Rekha Seshadri

List of Publications by Year
in descending order

67 papers	10,015 citations	136950 32 h-index	95266 68 g-index
79 all docs	79 docs citations	79 times ranked	12802 citing authors

#	Article	IF	Citations
1	Role of Mobile DNA in the Evolution of Vancomycin-Resistant Enterococcus faecalis. Science, 2003, 299, 2071-2074.	12.6	849
2	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. Nucleic Acids Research, 2019, 47, D666-D677.	14.5	799
3	Genome sequence of the dissimilatory metal ionâ€"reducing bacterium Shewanella oneidensis. Nature Biotechnology, 2002, 20, 1118-1123.	17.5	771
4	Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5. Nature Biotechnology, 2005, 23, 873-878.	17.5	615
5	The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough. Nature Biotechnology, 2004, 22, 554-559.	17.5	559
6	Complete genome sequence of the Q-fever pathogenCoxiellaburnetii. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5455-5460.	7.1	506
7	New insights from uncultivated genomes of the global human gut microbiome. Nature, 2019, 568, 505-510.	27.8	505
8	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
9	Comparative Genomics of Emerging Human Ehrlichiosis Agents. PLoS Genetics, 2006, 2, e21.	3.5	423
10	The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13148-13153.	7.1	422
11	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	17.5	414
12	Genome Sequence of the PCE-Dechlorinating BacteriumDehalococcoides ethenogenes. Science, 2005, 307, 105-108.	12.6	402
13	CAMERA: A Community Resource for Metagenomics. PLoS Biology, 2007, 5, e75.	5.6	344
14	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. Nucleic Acids Research, 2021, 49, D751-D763.	14.5	332
15	Genome Sequence of Aeromonas hydrophila ATCC 7966 T : Jack of All Trades. Journal of Bacteriology, 2006, 188, 8272-8282.	2.2	317
16	Skewed genomic variability in strains of the toxigenic bacterial pathogen, Clostridium perfringens. Genome Research, 2006, 16, 1031-1040.	5.5	281
17	Genomic Insights into Methanotrophy: The Complete Genome Sequence of Methylococcus capsulatus (Bath). PLoS Biology, 2004, 2, e303.	5.6	275
18	Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5646-5651.	7.1	251

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19	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	17.5	222
20	Bacterial Genomics and Pathogen Evolution. Cell, 2006, 124, 703-714.	28.9	122
21	Massive dominance of Epsilonproteobacteria in formation waters from a Canadian oil sands reservoir containing severely biodegraded oil. Environmental Microbiology, 2012, 14, 387-404.	3.8	117
22	Genome Degradation in Brucella ovis Corresponds with Narrowing of Its Host Range and Tissue Tropism. PLoS ONE, 2009, 4, e5519.	2.5	110
23	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. Microbiome, 2020, 8, 22.	11.1	91
24	Complete and Draft Genome Sequences of Six Members of the Aquificales. Journal of Bacteriology, 2009, 191, 1992-1993.	2.2	76
25	IMG-ABC v.5.0: an update to the IMG/Atlas of Biosynthetic Gene Clusters Knowledgebase. Nucleic Acids Research, 2020, 48, D422-D430.	14.5	64
26	Symbiotic Burkholderia Species Show Diverse Arrangements of nif/fix and nod Genes and Lack Typical High-Affinity Cytochrome cbb3 Oxidase Genes. Molecular Plant-Microbe Interactions, 2016, 29, 609-619.	2.6	62
27	DOE JGI Metagenome Workflow. MSystems, 2021, 6, .	3.8	56
28	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
29	Limited Role for Iron Regulation in Coxiella burnetii Pathogenesis. Infection and Immunity, 2008, 76, 2189-2201.	2.2	47
30	Identification and Cloning of Immunodominant Antigens of Coxiella burnetii. Infection and Immunity, 2004, 72, 844-852.	2.2	44
31	Sugar metabolism by Brucellae. Veterinary Microbiology, 2002, 90, 249-261.	1.9	40
32	Differential Expression of Translational Elements by Life Cycle Variants of Coxiella burnetii. Infection and Immunity, 1999, 67, 6026-6033.	2.2	39
33	Characterization of a Stress-Induced Alternate Sigma Factor, RpoS, of Coxiella burnetii and Its Expression during the Development Cycle. Infection and Immunity, 2001, 69, 4874-4883.	2.2	38
34	Metagenomic investigation of the geologically unique <scp>H</scp>ellenic <scp>V</scp>olcanic <scp>A</scp>rc reveals a distinctive ecosystem with unexpected physiology. Environmental Microbiology, 2016, 18, 1122-1136.	3.8	37
35	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. Scientific Reports, 2015, 5, 16825.	3.3	33
36	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. Animal Microbiome, 2019, 1, 15.	3.8	27

