

ARG-ANNOT, a New Bioinformatic Tool To Discover Antimicrobial Genomes

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Counting the Homeless. <i>Evaluation Review</i> , 1992, 16, 409-417.	0.4	9
2	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , 2014, 6, 90.	3.6	953
3	First Complete Genome Sequence of <i>Staphylococcus xylosus</i> , a Meat Starter Culture and a Host to Propagate <i>Staphylococcus aureus</i> Phages. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
4	Worldwide emergence of colistin resistance in <i>Klebsiella pneumoniae</i> from healthy humans and patients in Lao PDR, Thailand, Israel, Nigeria and France owing to inactivation of the PhoP/PhoQ regulator mgrB: an epidemiological and molecular study. <i>International Journal of Antimicrobial Agents</i> , 2014, 44, 500-507.	1.1	246
5	Comparison of the Web Tools ARG-ANNOT and ResFinder for Detection of Resistance Genes in Bacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4986-4986.	1.4	45
6	Characterizing the genetic basis of bacterial phenotypes using genome-wide association studies: a new direction for bacteriology. <i>Genome Medicine</i> , 2014, 6, 109.	3.6	105
7	Genome analysis of NDM-1 producing <i>Morganella morganii</i> clinical isolate. <i>Expert Review of Anti-Infective Therapy</i> , 2014, 12, 1297-1305.	2.0	34
8	Reply to "Comparison of the Web Tools ARG-ANNOT and ResFinder for Detection of Resistance Genes in Bacteria". <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4987-4987.	1.4	6
9	Assessing the genetic diversity of Cu resistance in mine tailings through high-throughput recovery of full-length copA genes. <i>Scientific Reports</i> , 2015, 5, 13258.	1.6	27
10	ISMMapper: identifying transposase insertion sites in bacterial genomes from short read sequence data. <i>BMC Genomics</i> , 2015, 16, 667.	1.2	119
11	Comparative genome analysis of the candidate functional starter culture strains <i>Lactobacillus fermentum</i> 222 and <i>Lactobacillus plantarum</i> 80 for controlled cocoa bean fermentation processes. <i>BMC Genomics</i> , 2015, 16, 766.	1.2	56
12	Draft Genome Sequence of a Clinical Isolate of <i>Serratia marcescens</i> , Strain AH0650_Sm1. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
13	Search Engine for Antimicrobial Resistance: A Cloud Compatible Pipeline and Web Interface for Rapidly Detecting Antimicrobial Resistance Genes Directly from Sequence Data. <i>PLoS ONE</i> , 2015, 10, e0133492.	1.1	62
14	Acquisition of extended-spectrum cephalosporin- and colistin-resistant <i>Salmonella enterica</i> subsp. <i>enterica</i> serotype Newport by pilgrims during Hajj. <i>International Journal of Antimicrobial Agents</i> , 2015, 45, 600-604.	1.1	52
15	Whole-Genome Sequence of <i>Chryseobacterium oranimense</i> , a Colistin-Resistant Bacterium Isolated from a Cystic Fibrosis Patient in France. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1696-1706.	1.4	29
16	Bioinformatics of antimicrobial resistance in the age of molecular epidemiology. <i>Current Opinion in Microbiology</i> , 2015, 27, 45-50.	2.3	103
17	MALDI-TOF MS as a Tool To Detect a Nosocomial Outbreak of Extended-Spectrum- β -Lactamase- and ArmA Methyltransferase-Producing <i>Enterobacter cloacae</i> Clinical Isolates in Algeria. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6477-6483.	1.4	32
18	Detection of expanded-spectrum β -lactamases in Gram-negative bacteria in the 21st century. <i>Expert Review of Anti-Infective Therapy</i> , 2015, 13, 1139-1158.	2.0	21

