

# Rup Lal

## List of Publications by Year in descending order

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232  
papers

7,079  
citations

61984

43  
h-index

88630

70  
g-index

239  
all docs

239  
docs citations

239  
times ranked

5420  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hexachlorocyclohexane (HCH) as new Stockholm Convention POPs—a global perspective on the management of Lindane and its waste isomers. <i>Environmental Science and Pollution Research</i> , 2011, 18, 152-162.	5.3	359
2	Biochemistry of Microbial Degradation of Hexachlorocyclohexane and Prospects for Bioremediation. <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 58-80.	6.6	331
3	Cloning and Characterization of lin Genes Responsible for the Degradation of Hexachlorocyclohexane Isomers by <i>Sphingomonas paucimobilis</i> Strain B90. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6021-6028.	3.1	173
4	High Throughput Sequencing: An Overview of Sequencing Chemistry. <i>Indian Journal of Microbiology</i> , 2016, 56, 394-404.	2.7	169
5	Bioactive compounds from marine actinomycetes. <i>Indian Journal of Microbiology</i> , 2008, 48, 410-431.	2.7	151
6	The enzymatic basis for pesticide bioremediation. <i>Indian Journal of Microbiology</i> , 2008, 48, 65-79.	2.7	144
7	Organization of lin Genes and IS 6100 among Different Strains of Hexachlorocyclohexane-Degrading <i>Sphingomonas paucimobilis</i> : Evidence for Horizontal Gene Transfer. <i>Journal of Bacteriology</i> , 2004, 186, 2225-2235.	2.2	138
8	Diversity, distribution and divergence of lin genes in hexachlorocyclohexane-degrading sphingomonads. <i>Trends in Biotechnology</i> , 2006, 24, 121-130.	9.3	129
9	Fish Gut Microbiome: Current Approaches and Future Perspectives. <i>Indian Journal of Microbiology</i> , 2018, 58, 397-414.	2.7	121
10	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. <i>Environmental Microbiology</i> , 2018, 20, 402-419.	3.8	120
11	Hexachlorocyclohexane-degrading bacterial strains <i>Sphingomonas paucimobilis</i> B90A, UT26 and Sp+, having similar lin genes, represent three distinct species, <i>Sphingobium indicum</i> sp. nov., <i>Sphingobium japonicum</i> sp. nov. and <i>Sphingobium francense</i> sp. nov., and reclassification of [ <i>Sphingomonas</i> ] <i>chungbukensis</i> as <i>Sphingobium chungbukense</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1965-1972.	1.7	116
12	The urgent need for microbiology literacy in society. <i>Environmental Microbiology</i> , 2019, 21, 1513-1528.	3.8	99
13	Comparative Metagenomic Analysis of Soil Microbial Communities across Three Hexachlorocyclohexane Contamination Levels. <i>PLoS ONE</i> , 2012, 7, e46219.	2.5	97
14	Enantioselective Transformation of $\hat{1}\pm$ -Hexachlorocyclohexane by the Dehydrochlorinases LinA1 and LinA2 from the Soil Bacterium <i>Sphingomonas paucimobilis</i> B90A. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8514-8518.	3.1	93
15	Biochemical and Molecular Basis of Pesticide Degradation by Microorganisms. <i>Critical Reviews in Biotechnology</i> , 1999, 19, 197-225.	9.0	91
16	Haloalkane Dehalogenase LinB Is Responsible for $\hat{1}2$ - and $\hat{1}^{\prime}$ -Hexachlorocyclohexane Transformation in <i>Sphingobium indicum</i> B90A. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5720-5727.	3.1	90
17	Evaluation of hexachlorocyclohexane contamination from the last lindane production plant operating in India. <i>Environmental Science and Pollution Research</i> , 2011, 18, 586-597.	5.3	87
18	<i>Devosia chinhatensis</i> sp. nov., isolated from a hexachlorocyclohexane (HCH) dump site in India. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 861-865.	1.7	82

