

# Scott A Beatson

## List of Publications by Citations

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161  
papers

11,591  
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47  
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186  
ext. papers

15,035  
ext. citations

6.4  
avg, IF

6.16  
L-index

#	Paper	IF	Citations
161	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , <b>2004</b> , 428, 493-521	50.4	1689
160	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. <i>BMC Genomics</i> , <b>2011</b> , 12, 402	4.5	1617
159	Easyfig: a genome comparison visualizer. <i>Bioinformatics</i> , <b>2011</b> , 27, 1009-10	7.2	1590
158	An extensive repertoire of type III secretion effectors in Escherichia coli O157 and the role of lambdoid phages in their dissemination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 14941-6	11.5	370
157	Global dissemination of a multidrug resistant Escherichia coli clone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 5694-9	11.5	354
156	Effect of Piperacillin-Tazobactam vs Meropenem on 30-Day Mortality for Patients With E coli or Klebsiella pneumoniae Bloodstream Infection and Ceftriaxone Resistance: A Randomized Clinical Trial. <i>JAMA - Journal of the American Medical Association</i> , <b>2018</b> , 320, 984-994	27.4	339
155	Antimicrobial Resistance in ESKAPE Pathogens. <i>Clinical Microbiology Reviews</i> , <b>2020</b> , 33,	34	290
154	Accelerated evolution of the Prdm9 speciation gene across diverse metazoan taxa. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000753	6	203
153	Characterization of a complex chemosensory signal transduction system which controls twitching motility in Pseudomonas aeruginosa. <i>Molecular Microbiology</i> , <b>2004</b> , 52, 873-93	4.1	167
152	Insights into a multidrug resistant Escherichia coli pathogen of the globally disseminated ST131 lineage: genome analysis and virulence mechanisms. <i>PLoS ONE</i> , <b>2011</b> , 6, e26578	3.7	149
151	Differential regulation of twitching motility and elastase production by Vfr in Pseudomonas aeruginosa. <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 3605-13	3.5	148
150	A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic Escherichia coli strain H10407. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5822-31	3.5	141
149	FpvB, an alternative type I ferripyoverdine receptor of Pseudomonas aeruginosa. <i>Microbiology (United Kingdom)</i> , <b>2004</b> , 150, 1671-1680	2.9	129
148	Bioinformatics, genomics and evolution of non-flagellar type-III secretion systems: a Darwinian perspective. <i>FEMS Microbiology Reviews</i> , <b>2005</b> , 29, 201-29	15.1	124
147	Sequential Acquisition of Virulence and Fluoroquinolone Resistance Has Shaped the Evolution of Escherichia coli ST131. <i>MBio</i> , <b>2016</b> , 7, e00347-16	7.8	121
146	Quorum sensing is not required for twitching motility in Pseudomonas aeruginosa. <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 3598-604	3.5	115
145	Chaperone-usher fimbriae of Escherichia coli. <i>PLoS ONE</i> , <b>2013</b> , 8, e52835	3.7	111

