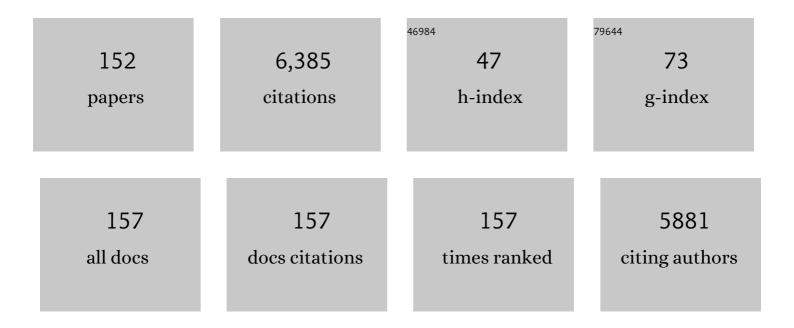
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	<scp>XRCC1</scp> counteracts poly(ADP ribose)polymerase (PARP) poisons, olaparib and talazoparib, and a clinical alkylating agent, temozolomide, by promoting the removal of trapped <scp>PARP1</scp> from broken <scp>DNA</scp> . Genes To Cells, 2022, 27, 331-344.	0.5	12
2	Division of labor of Y-family polymerases in translesion-DNA synthesis for distinct types of DNA damage. PLoS ONE, 2021, 16, e0252587.	1.1	6
3	XRCC1 prevents toxic PARP1 trapping during DNA base excision repair. Molecular Cell, 2021, 81, 3018-3030.e5.	4.5	80
4	Replication-dependent cytotoxicity and Spartan-mediated repair of trapped PARP1–DNA complexes. Nucleic Acids Research, 2021, 49, 10493-10506.	6.5	16
5	Restoration of ligatable "clean―double-strand break ends is the rate-limiting step in the rejoining of ionizing-radiation-induced DNA breakage. DNA Repair, 2020, 93, 102913.	1.3	5
6	Genetic evidence for the involvement of mismatch repair proteins, PMS2 and MLH3, in a late step of homologous recombination. Journal of Biological Chemistry, 2020, 295, 17460-17475.	1.6	18
7	UBC13-Mediated Ubiquitin Signaling Promotes Removal of Blocking Adducts from DNA Double-Strand Breaks. IScience, 2020, 23, 101027.	1.9	17
8	Transcriptome Analysis of Zygotic Induction During Conjugative Transfer of Plasmid RP4. Frontiers in Microbiology, 2020, 11, 1125.	1.5	3
9	A transcriptional regulator, IscR, of Burkholderia multivorans acts as both repressor and activator for transcription of iron-sulfur cluster-biosynthetic isc operon. Research in Microbiology, 2020, 171, 319-330.	1.0	2
10	Estrogen Induces Mammary Ductal Dysplasia via the Upregulation of Myc Expression in a DNA-Repair-Deficient Condition. IScience, 2020, 23, 100821.	1.9	9
11	Expression of an alcohol dehydrogenase gene in a heterotrophic bacterium induces carbon dioxide-dependent high-yield growth under oligotrophic conditions. Microbiology (United Kingdom), 2020, 166, 531-545.	0.7	2
12	Complete Genome Sequence of <i>Thalassococcus</i> sp. Strain S3, a Marine <i>Roseobacter</i> Clade Member Capable of Degrading Carbazole. Microbiology Resource Announcements, 2019, 8, .	0.3	5
13	Type II DNA Topoisomerases Cause Spontaneous Double-Strand Breaks in Genomic DNA. Genes, 2019, 10, 868.	1.0	60
14	Complete Genome Sequence of Bacillus licheniformis TAB7, a Compost-Deodorizing Strain with Potential for Plant Growth Promotion. Microbiology Resource Announcements, 2019, 8, .	0.3	4
15	Complete Genome Sequence of an Anaerobic Benzene-Degrading Bacterium, <i>Azoarcus</i> sp. Strain DN11. Microbiology Resource Announcements, 2019, 8, .	0.3	7
16	Lessons from the genomes of lindaneâ€degrading sphingomonads. Environmental Microbiology Reports, 2019, 11, 630-644.	1.0	28
17	PDIP38/PolDIP2 controls the DNA damage tolerance pathways by increasing the relative usage of translesion DNA synthesis over template switching. PLoS ONE, 2019, 14, e0213383.	1.1	15
18	Mobile Genetic Elements Involved in the Evolution of Bacteria that Degrade Recalcitrant Xenobiotic		1

Mobile Genetic Elements Involve Compounds. , 2019, , 215-244.

