

Masataka Tsuda

List of Publications by Year in descending order

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152
papers

6,385
citations

46984

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79644

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157
all docs

157
docs citations

157
times ranked

5881
citing authors

#	ARTICLE	IF	CITATIONS
1	Design and Experimental Application of a Novel Non-Degenerate Universal Primer Set that Amplifies Prokaryotic 16S rRNA Genes with a Low Possibility to Amplify Eukaryotic rRNA Genes. <i>DNA Research</i> , 2014, 21, 217-227.	1.5	432
2	Redesigning dehalogenase access tunnels as a strategy for degrading an anthropogenic substrate. <i>Nature Chemical Biology</i> , 2009, 5, 727-733.	3.9	238
3	GenomeMatcher: A graphical user interface for DNA sequence comparison. <i>BMC Bioinformatics</i> , 2008, 9, 376.	1.2	233
4	Revised nomenclature for transposable genetic elements. <i>Plasmid</i> , 2008, 60, 167-173.	0.4	222
5	Aerobic degradation of lindane ($\hat{1}^3$ -hexachlorocyclohexane) in bacteria and its biochemical and molecular basis. <i>Applied Microbiology and Biotechnology</i> , 2007, 76, 741-752.	1.7	192
6	Involvement of SLX4 in interstrand cross-link repair is regulated by the Fanconi anemia pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6492-6496.	3.3	169
7	Identification of the urease operon in <i>Helicobacter pylori</i> and its control by mRNA decay in response to pH. <i>Molecular Microbiology</i> , 2000, 36, 1071-1084.	1.2	154
8	Mre11 Is Essential for the Removal of Lethal Topoisomerase 2 Covalent Cleavage Complexes. <i>Molecular Cell</i> , 2016, 64, 580-592.	4.5	144
9	Genetic analysis of a transposon carrying toluene degrading genes on a TOL plasmid pWWO. <i>Molecular Genetics and Genomics</i> , 1987, 210, 270-276.	2.4	118
10	Complete Genome Sequence of <i>Acidovorax</i> sp. Strain KKS102, a Polychlorinated-Biphenyl Degradator. <i>Journal of Bacteriology</i> , 2012, 194, 6970-6971.	1.0	117
11	Modification of Activity and Specificity of Haloalkane Dehalogenase from <i>Sphingomonas paucimobilis</i> UT26 by Engineering of Its Entrance Tunnel. <i>Journal of Biological Chemistry</i> , 2003, 278, 52622-52628.	1.6	115
12	Characterization of the MexC-MexD-OprJ Multidrug Efflux System in $\hat{1}^m$ <i>mexA-mexB-oprM</i> Mutants of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 1938-1943.	1.4	102
13	Naphthalene degrading genes on plasmid NAH7 are on a defective transposon. <i>Molecular Genetics and Genomics</i> , 1990, 223, 33-39.	2.4	101
14	Strategies for bioremediation of polychlorinated biphenyls. <i>Applied Microbiology and Biotechnology</i> , 2004, 65, 250-8.	1.7	99
15	Genomic and Functional Analysis of the IncP-9 Naphthalene-Catabolic Plasmid NAH7 and Its Transposon Tn 4655 Suggests Catabolic Gene Spread by a Tyrosine Recombinase. <i>Journal of Bacteriology</i> , 2006, 188, 4057-4067.	1.0	98
16	Repriming by PrimPol is critical for DNA replication restart downstream of lesions and chain-terminating nucleosides. <i>Cell Cycle</i> , 2016, 15, 1997-2008.	1.3	88
17	High frequency mobilization of the chromosome of <i>Escherichia coli</i> by a mutant of plasmid RP4 temperature-sensitive for maintenance. <i>Molecular Genetics and Genomics</i> , 1980, 180, 47-56.	2.4	85
18	Fiber-Optic-Based Biomonitoring of Benzene Derivatives by Recombinant <i>E. coli</i> Bearing Luciferase Gene-Fused TOL-Plasmid Immobilized on the Fiber-Optic End. <i>Analytical Chemistry</i> , 1997, 69, 2600-2605.	3.2	80