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19	Description of <i>Sphingobium fuliginis</i> sp. nov., a phenanthrene-degrading bacterium from a fly ash dumping site, and reclassification of <i>Sphingomonas cloacae</i> as <i>Sphingobium cloacae</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2147-2152.	1.7	75
20	Comparative Genomic Analysis Reveals Habitat-Specific Genes and Regulatory Hubs within the Genus <i>Novosphingobium</i> . MSystems, 2017, 2, .	3.8	75
21	<i>Sphingobium ummariense</i> sp. nov., a hexachlorocyclohexane (HCH)-degrading bacterium, isolated from HCH-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 162-166.	1.7	73
22	Comparative genomic analysis of nine <i>Sphingobium</i> strains: insights into their evolution and hexachlorocyclohexane (HCH) degradation pathways. BMC Genomics, 2014, 15, 1014.	2.8	73
23	Enhanced biodegradation of hexachlorocyclohexane (HCH) in contaminated soils via inoculation with <i>Sphingobium indicum</i> B90A. Biodegradation, 2008, 19, 27-40.	3.0	71
24	Recent Advancements in the Development of Modern Probiotics for Restoring Human Gut Microbiome Dysbiosis. Indian Journal of Microbiology, 2020, 60, 12-25.	2.7	70
25	Enzymes and Operons Mediating Xenobiotic Degradation in Bacteria. Critical Reviews in Microbiology, 2001, 27, 133-166.	6.1	65
26	Reclassification of <i>Amycolatopsis mediterranei</i> DSM 46095 as <i>Amycolatopsis rifamycinica</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1145-1149.	1.7	61
27	Accumulation, Metabolism, and Effects of Organophosphorus Insecticides on Microorganisms. Advances in Applied Microbiology, 1982, 28, 149-200.	2.4	60
28	Comparative Genomic Analysis of Rapidly Evolving SARS-CoV-2 Reveals Mosaic Pattern of Phylogeographical Distribution. MSystems, 2020, 5, .	3.8	60
29	<i>Sphingobium quisquiliarum</i> sp. nov., a hexachlorocyclohexane (HCH)-degrading bacterium isolated from an HCH-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 429-433.	1.7	59
30	Degradation of alpha, beta, gamma and delta-hexachlorocyclohexanes by <i>Sphingomonas paucimobilis</i> . Biotechnology Letters, 1998, 20, 885-887.	2.2	57
31	<i>Rhizobium rosettiformans</i> sp. nov., isolated from a hexachlorocyclohexane dump site, and reclassification of <i>Blastobacter aggregatus</i> Hirsch and MÅller 1986 as <i>Rhizobium aggregatum</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 1218-1225.	1.7	57
32	Microbial taxonomy in the era of OMICS: application of DNA sequences, computational tools and techniques. Antonie Van Leeuwenhoek, 2017, 110, 1357-1371.	1.7	54
33	Defining the Environmental Adaptations of Genus <i>Devosia</i> : Insights into its Expansive Short Peptide Transport System and Positively Selected Genes. Scientific Reports, 2020, 10, 1151.	3.3	54
34	<i>Sphingobium chinhatense</i> sp. nov., a hexachlorocyclohexane (HCH)-degrading bacterium isolated from an HCH dumpsite. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 3140-3144.	1.7	53
35	Reconstructing an ancestral genotype of two hexachlorocyclohexane-degrading <i>Sphingobium</i> species using metagenomic sequence data. ISME Journal, 2014, 8, 398-408.	9.8	53
36	<i>Pseudomonas delhiensis</i> sp. nov., from a fly ash dumping site of a thermal power plant. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 527-531.	1.7	52