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19	Conjugative Transfer of IncP-9 Catabolic Plasmids Requires a Previously Uncharacterized Gene, mpfK , Whose Homologs Are Conserved in Various MPF T -Type Plasmids. Applied and Environmental Microbiology, 2019, 85, .	1.4	1
20	Properties and efficient scrap-and-build repairing of mechanically sheared 3' DNA ends. Communications Biology, 2019, 2, 409.	2.0	10
21	Suppression of substrate inhibition in phenanthrene-degrading Mycobacterium by co-cultivation with a non-degrading Burkholderia strain. Microbiology (United Kingdom), 2019, 165, 625-637.	0.7	4
22	Establishment of plasmid vector and allelic exchange mutagenesis systems in a mycobacterial strain that is able to degrade polycyclic aromatic hydrocarbon. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1169-1171.	0.6	1
23	SUMOylation of PCNA by PIAS1 and PIAS4 promotes template switch in the chicken and human B cell lines. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12793-12798.	3.3	30
24	BRCA1 ensures genome integrity by eliminating estrogen-induced pathological topoisomerase II–DNA complexes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10642-E10651.	3.3	75
25	Complete Genome Sequence of the Marine Carbazole-Degrading Bacterium Erythrobacter sp. Strain KY5. Microbiology Resource Announcements, 2018, 7, .	0.3	5
26	Optimization of single strand DNA incorporation reaction by Moloney murine leukaemia virus reverse transcriptase. DNA Research, 2018, 25, 477-487.	1.5	5
27	Efficient N-tailing of blunt DNA ends by Moloney murine leukemia virus reverse transcriptase. Scientific Reports, 2017, 7, 41769.	1.6	20
28	Complete Genome Sequence of <i>Bradyrhizobium diazoefficiens</i> USDA 122, a Nitrogen-Fixing Soybean Symbiont. Genome Announcements, 2017, 5, .	0.8	9
29	The Small Protein HemP Is a Transcriptional Activator for the Hemin Uptake Operon in Burkholderia multivorans ATCC 17616. Applied and Environmental Microbiology, 2017, 83, .	1.4	19
30	Compounds that enhance the tailing activity of Moloney murine leukemia virus reverse transcriptase. Scientific Reports, 2017, 7, 6520.	1.6	12
31	Host Range of the Conjugative Transfer System of IncP-9 Naphthalene-Catabolic Plasmid NAH7 and Characterization of Its <i>oriT</i> Region and Relaxase. Applied and Environmental Microbiology, 2017, 83, .	1.4	20
32	Complementation of aprataxin deficiency by base excision repair enzymes in mitochondrial extracts. Nucleic Acids Research, 2017, 45, 10079-10088.	6.5	24
33	Selective cytotoxicity of the anti-diabetic drug, metformin, in glucose-deprived chicken DT40 cells. PLoS ONE, 2017, 12, e0185141.	1.1	6
34	ALC1/CHD1L, a chromatin-remodeling enzyme, is required for efficient base excision repair. PLoS ONE, 2017, 12, e0188320.	1.1	34
35	The dominant role of proofreading exonuclease activity of replicative polymerase ε in cellular tolerance to cytarabine (Ara-C). Oncotarget, 2017, 8, 33457-33474.	0.8	24
36	土壌ç″°èŒå¢ã®åŒ−å¦çš"æ'¹ä¹±ã«å⁻¾ãı™ã,‹ãfãfẽ,¹ãf^性. Kagaku To Seibutsu, 2017, 55, 446-447.	0.0	0

#	Article	IF	CITATIONS
37	Complete Genome Sequence of Methylobacterium sp. Strain AMS5, an Isolate from a Soybean Stem. Genome Announcements, 2016, 4, .	0.8	7
38	Complete Genome Sequence of a γ-Hexachlorocyclohexane-Degrading Bacterium, Sphingobium sp. Strain MI1205. Genome Announcements, 2016, 4, .	0.8	7