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19	Characterization of the Replication, Maintenance, and Transfer Features of the IncP-7 Plasmid pCAR1, Which Carries Genes Involved in Carbazole and Dioxin Degradation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3206-3216.	1.4	80
20	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. <i>ISME Journal</i> , 2009, 3, 1335-1348.	4.4	80
21	XRCC1 prevents toxic PARP1 trapping during DNA base excision repair. <i>Molecular Cell</i> , 2021, 81, 3018-3030.e5.	4.5	80
22	Identification and characterization of Tn4653, a transposon covering the toluene transposon Tn4651 on TOL plasmid pWWO. <i>Molecular Genetics and Genomics</i> , 1988, 213, 72-77.	2.4	78
23	Isolation and characterization of naphthalene-catabolic genes and plasmids from oil-contaminated soil by using two cultivation-independent approaches. <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 501-510.	1.7	77
24	Identification and Characterization of Genes Involved in the Downstream Degradation Pathway of $\hat{1}$ -Hexachlorocyclohexane in <i>Sphingomonas paucimobilis</i> UT26. <i>Journal of Bacteriology</i> , 2005, 187, 847-853.	1.0	76
25	BRCA1 ensures genome integrity by eliminating estrogen-induced pathological topoisomerase II $\hat{1}$ -DNA complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10642-E10651.	3.3	75
26	A positive regulatory gene, pvdS, for expression of pyoverdinin biosynthetic genes in <i>Pseudomonas aeruginosa</i> PAO. <i>Molecular Genetics and Genomics</i> , 1995, 248, 17-24.	2.4	74
27	A Phylogenomic Study of the OCTase Genes in <i>Pseudomonas syringae</i> Pathovars: The Horizontal Transfer of the argK $\hat{1}$ -tox Cluster and the Evolutionary History of OCTase Genes on Their Genomes. <i>Journal of Molecular Evolution</i> , 2002, 54, 437-457.	0.8	73
28	Two Rhizobial Strains, <i>Mesorhizobium loti</i> MAFF303099 and <i>Bradyrhizobium japonicum</i> USDA110, Encode Haloalkane Dehalogenases with Novel Structures and Substrate Specificities. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4372-4379.	1.4	73
29	Degradation of $\hat{1}$ -Hexachlorocyclohexane by Haloalkane Dehalogenase LinB from <i>Sphingomonas paucimobilis</i> UT26. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2183-2185.	1.4	72
30	The Role of mex-Gene Products in Antibiotic Extrusion in <i>Pseudomonas aeruginosa</i> . <i>Biochemical and Biophysical Research Communications</i> , 1997, 233, 611-618.	1.0	71
31	Halide-Stabilizing Residues of Haloalkane Dehalogenases Studied by Quantum Mechanic Calculations and Site-Directed Mutagenesis. <i>Biochemistry</i> , 2002, 41, 14272-14280.	1.2	69
32	Mobile catabolic genes in bacteria. <i>Journal of Bioscience and Bioengineering</i> , 1999, 87, 401-410.	1.1	66
33	Complete Genome Sequence of the Representative $\hat{1}$ -Hexachlorocyclohexane-Degrading Bacterium <i>Sphingobium japonicum</i> UT26. <i>Journal of Bacteriology</i> , 2010, 192, 5852-5853.	1.0	66
34	Degradation of $\hat{1}$ -hexachlorocyclohexane by haloalkane dehalogenase LinB from $\hat{1}$ -hexachlorocyclohexane-utilizing bacterium <i>Sphingobium</i> sp. MI1205. <i>Archives of Microbiology</i> , 2007, 188, 313-325.	1.0	62
35	Type II DNA Topoisomerases Cause Spontaneous Double-Strand Breaks in Genomic DNA. <i>Genes</i> , 2019, 10, 868.	1.0	60
36	Complete Nucleotide Sequence of an Exogenously Isolated Plasmid, pLB1, Involved in $\hat{1}$ -Hexachlorocyclohexane Degradation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6923-6933.	1.4	58