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37	Exploring internal features of 16S rRNA gene for identification of clinically relevant species of the genus <i>Streptococcus</i> . <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2011, 10, 28.	3.8	52
38	Proposal to reclassify [ <i>Sphingomonas</i> ] <i>xenophaga</i> Stolz et al. 2000 and [ <i>Sphingomonas</i> ] <i>taejonensis</i> Lee et al. 2001 as <i>Sphingobium xenophagum</i> comb. nov. and <i>Sphingopyxis taejonensis</i> comb. nov., respectively. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 667-670.	1.7	51
39	Hydroxylated Metabolites of $\hat{1}^2$ - and $\hat{1}^7$ -Hexachlorocyclohexane: A Bacterial Formation, Stereochemical Configuration, and Occurrence in Groundwater at a Former Production Site. <i>Environmental Science &amp; Technology</i> , 2007, 41, 4292-4298.	10.0	51
40	<i>Acinetobacter indicus</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2883-2890.	1.7	48
41	From dengue to Zika: the wide spread of mosquito-borne arboviruses. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2019, 38, 3-14.	2.9	48
42	Rapid and solitary production of mono-rhamnolipid biosurfactant and biofilm inhibiting pyocyanin by a taxonomic outlier <i>Pseudomonas aeruginosa</i> strain CR1. <i>Journal of Biotechnology</i> , 2020, 307, 98-106.	3.8	48
43	<i>Devosia albogilva</i> sp. nov. and <i>Devosia crocina</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 795-799.	1.7	47
44	Arsenic rich Himalayan hot spring metagenomics reveal genetically novel predator-prey genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 812-823.	2.4	47
45	<i>Novosphingobium barchaimii</i> sp. nov., isolated from hexachlorocyclohexane-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 667-672.	1.7	46
46	<i>Sphingomonas histidinilytica</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 1038-1043.	1.7	45
47	<i>Sphingopyxis ummariensis</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 780-784.	1.7	44
48	<i>Sphingobium lactosutens</i> sp. nov., isolated from a hexachlorocyclohexane dump site and <i>Sphingobium abikonense</i> sp. nov., isolated from oil-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2291-2296.	1.7	42
49	New Metabolites in the Degradation of $\hat{1}^2$ - and $\hat{1}^3$ -Hexachlorocyclohexane (HCH): Pentachlorocyclohexenes Are Hydroxylated to Cyclohexenols and Cyclohexenediols by the Haloalkane Dehalogenase LinB from <i>Sphingobium indicum</i> B90A. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 6594-6603.	5.2	41
50	<i>Novosphingobium lindaniclasticum</i> sp. nov., a hexachlorocyclohexane (HCH)-degrading bacterium isolated from an HCH dumpsite. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2160-2167.	1.7	41
51	Phylogenetic analyses of phylum Actinobacteria based on whole genome sequences. <i>Research in Microbiology</i> , 2013, 164, 718-728.	2.1	40
52	<i>Pontibacter ramchanderi</i> sp. nov., isolated from hexachlorocyclohexane-contaminated pond sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2829-2834.	1.7	40
53	<i>Pontibacter lucknowensis</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 309-313.	1.7	40
54	Modification of Rifamycin Polyketide Backbone Leads to Improved Drug Activity against Rifampicin-resistant <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 21142-21152.	3.4	40

