

Scott A Beatson

List of Publications by Year in descending order

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159
papers

17,048
citations

38660

50
h-index

16605

123
g-index

188
all docs

188
docs citations

188
times ranked

20216
citing authors

#	ARTICLE	IF	CITATIONS
1	Easyfig: a genome comparison visualizer. <i>Bioinformatics</i> , 2011, 27, 1009-1010.	1.8	2,861
2	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. <i>BMC Genomics</i> , 2011, 12, 402.	1.2	2,691
3	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
4	Antimicrobial Resistance in ESKAPE Pathogens. <i>Clinical Microbiology Reviews</i> , 2020, 33, .	5.7	898
5	Effect of Piperacillin-Tazobactam vs Meropenem on 30-Day Mortality for Patients With <i>E coli</i> or <i>Klebsiella pneumoniae</i> Bloodstream Infection and Ceftriaxone Resistance. <i>JAMA - Journal of the American Medical Association</i> , 2018, 320, 984.	3.8	538
6	Global dissemination of a multidrug resistant <i>Escherichia coli</i> clone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5694-5699.	3.3	498
7	An extensive repertoire of type III secretion effectors in <i>Escherichia coli</i> 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> , 2006, 103, 14941-14946.	3.3	413
8	Accelerated Evolution of the Prdm9 Speciation Gene across Diverse Metazoan Taxa. <i>PLoS Genetics</i> , 2009, 5, e1000753.	1.5	256
9	Insights into a Multidrug Resistant <i>Escherichia coli</i> Pathogen of the Globally Disseminated ST131 Lineage: Genome Analysis and Virulence Mechanisms. <i>PLoS ONE</i> , 2011, 6, e26578.	1.1	209
10	Characterization of a complex chemosensory signal transduction system which controls twitching motility in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2004, 52, 873-893.	1.2	208
11	Chaperone-Usher Fimbriae of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2013, 8, e52835.	1.1	179
12	Differential Regulation of Twitching Motility and Elastase Production by Vfr in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002, 184, 3605-3613.	1.0	175
13	A Commensal Gone Bad: Complete Genome Sequence of the Prototypical Enterotoxigenic <i>Escherichia coli</i> Strain H10407. <i>Journal of Bacteriology</i> , 2010, 192, 5822-5831.	1.0	168
14	FpvB, an alternative type I ferripyoverdine receptor of <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 1311-1322.	0.7	164
15	Sequential Acquisition of Virulence and Fluoroquinolone Resistance Has Shaped the Evolution of <i>Escherichia coli</i> ST131. <i>MBio</i> , 2016, 7, e00347-16.	1.8	164
16	The Serum Resistome of a Globally Disseminated Multidrug Resistant Uropathogenic <i>Escherichia coli</i> Clone. <i>PLoS Genetics</i> , 2013, 9, e1003834.	1.5	146
17	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> , 2003, 149, 1311-1322.	0.7	141
18	Bioinformatics, genomics and evolution of non-flagellar type-III secretion systems: a Darwinian perspective. <i>FEMS Microbiology Reviews</i> , 2005, 29, 201-229.	3.9	135

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19	Variation in bacterial flagellins: from sequence to structure. <i>Trends in Microbiology</i> , 2006, 14, 151-155.	3.5	129
20	Quorum Sensing Is Not Required for Twitching Motility in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002, 184, 3598-3604.	1.0	121
21	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> , 2013, 208, 921-928.	1.9	116
22	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> , 2014, 9, e104400.	1.1	116
23	Stepwise evolution of pandrug-resistance in <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2015, 5, 15082.	1.6	115
24	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> , 2008, 10, 589-604.	1.8	112
25	Identification of IncA/C Plasmid Replication and Maintenance Genes and Development of a Plasmid Multilocus Sequence Typing Scheme. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	106
26	<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> , 2010, 192, 6001-6016.	1.0	104
27	Bioinformatics analysis of the locus for enterocyte effacement provides novel insights into type-III secretion. <i>BMC Microbiology</i> , 2005, 5, 9.	1.3	100
28	Identification of Type 3 Fimbriae in Uropathogenic <i>Escherichia coli</i> Reveals a Role in Biofilm Formation. <i>Journal of Bacteriology</i> , 2008, 190, 1054-1063.	1.0	98
29	Evolution and Comparative Genomics of Odorant- and Pheromone-Associated Genes in Rodents. <i>Genome Research</i> , 2004, 14, 591-602.	2.4	97
30	Genomic Evolution of the Pathogenic <i>Wolbachia</i> Strain, wMelPop. <i>Genome Biology and Evolution</i> , 2013, 5, 2189-2204.	1.1	96
31	Identification of type II and type III pyoverdine receptors from <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 821-831.	0.7	90
32	The co-transcriptome of uropathogenic <i>Escherichia coli</i> infected mouse macrophages reveals new insights into host-pathogen interactions. <i>Cellular Microbiology</i> , 2015, 17, 730-746.	1.1	90
33	<i>Pseudomonas aeruginosa</i> fimL regulates multiple virulence functions by intersecting with Vfr-modulated pathways. <i>Molecular Microbiology</i> , 2005, 55, 1357-1378.	1.2	85
34	Multiple antibiotic resistance gene recruitment onto the enterohemorrhagic <i>Escherichia coli</i> virulence plasmid. <i>FASEB Journal</i> , 2010, 24, 1160-1166.	0.2	85
35	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> , 2006, 15, 935-941.	3.1	84
36	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> , 2014, 187, 57-72.	2.1	83