39	Complete Genome Sequence of a γ-Hexachlorocyclohexane Degrader, Sphingobium sp. Strain TKS, Isolated from a γ-Hexachlorocyclohexane-Degrading Microbial Community. Genome Announcements, 2016, 4, .	0.8	9
40	Repriming by PrimPol is critical for DNA replication restart downstream of lesions and chain-terminating nucleosides. Cell Cycle, 2016, 15, 1997-2008.	1.3	88
41	Complete genome sequence of Burkholderia caribensis Bcrs1W (NBRC110739), a strain co-residing with phenanthrene degrader Mycobacterium sp. EPa45. Journal of Biotechnology, 2016, 228, 67-68.	1.9	7
42	Comparison of the complete genome sequences of four Î ³ -hexachlorocyclohexane-degrading bacterial strains: insights into the evolution of bacteria able to degrade a recalcitrant man-made pesticide. DNA Research, 2016, 23, 581-599.	1.5	29
43	Mre11 Is Essential for the Removal of Lethal Topoisomerase 2 Covalent Cleavage Complexes. Molecular Cell, 2016, 64, 580-592.	4.5	144
44	Complete Genome Sequence of Sphingopyxis macrogoltabida Strain 203N (NBRC 111659), a Polyethylene Glycol Degrader. Genome Announcements, 2016, 4, .	0.8	1
45	Complete Genome Sequence of Sphingopyxis terrae Strain 203-1 (NBRC 111660), a Polyethylene Glycol Degrader. Genome Announcements, 2016, 4, .	0.8	1
46	Biodegradation of γ-hexachlorocyclohexane by transgenic hairy root cultures of Cucurbita moschata that accumulate recombinant bacterial LinA. Plant Cell Reports, 2016, 35, 1963-1974.	2.8	14
47	In vivoevidence for translesion synthesis by the replicative DNA polymerase δ. Nucleic Acids Research, 2016, 44, gkw439.	6.5	33
48	Complete Genome Sequence of Polyvinyl Alcohol-Degrading Strain Sphingopyxis sp. 113P3 (NBRC 111507). Genome Announcements, 2015, 3, .	0.8	4
49	Complete Genome Sequence of Polypropylene Glycol- and Polyethylene Glycol-Degrading Sphingopyxis macrogoltabida Strain EY-1. Genome Announcements, 2015, 3, .	0.8	Ο
50	Complete Genome Sequence of Sphingopyxis macrogoltabida Type Strain NBRC 15033, Originally Isolated as a Polyethylene Glycol Degrader. Genome Announcements, 2015, 3, .	0.8	1
51	Complete Genome Sequence of a Polypropylene Glycol-Degrading Strain, Microbacterium sp. No. 7. Genome Announcements, 2015, 3, .	0.8	4
52	Properties and biotechnological applications of natural and engineered haloalkane dehalogenases. Applied Microbiology and Biotechnology, 2015, 99, 9865-9881.	1.7	53
53	Complete Genome Sequence of a Phenanthrene Degrader, Burkholderia sp. HB-1 (NBRC 110738). Genome Announcements, 2015, 3, .	0.8	6
54	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. DNA Research, 2015, 22, 413-424.	1.5	39

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55	Isolation of oxygenase genes for indigo-forming activity from an artificially polluted soil metagenome by functional screening using Pseudomonas putida strains as hosts. Applied Microbiology and Biotechnology, 2015, 99, 4453-4470.	1.7	48
56	The POLD3 subunit of DNA polymerase δ can promote translesion synthesis independently of DNA polymerase ζ. Nucleic Acids Research, 2015, 43, 1671-1683.	6.5	51
57	Bacterial clade with the ribosomal RNA operon on a small plasmid rather than the chromosome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14343-14347.	3.3	47
