

Joshua P Ramsay

List of Publications by Year in descending order

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53
papers

2,095
citations

394421

19
h-index

243625

44
g-index

54
all docs

54
docs citations

54
times ranked

2853
citing authors

#	ARTICLE	IF	CITATIONS
1	A census of mammalian imprinting. <i>Trends in Genetics</i> , 2005, 21, 457-465.	6.7	612
2	Statin therapy causes gut dysbiosis in mice through a PXR-dependent mechanism. <i>Microbiome</i> , 2017, 5, 95.	11.1	124
3	Excision and transfer of the <i>Mesorhizobium loti</i> R7A symbiosis island requires an integrase IntS, a novel recombination directionality factor RdfS, and a putative relaxase RlxS. <i>Molecular Microbiology</i> , 2006, 62, 723-734.	2.5	119
4	Diverse mobilization strategies facilitate transfer of non-conjugative mobile genetic elements. <i>Current Opinion in Microbiology</i> , 2017, 38, 1-9.	5.1	104
5	An updated view of plasmid conjugation and mobilization in <i>Staphylococcus</i> . <i>Mobile Genetic Elements</i> , 2016, 6, e1208317.	1.8	83
6	Origin-of-transfer sequences facilitate mobilisation of non-conjugative antimicrobial-resistance plasmids in <i>Staphylococcus aureus</i> . <i>Nucleic Acids Research</i> , 2015, 43, 7971-7983.	14.5	81
7	Ribosomal frameshifting and dual-target antiactivation restrict quorum-sensing-activated transfer of a mobile genetic element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4104-4109.	7.1	68
8	Assembly and transfer of tripartite integrative and conjugative genetic elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12268-12273.	7.1	64
9	The imprinted gene and parent-of-origin effect database now includes parental origin of de novo mutations. <i>Nucleic Acids Research</i> , 2006, 34, D29-D31.	14.5	57
10	A LuxRI-family regulatory system controls excision and transfer of the <i>Mesorhizobium loti</i> strain R7A symbiosis island by activating expression of two conserved hypothetical genes. <i>Molecular Microbiology</i> , 2009, 73, 1141-1155.	2.5	57
11	A quorum-sensing molecule acts as a morphogen controlling gas vesicle organelle biogenesis and adaptive flotation in an enterobacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14932-14937.	7.1	55
12	RNA-seq reveals the RNA binding proteins, Hfq and RsmA, play various roles in virulence, antibiotic production and genomic flux in <i>Serratia</i> sp. ATCC 39006. <i>BMC Genomics</i> , 2013, 14, 822.	2.8	50
13	A widely conserved molecular switch controls quorum sensing and symbiosis island transfer in <i>Mesorhizobium loti</i> through expression of a novel antiactivator. <i>Molecular Microbiology</i> , 2013, 87, 1-13.	2.5	50
14	Replication of Staphylococcal Resistance Plasmids. <i>Frontiers in Microbiology</i> , 2017, 8, 2279.	3.5	49
15	Molecular genetic and physical analysis of gas vesicles in buoyant enterobacteria. <i>Environmental Microbiology</i> , 2016, 18, 1264-1276.	3.8	45
16	The RNA chaperone, Hfq, controls two <i>luxR</i> -type regulators and plays a key role in pathogenesis and production of antibiotics in <i>Serratia</i> sp. ATCC 39006. <i>Environmental Microbiology</i> , 2011, 13, 2649-2666.	3.8	34
17	<i>Staphylococcus aureus</i> plasmids without mobilization genes are mobilized by a novel conjugative plasmid from community isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 649-652.	3.0	29
18	Staphylococcal Plasmids, Transposable and Integrative Elements. <i>Microbiology Spectrum</i> , 2018, 6, .	3.0	29

