

Ravi P Tiwari

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	The model legume <i>Medicago truncatula</i> A17 is poorly matched for N ₂ fixation with the sequenced microsymbiont <i>Sinorhizobium meliloti</i> 1021. <i>New Phytologist</i> , 2008, 179, 62-66.	3.5	115
2	Constructs for insertional mutagenesis, transcriptional signal localization and gene regulation studies in root nodule and other bacteria. <i>Microbiology (United Kingdom)</i> , 1999, 145, 1307-1316.	0.7	114
3	In situ lateral transfer of symbiosis islands results in rapid evolution of diverse competitive strains of mesorhizobia suboptimal in symbiotic nitrogen fixation on the pasture legume <i>Biserrula pelecinus</i> L.. <i>Environmental Microbiology</i> , 2007, 9, 2496-2511.	1.8	109
4	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer (Sinorhizobium) medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010, 2, 77-86.	1.5	100
5	ActP controls copper homeostasis in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> and <i>Sinorhizobium meliloti</i> preventing low pH-induced copper toxicity. <i>Molecular Microbiology</i> , 2002, 43, 981-991.	1.2	91
6	Rapid In Situ Evolution of Nodulating Strains for <i>Biserrula pelecinus</i> L. through Lateral Transfer of a Symbiosis Island from the Original Mesorhizobial Inoculant. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7365-7367.	1.4	83
7	Colonization of <i>Phaseolus vulgaris</i> nodules by <i>Agrobacterium</i> -like strains. <i>Canadian Journal of Microbiology</i> , 2005, 51, 105-111.	0.8	66
8	<i>Mesorhizobium australicum</i> sp. nov. and <i>Mesorhizobium opportunistum</i> sp. nov., isolated from <i>Biserrula pelecinus</i> L. in Australia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2140-2147.	0.8	65
9	An Essential Role for actA in Acid Tolerance of <i>Rhizobium Meliloti</i> . <i>Microbiology (United Kingdom)</i> , 1996, 142, 601-610.	0.7	62
10	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> .. <i>Standards in Genomic Sciences</i> , 2010, 2, 66-76.	1.5	60
11	Nodulation of legumes from the Thar desert of India and molecular characterization of their rhizobia. <i>Plant and Soil</i> , 2012, 357, 227-243.	1.8	57
12	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers.. <i>Standards in Genomic Sciences</i> , 2010, 2, 347-356.	1.5	53
13	The transcriptional regulator gene <i>phrR</i> in <i>Sinorhizobium meliloti</i> WSM419 is regulated by low pH and other stresses. <i>Microbiology (United Kingdom)</i> , 1998, 144, 3335-3342.	0.7	49
14	The <i>Sinorhizobium medicae</i> WSM419 <i>IpiA</i> gene is transcriptionally activated by <i>FsrR</i> and required to enhance survival in lethal acid conditions. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3049-3059.	0.7	42
15	Regulation of exopolysaccharide production in <i>Rhizobium leguminosarum</i> biovar <i>viciae</i> WSM710 involves <i>exoR</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 1951-1958.	0.7	40
16	<i>Mesorhizobium ciceri</i> biovar <i>biserrulae</i> , a novel biovar nodulating the pasture legume <i>Biserrula pelecinus</i> L.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 1041-1045.	0.8	40
17	<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.	0.7	26
18	Competitiveness and symbiotic effectiveness of a <i>R. gallicum</i> strain isolated from root nodules of <i>Phaseolus vulgaris</i> . <i>European Journal of Agronomy</i> , 2005, 22, 209-216.	1.9	25

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19	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. <i>Archives of Microbiology</i> , 2009, 191, 311-318.	1.0	24
20	Probing for pH-Regulated Proteins in <i>Sinorhizobium medicae</i> Using Proteomic Analysis. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 7, 140-147.	1.0	19
21	Probing for pH-Regulated Genes in <i>Sinorhizobium medicae</i> Using Transcriptional Analysis. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 7, 133-139.	1.0	17
22	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
23	<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.	0.7	13
24	Complete genome sequence of <i>Mesorhizobium opportunistum</i> type strain WSM2075T. <i>Standards in Genomic Sciences</i> , 2013, 9, 294-303.	1.5	12
25	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
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.	6.5	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	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
29	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
30	A helicase gene (helO) in <i>Rhizobium meliloti</i> WSM419. <i>FEMS Microbiology Letters</i> , 2006, 153, 43-49.	0.7	7
31	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
32	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
33	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
34	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
35	Genome sequence of the lupin-nodulating <i>Bradyrhizobium</i> sp. strain WSM1417. <i>Standards in Genomic Sciences</i> , 2013, 9, 273-282.	1.5	3
36	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

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37	Biserrula pelecinus L. is a promising forage legume for the central Ethiopian highlands. Grass and Forage Science, 2021, 76, 105-115.	1.2	2
38	High-quality permanent draft genome sequence of Bradyrhizobium sp. strain WSM1743 - an effective microsymbiont of an Indigofera sp. growing in Australia. Standards in Genomic Sciences, 2015, 10, 87.	1.5	1
39	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. Molecular Microbiology, 2017, 103, 829-844.	1.2	1
40	Genetic Circuits Involved in the Response of Root Nodule Bacteria to Low pH. Current Plant Science and Biotechnology in Agriculture, 2000, , 475-476.	0.0	1
41	Complete genome sequence of Mesorhizobium australicum type strain (WSM2073T). Standards in Genomic Sciences, 2013, 9, 1-15.	1.5	1
42	Genome sequence of the Ornithopus/Lupinus-nodulating Bradyrhizobium sp. strain WSM471. Standards in Genomic Sciences, 2013, 9, 254-263.	1.5	0