58	Complete Genome Sequence of a Phenanthrene Degrader, Mycobacterium sp. Strain EPa45 (NBRC) Tj ETQq0 0 () rgBT /Ov	erlock 10 Tf 5
59	Complete Genome Sequence of Pseudomonas aeruginosa MTB-1, Isolated from a Microbial Community Enriched by the Technical Formulation of Hexachlorocyclohexane. Genome Announcements, 2014, 2, .	0.8	7
60	Stepwise enhancement of catalytic performance of haloalkane dehalogenase LinB towards β-hexachlorocyclohexane. AMB Express, 2014, 4, 72.	1.4	11
61	Complete Genome Sequence of the Thermophilic Polychlorinated Biphenyl Degrader <i>Geobacillus</i> sp. Strain JF8 (NBRC 109937). Genome Announcements, 2014, 2, .	0.8	15
62	Identification of Burkholderia multivorans ATCC 17616 genetic determinants for fitness in soil by using signature-tagged mutagenesis. Microbiology (United Kingdom), 2014, 160, 883-891.	0.7	14
63	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. DNA Research, 2014, 21, 217-227.	1.5	432
64	Complete Genome Sequence of Pseudomonas sp. Strain TKP, Isolated from a γ-Hexachlorocyclohexane-Degrading Mixed Culture. Genome Announcements, 2014, 2, .	0.8	12
65	Mobile Catabolic Genetic Elements in Pseudomonads. , 2014, , 83-103.		5
66	Inhibitory effect ofPseudomonas putidanitrogen-related phosphotransferase system on conjugative transfer of IncP-9 plasmid fromEscherichia coli. FEMS Microbiology Letters, 2013, 345, 102-109.	0.7	6
67	Cointegrate-resolution of toluene-catabolic transposon Tn4651: Determination of crossover site and the segment required for full resolution activity. Plasmid, 2013, 69, 24-35.	0.4	19
68	Analysis of Extracellular Alginate Lyase (alyA) Expression and its Regulatory Region in a Marine Bacterial Strain, Pseudoalteromonas atlantica AR06, Using a gfp Gene Reporter System. Marine Biotechnology, 2013, 15, 349-356.	1.1	7
69	Crystal Structure and Site-Directed Mutagenesis Analyses of Haloalkane Dehalogenase LinB from Sphingobium sp. Strain MI1205. Journal of Bacteriology, 2013, 195, 2642-2651.	1.0	20
70	Complete Genome Sequence of Ralstonia pickettii DTP0602, a 2,4,6-Trichlorophenol Degrader. Genome Announcements, 2013, 1, .	0.8	10
71	Conjugal Transfer of Polychlorinated Biphenyl/Biphenyl Degradation Genes in Acidovorax sp. Strain KKS102, Which Are Located on an Integrative and Conjugative Element. Journal of Bacteriology, 2012, 194, 4237-4248.	1.0	42
72	Suppression of pleiotropic phenotypes of a Burkholderia multivorans fur mutant by oxyR mutation. Microbiology (United Kingdom), 2012, 158, 1284-1293.	0.7	11

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73	Complete Genome Sequence of Acidovorax sp. Strain KKS102, a Polychlorinated-Biphenyl Degrader. Journal of Bacteriology, 2012, 194, 6970-6971.	1.0	117
74	<scp>ParI</scp> , an orphan <scp>ParA</scp> family protein from <i><scp>P</scp>seudomonas putida</i> â€ <scp>KT</scp> 2440â€specific genomic island, interferes with the partition system of <scp>IncP</scp> â€7 plasmids. Environmental Microbiology, 2012, 14, 2946-2959.	1.8	18
75	Cloning of γ-hexachlorocyclohexane dehydrochlorinase gene with its flanking regions from soil by activity-based screening techniques. European Journal of Soil Biology, 2012, 52, 16-19.	1.4	5
76	Pivotal role of anthranilate dioxygenase genes in the adaptation of Burkholderia multivorans ATCC 17616 in soil. FEMS Microbiology Letters, 2012, 330, 46-55.	0.7	4