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55	Interplay of Human Gut Microbiome in Health and Wellness. Indian Journal of Microbiology, 2020, 60, 26-36.	2.7	40
56	Regulation and manipulation of the gene clusters encoding type-I PKs. Trends in Biotechnology, 2000, 18, 264-274.	9.3	39
57	Dynamics of Multiple lin Gene Expression in <i>Sphingomonas paucimobilis</i> B90A in Response to Different Hexachlorocyclohexane Isomers. Applied and Environmental Microbiology, 2004, 70, 6650-6656.	3.1	39
58	Laboratory and field scale bioremediation of hexachlorocyclohexane (HCH) contaminated soils by means of bioaugmentation and biostimulation. Biodegradation, 2016, 27, 179-193.	3.0	39
59	Genetic manipulations of microorganisms for the degradation of hexachlorocyclohexane. FEMS Microbiology Reviews, 1996, 19, 69-84.	8.6	38
60	<i>Pseudomonas</i> sp. to <i>Sphingobium indicum</i> : a journey of microbial degradation and bioremediation of Hexachlorocyclohexane. Indian Journal of Microbiology, 2008, 48, 3-18.	2.7	38
61	Metabolomics of hexachlorocyclohexane (<scp>HCH</scp>) transformation: ratio of <scp>LinA</scp> to <scp>LinB</scp> determines metabolic fate of <scp>HCH</scp> isomers. Environmental Microbiology, 2013, 15, 1040-1049.	3.8	38
62	<i>Pseudomonas panipatensis</i> sp. nov., isolated from an oil-contaminated site. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1339-1345.	1.7	36
63	Isotope fractionation approach to characterize the reactive transport processes governing the fate of hexachlorocyclohexanes at a contaminated site in India. Environment International, 2019, 132, 105036.	10.0	36
64	Comparative Genomic Analyses Reveal Core-Genome-Wide Genes Under Positive Selection and Major Regulatory Hubs in Outlier Strains of <i>Pseudomonas aeruginosa</i> . Frontiers in Microbiology, 2019, 10, 53.	3.5	36
65	Enzymatic Conversion of $\mu$ -Hexachlorocyclohexane and a Heptachlorocyclohexane Isomer, Two Neglected Components of Technical Hexachlorocyclohexane. Environmental Science & Technology, 2012, 46, 4051-4058.	10.0	35
66	<i>Pontibacter indicus</i> sp. nov., isolated from hexachlorocyclohexane-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 254-259.	1.7	35
67	<i>Sphingobium lucknowense</i> sp. nov., a hexachlorocyclohexane (HCH)-degrading bacterium isolated from HCH-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 618-623.	1.7	33
68	Comparative genomic analysis of novel <i>Acinetobacter</i> symbionts: A combined systems biology and genomics approach. Scientific Reports, 2016, 6, 29043.	3.3	33
69	Engineering Antibiotic Producers to Overcome the Limitations of Classical Strain Improvement Programs. Critical Reviews in Microbiology, 1996, 22, 201-255.	6.1	32
70	<i>Parapedobacter indicus</i> sp. nov., isolated from hexachlorocyclohexane-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 129-134.	1.7	32
71	Chicken Gut Microbiome and Human Health: Past Scenarios, Current Perspectives, and Futuristic Applications. Indian Journal of Microbiology, 2020, 60, 2-11.	2.7	32
72	Draft Genome Sequence of <i>Thermus</i> sp. Strain RL, Isolated from a Hot Water Spring Located atop the Himalayan Ranges at Manikaran, India. Journal of Bacteriology, 2012, 194, 3534-3534.	2.2	31