144	Proteome analysis of extracellular proteins regulated by the las and rhl quorum sensing systems in <i>Pseudomonas aeruginosa</i> PAO1. <i>Microbiology (United Kingdom)</i> , <b>2003</b> , 149, 1311-1322	2.9	111
143	The serum resistome of a globally disseminated multidrug resistant uropathogenic <i>Escherichia coli</i> clone. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003834	6	106
142	Variation in bacterial flagellins: from sequence to structure. <i>Trends in Microbiology</i> , <b>2006</b> , 14, 151-5	12.4	106
141	EhaA is a novel autotransporter protein of enterohemorrhagic <i>Escherichia coli</i> O157:H7 that contributes to adhesion and biofilm formation. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 589-604	5.2	101
140	A FimH inhibitor prevents acute bladder infection and treats chronic cystitis caused by multidrug-resistant uropathogenic <i>Escherichia coli</i> ST131. <i>Journal of Infectious Diseases</i> , <b>2013</b> , 208, 921-8	7	96
139	<i>Legionella pneumophila</i> strain 130b possesses a unique combination of type IV secretion systems and novel Dot/Icm secretion system effector proteins. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 6001-16	3.5	95
138	Bioinformatics analysis of the locus for enterocyte effacement provides novel insights into type-III secretion. <i>BMC Microbiology</i> , <b>2005</b> , 5, 9	4.5	95
137	Stepwise evolution of pandrug-resistance in <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , <b>2015</b> , 5, 15082	4.9	87
136	<i>Pseudomonas aeruginosa</i> fimL regulates multiple virulence functions by intersecting with Vfr-modulated pathways. <i>Molecular Microbiology</i> , <b>2005</b> , 55, 1357-78	4.1	79
135	Identification of type 3 fimbriae in uropathogenic <i>Escherichia coli</i> reveals a role in biofilm formation. <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 1054-63	3.5	78
134	Genomic evolution of the pathogenic <i>Wolbachia</i> strain, wMelPop. <i>Genome Biology and Evolution</i> , <b>2013</b> , 5, 2189-204	3.9	77
133	Evolutionary links between FliH/YscL-like proteins from bacterial type III secretion systems and second-stalk components of the FoF1 and vacuolar ATPases. <i>Protein Science</i> , <b>2006</b> , 15, 935-41	6.3	76
132	The complete genome sequence of <i>Escherichia coli</i> EC958: a high quality reference sequence for the globally disseminated multidrug resistant <i>E. coli</i> O25b:H4-ST131 clone. <i>PLoS ONE</i> , <b>2014</b> , 9, e104400	3.7	75
131	Identification of type II and type III pyoverdine receptors from <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , <b>2003</b> , 149, 821-831	2.9	75
130	Identification of IncA/C Plasmid Replication and Maintenance Genes and Development of a Plasmid Multilocus Sequence Typing Scheme. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2017</b> , 61,	5.9	73
129	Evolution and comparative genomics of odorant- and pheromone-associated genes in rodents. <i>Genome Research</i> , <b>2004</b> , 14, 591-602	9.7	72
128	UpaH is a newly identified autotransporter protein that contributes to biofilm formation and bladder colonization by uropathogenic <i>Escherichia coli</i> CFT073. <i>Infection and Immunity</i> , <b>2010</b> , 78, 1659-69	7	70
127	The Flag-2 locus, an ancestral gene cluster, is potentially associated with a novel flagellar system from <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 1430-40	3.5	69