77	Genomic organization and genomic structural rearrangements of Sphingobium japonicum UT26, an archetypal γ-hexachlorocyclohexane-degrading bacterium. Enzyme and Microbial Technology, 2011, 49, 499-508.	1.6	47
78	The <i>lin</i> Genes for γ-Hexachlorocyclohexane Degradation in <i>Sphingomonas</i> sp. MM-1 Proved to Be Dispersed across Multiple Plasmids. Bioscience, Biotechnology and Biochemistry, 2011, 75, 466-472.	0.6	53
79	Involvement of SLX4 in interstrand cross-link repair is regulated by the Fanconi anemia pathway. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6492-6496.	3.3	169
80	Complete Nucleotide Sequence of TOL Plasmid pDK1 Provides Evidence for Evolutionary History of IncP-7 Catabolic Plasmids. Journal of Bacteriology, 2010, 192, 5558-5558.	1.0	1
81	ã,²ãƒŽãƒè§£æžã,½ãƒ∙ãƒ^ã,¦ã,¨ã,¢GenomeMatcher. Kagaku To Seibutsu, 2010, 48, 313-319.	0.0	0
82	Analysis of extracellular alginate lyase and its gene from a marine bacterial strain, Pseudoalteromonas atlantica AR06. Applied Microbiology and Biotechnology, 2010, 86, 567-576.	1.7	47
83	Conjugative transfer of naphthalene-catabolic plasmid NAH7 regulated by nitrogen-related phosphotransferase system of recipient cells. Journal of Biotechnology, 2010, 150, 269-269.	1.9	0
84	ldentification of <i>Burkholderia multivorans</i> ATCC 17616 genes induced in soil environment by <i>in vivo</i> expression technology. Environmental Microbiology, 2010, 12, 2539-2558.	1.8	31
85	Complete Nucleotide Sequence of TOL Plasmid pDK1 Provides Evidence for Evolutionary History of IncP-7 Catabolic Plasmids. Journal of Bacteriology, 2010, 192, 4337-4347.	1.0	53
86	Complete Genome Sequence of the Representative γ-Hexachlorocyclohexane-Degrading Bacterium <i>Sphingobium japonicum</i> UT26. Journal of Bacteriology, 2010, 192, 5852-5853.	1.0	66
87	Optimization of the packing in the haloalkane dehalogenase crystal by seeding. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s293-s293.	0.3	0
88	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. ISME Journal, 2009, 3, 1335-1348.	4.4	80
89	Redesigning dehalogenase access tunnels as a strategy for degrading an anthropogenic substrate. Nature Chemical Biology, 2009, 5, 727-733.	3.9	238
90	Title is missing!. Kagaku To Seibutsu, 2009, 47, 35-42.	0.0	0

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91	Insertion sequence-based cassette PCR: cultivation-independent isolation of γ-hexachlorocyclohexane-degrading genes from soil DNA. Applied Microbiology and Biotechnology, 2008, 79, 627-632.	1.7	17
92	GenomeMatcher: A graphical user interface for DNA sequence comparison. BMC Bioinformatics, 2008, 9, 376.	1.2	233
93	Revised nomenclature for transposable genetic elements. Plasmid, 2008, 60, 167-173.	0.4	222
94	Pleiotropic roles of iron-responsive transcriptional regulator Fur in Burkholderia multivorans. Microbiology (United Kingdom), 2008, 154, 1763-1774.	0.7	39
95	Characterization of the <i>traD</i> Operon of Naphthalene-Catabolic Plasmid NAH7: a Host-Range Modifier in Conjugative Transfer. Journal of Bacteriology, 2008, 190, 6281-6289.	1.0	15
96	Construction of Signature-tagged Mutant Library in Mesorhizobium loti as a Powerful Tool for Functional Genomics. DNA Research, 2008, 15, 297-308.	1.5	41
