

Ryo Miyazaki

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

27
papers

810
citations

16
h-index

28
g-index

29
ext. papers

1,079
ext. citations

5.8
avg, IF

3.92
L-index

#	Paper	IF	Citations
27	Deep Sequencing Uncovers Caste-Associated Diversity of Symbionts in the Social Ant <i>Camponotus japonicus</i> . <i>MBio</i> , 2020 , 11,	7.8	3
26	Vast Differences in Strain-Level Diversity in the Gut Microbiota of Two Closely Related Honey Bee Species. <i>Current Biology</i> , 2020 , 30, 2520-2531.e7	6.3	28
25	Local Necrotic Cells Trigger Systemic Immune Activation via Gut Microbiome Dysbiosis in <i>Drosophila</i> . <i>Cell Reports</i> , 2020 , 32, 107938	10.6	4
24	Community analysis of gut microbiota in hornets, the largest eusocial wasps, <i>Vespa mandarinia</i> and <i>V. simillima</i> . <i>Scientific Reports</i> , 2019 , 9, 9830	4.9	17
23	A novel system of bacterial cell division arrest implicated in horizontal transmission of an integrative and conjugative element. <i>PLoS Genetics</i> , 2019 , 15, e1008445	6	2
22	Physiological and transcriptome changes induced by <i>Pseudomonas putida</i> acquisition of an integrative and conjugative element. <i>Scientific Reports</i> , 2018 , 8, 5550	4.9	9
21	The hidden life of integrative and conjugative elements. <i>FEMS Microbiology Reviews</i> , 2017 , 41, 512-537	15.1	86
20	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015 , 6, 101	5.7	21
19	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015 , 17, 91-104	5.2	30
18	An operon of three transcriptional regulators controls horizontal gene transfer of the integrative and conjugative element ICE _{clc} in <i>Pseudomonas knackmussii</i> B13. <i>PLoS Genetics</i> , 2014 , 10, e1004441	6	14
17	The TetR-type MfsR protein of the integrative and conjugative element (ICE) ICE _{clc} controls both a putative efflux system and initiation of ICE transfer. <i>Journal of Bacteriology</i> , 2014 , 196, 3971-9	3.5	7
16	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, 102-9 ^{2.9}	2.9	5
15	A new large-DNA-fragment delivery system based on integrase activity from an integrative and conjugative element. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 4440-7	4.8	17
14	Cell differentiation to "mating bodies" induced by an integrating and conjugative element in free-living bacteria. <i>Current Biology</i> , 2013 , 23, 255-9	6.3	24
13	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , 2013 , 7, 1173-86	11.9	96
12	Cellular variability of RpoS expression underlies subpopulation activation of an integrative and conjugative element. <i>PLoS Genetics</i> , 2012 , 8, e1002818	6	32
11	A dual functional origin of transfer in the ICE _{clc} genomic island of <i>Pseudomonas knackmussii</i> B13. <i>Molecular Microbiology</i> , 2011 , 79, 743-58	4.1	28

10	How can a dual oriT system contribute to efficient transfer of an integrative and conjugative element?. <i>Mobile Genetic Elements</i> , 2011 , 1, 82-84		4
9	Intracellular excision and reintegration dynamics of the ICE _{clc} genomic island of <i>Pseudomonas knackmussii</i> sp. strain B13. <i>Molecular Microbiology</i> , 2009 , 72, 1293-306	4.1	43
8	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. <i>ISME Journal</i> , 2009 , 3, 1335-48	11.9	68
7	Characterization of the traD operon of naphthalene-catabolic plasmid NAH7: a host-range modifier in conjugative transfer. <i>Journal of Bacteriology</i> , 2008 , 190, 6281-9	3.5	11
6	Insertion sequence-based cassette PCR: cultivation-independent isolation of gamma-hexachlorocyclohexane-degrading genes from soil DNA. <i>Applied Microbiology and Biotechnology</i> , 2008 , 79, 627-32	5.7	14
5	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, 501-10	5.7	70
4	Genomic and functional analysis of the IncP-9 naphthalene-catabolic plasmid NAH7 and its transposon Tn4655 suggests catabolic gene spread by a tyrosine recombinase. <i>Journal of Bacteriology</i> , 2006 , 188, 4057-67	3.5	84
3	Complete nucleotide sequence of an exogenously isolated plasmid, pLB1, involved in gamma-hexachlorocyclohexane degradation. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6923-33 ^{4.8}		55
2	Distribution of gamma-hexachlorocyclohexane-degrading genes on three replicons in <i>Sphingobium japonicum</i> UT26. <i>FEMS Microbiology Letters</i> , 2006 , 256, 112-8	2.9	35
1	Vast differences in strain-level diversity in the gut microbiota of two closely related honey bee species		2