126	Heat resistance and salt hypersensitivity in <i>Lactococcus lactis</i> due to spontaneous mutation of lmg_1816 (gdpP) induced by high-temperature growth. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 7753-9	4.8	61
125	Multiple antibiotic resistance gene recruitment onto the enterohemorrhagic <i>Escherichia coli</i> virulence plasmid. <i>FASEB Journal</i> , <b>2010</b> , 24, 1160-6	0.9	60
124	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing <i>Escherichia coli</i> (STEC) in global food production systems. <i>International Journal of Food Microbiology</i> , <b>2014</b> , 187, 57-72	5.8	58
123	Identification of novel vaccine candidates against multidrug-resistant <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e77631	3.7	56
122	An interactive web-based <i>Pseudomonas aeruginosa</i> genome database: discovery of new genes, pathways and structures. <i>Microbiology (United Kingdom)</i> , <b>2000</b> , 146 (Pt 10), 2351-2364	2.9	56
121	The co-transcriptome of uropathogenic <i>Escherichia coli</i> -infected mouse macrophages reveals new insights into host-pathogen interactions. <i>Cellular Microbiology</i> , <b>2015</b> , 17, 730-46	3.9	55
120	Cadherin-like domains in alpha-dystroglycan, alpha/epsilon-sarcoglycan and yeast and bacterial proteins. <i>Current Biology</i> , <b>2002</b> , 12, R197-9	6.3	50
119	Draft genome sequence of the male-killing <i>Wolbachia</i> strain wBol1 reveals recent horizontal gene transfers from diverse sources. <i>BMC Genomics</i> , <b>2013</b> , 14, 20	4.5	49
118	Molecular analysis of the <i>Acinetobacter baumannii</i> biofilm-associated protein. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 6535-43	4.8	49
117	Protein secretion systems in <i>Fusobacterium nucleatum</i> : genomic identification of Type 4 piliation and complete Type V pathways brings new insight into mechanisms of pathogenesis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2005</b> , 1713, 92-112	3.8	49
116	Conjugative plasmid transfer and adhesion dynamics in an <i>Escherichia coli</i> biofilm. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 6783-91	4.8	48
115	Analysis of a <i>Streptococcus pyogenes</i> puerperal sepsis cluster by use of whole-genome sequencing. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 2224-8	9.7	47
114	Lysogeny with Shiga toxin 2-encoding bacteriophages represses type III secretion in enterohemorrhagic <i>Escherichia coli</i> . <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002672	7.6	46
113	<i>Galleria mellonella</i> infection model demonstrates high lethality of ST69 and ST127 uropathogenic <i>E. coli</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e101547	3.7	45
112	Transfer of scarlet fever-associated elements into the group A <i>Streptococcus</i> M1T1 clone. <i>Scientific Reports</i> , <b>2015</b> , 5, 15877	4.9	41
111	Tracing the evolutionary history of the pandemic group A streptococcal M1T1 clone. <i>FASEB Journal</i> , <b>2012</b> , 26, 4675-84	0.9	41
110	The metabolic enzyme AdhE controls the virulence of <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , <b>2014</b> , 93, 199-211	4.1	40
109	Molecular analysis of type 3 fimbrial genes from <i>Escherichia coli</i> , <i>Klebsiella</i> and <i>Citrobacter</i> species. <i>BMC Microbiology</i> , <b>2010</b> , 10, 183	4.5	39

108	Prevalence of pathogenicity island IICFT073 genes among extraintestinal clinical isolates of <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , <b>2005</b> , 43, 2425-34	9.7	39
107	Transcriptional regulators of the GAD acid stress island are carried by effector protein-encoding prophages and indirectly control type III secretion in enterohemorrhagic <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , <b>2011</b> , 80, 1349-65	4.1	38
106	Hospital-wide Eradication of a Nosocomial <i>Legionella pneumophila</i> Serogroup 1 Outbreak. <i>Clinical Infectious Diseases</i> , <b>2016</b> , 62, 273-279	11.6	37
105	Whole genome analysis of cephalosporin-resistant <i>Escherichia coli</i> from bloodstream infections in Australia, New Zealand and Singapore: high prevalence of CMY-2 producers and ST131 carrying blaCTX-M-15 and blaCTX-M-27. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2018</b> , 73, 634-642	5.1	36
104	Population dynamics of an <i>Escherichia coli</i> ST131 lineage during recurrent urinary tract infection. <i>Nature Communications</i> , <b>2019</b> , 10, 3643	17.4	36
103	Mechanisms Involved in Acquisition of blaNDM Genes by IncA/C2 and IncFIY Plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 4082-8	5.9	34
102	Comparative genomics of the <i>Staphylococcus intermedius</i> group of animal pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2012</b> , 2, 44	5.9	33
101	Origin of the diversity in DNA recognition domains in phasevarion associated modA genes of pathogenic <i>Neisseria</i> and <i>Haemophilus influenzae</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e32337	3.7	32
100	Molecular characterization of a multidrug resistance IncF plasmid from the globally disseminated <i>Escherichia coli</i> ST131 clone. <i>PLoS ONE</i> , <b>2015</b> , 10, e0122369	3.7	32
99	Genome sequence of the emerging pathogen <i>Aeromonas caviae</i> . <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 1286-7	5.7	30
98	Discovery of -Mediated Colistin Resistance in a Highly Virulent <i>Escherichia coli</i> Lineage. <i>MSphere</i> , <b>2018</b> , 3,	5	30
97	Genome-Wide Discovery of Genes Required for Capsule Production by Uropathogenic. <i>MBio</i> , <b>2017</b> , 8,	7.8	29
96	UafB is a serine-rich repeat adhesin of <i>Staphylococcus saprophyticus</i> that mediates binding to fibronectin, fibrinogen and human uroepithelial cells. <i>Microbiology (United Kingdom)</i> , <b>2011</b> , 157, 1161-1175	2.9	29
95	Regulatory interplay between pap operons in uropathogenic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , <b>2008</b> , 67, 996-1011	4.1	29
94	The host metabolite D-serine contributes to bacterial niche specificity through gene selection. <i>ISME Journal</i> , <b>2015</b> , 9, 1039-51	11.9	28
93	Modifications in the pmrB gene are the primary mechanism for the development of chromosomally encoded resistance to polymyxins in uropathogenic <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2017</b> , 72, 2729-2736	5.1	28
92	Molecular Characterization of the Multidrug Resistant <i>Escherichia coli</i> ST131 Clone. <i>Pathogens</i> , <b>2015</b> , 4, 422-30	4.5	28
91	Sub-inhibitory concentrations of ceftazidime and tobramycin reduce the quorum sensing signals of <i>Pseudomonas aeruginosa</i> . <i>Pathology</i> , <b>2004</b> , 36, 571-5	1.6	27