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73	Genome Sequence of <i>Sphingobium indicum</i> B90A, a Hexachlorocyclohexane-Degrading Bacterium. <i>Journal of Bacteriology</i> , 2012, 194, 4471-4472.	2.2	31
74	Development of an Improved Cloning Vector and Transformation System in <i>Amycolatopsis mediterranei</i> ( <i>Nocardia mediterranei</i> ).. <i>Journal of Antibiotics</i> , 1998, 51, 161-169.	2.0	30
75	Bacterial diversity of Drass, cold desert in Western Himalaya, and its comparison with Antarctic and Arctic. <i>Archives of Microbiology</i> , 2015, 197, 851-860.	2.2	30
76	<i>Pseudoxanthomonas indica</i> sp. nov., isolated from a hexachlorocyclohexane dumpsite. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2107-2111.	1.7	30
77	Isolation of Three Xylanase-Producing Strains of Actinomycetes and Their Identification Using Molecular Methods. <i>Current Microbiology</i> , 2006, 53, 178-182.	2.2	29
78	<i>Sphingobium baderi</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 673-678.	1.7	29
79	Genetics and Genomics of the Genus <i>Amycolatopsis</i> . <i>Indian Journal of Microbiology</i> , 2016, 56, 233-246.	2.7	28
80	<i>Sphingomonas laterariae</i> sp. nov., isolated from a hexachlorocyclohexane-contaminated dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2891-2896.	1.7	27
81	Bacterial and Archaeal Viruses of Himalayan Hot Springs at Manikaran Modulate Host Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 3095.	3.5	27
82	Enantiomer and Carbon Isotope Fractionation of $\pm$ -Hexachlorocyclohexane by <i>Sphingobium indicum</i> Strain B90A and the Corresponding Enzymes. <i>Environmental Science &amp; Technology</i> , 2019, 53, 8715-8724.	10.0	27
83	Residues of organochlorine insecticides in Delhi vegetables. <i>Bulletin of Environmental Contamination and Toxicology</i> , 1989, 42-42, 45-49.	2.7	26
84	Recent trends in rifamycin research. <i>BioEssays</i> , 1994, 16, 211-216.	2.5	26
85	Whole Genome Sequence of the Rifamycin B-Producing Strain <i>Amycolatopsis mediterranei</i> S699. <i>Journal of Bacteriology</i> , 2011, 193, 5562-5563.	2.2	26
86	Draft Genome Sequence of <i>Sphingobium chinhatense</i> Strain IP26 T , Isolated from a Hexachlorocyclohexane Dumpsite. <i>Genome Announcements</i> , 2013, 1, .	0.8	26
87	Visualizing the invisible: class excursions to ignite children's enthusiasm for microbes. <i>Microbial Biotechnology</i> , 2020, 13, 844-887.	4.2	26
88	<i>Flavobacterium ummariense</i> sp. nov., isolated from hexachlorocyclohexane-contaminated soil, and emended description of <i>Flavobacterium cети</i> Vela et al. 2007. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2674-2679.	1.7	25
89	<i>Sphingopyxis indica</i> sp. nov., isolated from a high dose point hexachlorocyclohexane (HCH)-contaminated dumpsite. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2186-2191.	1.7	25
90	<i>Rhizobium populi</i> sp. nov., an endophytic bacterium isolated from <i>Populus euphratica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3215-3221.	1.7	25

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91	<i>Pontibacter chinhatensis</i> sp. nov., isolated from pond sediment containing discarded hexachlorocyclohexane isomer waste. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2248-2254.	1.7	25
92	From bacterial genomics to metagenomics: concept, tools and recent advances. <i>Indian Journal of Microbiology</i> , 2008, 48, 173-194.	2.7	24
93	<i>Microbacterium amylolyticum</i> sp. nov., isolated from soil from an industrial waste site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2114-2120.	1.7	24
94	<i>Fictibacillus halophilus</i> sp. nov., from a microbial mat of a hot spring atop the Himalayan Range. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2409-2416.	1.7	24
95	<i>Devosia lucknowensis</i> sp. nov., a bacterium isolated from hexachlorocyclohexane (HCH) contaminated pond soil. <i>Journal of Microbiology</i> , 2013, 51, 689-694.	2.8	23
96	Kinetic Isotope Effects of the Enzymatic Transformation of $\hat{1}^3$ -Hexachlorocyclohexane by the Lindane Dehydrochlorinase Variants LinA1 and LinA2. <i>Environmental Science &amp; Technology</i> , 2019, 53, 2353-2363.	10.0	23
97	Comparative Genomics and Integrated Network Approach Unveiled Undirected Phylogeny Patterns, Co-mutational Hot Spots, Functional Cross Talk, and Regulatory Interactions in SARS-CoV-2. <i>MSystems</i> , 2021, 6, .	3.8	23
98	<i>Sphingopyxis flava</i> sp. nov., isolated from a hexachlorocyclohexane (HCH)-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3720-3726.	1.7	23
99	<i>Tessaracoccus flavus</i> sp. nov., isolated from the drainage system of a lindane-producing factory. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1862-1868.	1.7	23
100	Compound-Specific Isotope Analysis and Enantiomer Fractionation to Characterize the Transformation of Hexachlorocyclohexane Isomers in a Soil-Wheat Pot System. <i>Environmental Science &amp; Technology</i> , 2020, 54, 8690-8698.	10.0	22
101	The Importance of Homologous Recombination in the Generation of Large Deletions in Hybrid Plasmids in <i>Amycolatopsis mediterranei</i> . <i>Plasmid</i> , 2000, 43, 1-11.	1.4	21
102	<i>Microbacterium lindanitolerans</i> sp. nov., isolated from hexachlorocyclohexane-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 2634-2638.	1.7	21
103	Response and resilience of soil microbial communities inhabiting in edible oil stress/contamination from industrial estates. <i>BMC Microbiology</i> , 2016, 16, 50.	3.3	21
104	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38.	2.7	21
105	The Human Microbiome Project. <i>Indian Journal of Microbiology</i> , 2012, 52, 315-315.	2.7	20
106	Draft Genome Sequence of <i>Sphingobium quisquiliarum</i> Strain P25 T , a Novel Hexachlorocyclohexane (HCH)-Degrading Bacterium Isolated from an HCH Dumpsite. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
107	Draft Genome Sequence of <i>Cellulosimicrobium</i> sp. Strain MM, Isolated from Arsenic-Rich Microbial Mats of a Himalayan Hot Spring. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
108	Hexachlorocyclohexane: persistence, toxicity and decontamination. <i>Reviews on Environmental Health</i> , 2014, 29, 49-52.	2.4	20



