Standards in Genomic Sciences</i> , 2013, 9, 304-314.	1.5	12
25	Genome sequence of the <i>Lotus corniculatus</i> microsymbiont <i>Mesorhizobium loti</i> strain R88B. <i>Standards in Genomic Sciences</i> , 2014, 9, 3.	1.5	12
26	Uracil DNA glycosylase (UDG) activities in <i>Bradyrhizobium diazoefficiens</i> : characterization of a new class of UDG with broad substrate specificity. <i>Nucleic Acids Research</i> , 2017, 45, 5863-5876.	14.5	12
27	Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013, 9, 410-419.	1.5	11
28	High-quality permanent draft genome sequence of the <i>Bradyrhizobium elkanii</i> type strain USDA 76T, isolated from <i>Glycine max</i> (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017, 12, 26.	1.5	11
29	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , 2013, 9, 243-253.	1.5	10
30	Genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia sprentiae</i> strain WSM5005T. <i>Standards in Genomic Sciences</i> , 2013, 9, 385-394.	1.5	9
31	High-quality permanent draft genome sequence of <i>Rhizobium sullae</i> strain WSM1592; a <i>Hedysarum coronarium</i> microsymbiont from Sassari, Italy. <i>Standards in Genomic Sciences</i> , 2015, 10, 44.	1.5	9
32	A helicase gene ( <i>helO</i> ) in <i>Rhizobium meliloti</i> WSM419. <i>FEMS Microbiology Letters</i> , 2006, 153, 43-49.	1.8	7
33	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557T. <i>Standards in Genomic Sciences</i> , 2013, 9, 540-550.	1.5	7
34	High-quality permanent draft genome sequence of <i>Ensifer</i> sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (Khejri) native to the Thar Desert of India. <i>Standards in Genomic Sciences</i> , 2016, 11, 43.	1.5	7
35	Genome sequence of <i>Burkholderia mimosarum</i> strain LMG 23256T, a <i>Mimosa pigra</i> microsymbiont from Anso, Taiwan. <i>Standards in Genomic Sciences</i> , 2013, 9, 484-494.	1.5	6
36	Genome sequence of <i>Ensifer arboris</i> strain LMG 14919T; a microsymbiont of the legume <i>Prosopis chilensis</i> growing in Kostj, Sudan. <i>Standards in Genomic Sciences</i> , 2013, 9, 473-483.	1.5	6

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37	Genome sequence of <i>Microvirga lupini</i> strain LUT6T, a novel <i>Lupinus albus</i> alphaproteobacterial microsymbiont from Texas. <i>Standards in Genomic Sciences</i> , 2014, 9, 1159-1167.	1.5	6
38	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Cupriavidus</i> sp. strain UYPR2.512. <i>Standards in Genomic Sciences</i> , 2015, 10, 13.	1.5	6
39	High-quality permanent draft genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia</i> sp. strain WSM4176. <i>Standards in Genomic Sciences</i> , 2015, 10, 79.	1.5	5
40	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Tv2a.2, a microsymbiont of <i>Tachigali versicolor</i> discovered in Barro Colorado Island of Panama. <i>Standards in Genomic Sciences</i> , 2015, 10, 27.	1.5	5
41	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> Strain WSM1284, an Efficient Nitrogen-Fixing Microsymbiont of the Pasture Legume <i>Biserrula pelecinus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
42	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI565.. <i>Standards in Genomic Sciences</i> , 2013, 9, 220-231.	1.5	4
43	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. <i>Standards in Genomic Sciences</i> , 2013, 9, 264-272.	1.5	4
44	High-quality permanent draft genome sequence of <i>Ensifer meliloti</i> strain 4H41, an effective salt- and drought-tolerant microsymbiont of <i>Phaseolus vulgaris</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 34.	1.5	4
45	Complete Genome Sequences of <i>Trifolium</i> spp. Inoculant Strains <i>Rhizobium leguminosarum</i> sv. <i>trifolii</i> TA1 and CC275e: Resources for Genomic Study of the <i>Rhizobium</i> - <i>Trifolium</i> Symbiosis. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 131-134.	2.6	4
46	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI943.. <i>Standards in Genomic Sciences</i> , 2013, 9, 232-242.	1.5	3
47	Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. <i>Standards in Genomic Sciences</i> , 2013, 9, 283-293.	1.5	3
48	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2230 from Karjini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2013, 9, 551-561.	1.5	3
49	Genome sequence of the dark pink pigmented <i>Listia bainesii</i> microsymbiont <i>Methylobacterium</i> sp. WSM2598. <i>Standards in Genomic Sciences</i> , 2014, 9, 5.	1.5	3