97	Region-Specific Insertion of Transposons in Combination with Selection for High Plasmid Transferability and Stability Accounts for the Structural Similarity of IncP-1 Plasmids. Journal of Bacteriology, 2007, 189, 3091-3098.	1.0	52
98	Identification and Characterization of Genes Encoding a Putative ABC-Type Transporter Essential for Utilization of γ-Hexachlorocyclohexane in Sphingobium japonicum UT26. Journal of Bacteriology, 2007, 189, 3712-3720.	1.0	56
99	The identification of catalytic pentad in the haloalkane dehalogenase DhmA from Mycobacterium avium N85: Reaction mechanism and molecular evolution. Journal of Structural Biology, 2007, 157, 384-392.	1.3	14
100	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. Journal of Molecular Biology, 2007, 369, 11-26.	2.0	50
101	Crystallization and preliminary crystallographic analysis of a haloalkane dehalogenase, DbjA, fromBradyrhizobium japonicumUSDA110. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 294-296.	0.7	11
102	Degradation of β-hexachlorocyclohexane by haloalkane dehalogenase LinB from γ-hexachlorocyclohexane-utilizing bacterium Sphingobium sp. MI1205. Archives of Microbiology, 2007, 188, 313-325.	1.0	62
103	Isolation and characterization of naphthalene-catabolic genes and plasmids from oil-contaminated soil by using two cultivation-independent approaches. Applied Microbiology and Biotechnology, 2007, 74, 501-510.	1.7	77
104	Aerobic degradation of lindane (γ-hexachlorocyclohexane) in bacteria and its biochemical and model and molecular basis. Applied Microbiology and Biotechnology, 2007, 76, 741-752.	1.7	192
105	Growth Inhibition by Metabolites of γ-Hexachlorocyclohexane inSphingobium japonicumUT26. Bioscience, Biotechnology and Biochemistry, 2006, 70, 1029-1032.	0.6	17
106	Global Gene Expression in Bradyrhizobium japonicum Cultured with Vanillin, Vanillate, 4-Hydroxybenzoate and Protocatechuate. Microbes and Environments, 2006, 21, 240-250.	0.7	22
107	Distribution of γ-hexachlorocyclohexane-degrading genes on three replicons inSphingobium japonicumUT26. FEMS Microbiology Letters, 2006, 256, 112-118.	0.7	36
108	Identification of a response regulator gene for catabolite control from a PCB-degrading beta-proteobacteria, Acidovorax sp. KKS102. Molecular Microbiology, 2006, 60, 1563-1575.	1.2	51

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109	Comparative Analysis of argK-tox Clusters and Their Flanking Regions in Phaseolotoxin-Producing Pseudomonas syringae Pathovars. Journal of Molecular Evolution, 2006, 63, 401-414.	0.8	35
110	Functional Analysis of Unique Class II Insertion Sequence IS 1071. Applied and Environmental Microbiology, 2006, 72, 291-297.	1.4	36
111	Characterization of the Replication, Maintenance, and Transfer Features of the IncP-7 Plasmid pCAR1, Which Carries Genes Involved in Carbazole and Dioxin Degradation. Applied and Environmental Microbiology, 2006, 72, 3206-3216.	1.4	80
112	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. Journal of Bacteriology, 2006, 188, 4057-4067.	1.0	98
113	Complete Nucleotide Sequence of an Exogenously Isolated Plasmid, pLB1, Involved in γ-Hexachlorocyclohexane Degradation. Applied and Environmental Microbiology, 2006, 72, 6923-6933.	1.4	58
114	Recipient Range of IncP-7 Conjugative Plasmid pCAR2 from Pseudomonas putida HS01 is Broader than from Other Pseudomonas Strains. Biotechnology Letters, 2005, 27, 1847-1853.	1.1	57
