

# Rekha Seshadri

## List of Publications by Year in descending order

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67  
papers

10,015  
citations

156536

32  
h-index

107981

68  
g-index

79  
all docs

79  
docs citations

79  
times ranked

14290  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of Mobile DNA in the Evolution of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003, 299, 2071-2074.	6.0	849
2	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	6.5	799
3	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	9.4	771
4	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	9.4	615
5	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	9.4	559
6	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5455-5460.	3.3	506
7	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	13.7	505
8	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
9	Comparative Genomics of Emerging Human Ehrlichiosis Agents. <i>PLoS Genetics</i> , 2006, 2, e21.	1.5	423
10	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13148-13153.	3.3	422
11	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	9.4	414
12	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	6.0	402
13	CAMERA: A Community Resource for Metagenomics. <i>PLoS Biology</i> , 2007, 5, e75.	2.6	344
14	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , 2021, 49, D751-D763.	6.5	332
15	Genome Sequence of <i>Aeromonas hydrophila</i> ATCC 7966 T : Jack of All Trades. <i>Journal of Bacteriology</i> , 2006, 188, 8272-8282.	1.0	317
16	Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006, 16, 1031-1040.	2.4	281
17	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	2.6	275
18	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	3.3	251

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19	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
20	Bacterial Genomics and Pathogen Evolution. <i>Cell</i> , 2006, 124, 703-714.	13.5	122
21	Massive dominance of <i>Epsilonproteobacteria</i> in formation waters from a Canadian oil sands reservoir containing severely biodegraded oil. <i>Environmental Microbiology</i> , 2012, 14, 387-404.	1.8	117
22	Genome Degradation in <i>Brucella ovis</i> Corresponds with Narrowing of Its Host Range and Tissue Tropism. <i>PLoS ONE</i> , 2009, 4, e5519.	1.1	110
23	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	4.9	91
24	Complete and Draft Genome Sequences of Six Members of the <i>Aquificales</i> . <i>Journal of Bacteriology</i> , 2009, 191, 1992-1993.	1.0	76
25	IMG-ABC v.5.0: an update to the IMG/Atlas of Biosynthetic Gene Clusters Knowledgebase. <i>Nucleic Acids Research</i> , 2020, 48, D422-D430.	6.5	64
26	Symbiotic <i>Burkholderia</i> Species Show Diverse Arrangements of <i>nif/fix</i> and <i>nod</i> Genes and Lack Typical High-Affinity Cytochrome <i>cbb3</i> Oxidase Genes. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 609-619.	1.4	62
27	DOE JGI Metagenome Workflow. <i>MSystems</i> , 2021, 6, .	1.7	56
28	A Genomic Encyclopedia of the Root Nodule Bacteria: assessing genetic diversity through a systematic biogeographic survey. <i>Standards in Genomic Sciences</i> , 2015, 10, 14.	1.5	55
29	Limited Role for Iron Regulation in <i>Coxiella burnetii</i> Pathogenesis. <i>Infection and Immunity</i> , 2008, 76, 2189-2201.	1.0	47
30	Identification and Cloning of Immunodominant Antigens of <i>Coxiella burnetii</i> . <i>Infection and Immunity</i> , 2004, 72, 844-852.	1.0	44
31	Sugar metabolism by <i>Brucellae</i> . <i>Veterinary Microbiology</i> , 2002, 90, 249-261.	0.8	40
32	Differential Expression of Translational Elements by Life Cycle Variants of <i>Coxiella burnetii</i> . <i>Infection and Immunity</i> , 1999, 67, 6026-6033.	1.0	39
33	Characterization of a Stress-Induced Alternate Sigma Factor, RpoS, of <i>Coxiella burnetii</i> and Its Expression during the Development Cycle. <i>Infection and Immunity</i> , 2001, 69, 4874-4883.	1.0	38
34	Metagenomic investigation of the geologically unique <i>Hellenic Volcanic Arc</i> reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016, 18, 1122-1136.	1.8	37
35	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. <i>Scientific Reports</i> , 2015, 5, 16825.	1.6	33
36	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. <i>Animal Microbiome</i> , 2019, 1, 15.	1.5	27

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37	A Comparison of Microbial Genome Web Portals. <i>Frontiers in Microbiology</i> , 2019, 10, 208.	1.5	22
38	Genome Analysis of <i>Coxiella burnetii</i> Species: Insights into Pathogenesis and Evolution and Implications for Biodefense. <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 442-450.	1.8	20
39	Shotgun metagenomic analysis of microbial communities from the Loxahatchee nature preserve in the Florida Everglades. <i>Environmental Microbiomes</i> , 2020, 15, 2.	2.2	20
40	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.	1.2	18
41	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
42	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
43	Bacteria to the rescue. <i>Nature Biotechnology</i> , 2005, 23, 1236-1237.	9.4	7
44	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
45	Preliminary Assessment of Genome Differences between the Reference Nine Mile Isolate and Two Human Endocarditis Isolates of <i>Coxiella burnetii</i> . <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 64-67.	1.8	6
46	Cloning, expression, and purification of <i>Brucella suis</i> outer membrane proteins. <i>Protein Expression and Purification</i> , 2005, 40, 134-141.	0.6	6
47	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
48	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
49	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
50	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
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	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
54	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

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55	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
56	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
57	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
58	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
59	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.	1.5	2
60	Fur-Regulated Genes in <i>Coxiella burnetii</i> . <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 68-72.	1.8	1
61	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
62	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
63	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
64	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.	1.2	1
65	A bacterial toolkit for plants. <i>Nature Reviews Microbiology</i> , 2020, 18, 124-124.	13.6	1
66	INTRODUCING CAMERA. <i>Limnology and Oceanography Bulletin</i> , 2007, 16, 45-45.	0.2	0
67	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