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37	Identification of Novel Vaccine Candidates against Multidrug-Resistant <i>Acinetobacter baumannii</i> . PLoS ONE, 2013, 8, e77631.	1.1	80
38	The Flag-2 Locus, an Ancestral Gene Cluster, Is Potentially Associated with a Novel Flagellar System from <i>Escherichia coli</i> . Journal of Bacteriology, 2005, 187, 1430-1440.	1.0	78
39	Heat Resistance and Salt Hypersensitivity in <i>Lactococcus lactis</i> Due to Spontaneous Mutation of <i>llmg_1816</i> (<i>gdpP</i>) Induced by High-Temperature Growth. Applied and Environmental Microbiology, 2012, 78, 7753-7759.	1.4	78
40	UpaH Is a Newly Identified Autotransporter Protein That Contributes to Biofilm Formation and Bladder Colonization by Uropathogenic <i>Escherichia coli</i> CFT073. Infection and Immunity, 2010, 78, 1659-1669.	1.0	77
41	Population dynamics of an <i>Escherichia coli</i> ST131 lineage during recurrent urinary tract infection. Nature Communications, 2019, 10, 3643.	5.8	76
42	Molecular Analysis of the <i>Acinetobacter baumannii</i> Biofilm-Associated Protein. Applied and Environmental Microbiology, 2013, 79, 6535-6543.	1.4	68
43	Draft genome sequence of the male-killing <i>Wolbachia</i> strain wBol1 reveals recent horizontal gene transfers from diverse sources. BMC Genomics, 2013, 14, 20.	1.2	65
44	Molecular analysis of type 3 fimbrial genes from <i>Escherichia coli</i> , <i>Klebsiella</i> and <i>Citrobacter</i> species. BMC Microbiology, 2010, 10, 183.	1.3	64
45	An interactive web-based <i>Pseudomonas aeruginosa</i> genome database: discovery of new genes, pathways and structures. Microbiology (United Kingdom), 2000, 146, 2351-2364.	0.7	59
46	<i>Galleria mellonella</i> Infection Model Demonstrates High Lethality of ST69 and ST127 Uropathogenic <i>E. coli</i> . PLoS ONE, 2014, 9, e101547.	1.1	59
47	Cadherin-like domains in α -dystroglycan, β -sarcoglycan and yeast and bacterial proteins. Current Biology, 2002, 12, R197-R199.	1.8	58
48	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. Biochimica Et Biophysica Acta - Biomembranes, 2005, 1713, 92-112.	1.4	57
49	Lysogeny with Shiga Toxin 2-Encoding Bacteriophages Represses Type III Secretion in Enterohemorrhagic <i>Escherichia coli</i> . PLoS Pathogens, 2012, 8, e1002672.	2.1	57
50	Transfer of scarlet fever-associated elements into the group A <i>Streptococcus</i> MIT1 clone. Scientific Reports, 2015, 5, 15877.	1.6	57
51	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. Journal of Antimicrobial Chemotherapy, 2018, 73, 634-642.	1.3	56
52	Analysis of a <i>Streptococcus pyogenes</i> Puerperal Sepsis Cluster by Use of Whole-Genome Sequencing. Journal of Clinical Microbiology, 2012, 50, 2224-2228.	1.8	55
53	Conjugative Plasmid Transfer and Adhesion Dynamics in an <i>Escherichia coli</i> Biofilm. Applied and Environmental Microbiology, 2009, 75, 6783-6791.	1.4	54
54	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering. PLoS Pathogens, 2020, 16, e1008287.	2.1	51