115	Identification and Characterization of Genes Involved in the Downstream Degradation Pathway of γ-Hexachlorocyclohexane in Sphingomonas paucimobilis UT26. Journal of Bacteriology, 2005, 187, 847-853.	1.0	76
116	Two Rhizobial Strains, Mesorhizobium loti MAFF303099 and Bradyrhizobium japonicum USDA110, Encode Haloalkane Dehalogenases with Novel Structures and Substrate Specificities. Applied and Environmental Microbiology, 2005, 71, 4372-4379.	1.4	73
117	Degradation of β-Hexachlorocyclohexane by Haloalkane Dehalogenase LinB from Sphingomonas paucimobilis UT26. Applied and Environmental Microbiology, 2005, 71, 2183-2185.	1.4	72
118	High-Temperature-Induced Transposition of Insertion Elements in Burkholderia multivorans ATCC 17616. Applied and Environmental Microbiology, 2005, 71, 1822-1828.	1.4	48
119	Organization and localization of the dnaA and dnaK gene regions on the multichromosomal genome of Burkholderia multivorans ATCC 17616. Journal of Bioscience and Bioengineering, 2005, 99, 603-610.	1.1	9
120	Identification of Insertion Sequence from a γ-Hexachlorocyclohexane Degrading Bacterium,Sphingomonas paucimobilisUT26. Bioscience, Biotechnology and Biochemistry, 2005, 69, 216-219.	0.6	3
121	Strategies for bioremediation of polychlorinated biphenyls. Applied Microbiology and Biotechnology, 2004, 65, 250-8.	1.7	99
122	Structure of Haloacetate-Catabolic IncP-1β Plasmid pUO1 and Genetic Mobility of Its Residing Haloacetate-Catabolic Transposon. Journal of Bacteriology, 2003, 185, 6741-6745.	1.0	53
123	Reconstruction of Mycobacterial Dehalogenase Rv2579 by Cumulative Mutagenesis of Haloalkane Dehalogenase LinB. Applied and Environmental Microbiology, 2003, 69, 2349-2355.	1.4	21
124	Modification of Activity and Specificity of Haloalkane Dehalogenase from Sphingomonas paucimobilis UT26 by Engineering of Its Entrance Tunnel. Journal of Biological Chemistry, 2003, 278, 52622-52628.	1.6	115
125	Distribution and Organization of Auxotrophic Genes on the Multichromosomal Genome of Burkholderia multivorans ATCC 17616. Journal of Bacteriology, 2003, 185, 3333-3343.	1.0	34
126	Characterization of a Class II Defective Transposon Carrying Two Haloacetate Dehalogenase Genes from Delftia acidovorans Plasmid pUO1. Applied and Environmental Microbiology, 2002, 68, 2307-2315.	1.4	34

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127	Site-Specific Recombination System Encoded by Toluene Catabolic Transposon Tn 4651. Journal of Bacteriology, 2002, 184, 4757-4766.	1.0	20
128	Halide-Stabilizing Residues of Haloalkane Dehalogenases Studied by Quantum Mechanic Calculations and Site-Directed Mutagenesisâ€. Biochemistry, 2002, 41, 14272-14280.	1.2	69
129	A Phylogenomic Study of the OCTase Genes in Pseudomonas syringae Pathovars: The Horizontal Transfer of the argK–tox Cluster and the Evolutionary History of OCTase Genes on Their Genomes. Journal of Molecular Evolution, 2002, 54, 437-457.	0.8	73
130	Ironâ€Mediated Regulation of Alkaline Proteinase Production in <i>Pseudomonas aeruginosa</i> . Microbiology and Immunology, 2001, 45, 579-590.	0.7	34
131	Identification and Characterization of Tn 4656 , a Novel Class II Transposon Carrying a Set of Toluene-Degrading Genes from TOL Plasmid pWW53. Journal of Bacteriology, 2001, 183, 6215-6224.	1.0	30
