

INTEGRALL: a database and search engine for integrons

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Worldwide Prevalence of Class 2 Integrases outside the Clinical Setting Is Associated with Human Impact. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5100-5110.	3.1	41
2	Context-driven discovery of gene cassettes in mobile integrons using a computational grammar. <i>BMC Bioinformatics</i> , 2009, 10, 281.	2.6	17
3	ACLAME: A CLAssification of Mobile genetic Elements, update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D57-D61.	14.5	289
4	Wastewater bacterial communities bring together broad-host range plasmids, integrons and a wide diversity of uncharacterized gene cassettes. <i>Research in Microbiology</i> , 2010, 161, 58-66.	2.1	89
5	Actualit�s sur les int�grons de r�sistance aux antibiotiques: mise au point. <i>Journal Des Anti-infectieux</i> , 2011, 13, 133-144.	0.1	5
6	Pyrosequencing of Antibiotic-Contaminated River Sediments Reveals High Levels of Resistance and Gene Transfer Elements. <i>PLoS ONE</i> , 2011, 6, e17038.	2.5	452
8	Gene flow, mobile genetic elements and the recruitment of antibiotic resistance genes into Gram-negative pathogens. <i>FEMS Microbiology Reviews</i> , 2011, 35, 790-819.	8.6	530
9	Analysis of antibiotic resistance regions in Gram-negative bacteria. <i>FEMS Microbiology Reviews</i> , 2011, 35, 820-855.	8.6	290
10	Characterization and horizontal transfer of class 1 integrons in Salmonella strains isolated from food products of animal origin. <i>International Journal of Food Microbiology</i> , 2011, 149, 274-277.	4.7	24
11	The influence of the accessory genome on bacterial pathogen evolution. <i>Mobile Genetic Elements</i> , 2011, 1, 55-65.	1.8	125
12	RAC: Repository of Antibiotic resistance Cassettes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar054-bar054.	3.0	57
13	Computational inference of grammars for larger-than-gene structures from annotated gene sequences. <i>Bioinformatics</i> , 2011, 27, 791-796.	4.1	6
14	Evolution of an Incompatibility Group IncA/C Plasmid Harboring <i>bla</i> _{CMY-16} and <i>qnrA6</i> Genes and Its Transfer through Three Clones of <i>Providencia stuartii</i> during a Two-Year Outbreak in a Tunisian Burn Unit. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1342-1349.	3.2	30
15	Two Novel Class I Integron Arrays Containing IMP-18 Metallo- β -Lactamase Gene in <i>Pseudomonas aeruginosa</i> Clinical Isolates from Puerto Rico. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2119-2121.	3.2	18
16	Detection and Characterization of VIM-31, a New Variant of VIM-2 with Tyr224His and His252Arg Mutations, in a Clinical Isolate of <i>Enterobacter cloacae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 3283-3287.	3.2	14
17	Integrons. <i>Mobile Genetic Elements</i> , 2012, 2, 211-223.	1.8	139
18	Novel gene cassettes and integrons in antibiotic-resistant bacteria isolated from urban wastewaters. <i>Research in Microbiology</i> , 2012, 163, 92-100.	2.1	77
19	Analysis of Drug Resistance Determinants in <i>Klebsiella pneumoniae</i> Isolates from a Tertiary-Care Hospital in Beijing, China. <i>PLoS ONE</i> , 2012, 7, e42280.	2.5	41

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20	Clonal Spread of Carbapenem Non-susceptible <i>Acinetobacter baumannii</i> in an Intensive Care Unit in a Teaching Hospital in China. <i>Annals of Laboratory Medicine</i> , 2012, 32, 413-419.	2.5	17
21	Beta-lactams resistance and presence of class 1 integron in <i>Pseudomonas</i> spp. isolated from untreated hospital effluents in Brazil. <i>Antonie Van Leeuwenhoek</i> , 2012, 102, 73-81.	1.7	32
22	Antibiotic-resistant <i>Escherichia coli</i> in karstic systems: a biological indicator of the origin of fecal contamination?. <i>FEMS Microbiology Ecology</i> , 2012, 81, 267-280.	2.7	24
23	Broad diversity of conjugative plasmids in integron-carrying bacteria from wastewater environments. <i>FEMS Microbiology Letters</i> , 2012, 330, 157-164.	1.8	43
24	The gain and loss of chromosomal integron systems in the <i>Treponema</i> species. <i>BMC Evolutionary Biology</i> , 2013, 13, 16.	3.2	20
25	Distinguishable Epidemics of Multidrug-Resistant <i>Salmonella</i> Typhimurium DT104 in Different Hosts. <i>Science</i> , 2013, 341, 1514-1517.	12.6	310
26	Integron attI1 Sites, Not Riboswitches, Associate with Antibiotic Resistance Genes. <i>Cell</i> , 2013, 153, 1417-1418.	28.9	19
27	Comparative genomics of IncP-1 μ plasmids from water environments reveals diverse and unique accessory genetic elements. <i>Plasmid</i> , 2013, 70, 412-419.	1.4	12