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55	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> , 2011, 80, 1349-1365.	1.2	50
56	The metabolic enzyme <i>AdhE</i> controls the virulence of <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , 2014, 93, 199-211.	1.2	49
57	Mechanisms Involved in Acquisition of <i>bla</i> _{NDM} Genes by IncA/C ₂ and IncFII _Y Plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4082-4088.	1.4	49
58	Hospital-wide Eradication of a Nosocomial <i>Legionella pneumophila</i> Serogroup 1 Outbreak. <i>Clinical Infectious Diseases</i> , 2016, 62, 273-279.	2.9	49
59	Tracing the evolutionary history of the pandemic group A streptococcal MIT1 clone. <i>FASEB Journal</i> , 2012, 26, 4675-4684.	0.2	48
60	Discovery of <i>mcr-1</i> -Mediated Colistin Resistance in a Highly Virulent <i>Escherichia coli</i> Lineage. <i>MSphere</i> , 2018, 3, .	1.3	48
61	Molecular Characterization of a Multidrug Resistance IncF Plasmid from the Globally Disseminated <i>Escherichia coli</i> ST131 Clone. <i>PLoS ONE</i> , 2015, 10, e0122369.	1.1	48
62	Omics Approaches to Study Uropathogenic <i>Escherichia coli</i> Virulence. <i>Trends in Microbiology</i> , 2017, 25, 729-740.	3.5	46
63	Prevalence of Pathogenicity Island II CFT073 Genes among Extraintestinal Clinical Isolates of <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 2425-2434.	1.8	45
64	Comparative Genomics of the <i>Staphylococcus intermedius</i> Group of Animal Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 44.	1.8	45
65	The host metabolite D-serine contributes to bacterial niche specificity through gene selection. <i>ISME Journal</i> , 2015, 9, 1039-1051.	4.4	43
66	A Novel Protective Vaccine Antigen from the Core <i>Escherichia coli</i> Genome. <i>MSphere</i> , 2016, 1, .	1.3	43
67	Genome-Wide Discovery of Genes Required for Capsule Production by Uropathogenic <i>Escherichia coli</i> . <i>MBio</i> , 2017, 8, .	1.8	43
68	Modifications in the <i>pmrB</i> 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> , 2017, 72, 2729-2736.	1.3	41
69	Genome Sequence of the Emerging Pathogen <i>Aeromonas caviae</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1286-1287.	1.0	39
70	Molecular Characterization of the Multidrug Resistant <i>Escherichia coli</i> ST131 Clone. <i>Pathogens</i> , 2015, 4, 422-430.	1.2	39
71	Origin of the Diversity in DNA Recognition Domains in Phasevarion Associated <i>modA</i> Genes of Pathogenic <i>Neisseria</i> and <i>Haemophilus influenzae</i> . <i>PLoS ONE</i> , 2012, 7, e32337.	1.1	38
72	Companion Animals Are Spillover Hosts of the Multidrug-Resistant Human Extraintestinal <i>Escherichia coli</i> Pandemic Clones ST131 and ST1193. <i>Frontiers in Microbiology</i> , 2020, 11, 1968.	1.5	38

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73	Genomic Investigation Reveals Contaminated Detergent as the Source of an Extended-Spectrum-β-Lactamase-Producing <i>Klebsiella michiganensis</i> Outbreak in a Neonatal Unit. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	37
74	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> , 2011, 157, 1161-1175.	0.7	36
75	Repurposing a neurodegenerative disease drug to treat Gram-negative antibiotic-resistant bacterial sepsis. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	36
76	Tracking antibiotic resistance. <i>Science</i> , 2014, 345, 1454-1455.	6.0	35
77	Discovery of New Genes Involved in Curli Production by a Uropathogenic <i>Escherichia coli</i> Strain from the Highly Virulent O45:K1:H7 Lineage. <i>MBio</i> , 2018, 9, .	1.8	35
78	The role of H4 flagella in <i>Escherichia coli</i> ST131 virulence. <i>Scientific Reports</i> , 2015, 5, 16149.	1.6	34
79	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing <i>Enterobacter hormaechei</i> . <i>Nature Communications</i> , 2020, 11, 466.	5.8	34
80	Regulatory interplay between <i>pap</i> operons in uropathogenic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2008, 67, 996-1011.	1.2	33
81	Microevolution of <i>Streptococcus agalactiae</i> ST-261 from Australia Indicates Dissemination via Imported Tilapia and Ongoing Adaptation to Marine Hosts or Environment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	33
82	Sub-inhibitory concentrations of ceftazidime and tobramycin reduce the quorum sensing signals of <i>Pseudomonas aeruginosa</i> . <i>Pathology</i> , 2004, 36, 571-575.	0.3	32
83	uPEPperoni: An online tool for upstream open reading frame location and analysis of transcript conservation. <i>BMC Bioinformatics</i> , 2014, 15, 36.	1.2	32
84	Molecular Characterization of the Vacuolating Autotransporter Toxin in Uropathogenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2016, 198, 1487-1498.	1.0	31
85	Within-host whole genome analysis of an antibiotic resistant <i>Pseudomonas aeruginosa</i> strain sub-type in cystic fibrosis. <i>PLoS ONE</i> , 2017, 12, e0172179.	1.1	31
86	Novel genes associated with enhanced motility of <i>Escherichia coli</i> ST131. <i>PLoS ONE</i> , 2017, 12, e0176290.	1.1	31
87	Mutual Exclusivity of Hyaluronan and Hyaluronidase in Invasive Group A <i>Streptococcus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 32303-32315.	1.6	30
88	Lineage-Specific Methyltransferases Define the Methylome of the Globally Disseminated <i>Escherichia coli</i> ST131 Clone. <i>MBio</i> , 2015, 6, e01602-15.	1.8	27
89	Increased S-Nitrosylation and Proteasomal Degradation of Caspase-3 during Infection Contribute to the Persistence of Adherent Invasive <i>Escherichia coli</i> (AIEC) in Immune Cells. <i>PLoS ONE</i> , 2013, 8, e68386.	1.1	26
90	Genome analysis and CRISPR typing of <i>Salmonella enterica</i> serovar Virchow. <i>BMC Genomics</i> , 2014, 15, 389.	1.2	25