50	Genome sequence of the <i>Medicago</i> -nodulating <i>Ensifer meliloti</i> commercial inoculant strain RRI128. <i>Standards in Genomic Sciences</i> , 2014, 9, 602-613.	1.5	3
51	High-quality permanent draft genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> strain GB30; an effective microsymbiont of <i>Pisum sativum</i> growing in Poland. <i>Standards in Genomic Sciences</i> , 2015, 10, 36.	1.5	3
52	Genome sequence of <i>Bradyrhizobium</i> sp. WSM1253; a microsymbiont of <i>Ornithopus compressus</i> from the Greek Island of Sifnos. <i>Standards in Genomic Sciences</i> , 2015, 10, 113.	1.5	3
53	Genome sequence of <i>Ensifer medicae</i> strain WSM1115; an acid-tolerant <i>Medicago</i> -nodulating microsymbiont from Samothraki, Greece. <i>Standards in Genomic Sciences</i> , 2013, 9, 514-526.	1.5	2
54	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2232 from Karjini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2013, 9, 1168-1180.	1.5	2

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55	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Burkholderia</i> sp. strain UYPR1.413. <i>Standards in Genomic Sciences</i> , 2015, 10, 31.	1.5	2
56	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Ai1a-2; a microsymbiont of <i>Andira inermis</i> discovered in Costa Rica. <i>Standards in Genomic Sciences</i> , 2015, 10, 33.	1.5	2
57	High-quality permanent draft genome sequence of the <i>Mimosa asperata</i> - nodulating <i>Cupriavidus</i> sp. strain AMP6. <i>Standards in Genomic Sciences</i> , 2015, 10, 80.	1.5	2
58	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Th.b2, a microsymbiont of <i>Amphicarpaea bracteata</i> collected in Johnson City, New York. <i>Standards in Genomic Sciences</i> , 2015, 10, 24.	1.5	2
59	High-Quality draft genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain CJ3Sym. <i>Standards in Genomic Sciences</i> , 2015, 10, 54.	1.5	2
60	High-quality draft genome sequence of <i>Rhizobium mesoamericanum</i> strain STM6155, a <i>Mimosa pudica</i> microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , 2017, 12, 7.	1.5	2
61	The Genome of the Acid Soil-Adapted Strain <i>Rhizobium favelukesii</i> OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host. <i>Frontiers in Microbiology</i> , 2022, 13, 735911.	3.5	2
62	Genome sequence of <i>Ensifer medicae</i> strain WSM1369; an effective microsymbiont of the annual legume <i>Medicago sphaerocarpos</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 420-430.	1.5	1
63	High-quality permanent draft genome sequence of the <i>Lebeckia</i> - nodulating <i>Burkholderia dilworthii</i> strain WSM3556T. <i>Standards in Genomic Sciences</i> , 2015, 10, 64.	1.5	1
64	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. strain WSM1743 - an effective microsymbiont of an <i>Indigofera</i> sp. growing in Australia. <i>Standards in Genomic Sciences</i> , 2015, 10, 87.	1.5	1
65	High-quality permanent draft genome sequence of <i>Ensifer medicae</i> strain WSM244, a microsymbiont isolated from <i>Medicago polymorpha</i> growing in alkaline soil. <i>Standards in Genomic Sciences</i> , 2015, 10, 126.	1.5	1
66	Evolution of a multi-step phosphorelay signal transduction system in <i>Ensifer</i> : recruitment of the sigma factor RpoN and a novel enhancer-binding protein triggers acid-activated gene expression. <i>Molecular Microbiology</i> , 2017, 103, 829-844.	2.5	1
67	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013, 9, 254-263.	1.5	0
68	Genome sequence of <i>Ensifer medicae</i> Di28; an effective N <sub>2</sub> -fixing microsymbiont of <i>Medicago murex</i> and <i>M. polymorpha</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 4.	1.5	0
69	High-quality draft genome sequence of <i>Ensifer meliloti</i> Mlalz-1, a microsymbiont of <i>Medicago laciniata</i> (L.) miller collected in Lanzarote, Canary Islands, Spain. <i>Standards in Genomic Sciences</i> , 2017, 12, 58.	1.5	0
70	The complete mitochondrial genome of the vulnerable Australian crest-tailed mulgara ( <i>Dasyercus</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.4	0
71	The complete mitochondrial genome of the Australian Common Rock Rat, <i>Zyzomys argurus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2486-2488.	0.4	0
72	The complete mitochondrial genome of the Australian ghost bat <i>Macroderma gigas</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2630-2631.	0.4	0