132	Identification of the urease operon in Helicobacter pylori and its control by mRNA decay in response to pH. Molecular Microbiology, 2000, 36, 1071-1084.	1.2	154
133	Mobile catabolic genes in bacteria. Journal of Bioscience and Bioengineering, 1999, 87, 401-410.	1.1	66
134	Cloning and characterization of the thiD/J gene of Escherichia coli encoding a thiamin-synthesizing bifunctional enzyme, hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase. Microbiology (United Kingdom), 1999, 145, 495-501.	0.7	49
135	Nucleotide Sequence and Characterization of cdrA, a Cell Division-Related Gene of Helicobacter pylori. Journal of Bacteriology, 1999, 181, 5134-5134.	1.0	0
136	Functional replacement of OprJ by OprM in the MexCD-OprJ multidrug efflux system ofPseudomonas aeruginosa. FEMS Microbiology Letters, 1998, 165, 21-27.	0.7	52
137	Use of a transposon-encoded site-specific resolution system for construction of large and defined deletion mutations in bacterial chromosome. Gene, 1998, 207, 33-41.	1.0	28
138	Characterization of the MexC-MexD-OprJ Multidrug Efflux System in Δ <i>mexA-mexB-oprM</i> Mutants of <i>Pseudomonas aeruginosa</i> . Antimicrobial Agents and Chemotherapy, 1998, 42, 1938-1943.	1.4	102
139	Nucleotide Sequence and Characterization of cdrA , a Cell Division-Related Gene of Helicobacter pylori. Journal of Bacteriology, 1998, 180, 5263-5268.	1.0	37
140	Fiber-Optic-Based Biomonitoring of Benzene Derivatives by RecombinantE.coliBearing Luciferase Gene-Fused TOL-Plasmid Immobilized on the Fiber-Optic End. Analytical Chemistry, 1997, 69, 2600-2605.	3.2	80
141	The Role ofmex-Gene Products in Antibiotic Extrusion inPseudomonas aeruginosa. Biochemical and Biophysical Research Communications, 1997, 233, 611-618.	1.0	71
142	A genetic analysis system of Burkholderia cepacia: construction of mobilizable transposons and a cloning vector. Gene, 1996, 174, 191-194.	1.0	18
143	A positive regulatory gene,pvdS, for expression of pyoverdin biosynthetic genes inPseudomonas aeruginosa PAO. Molecular Genetics and Genomics, 1995, 248, 17-24.	2.4	74
144	Genetic Transformation in <i>Helicobacter pylori</i> . Microbiology and Immunology, 1993, 37, 85-89.	0.7	55

#	Article	IF	CITATIONS
145	Tol Plasmid: Organization And Regulation Of Gene Expression. , 1992, , 139-142.		0
146	Naphthalene degrading genes on plasmid NAH7 are on a defective transposon. Molecular Genetics and Genomics, 1990, 223, 33-39.	2.4	101
147	Identification and characterization of Tn4653, a transposon covering the toluene transposon Tn4651 on TOL plasmid pWW0. Molecular Genetics and Genomics, 1988, 213, 72-77.	2.4	78
148	Genetic analysis of a transposon carrying toluene degrading genes on a TOL plasmid pWWO. Molecular Genetics and Genomics, 1987, 210, 270-276.	2.4	118
149	Tn501 insertion mutagenesis in Pseudomonas aeruginosa PAO. Molecular Genetics and Genomics, 1984, 196, 494-500.	2.4	27
150	Tn1 insertion mutagenesis in Escherichia coli K-12 using a temperature-sensitive mutant of plasmid RP4. Molecular Genetics and Genomics, 1981, 184, 52-55.	2.4	16
151	High frequency mobilization of the chromosome of Escherichia coli by a mutant of plasmid RP4 temperature-Sensitive for maintenance. Molecular Genetics and Genomics, 1980, 180, 47-56.	2.4	85
152	Biodegradation of Organochlorine Pesticides. , 0, , 5.1.2-1-5.1.2-30.		7