90	A Novel Protective Vaccine Antigen from the Core Genome. <i>MSphere</i> , <b>2016</b> , 1,	5	26
89	The role of H4 flagella in Escherichia coli ST131 virulence. <i>Scientific Reports</i> , <b>2015</b> , 5, 16149	4.9	24
88	Increased S-nitrosylation and proteasomal degradation of caspase-3 during infection contribute to the persistence of adherent invasive Escherichia coli (AIEC) in immune cells. <i>PLoS ONE</i> , <b>2013</b> , 8, e68386	3.7	24
87	Within-host whole genome analysis of an antibiotic resistant Pseudomonas aeruginosa strain sub-type in cystic fibrosis. <i>PLoS ONE</i> , <b>2017</b> , 12, e0172179	3.7	23
86	Mutual exclusivity of hyaluronan and hyaluronidase in invasive group A Streptococcus. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 32303-32315	5.4	23
85	Microbiology. Tracking antibiotic resistance. <i>Science</i> , <b>2014</b> , 345, 1454-5	33.3	23
84	Zocin A immunity factor: a femA-like gene found in a group C streptococcus. <i>FEMS Microbiology Letters</i> , <b>1998</b> , 163, 73-7	2.9	23
83	uPEPperoni: an online tool for upstream open reading frame location and analysis of transcript conservation. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 36	3.6	22
82	Characterization of EhaJ, a New Autotransporter Protein from Enterohemorrhagic and Enteropathogenic Escherichia coli. <i>Frontiers in Microbiology</i> , <b>2011</b> , 2, 120	5.7	22
81	Molecular Characterization of the Vacuolating Autotransporter Toxin in Uropathogenic Escherichia coli. <i>Journal of Bacteriology</i> , <b>2016</b> , 198, 1487-98	3.5	21
80	Genome analysis and CRISPR typing of Salmonella enterica serovar Virchow. <i>BMC Genomics</i> , <b>2014</b> , 15, 389	4.5	21
79	Lineage-Specific Methyltransferases Define the Methylome of the Globally Disseminated Escherichia coli ST131 Clone. <i>MBio</i> , <b>2015</b> , 6, e01602-15	7.8	21
78	Secretion of flagellin by the LEE-encoded type III secretion system of enteropathogenic Escherichia coli. <i>BMC Microbiology</i> , <b>2009</b> , 9, 30	4.5	21
77	Discovery of New Genes Involved in Curli Production by a Uropathogenic Escherichia coli Strain from the Highly Virulent O45:K1:H7 Lineage. <i>MBio</i> , <b>2018</b> , 9,	7.8	20
76	Molecular analysis of asymptomatic bacteriuria Escherichia coli strain VR50 reveals adaptation to the urinary tract by gene acquisition. <i>Infection and Immunity</i> , <b>2015</b> , 83, 1749-64	3.7	20
75	Novel genes associated with enhanced motility of Escherichia coli ST131. <i>PLoS ONE</i> , <b>2017</b> , 12, e0176290	3.7	20
74	New plasmids and putative virulence factors from the draft genome of an Australian clinical isolate of Photobacterium asymbiotica. <i>FEMS Microbiology Letters</i> , <b>2010</b> , 309, 136-43	2.9	19
73	Companion Animals Are Spillover Hosts of the Multidrug-Resistant Human Extraintestinal Pandemic Clones ST131 and ST1193. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1968	5.7	19