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37	Recipient Range of IncP-7 Conjugative Plasmid pCAR2 from <i>Pseudomonas putida</i> HS01 is Broader than from Other <i>Pseudomonas</i> Strains. <i>Biotechnology Letters</i> , 2005, 27, 1847-1853.	1.1	57
38	Identification and Characterization of Genes Encoding a Putative ABC-Type Transporter Essential for Utilization of \hat{I}^3 -Hexachlorocyclohexane in <i>Sphingobium japonicum</i> UT26. <i>Journal of Bacteriology</i> , 2007, 189, 3712-3720.	1.0	56
39	Genetic Transformation in <i>Helicobacter pylori</i> . <i>Microbiology and Immunology</i> , 1993, 37, 85-89.	0.7	55
40	Structure of Haloacetate-Catabolic IncP-1 \hat{I}^2 Plasmid pUO1 and Genetic Mobility of Its Residing Haloacetate-Catabolic Transposon. <i>Journal of Bacteriology</i> , 2003, 185, 6741-6745.	1.0	53
41	Complete Nucleotide Sequence of TOL Plasmid pDK1 Provides Evidence for Evolutionary History of IncP-7 Catabolic Plasmids. <i>Journal of Bacteriology</i> , 2010, 192, 4337-4347.	1.0	53
42	The <i>lin</i> Genes for \hat{I}^3 -Hexachlorocyclohexane Degradation in <i>Sphingomonas</i> sp. MM-1 Proved to Be Dispersed across Multiple Plasmids. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 466-472.	0.6	53
43	Properties and biotechnological applications of natural and engineered haloalkane dehalogenases. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9865-9881.	1.7	53
44	Functional replacement of OprJ by OprM in the MexCD-OprJ multidrug efflux system of <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 1998, 165, 21-27.	0.7	52
45	Region-Specific Insertion of Transposons in Combination with Selection for High Plasmid Transferability and Stability Accounts for the Structural Similarity of IncP-1 Plasmids. <i>Journal of Bacteriology</i> , 2007, 189, 3091-3098.	1.0	52
46	Identification of a response regulator gene for catabolite control from a PCB-degrading beta-proteobacteria, <i>Acidovorax</i> sp. KKS102. <i>Molecular Microbiology</i> , 2006, 60, 1563-1575.	1.2	51
47	The POLD3 subunit of DNA polymerase \hat{I} can promote translesion synthesis independently of DNA polymerase $\hat{I}\eta$. <i>Nucleic Acids Research</i> , 2015, 43, 1671-1683.	6.5	51
48	Complete Sequence Determination Combined with Analysis of Transposition/Site-specific Recombination Events to Explain Genetic Organization of IncP-7 TOL Plasmid pWW53 and Related Mobile Genetic Elements. <i>Journal of Molecular Biology</i> , 2007, 369, 11-26.	2.0	50
49	Cloning and characterization of the <i>thiD/J</i> gene of <i>Escherichia coli</i> encoding a thiamin-synthesizing bifunctional enzyme, hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase. <i>Microbiology (United Kingdom)</i> , 1999, 145, 495-501.	0.7	49
50	High-Temperature-Induced Transposition of Insertion Elements in <i>Burkholderia multivorans</i> ATCC 17616. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1822-1828.	1.4	48
51	Isolation of oxygenase genes for indigo-forming activity from an artificially polluted soil metagenome by functional screening using <i>Pseudomonas putida</i> strains as hosts. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 4453-4470.	1.7	48
52	Analysis of extracellular alginate lyase and its gene from a marine bacterial strain, <i>Pseudoalteromonas atlantica</i> AR06. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 567-576.	1.7	47
53	Genomic organization and genomic structural rearrangements of <i>Sphingobium japonicum</i> UT26, an archetypal \hat{I}^3 -hexachlorocyclohexane-degrading bacterium. <i>Enzyme and Microbial Technology</i> , 2011, 49, 499-508.	1.6	47
54	Bacterial clade with the ribosomal RNA operon on a small plasmid rather than the chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14343-14347.	3.3	47