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19	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3574-81.	3.3	942
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21	Whole-genome assembly of <i>Akkermansia muciniphila</i> sequenced directly from human stool. Biology Direct, 2015, 10, 5.	1.9	32
22	SISPA-Seq for rapid whole genome surveys of bacterial isolates. Infection, Genetics and Evolution, 2015, 32, 191-198.	1.0	16
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24	The human gut resistome. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140087.	1.8	275
25	Whole genome sequencing in clinical and public health microbiology. Pathology, 2015, 47, 199-210.	0.3	226
26	Applying meta-pathway analyses through metagenomics to identify the functional properties of the major bacterial communities of a single spontaneous cocoa bean fermentation process sample. Food Microbiology, 2015, 50, 54-63.	2.1	88
27	Next-Generation Sequencing for Infectious Disease Diagnosis and Management. Journal of Molecular Diagnostics, 2015, 17, 623-634.	1.2	151
28	Complete Genome Sequence of the Clinical Strain <i>Acinetobacter baumannii</i> R2090 Carrying the Chromosomally Encoded Metallo- β -Lactamase Gene <i>bla</i> _{NDM-1} . Genome Announcements, 2015, 3, .	0.8	1
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32	<i>Bacillus niameyensis</i> sp. nov., a new bacterial species isolated from human gut. New Microbes and New Infections, 2015, 8, 61-69.	0.8	7
33	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Orion Strain CRJGF_00093 (Phylum <i>Gammaproteobacteria</i>). Genome Announcements, 2016, 4, .	0.8	6
34	Functional characterization of the <i>Mycobacterium abscessus</i> genome coupled with condition specific transcriptomics reveals conserved molecular strategies for host adaptation and persistence. BMC Genomics, 2016, 17, 553.	1.2	76
35	Genomic Tools for Customized Recovery and Detection of Foodborne Shiga Toxigenic <i>Escherichia coli</i> . Journal of Food Protection, 2016, 79, 2066-2077.	0.8	14
36	In silico serotyping of <i>E. coli</i> from short read data identifies limited novel O-loci but extensive diversity of O:H serotype combinations within and between pathogenic lineages. Microbial Genomics, 2016, 2, e000064.	1.0	110

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38	Resistome diversity in cattle and the environment decreases during beef production. ELife, 2016, 5, e13195.	2.8	126
39	Genome Sequence of <i>Vibrio parahaemolyticus</i> VP152 Strain Isolated from <i>Penaeus indicus</i> in Malaysia. Frontiers in Microbiology, 2016, 7, 1410.	1.5	7
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42	Carbapenem-Resistant Bacteria Recovered from Faeces of Dairy Cattle in the High Plains Region of the USA. PLoS ONE, 2016, 11, e0147363.	1.1	64
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44	Draft Genome Sequence of <i>Mycobacterium wolinskyi</i> , a Rapid-Growing Species of Nontuberculous Mycobacteria. Genome Announcements, 2016, 4, .	0.8	3
45	SSTAR, a Stand-Alone Easy-To-Use Antimicrobial Resistance Gene Predictor. MSphere, 2016, 1, .	1.3	61
46	A genome-wide association study identifies a horizontally transferred bacterial surface adhesin gene associated with antimicrobial resistant strains. Scientific Reports, 2016, 6, 37811.	1.6	19
47	Carriage of ESBL/AmpC-producing or ciprofloxacin non-susceptible <i>Escherichia coli</i> and <i>Klebsiella</i> spp. in healthy people in Norway. Antimicrobial Resistance and Infection Control, 2016, 5, 57.	1.5	41
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51	Fortuitous diagnosis of NDM-1-producing <i>Acinetobacter pittii</i> carriage in a patient from France with no recent history of travel. Journal of Antimicrobial Chemotherapy, 2016, 72, dkw505.	1.3	9
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56	Biological and Epidemiological Features of Antibiotic-Resistant <i>Streptococcus pneumoniae</i> in Pre- and Post-Conjugate Vaccine Eras: a United States Perspective. <i>Clinical Microbiology Reviews</i> , 2016, 29, 525-552.	5.7	240
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71	Draft Genome Sequence for a Clinical Isolate of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	3
72	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Kiambu Strain CRJJGF_00061 (Phylum Gammaproteobacteria). <i>Genome Announcements</i> , 2016, 4, .	0.8	4

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89	Safety evaluation of AB-LIFEÂ® (<i>Lactobacillus plantarum</i> CECT 7527, 7528 and 7529): Antibiotic resistance and 90-day repeated-dose study in rats. <i>Food and Chemical Toxicology</i> , 2016, 92, 117-128.	1.8	31
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101	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. <i>ISME Journal</i> , 2017, 11, 237-247.	4.4	298
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110	MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580.	6.5	328
111	Draft Genome Sequences of Clinical Isolates of Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	2
112	Global Molecular Epidemiology of IMP-Producing Enterobacteriaceae. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	61
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128	Low Frequency of Ceftazidime-Avibactam Resistance among Enterobacteriaceae Isolates Carrying <i>bla</i> _{KPC} Collected in U.S. Hospitals from 2012 to 2015. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	47
129	Protracted Regional Dissemination of GIM-1-Producing <i>Serratia marcescens</i> in Western Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	6
130	New Laboratory Tools for Emerging Bacterial Challenges. <i>Clinical Infectious Diseases</i> , 2017, 65, S39-S49.	2.9	3
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133	Population and Whole Genome Sequence Based Characterization of Invasive Group A Streptococci Recovered in the United States during 2015. <i>MBio</i> , 2017, 8, .	1.8	110
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