72	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008287	7.6	18
71	GIFT domains: linking eukaryotic intraflagellar transport and glycosylation to bacterial gliding. <i>Trends in Biochemical Sciences</i> , <b>2004</b> , 29, 396-9	10.3	18
70	A minimal tiling path cosmid library for functional analysis of the Pseudomonas aeruginosa PAO1 genome. <i>Microbial &amp; Comparative Genomics</i> , <b>2000</b> , 5, 189-203		18
69	Microevolution of Streptococcus agalactiae ST-261 from Australia Indicates Dissemination via Imported Tilapia and Ongoing Adaptation to Marine Hosts or Environment. <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	17
68	Acquisition of the Sda1-encoding bacteriophage does not enhance virulence of the serotype M1 Streptococcus pyogenes strain SF370. <i>Infection and Immunity</i> , <b>2013</b> , 81, 2062-9	3.7	17
67	A distinct and divergent lineage of genomic island-associated Type IV Secretion Systems in Legionella. <i>PLoS ONE</i> , <b>2013</b> , 8, e82221	3.7	17
66	Discovery and Characterization of Human-Urine Utilization by Asymptomatic-Bacteriuria-Causing Streptococcus agalactiae. <i>Infection and Immunity</i> , <b>2016</b> , 84, 307-19	3.7	15
65	The Intimin-Like Protein FdeC Is Regulated by H-NS and Temperature in Enterohemorrhagic Escherichia coli. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 7337-47	4.8	15
64	Characterisation of a cell wall-anchored protein of Staphylococcus saprophyticus associated with linoleic acid resistance. <i>BMC Microbiology</i> , <b>2012</b> , 12, 8	4.5	15
63	The comparative in-vitro activity of roxithromycin and other antibiotics against Bordetella pertussis. <i>Journal of Antimicrobial Chemotherapy</i> , <b>1998</b> , 41 Suppl B, 23-7	5.1	15
62	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium Starkeya novella type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 7, 44-58		15
61	Genomic Investigation Reveals Contaminated Detergent as the Source of an Extended-Spectrum-β-Lactamase-Producing Klebsiella michiganensis Outbreak in a Neonatal Unit. <i>Journal of Clinical Microbiology</i> , <b>2020</b> , 58,	9.7	15
60	OMIC Approaches to Study Uropathogenic Escherichia coli Virulence. <i>Trends in Microbiology</i> , <b>2017</b> , 25, 729-740	12.4	14
59	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing Enterobacter hormaechei. <i>Nature Communications</i> , <b>2020</b> , 11, 466	17.4	14
58	Stability of active prophages in industrial Lactococcus lactis strains in the presence of heat, acid, osmotic, oxidative and antibiotic stressors. <i>International Journal of Food Microbiology</i> , <b>2016</b> , 220, 26-32	5.8	14
57	Genetic variation in IRF4 expression modulates growth characteristics, tyrosinase expression and interferon-gamma response in melanocytic cells. <i>Pigment Cell and Melanoma Research</i> , <b>2018</b> , 31, 51-63	4.5	13
56	Repurposing a neurodegenerative disease drug to treat Gram-negative antibiotic-resistant bacterial sepsis. <i>Science Translational Medicine</i> , <b>2020</b> , 12,	17.5	13
55	Comprehensive analysis of type 1 fimbriae regulation in fimB-null strains from the multidrug resistant Escherichia coli ST131 clone. <i>Molecular Microbiology</i> , <b>2016</b> , 101, 1069-87	4.1	13