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55	Conjugal Transfer of Polychlorinated Biphenyl/Biphenyl Degradation Genes in <i>Acidovorax</i> sp. Strain KKS102, Which Are Located on an Integrative and Conjugative Element. <i>Journal of Bacteriology</i> , 2012, 194, 4237-4248.	1.0	42
56	Construction of Signature-tagged Mutant Library in <i>Mesorhizobium loti</i> as a Powerful Tool for Functional Genomics. <i>DNA Research</i> , 2008, 15, 297-308.	1.5	41
57	Pleiotropic roles of iron-responsive transcriptional regulator Fur in <i>Burkholderia multivorans</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 1763-1774.	0.7	39
58	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. <i>DNA Research</i> , 2015, 22, 413-424.	1.5	39
59	Nucleotide Sequence and Characterization of <i>cdrA</i> , a Cell Division-Related Gene of <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 1998, 180, 5263-5268.	1.0	37
60	Distribution of γ -hexachlorocyclohexane-degrading genes on three replicons in <i>Sphingobium japonicum</i> UT26. <i>FEMS Microbiology Letters</i> , 2006, 256, 112-118.	0.7	36
61	Functional Analysis of Unique Class II Insertion Sequence IS 1071. <i>Applied and Environmental Microbiology</i> , 2006, 72, 291-297.	1.4	36
62	Comparative Analysis of <i>argK-tox</i> Clusters and Their Flanking Regions in Phaseolotoxin-Producing <i>Pseudomonas syringae</i> Pathovars. <i>Journal of Molecular Evolution</i> , 2006, 63, 401-414.	0.8	35
63	Iron-Mediated Regulation of Alkaline Proteinase Production in <i>Pseudomonas aeruginosa</i> . <i>Microbiology and Immunology</i> , 2001, 45, 579-590.	0.7	34
64	Characterization of a Class II Defective Transposon Carrying Two Haloacetate Dehalogenase Genes from <i>Delftia acidovorans</i> Plasmid pUO1. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2307-2315.	1.4	34
65	Distribution and Organization of Auxotrophic Genes on the Multichromosomal Genome of <i>Burkholderia multivorans</i> ATCC 17616. <i>Journal of Bacteriology</i> , 2003, 185, 3333-3343.	1.0	34
66	ALC1/CHD1L, a chromatin-remodeling enzyme, is required for efficient base excision repair. <i>PLoS ONE</i> , 2017, 12, e0188320.	1.1	34
67	In vivo evidence for translesion synthesis by the replicative DNA polymerase $\hat{\nu}$. <i>Nucleic Acids Research</i> , 2016, 44, gkw439.	6.5	33
68	Identification of <i>Burkholderia multivorans</i> ATCC 17616 genes induced in soil environment by <i>in vivo</i> expression technology. <i>Environmental Microbiology</i> , 2010, 12, 2539-2558.	1.8	31
69	Identification and Characterization of Tn 4656, a Novel Class II Transposon Carrying a Set of Toluene-Degrading Genes from TOL Plasmid pWW53. <i>Journal of Bacteriology</i> , 2001, 183, 6215-6224.	1.0	30
70	SUMOylation of PCNA by PIAS1 and PIAS4 promotes template switch in the chicken and human B cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12793-12798.	3.3	30
71	Comparison of the complete genome sequences of four $\hat{\nu}$ -hexachlorocyclohexane-degrading bacterial strains: insights into the evolution of bacteria able to degrade a recalcitrant man-made pesticide. <i>DNA Research</i> , 2016, 23, 581-599.	1.5	29
72	Use of a transposon-encoded site-specific resolution system for construction of large and defined deletion mutations in bacterial chromosome. <i>Gene</i> , 1998, 207, 33-41.	1.0	28