28	Genetic diversity and antimicrobial resistance of <i>Escherichia coli</i> from Tagus estuary (Portugal). <i>Science of the Total Environment</i> , 2013, 461-462, 65-71.	8.0	41
29	GES-18, a New Carbapenem-Hydrolyzing GES-Type β -Lactamase from <i>Pseudomonas aeruginosa</i> That Contains Ile80 and Ser170 Residues. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 396-401.	3.2	36
30	Metagenomic insights into chlorination effects on microbial antibiotic resistance in drinking water. <i>Water Research</i> , 2013, 47, 111-120.	11.3	423
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33	Metagenomic Profiles of Antibiotic Resistance Genes (ARGs) between Human Impacted Estuary and Deep Ocean Sediments. <i>Environmental Science & Technology</i> , 2013, 47, 12753-12760.	10.0	329
34	Identical Miniature Inverted Repeat Transposable Elements Flank Class 1 Integrons in Clinical Isolates of <i>Acinetobacter</i> spp. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2382-2384.	3.9	16
35	Metagenomic analysis reveals significant changes of microbial compositions and protective functions during drinking water treatment. <i>Scientific Reports</i> , 2013, 3, 3550.	3.3	116
36	Structural Diversity of Class 1 Integrons and Their Associated Gene Cassettes in <i>Klebsiella pneumoniae</i> Isolates from a Hospital in China. <i>PLoS ONE</i> , 2013, 8, e75805.	2.5	41
37	Resistance Determinants and Mobile Genetic Elements of an NDM-1-Encoding <i>Klebsiella pneumoniae</i> Strain. <i>PLoS ONE</i> , 2014, 9, e99209.	2.5	123

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38	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
39	Characterization of Antibiotic Resistance in Escherichia coli Isolated from Shrimps and Their Environment. Journal of Food Protection, 2014, 77, 1394-1401.	1.7	33
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48	An overview of the domestication and impact of the <i>Salmonella</i> mobilome. Critical Reviews in Microbiology, 2014, 40, 63-75.	6.1	14
49	The Integron: Adaptation On Demand. Microbiology Spectrum, 2015, 3, MDNA3-0019-2014.	3.0	95
50	Stepwise evolution of pandrug-resistance in Klebsiella pneumoniae. Scientific Reports, 2015, 5, 15082.	3.3	115
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57	Low Prevalence of Carbapenem-Resistant Bacteria in River Water: Resistance Is Mostly Related to Intrinsic Mechanisms. <i>Microbial Drug Resistance</i> , 2015, 21, 497-506.	2.0	77
58	Pan-genome dynamics of <i>Pseudomonas</i> gene complements enriched across hexachlorocyclohexane dumpsite. <i>BMC Genomics</i> , 2015, 16, 313.	2.8	19
59	Acquired metallo- β -lactamases and their genetic association with class 1 integrons and IS _{CR} elements in Gram-negative bacteria. <i>Future Microbiology</i> , 2015, 10, 873-887.	2.0	38
60	Distribution of Integrons and Gene Cassettes Among Uropathogenic and Diarrheagenic <i>Escherichia coli</i> Isolates in Iran. <i>Microbial Drug Resistance</i> , 2015, 21, 435-440.	2.0	20
61	Sequencing of plasmids pAMBL1 and pAMBL2 from <i>Pseudomonas aeruginosa</i> reveals a <i>bla</i> _{VIM-1} amplification causing high-level carbapenem resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 3000-3003.	3.0	35
62	Antibiotic resistance and prevalence of class 1 and 2 integrons in <i>Escherichia coli</i> isolated from two wastewater treatment plants, and their receiving waters (Gulf of Gdansk, Baltic Sea, Poland). <i>Environmental Science and Pollution Research</i> , 2015, 22, 2018-2030.	5.3	82
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68	Complete Nucleotide Sequence of the IncN Plasmid Encoding IMP-6 and CTX-M-2 from Emerging Carbapenem-Resistant Enterobacteriaceae in Japan. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1356-1359.	3.2	39
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71	Clusters of Antibiotic Resistance Genes Enriched Together Stay Together in Swine Agriculture. <i>MBio</i> , 2016, 7, e02214-15.	4.1	201
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75	The importance of integrons for development and propagation of resistance in <i>Shigella</i> : the case of Latin America. <i>Brazilian Journal of Microbiology</i> , 2016, 47, 800-806.	2.0	10
76	Identification and analysis of integrons and cassette arrays in bacterial genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4539-4550.	14.5	235
77	Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. <i>Science of the Total Environment</i> , 2016, 572, 697-712.	8.0	213
78	HattCI: Fast and Accurate <i>attC</i> site Identification Using Hidden Markov Models. <i>Journal of Computational Biology</i> , 2016, 23, 891-902.	1.6	20