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19	Comprehensive overexpression analysis of cyclic-di-GMP signalling proteins in the phytopathogen <i>Pectobacterium atrosepticum</i> reveals diverse effects on motility and virulence phenotypes. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1427-1439.	1.8	23
20	Evolutionary persistence of tripartite integrative and conjugative elements. <i>Plasmid</i> , 2017, 92, 30-36.	1.4	21
21	Sequential induction of three recombination directionality factors directs assembly of tripartite integrative and conjugative elements. <i>PLoS Genetics</i> , 2018, 14, e1007292.	3.5	20
22	Draft Genome Sequence of <i>Serratia</i> sp. Strain ATCC 39006, a Model Bacterium for Analysis of the Biosynthesis and Regulation of Prodigiosin, a Carbapenem, and Gas Vesicles. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
23	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> Strain CC1192, an Efficient Nitrogen-Fixing Microsymbiont of <i>Cicer arietinum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	19
24	Processing of Nonconjugative Resistance Plasmids by Conjugation Nicking Enzyme of Staphylococci. <i>Journal of Bacteriology</i> , 2016, 198, 888-897.	2.2	18
25	Complete genome sequence of <i>Acidihalobacter prosperus</i> strain F5, an extremely acidophilic, iron- and sulfur-oxidizing halophile with potential industrial applicability in saline water bioleaching of chalcopyrite. <i>Journal of Biotechnology</i> , 2017, 262, 56-59.	3.8	17
26	Survival of antibiotic resistant bacteria following artificial solar radiation of secondary wastewater effluent. <i>Science of the Total Environment</i> , 2018, 626, 1005-1011.	8.0	17
27	High-throughput β -galactosidase and β -glucuronidase Assays Using Fluorogenic Substrates. <i>Bio-protocol</i> , 2013, 3, .	0.4	17
28	An epigenetic switch activates bacterial quorum sensing and horizontal transfer of an integrative and conjugative element. <i>Nucleic Acids Research</i> , 2022, 50, 975-988.	14.5	17
29	Quorum sensing-controlled buoyancy through gas vesicles: Intracellular bacterial microcompartments for environmental adaptation. <i>Communicative and Integrative Biology</i> , 2012, 5, 96-98.	1.4	16
30	Evolution of Diverse Effective N ₂ -Fixing Microsymbionts of <i>Cicer arietinum</i> following Horizontal Transfer of the <i>Mesorhizobium ciceri</i> CC1192 Symbiosis Integrative and Conjugative Element. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	16
31	Draft Genome Sequence of the Acidophilic, Halotolerant, and Iron/Sulfur-Oxidizing <i>Acidihalobacter prosperus</i> DSM 14174 (Strain V6). <i>Genome Announcements</i> , 2017, 5, .	0.8	15
32	<i>Pseudomonas aeruginosa</i> Resistance to Bacteriophages and Its Prevention by Strategic Therapeutic Cocktail Formulation. <i>Antibiotics</i> , 2021, 10, 145.	3.7	14
33	A Plasmid-Transposon Hybrid Mutagenesis System Effective in a Broad Range of Enterobacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1442.	3.5	13
34	Comparative analysis of integrative and conjugative mobile genetic elements in the genus <i>Mesorhizobium</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	13
35	Evolution of a 72-Kilobase Cointegrant, Conjugative Multiresistance Plasmid in Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates from the Early 1990s. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	12
36	Multiple introductions of methicillin-resistant <i>Staphylococcus aureus</i> ST612 into Western Australia associated both with human and equine reservoirs. <i>International Journal of Antimicrobial Agents</i> , 2019, 54, 681-685.	2.5	9

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37	Immunogenicity and protective potential of <i>Bordetella pertussis</i> biofilm and its associated antigens in a murine model. <i>Cellular Immunology</i> , 2019, 337, 42-47.	3.0	9
38	Dissecting the regulation of bile-induced biofilm formation in <i>Staphylococcus aureus</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 1398-1406.	1.8	9
39	Silencing quorum sensing and ICE mobility through antiactivation and ribosomal frameshifting. <i>Mobile Genetic Elements</i> , 2015, 5, 103-108.	1.8	8
40	Evolving origin-of-transfer sequences on staphylococcal conjugative and mobilizable plasmids whoâ€™s mimicking whom?. <i>Nucleic Acids Research</i> , 2021, 49, 5177-5188.	14.5	8
41	Identification and characterisation of fosfomycin resistance in <i>Escherichia coli</i> urinary tract infection isolates from Australia. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106121.	2.5	7
42	Symbiosis islands of Loteae-nodulating <i>Mesorhizobium</i> comprise three radiating lineages with concordant nod gene complements and nodulation host-range groupings. <i>Microbial Genomics</i> , 2020, 6, .	2.0	7
43	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> WSM1497, an Efficient Nitrogen-Fixing Microsymbiont of the Forage Legume <i>Biserrula pelecinus</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	6
44	Draft Genome Sequence of <i>Acidihalobacter ferrooxidans</i> DSM 14175 (Strain V8), a New Iron- and Sulfur-Oxidizing, Halotolerant, Acidophilic Species. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
45	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> Strain WSM1284, an Efficient Nitrogen-Fixing Microsymbiont of the Pasture Legume <i>Biserrula pelecinus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
46	Complete Genome Sequence of a <i>Staphylococcus aureus</i> Sequence Type 612 Isolate from an Australian Horse. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	4
47	Delineation of the integrase-attachment and origin-of-transfer regions of the symbiosis island ICEMISymR7A. <i>Plasmid</i> , 2019, 104, 102416.	1.4	4
48	Replicating methicillin resistance?. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 874-875.	8.2	3
49	An in vitro study into the antimicrobial and cytotoxic effect of Acticoatâ„¢ dressings supplemented with chlorhexidine. <i>Burns</i> , 2022, 48, 941-951.	1.9	3
50	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> AB550, an Environmental Solar Radiation- and Multidrug-Resistant Strain Isolated in Western Australia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
51	<i>Staphylococcal Plasmids, Transposable and Integrative Elements.</i> , 0, , 499-520.		1
52	Complete Genome Sequences of Three of the Earliest Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Strains Isolated in Remote Western Australia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0079721.	0.6	1
53	Complete Genome Sequence of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 1, SCC <i>mec</i> IV[2B], Isolated in the 1990s from Northern Western Australia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0079621.	0.6	0