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73	Lessons from the genomes of lindane-degrading sphingomonads. <i>Environmental Microbiology Reports</i> , 2019, 11, 630-644.	1.0	28
74	Tn501 insertion mutagenesis in <i>Pseudomonas aeruginosa</i> PAO. <i>Molecular Genetics and Genomics</i> , 1984, 196, 494-500.	2.4	27
75	Complementation of aprataxin deficiency by base excision repair enzymes in mitochondrial extracts. <i>Nucleic Acids Research</i> , 2017, 45, 10079-10088.	6.5	24
76	The dominant role of proofreading exonuclease activity of replicative polymerase μ in cellular tolerance to cytarabine (Ara-C). <i>Oncotarget</i> , 2017, 8, 33457-33474.	0.8	24
77	Global Gene Expression in <i>Bradyrhizobium japonicum</i> Cultured with Vanillin, Vanillate, 4-Hydroxybenzoate and Protocatechuate. <i>Microbes and Environments</i> , 2006, 21, 240-250.	0.7	22
78	Reconstruction of Mycobacterial Dehalogenase Rv2579 by Cumulative Mutagenesis of Haloalkane Dehalogenase LinB. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2349-2355.	1.4	21
79	Site-Specific Recombination System Encoded by Toluene Catabolic Transposon Tn 4651. <i>Journal of Bacteriology</i> , 2002, 184, 4757-4766.	1.0	20
80	Crystal Structure and Site-Directed Mutagenesis Analyses of Haloalkane Dehalogenase LinB from <i>Sphingobium</i> sp. Strain MI1205. <i>Journal of Bacteriology</i> , 2013, 195, 2642-2651.	1.0	20
81	Efficient N-tailing of blunt DNA ends by Moloney murine leukemia virus reverse transcriptase. <i>Scientific Reports</i> , 2017, 7, 41769.	1.6	20
82	Host Range of the Conjugative Transfer System of IncP-9 Naphthalene-Catabolic Plasmid NAH7 and Characterization of Its <i>oriT</i> Region and Relaxase. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	20
83	Cointegrate-resolution of toluene-catabolic transposon Tn4651: Determination of crossover site and the segment required for full resolution activity. <i>Plasmid</i> , 2013, 69, 24-35.	0.4	19
84	The Small Protein HemP Is a Transcriptional Activator for the Hemin Uptake Operon in <i>Burkholderia multivorans</i> ATCC 17616. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	19
85	A genetic analysis system of <i>Burkholderia cepacia</i> : construction of mobilizable transposons and a cloning vector. <i>Gene</i> , 1996, 174, 191-194.	1.0	18
86	<i>ParK</i> , an orphan <i>ParA</i> family protein from <i>Pseudomonas putida</i> ... <i>KT</i> -specific genomic island, interferes with the partition system of <i>IncP</i> plasmids. <i>Environmental Microbiology</i> , 2012, 14, 2946-2959.	1.8	18
87	Genetic evidence for the involvement of mismatch repair proteins, PMS2 and MLH3, in a late step of homologous recombination. <i>Journal of Biological Chemistry</i> , 2020, 295, 17460-17475.	1.6	18
88	Growth Inhibition by Metabolites of β -Hexachlorocyclohexane in <i>Sphingobium japonicum</i> UT26. <i>Bioscience, Biotechnology and Biochemistry</i> , 2006, 70, 1029-1032.	0.6	17
89	Insertion sequence-based cassette PCR: cultivation-independent isolation of β -hexachlorocyclohexane-degrading genes from soil DNA. <i>Applied Microbiology and Biotechnology</i> , 2008, 79, 627-632.	1.7	17
90	UBC13-Mediated Ubiquitin Signaling Promotes Removal of Blocking Adducts from DNA Double-Strand Breaks. <i>IScience</i> , 2020, 23, 101027.	1.9	17

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91	Tn1 insertion mutagenesis in <i>Escherichia coli</i> K-12 using a temperature-sensitive mutant of plasmid RP4. <i>Molecular Genetics and Genomics</i> , 1981, 184, 52-55.	2.4	16
92	Replication-dependent cytotoxicity and Spartan-mediated repair of trapped PARP1-DNA complexes. <i>Nucleic Acids Research</i> , 2021, 49, 10493-10506.	6.5	16
93	Characterization of the <i>traD</i> Operon of Naphthalene-Catabolic Plasmid NAH7: a Host-Range Modifier in Conjugative Transfer. <i>Journal of Bacteriology</i> , 2008, 190, 6281-6289.	1.0	15
94	Complete Genome Sequence of the Thermophilic Polychlorinated Biphenyl Degradator <i>Geobacillus</i> sp. Strain JF8 (NBRC 109937). <i>Genome Announcements</i> , 2014, 2, .	0.8	15
95	PDIP38/PolDIP2 controls the DNA damage tolerance pathways by increasing the relative usage of translesion DNA synthesis over template switching. <i>PLoS ONE</i> , 2019, 14, e0213383.	1.1	15
96	The identification of catalytic pentad in the haloalkane dehalogenase DhmA from <i>Mycobacterium avium</i> N85: Reaction mechanism and molecular evolution. <i>Journal of Structural Biology</i> , 2007, 157, 384-392.	1.3	14
97	Identification of <i>Burkholderia multivorans</i> ATCC 17616 genetic determinants for fitness in soil by using signature-tagged mutagenesis. <i>Microbiology (United Kingdom)</i> , 2014, 160, 883-891.	0.7	14
98	Biodegradation of $\hat{1}^3$ -hexachlorocyclohexane by transgenic hairy root cultures of <i>Cucurbita moschata</i> that accumulate recombinant bacterial LinA. <i>Plant Cell Reports</i> , 2016, 35, 1963-1974.	2.8	14
99	Complete Genome Sequence of <i>Pseudomonas</i> sp. Strain TKP, Isolated from a $\hat{1}^3$ -Hexachlorocyclohexane-Degrading Mixed Culture. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
100	Compounds that enhance the tailing activity of Moloney murine leukemia virus reverse transcriptase. <i>Scientific Reports</i> , 2017, 7, 6520.	1.6	12
101	<i>XRCC1</i> counteracts poly(ADP ribose)polymerase (PARP) poisons, olaparib and talazoparib, and a clinical alkylating agent, temozolomide, by promoting the removal of trapped PARP1 from broken DNA. <i>Genes To Cells</i> , 2022, 27, 331-344.	0.5	12
102	Crystallization and preliminary crystallographic analysis of a haloalkane dehalogenase, DbjA, from <i>Bradyrhizobium japonicum</i> USDA110. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 294-296.	0.7	11
103	Suppression of pleiotropic phenotypes of a <i>Burkholderia multivorans fur</i> mutant by <i>oxyR</i> mutation. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1284-1293.	0.7	11
104	Stepwise enhancement of catalytic performance of haloalkane dehalogenase LinB towards $\hat{1}^2$ -hexachlorocyclohexane. <i>AMB Express</i> , 2014, 4, 72.	1.4	11
105	Complete Genome Sequence of <i>Ralstonia pickettii</i> DTP0602, a 2,4,6-Trichlorophenol Degradator. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
106	Properties and efficient scrap-and-build repairing of mechanically sheared 3' DNA ends. <i>Communications Biology</i> , 2019, 2, 409.	2.0	10
107	Organization and localization of the <i>dnaA</i> and <i>dnaK</i> gene regions on the multichromosomal genome of <i>Burkholderia multivorans</i> ATCC 17616. <i>Journal of Bioscience and Bioengineering</i> , 2005, 99, 603-610.	1.1	9
108	Complete Genome Sequence of a $\hat{1}^3$ -Hexachlorocyclohexane Degradator, <i>Sphingobium</i> sp. Strain TKS, Isolated from a $\hat{1}^3$ -Hexachlorocyclohexane-Degrading Microbial Community. <i>Genome Announcements</i> , 2016, 4, .	0.8	9