54	Use of whole genome sequencing to investigate an increase in <i>Neisseria gonorrhoeae</i> infection among women in urban areas of Australia. <i>Scientific Reports</i> , <b>2018</b> , 8, 1503	4.9	12
53	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 7, 44-58		12
52	Genomic Comparison of Two O111:H- Enterohemorrhagic <i>Escherichia coli</i> Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. <i>Infection and Immunity</i> , <b>2016</b> , 84, 775-81	3.7	11
51	Epidemiology. Outsmarting outbreaks. <i>Science</i> , <b>2012</b> , 338, 1161-2	33.3	11
50	Molecular and Structural Characterization of a Novel <i>Escherichia coli</i> Interleukin Receptor Mimic Protein. <i>MBio</i> , <b>2016</b> , 7, e02046	7.8	11
49	Detection of Epidemic Scarlet Fever Group A <i>Streptococcus</i> in Australia. <i>Clinical Infectious Diseases</i> , <b>2019</b> , 69, 1232-1234	11.6	10
48	Streptococcal collagen-like protein A and general stress protein 24 are immunomodulating virulence factors of group A <i>Streptococcus</i> . <i>FASEB Journal</i> , <b>2013</b> , 27, 2633-43	0.9	10
47	Extragenic suppressor mutations that restore twitching motility to <i>fimL</i> mutants of <i>Pseudomonas aeruginosa</i> are associated with elevated intracellular cyclic AMP levels. <i>MicrobiologyOpen</i> , <b>2012</b> , 1, 490-501	3.4	10
46	Physical and Linkage Maps for <i>Drosophila serrata</i> , a Model Species for Studies of Clinal Adaptation and Sexual Selection. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 287-97	3.2	10
45	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <i>BMC Genomics</i> , <b>2018</b> , 19, 644	4.5	10
44	Variation in hemolysin A expression between uropathogenic isolates determines NLRP3-dependent -independent macrophage cell death and host colonization. <i>FASEB Journal</i> , <b>2019</b> , 33, 7437-7450	0.9	9
43	Third-generation cephalosporin resistance conferred by a chromosomally encoded <i>bla</i> CMY-23 gene in the <i>Escherichia coli</i> ST131 reference strain EC958. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 1969-72	5.1	9
42	Contiguity: Contig adjacency graph construction and visualisation		9
41	Differential Regulation of the Surface-Exposed and Secreted SsIE Lipoprotein in Extraintestinal Pathogenic <i>Escherichia coli</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0162391	3.7	8
40	Genomic analysis of carbapenemase-producing in Queensland reveals widespread transmission of on an IncHI2 plasmid. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	7
39	SMRT sequencing reveals differential patterns of methylation in two O111:H- STEC isolates from a hemolytic uremic syndrome outbreak in Australia. <i>Scientific Reports</i> , <b>2019</b> , 9, 9436	4.9	6
38	Complex Multilevel Control of Hemolysin Production by Uropathogenic <i>Escherichia coli</i> . <i>MBio</i> , <b>2019</b> , 10,	7.8	6
37	Complete Genome Sequence of Serotype III Sequence Type 17 Strain 874391. <i>Genome Announcements</i> , <b>2017</b> , 5,		6