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37	A Comparison of Microbial Genome Web Portals. Frontiers in Microbiology, 2019, 10, 208.	3.5	22
38	Genome Analysis of Coxiella burnetii Species: Insights into Pathogenesis and Evolution and Implications for Biodefense. Annals of the New York Academy of Sciences, 2005, 1063, 442-450.	3.8	20
39	Shotgun metagenomic analysis of microbial communities from the Loxahatchee nature preserve in the Florida Everglades. Environmental Microbiomes, 2020, 15, 2.	5.0	20
40	Novel heavy metal resistance gene clusters are present in the genome of Cupriavidus neocaledonicus STM 6070, a new species of Mimosa pudica microsymbiont isolated from heavy-metal-rich mining site soil. BMC Genomics, 2020, 21, 214.	2.8	18
41	High-quality permanent draft genome sequence of the Bradyrhizobium elkanii type strain USDA 76T, isolated from Glycine max (L.) Merr. Standards in Genomic Sciences, 2017, 12, 26.	1.5	11
42	High-quality permanent draft genome sequence of Rhizobium sullae strain WSM1592; a Hedysarum coronarium microsymbiont from Sassari, Italy. Standards in Genomic Sciences, 2015, 10, 44.	1.5	9
43	Bacteria to the rescue. Nature Biotechnology, 2005, 23, 1236-1237.	17.5	7
44	High-quality permanent draft genome sequence of Ensifer sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (Khejri) native to the Thar Desert of India. Standards in Genomic Sciences, 2016, 11, 43.	1.5	7
45	Preliminary Assessment of Genome Differences between the Reference Nine Mile Isolate and Two Human Endocarditis Isolates of Coxiella burnetii. Annals of the New York Academy of Sciences, 2005, 1063, 64-67.	3.8	6
46	Cloning, expression, and purification of Brucella suis outer membrane proteins. Protein Expression and Purification, 2005, 40, 134-141.	1.3	6
47	High-quality permanent draft genome sequence of the Parapiptadenia rigida-nodulating Cupriavidus sp. strain UYPR2.512. Standards in Genomic Sciences, 2015, 10, 13.	1.5	6
48	High-quality permanent draft genome sequence of the Lebeckia ambigua-nodulating Burkholderia sp. strain WSM4176. Standards in Genomic Sciences, 2015, 10, 79.	1.5	5
49	High-quality permanent draft genome sequence of Bradyrhizobium sp. Tv2a.2, a microsymbiont of Tachigali versicolor discovered in Barro Colorado Island of Panama. Standards in Genomic Sciences, 2015, 10, 27.	1.5	5
50	High-quality permanent draft genome sequence of Ensifer meliloti strain 4H41, an effective salt- and drought-tolerant microsymbiont of Phaseolus vulgaris. Standards in Genomic Sciences, 2015, 10, 34.	1.5	4
51	High-quality permanent draft genome sequence of Rhizobium leguminosarum bv. viciae strain GB30; an effective microsymbiont of Pisum sativum growing in Poland. Standards in Genomic Sciences, 2015, 10, 36.	1.5	3
52	Genome sequence of Bradyrhizobium sp. WSM1253; a microsymbiont of Ornithopus compressus from the Greek Island of Sifnos. Standards in Genomic Sciences, 2015, 10, 113.	1.5	3
53	High-quality permanent draft genome sequence of the Parapiptadenia rigida-nodulating Burkholderia sp. strain UYPR1.413. Standards in Genomic Sciences, 2015, 10, 31.	1.5	2
54	High-quality permanent draft genome sequence of Bradyrhizobium sp. Ai1a-2; a microsymbiont of Andira inermis discovered in Costa Rica. Standards in Genomic Sciences, 2015, 10, 33.	1.5	2

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55	High-quality permanent draft genome sequence of the Mimosa asperata - nodulating Cupriavidus sp. strain AMP6. Standards in Genomic Sciences, 2015, 10, 80.	1.5	2
56	High-quality permanent draft genome sequence of Bradyrhizobium sp. Th.b2, a microsymbiont of Amphicarpaea bracteata collected in Johnson City, New York. Standards in Genomic Sciences, 2015, 10, 24.	1.5	2
57	High-Quality draft genome sequence of the Lotus spp. microsymbiont Mesorhizobium loti strain CJ3Sym. Standards in Genomic Sciences, 2015, 10, 54.	1.5	2
58	High-quality draft genome sequence of Rhizobium mesoamericanum strain STM6155, a Mimosa pudica microsymbiont from New Caledonia. Standards in Genomic Sciences, 2017, 12, 7.	1.5	2
59	The Genome of the Acid Soil-Adapted Strain Rhizobium favelukesii OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host. Frontiers in Microbiology, 2022, 13, 735911.	3.5	2
60	Fur-Regulated Genes in Coxiella burnetii. Annals of the New York Academy of Sciences, 2005, 1063, 68-72.	3.8	1
61	High-quality permanent draft genome sequence of the Lebeckia - nodulating Burkholderia dilworthii strain WSM3556T. Standards in Genomic Sciences, 2015, 10, 64.	1.5	1
62	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
63	High-quality permanent draft genome sequence of Ensifer medicae strain WSM244, a microsymbiont isolated from Medicago polymorpha growing in alkaline soil. Standards in Genomic Sciences, 2015, 10, 126.	1.5	1
64	Evolution of a multiâ€step phosphorelay signal transduction system in Ensifer: recruitment of the sigma factor RpoN and a novel enhancerâ€binding protein triggers acidâ€activated gene expression. Molecular Microbiology, 2017, 103, 829-844.	2.5	1
65	A bacterial toolkit for plants. Nature Reviews Microbiology, 2020, 18, 124-124.	28.6	1
66	INTRODUCING CAMERA. Limnology and Oceanography Bulletin, 2007, 16, 45-45.	0.4	0
67	High-quality draft genome sequence of Ensifer meliloti Mlalz-1, a microsymbiont of Medicago laciniata (L.) miller collected in Lanzarote, Canary Islands, Spain. Standards in Genomic Sciences, 2017, 12, 58.	1.5	0