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109	<i>Thermus parvatiensis</i> RLT sp. nov., Isolated from a Hot Water Spring, Located Atop the Himalayan Ranges at Manikaran, India. <i>Indian Journal of Microbiology</i> , 2015, 55, 357-365.	2.7	20
110	(Meta)genomic insights into the pathogenome of <i>Cellulosimicrobium cellulans</i> . <i>Scientific Reports</i> , 2016, 6, 25527.	3.3	20
111	Assessing Aerobic Biotransformation of Hexachlorocyclohexane Isomers by Compound-Specific Isotope Analysis. <i>Environmental Science &amp; Technology</i> , 2019, 53, 7419-7431.	10.0	20
112	<i>Luteimonas tolerans</i> sp. nov., isolated from hexachlorocyclohexane-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1851-1856.	1.7	20
113	Bioaccumulation, metabolism, and effects of DDT, fenitrothion, and chlorpyrifos on <i>Saccharomyces cerevisiae</i> . <i>Archives of Environmental Contamination and Toxicology</i> , 1987, 16, 753-757.	4.1	19
114	Evolution of mercuric reductase ( <i>merA</i> ) gene: A case of horizontal gene transfer. <i>Microbiology</i> , 2010, 79, 500-508.	1.2	19
115	<i>Sphingomonas indica</i> sp. nov., isolated from hexachlorocyclohexane (HCH)-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2997-3002.	1.7	19
116	Draft Genome Sequence of <i>Sphingobium</i> sp. Strain HDIPO4, an Avid Degradar of Hexachlorocyclohexane. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
117	Pan-genome dynamics of <i>Pseudomonas</i> gene complements enriched across hexachlorocyclohexane dumpsite. <i>BMC Genomics</i> , 2015, 16, 313.	2.8	19
118	Competing $S_N2$ and E2 reaction pathways for hexachlorocyclohexane degradation in the gas phase, solution and enzymes. <i>Chemical Communications</i> , 2011, 47, 976-978.	4.1	18
119	<i>Sphingobium czechense</i> sp. nov., isolated from a hexachlorocyclohexane dump site. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 723-728.	1.7	18
120	Codon usage bias in phylum Actinobacteria: relevance to environmental adaptation and host pathogenicity. <i>Research in Microbiology</i> , 2016, 167, 669-677.	2.1	17
121	Genome Organization of <i>Sphingobium indicum</i> B90A: An Archetypal Hexachlorocyclohexane (HCH) Degrading Genotype. <i>Genome Biology and Evolution</i> , 2017, 9, 2191-2197.	2.5	17
122	Comparative genomics of <i>Sphingopyxis</i> spp. unravelled functional attributes. <i>Genomics</i> , 2020, 112, 1956-1969.	2.9	17
123	<i>Pontibacter aurantiacus</i> sp. nov. isolated from hexachlorocyclohexane (HCH) contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1400-1407.	1.7	17
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