79	Unraveling genomic and phenotypic nature of multidrug-resistant (MDR) <i>Pseudomonas aeruginosa</i> VRFPA04 isolated from keratitis patient. <i>Microbiological Research</i> , 2016, 193, 140-149.	5.3	24
80	Efficiency of integron cassette insertion in correct orientation is ensured by the interplay of the three unpaired features of <i>attC</i> recombination sites. <i>Nucleic Acids Research</i> , 2016, 44, 7792-7803.	14.5	38
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82	Co-selection of antibiotic and metal(loid) resistance in gram-negative epiphytic bacteria from contaminated salt marshes. <i>Marine Pollution Bulletin</i> , 2016, 109, 427-434.	5.0	38
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88	Whole-genome typing and characterization of <i>bla</i> _{VIM19} -harbouring ST383 <i>Klebsiella pneumoniae</i> by PFGE, whole-genome mapping and WGS. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 1501-1509.	3.0	14
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90	VRprofile: gene-cluster-detection-based profiling of virulence and antibiotic resistance traits encoded within genome sequences of pathogenic bacteria. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw141.	6.5	100
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93	Identification of beta-Lactamases and beta-Lactam-Related Proteins in Human Pathogenic Bacteria using a Computational Search Approach. <i>Current Microbiology</i> , 2017, 74, 915-920.	2.2	2
94	Detection of the florfenicol resistance gene floR in <i>Chryseobacterium</i> isolates from rainbow trout. Exception to the general rule?. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	17
95	Occurrence of a novel class 1 integron harboring qnrVC4 in <i>Salmonella</i> Rissen. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 282-286.	1.8	15
96	Insertion sequences enrichment in extreme Red sea brine pool vent. <i>Extremophiles</i> , 2017, 21, 271-282.	2.3	3
97	<i>attI1</i> -Located Small Open Reading Frames ORF-17 and ORF-11 in a Class 1 Integron Affect Expression of a Gene Cassette Possessing a Canonical Shine-Dalgarno Sequence. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	7
98	Complete Genome Sequences of Two <i>Pseudomonas aeruginosa</i> Strains Isolated from Children with Bacteremia. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
99	Molecular Characterization of Carbapenemase-Producing <i>Pseudomonas aeruginosa</i> of Czech Origin and Evidence for Clonal Spread of Extensively Resistant Sequence Type 357 Expressing IMP-7 Metallo-β-Lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	45
100	Structural genomics of pNDM-BTR harboring <i>In191</i> and <i>Tn6360</i> , and other <i>bla</i> _{NDM} -carrying <i>IncN1</i> plasmids. <i>Future Microbiology</i> , 2017, 12, 1271-1281.	2.0	18
101	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> 704SK6, an OXA-48- and CTX-M-15-Encoding Wastewater Isolate. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
102	Complete Genome Sequences of Four Extensively Drug-Resistant <i>Pseudomonas aeruginosa</i> Strains, Isolated from Adults with Ventilator-Associated Pneumonia at a Tertiary Referral Hospital in Mexico City. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
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105	Novel class 1 Integrons and sequence types in VIM-2 and VIM-11-producing clinical strains of <i>Enterobacter cloacae</i> . <i>Infection, Genetics and Evolution</i> , 2017, 54, 374-378.	2.3	10
106	Genomic characterization of novel <i>IncFII</i> -type multidrug resistant plasmids p0716-KPC and p12181-KPC from <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2017, 7, 5830.	3.3	23
107	Detection of 224 candidate structured RNAs by comparative analysis of specific subsets of intergenic regions. <i>Nucleic Acids Research</i> , 2017, 45, 10811-10823.	14.5	116
108	Complete Genome Sequence of <i>Achromobacter denitrificans</i> PR1. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
109	Comparative genomics of type 1 <i>IncC</i> plasmids from China. <i>Future Microbiology</i> , 2017, 12, 1511-1522.	2.0	11

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110	Evolution and comparative genomics of pAQU-like conjugative plasmids in <i>Vibrio</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2503-2506.	3.0	11
111	Characterization of antibiotic resistant and pathogenic <i>Escherichia coli</i> in irrigation water and vegetables in household farms. <i>International Journal of Food Microbiology</i> , 2017, 257, 192-200.	4.7	95