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109	Complete Genome Sequence of <i>Bradyrhizobium diazoefficiens</i> USDA 122, a Nitrogen-Fixing Soybean Symbiont. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
110	Estrogen Induces Mammary Ductal Dysplasia via the Upregulation of Myc Expression in a DNA-Repair-Deficient Condition. <i>IScience</i> , 2020, 23, 100821.	1.9	9
111	Analysis of Extracellular Alginate Lyase (<i>alyA</i>) Expression and its Regulatory Region in a Marine Bacterial Strain, <i>Pseudoalteromonas atlantica</i> AR06, Using a <i>gfp</i> Gene Reporter System. <i>Marine Biotechnology</i> , 2013, 15, 349-356.	1.1	7
112	Complete Genome Sequence of <i>Pseudomonas aeruginosa</i> MTB-1, Isolated from a Microbial Community Enriched by the Technical Formulation of Hexachlorocyclohexane. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
113	Biodegradation of Organochlorine Pesticides. , 0, , 5.1.2-1-5.1.2-30.		7
114	Complete Genome Sequence of a Phenanthrene Degradar, <i>Mycobacterium</i> sp. Strain EPA45 (NBRC) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	7
115	Complete Genome Sequence of <i>Methylobacterium</i> sp. Strain AMS5, an Isolate from a Soybean Stem. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
116	Complete Genome Sequence of a $\hat{1}^3$ -Hexachlorocyclohexane-Degrading Bacterium, <i>Sphingobium</i> sp. Strain MI1205. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
117	Complete genome sequence of <i>Burkholderia caribensis</i> Bcrs1W (NBRC110739), a strain co-residing with phenanthrene degrader <i>Mycobacterium</i> sp. EPA45. <i>Journal of Biotechnology</i> , 2016, 228, 67-68.	1.9	7
118	Complete Genome Sequence of an Anaerobic Benzene-Degrading Bacterium, <i>Azoarcus</i> sp. Strain DN11. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
119	Inhibitory effect of <i>Pseudomonas putida</i> nitrogen-related phosphotransferase system on conjugative transfer of IncP-9 plasmid from <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2013, 345, 102-109.	0.7	6
120	Complete Genome Sequence of a Phenanthrene Degradar, <i>Burkholderia</i> sp. HB-1 (NBRC 110738). <i>Genome Announcements</i> , 2015, 3, .	0.8	6
121	Selective cytotoxicity of the anti-diabetic drug, metformin, in glucose-deprived chicken DT40 cells. <i>PLoS ONE</i> , 2017, 12, e0185141.	1.1	6
122	Division of labor of Y-family polymerases in translesion-DNA synthesis for distinct types of DNA damage. <i>PLoS ONE</i> , 2021, 16, e0252587.	1.1	6
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