36	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1340-1348	26.6	6
35	Genomic surveillance, characterization and intervention of a polymicrobial multidrug-resistant outbreak in critical care. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	6
34	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing $\beta$ proteobacterium Thioalkalimicrobium cyclicum type strain ALM 1 (DSM 14477(T)). <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 38		5
33	Genome Sequence of Hydrothermal Arsenic-Respiring Bacterium <i>Marinobacter santoriniensis</i> NKSG1T. <i>Genome Announcements</i> , <b>2013</b> , 1,		5
32	Diving Deep Into Hospital-Acquired <i>Legionella pneumophila</i> With Whole-Genome Sequencing. <i>Clinical Infectious Diseases</i> , <b>2017</b> , 64, 1260-1262	11.6	4
31	Control of Bacterial Sulfite Detoxification by Conserved and Species-Specific Regulatory Circuits. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 960	5.7	4
30	Novel insights into pasteurellosis in captive pinnipeds. <i>Veterinary Microbiology</i> , <b>2019</b> , 231, 232-237	3.3	4
29	Identification of a haemolysin-like peptide with antibacterial activity using the draft genome sequence of <i>Staphylococcus epidermidis</i> strain A487. <i>FEMS Immunology and Medical Microbiology</i> , <b>2011</b> , 62, 273-82		4
28	Contiguity: Contig adjacency graph construction and visualisation		4
27	Phase variation in <i>latB</i> associated with a fatal <i>Pasteurella multocida</i> outbreak in captive squirrel gliders. <i>Veterinary Microbiology</i> , <b>2020</b> , 243, 108612	3.3	3
26	Draft Genome Sequence of <i>Pseudomonas fluorescens</i> SRM1, an Isolate from Spoiled Raw Milk. <i>Genome Announcements</i> , <b>2015</b> , 3,		3
25	Using genomics to understand inter- and intra- outbreak diversity of isolates associated with fowl cholera in meat chickens. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	3
24	Sequential acquisition of virulence and fluoroquinolone resistance has shaped the evolution of <i>Escherichia coli</i> ST131		3
23	Emergence and impact of <i>oprD</i> mutations in <i>Pseudomonas aeruginosa</i> strains in cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , <b>2021</b> ,	4.1	3
22	Whole-genome sequencing as an improved means of investigating <i>Neisseria gonorrhoeae</i> treatment failures. <i>Sexual Health</i> , <b>2019</b> , 16, 500-507	2	2
21	Differential Afa/Dr Fimbriae Expression in the Multidrug-Resistant <i>Escherichia coli</i> ST131 Clone.. <i>MBio</i> , <b>2022</b> , e0351921	7.8	2
20	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing <i>Enterobacter hormaechei</i>		2
19	Multiple evolutionary trajectories for non-O157 Shiga toxigenic <i>Escherichia coli</i>		2

18	Genomic characterisation and context of the bla <sub>NDM-1</sub> carbapenemase in Escherichia coli ST101		2
17	Fatal Respiratory Diphtheria Caused by $\beta$ -Lactam-Resistant <i>Corynebacterium diphtheriae</i> . <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, e4531-e4538	11.6	2
16	Rescuing Tetracycline Class Antibiotics for the Treatment of Multidrug-Resistant <i>Acinetobacter baumannii</i> Pulmonary Infection.. <i>MBio</i> , <b>2022</b> , e0351721	7.8	1
15	Plasmid-mediated ciprofloxacin resistance imparts a selective advantage on ST131. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , AAC0214621	5.9	1
14	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre		1
13	Strain and lineage-level methylome heterogeneity in the multi-drug resistant pathogenic <i>Escherichia coli</i> ST101 clone		1
12	Molecular Epidemiology of Clinical and Colonizing Methicillin-Resistant Isolates in Companion Animals. <i>Frontiers in Veterinary Science</i> , <b>2021</b> , 8, 620491	3.1	1
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9	Outbreak of multi-drug-resistant (MDR) <i>Shigella flexneri</i> in northern Australia due to an endemic regional clone acquiring an IncFII plasmid. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , <b>2021</b> , 40, 279-286	5.3	0
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5	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering <b>2020</b> , 16, e1008287		
4	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering <b>2020</b> , 16, e1008287		
3	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering <b>2020</b> , 16, e1008287		
2	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering <b>2020</b> , 16, e1008287		
1	SRA Down Under: Cache and Analysis Platform for Infectious Disease. <i>Studies in Health Technology and Informatics</i> , <b>2019</b> , 266, 76-82	0.5	