112	OXA-427, a new plasmid-borne carbapenem-hydrolysing class D β -lactamase in Enterobacteriaceae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2469-2477.	3.0	24
113	Characterization of the Complete Nucleotide Sequences of IncA/C ₂ Plasmids Carrying In809-Like Integrons from Enterobacteriaceae Isolates of Wildlife Origin. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	35
114	Metagenomic analysis reveals wastewater treatment plants as hotspots of antibiotic resistance genes and mobile genetic elements. <i>Water Research</i> , 2017, 123, 468-478.	11.3	604
115	Genomics and the evolution of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 92-107.	3.8	50
116	Dynamic stepwise opening of integron attC DNA hairpins by SSB prevents toxicity and ensures functionality. <i>Nucleic Acids Research</i> , 2017, 45, 10555-10563.	14.5	23
117	Sequencing of blaIMP-Carrying IncN2 Plasmids, and Comparative Genomics of IncN2 Plasmids Harboring Class 1 Integrons. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 102.	3.9	22
118	Gene Expression in Class 2 Integrons Is SOS-Independent and Involves Two Pc Promoters. <i>Frontiers in Microbiology</i> , 2017, 8, 1499.	3.5	13
119	Characterization of Four Multidrug Resistance Plasmids Captured from the Sediments of an Urban Coastal Wetland. <i>Frontiers in Microbiology</i> , 2017, 8, 1922.	3.5	33
120	Molecular Characteristics of First IMP-4-Producing <i>Enterobacter cloacae</i> Sequence Type 74 and 194 in Korea. <i>Frontiers in Microbiology</i> , 2017, 8, 2343.	3.5	19
121	Genetic characterization of novel class 1 Integrons In0, In1069 and In1287 to In1290, and the inference of In1069-associated integron evolution in Enterobacteriaceae. <i>Antimicrobial Resistance and Infection Control</i> , 2017, 6, 84.	4.1	8
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124	Impact of Wastewater Treatment on the Prevalence of Integrons and the Genetic Diversity of Integron Gene Cassettes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	62
125	Characteristics of Carbapenemase-Producing Enterobacteriaceae in Wastewater Revealed by Genomic Analysis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	58
126	pSTM6-275, a Conjugative IncHI2 Plasmid of <i>Salmonella enterica</i> That Confers Antibiotic and Heavy-Metal Resistance under Changing Physiological Conditions. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	44
127	Automated annotation of mobile antibiotic resistance in Gram-negative bacteria: the Multiple Antibiotic Resistance Annotator (MARA) and database. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 883-890.	3.0	57

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128	A Practical Guide for Comparative Genomics of Mobile Genetic Elements in Prokaryotic Genomes. <i>Methods in Molecular Biology</i> , 2018, 1704, 213-242.	0.9	15
129	Draft Genome Sequence of Singapore <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> Isolate DS32358_14, Which Contains the Carbapenemase Gene <i>bla</i> _{VIM-1} . <i>Genome Announcements</i> , 2018, 6, .	0.8	0
130	Nucleotide sequence analysis of NPS-1 β -lactamase and a novel integron (In1427)-carrying transposon in an MDR <i>Pseudomonas aeruginosa</i> keratitis strain. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1724-1726.	3.0	14
131	Antibiotic resistance genes show enhanced mobilization through suspended growth and biofilm-based wastewater treatment processes. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	39
132	Integrons in Enterobacteriaceae : diversity, distribution and epidemiology. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 167-176.	2.5	76
133	Coexistence of two novel resistance plasmids, <i>bla</i> _{KPC-2} -carrying p14057A and <i>tetA</i> (A) -carrying p14057B, in <i>Pseudomonas aeruginosa</i> . <i>Virulence</i> , 2018, 9, 306-311.	4.4	18
134	Complete sequence of pBM413, a novel multidrug resistance megaplasmid carrying qnrVC6 and bla IMP-45 from <i>pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 145-150.	2.5	55
135	Distribution of ARGs and MGEs among glacial soil, permafrost, and sediment using metagenomic analysis. <i>Environmental Pollution</i> , 2018, 234, 339-346.	7.5	69
136	Co-occurrence of 3 different resistance plasmids in a multi-drug resistant <i>Cronobacter sakazakii</i> isolate causing neonatal infections. <i>Virulence</i> , 2018, 9, 110-120.	4.4	36
137	Comparative genomics analysis of pTEM-2262, an MDR plasmid from <i>Citrobacter freundii</i> , harboring two unclassified replicons. <i>Future Microbiology</i> , 2018, 13, 1657-1668.	2.0	3
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