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91	MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. <i>BMC Genomics</i> , 2021, 22, 474.	1.2	25
92	Zoocin A immunity factor: afemA-like gene found in a group C streptococcus. <i>FEMS Microbiology Letters</i> , 1998, 163, 73-77.	0.7	24
93	Characterization of Ehaj, a New Autotransporter Protein from Enterohemorrhagic and Enteropathogenic <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 120.	1.5	24
94	Molecular Analysis of Asymptomatic Bacteriuria <i>Escherichia coli</i> Strain VR50 Reveals Adaptation to the Urinary Tract by Gene Acquisition. <i>Infection and Immunity</i> , 2015, 83, 1749-1764.	1.0	24
95	Discovery and Characterization of Human-Urine Utilization by Asymptomatic-Bacteriuria-Causing <i>Streptococcus agalactiae</i> . <i>Infection and Immunity</i> , 2016, 84, 307-319.	1.0	24
96	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> , 2018, 8, 1503.	1.6	23
97	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. <i>Nature Microbiology</i> , 2020, 5, 1340-1348.	5.9	23
98	Secretion of flagellin by the LEE-encoded type III secretion system of enteropathogenic <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2009, 9, 30.	1.3	22
99	New plasmids and putative virulence factors from the draft genome of an Australian clinical isolate of <i>Photorhabdus asymbiotica</i> . <i>FEMS Microbiology Letters</i> , 2010, 309, no-no.	0.7	22
100	Genomic surveillance, characterization and intervention of a polymicrobial multidrug-resistant outbreak in critical care. <i>Microbial Genomics</i> , 2021, 7, .	1.0	22
101	Comprehensive analysis of type 1 fimbriae regulation in <i>fimB</i> null strains from the multidrug resistant <i>Escherichia coli</i> ST131 clone. <i>Molecular Microbiology</i> , 2016, 101, 1069-1087.	1.2	21
102	GIFT domains: linking eukaryotic intraflagellar transport and glycosylation to bacterial gliding. <i>Trends in Biochemical Sciences</i> , 2004, 29, 396-399.	3.7	20
103	The Intimin-Like Protein FdeC Is Regulated by H-NS and Temperature in Enterohemorrhagic <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 7337-7347.	1.4	20
104	The comparative in-vitro activity of roxithromycin and other antibiotics against <i>Bordetella pertussis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 1998, 41, 23-27.	1.3	19
105	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> , 2012, 2, 287-297.	0.8	19
106	Characterisation of a cell wall-anchored protein of <i>Staphylococcus saprophyticus</i> associated with linoleic acid resistance. <i>BMC Microbiology</i> , 2012, 12, 8.	1.3	19
107	Acquisition of the Sda1-Encoding Bacteriophage Does Not Enhance Virulence of the Serotype M1 <i>Streptococcus pyogenes</i> Strain SF370. <i>Infection and Immunity</i> , 2013, 81, 2062-2069.	1.0	19
108	A Distinct and Divergent Lineage of Genomic Island-Associated Type IV Secretion Systems in <i>Legionella</i> . <i>PLoS ONE</i> , 2013, 8, e82221.	1.1	19

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109	Genetic variation in <sc>IRF</sc>4 expression modulates growth characteristics, tyrosinase expression and interferonâ€šgamma response in melanocytic cells. Pigment Cell and Melanoma Research, 2018, 31, 51-63.	1.5	19
110	Detection of Epidemic Scarlet Fever Group A Streptococcus in Australia. Clinical Infectious Diseases, 2019, 69, 1232-1234.	2.9	19
111	Genomic analysis of carbapenemase-producing Enterobacteriaceae in Queensland reveals widespread transmission of bla IMP-4 on an IncHI2 plasmid. Microbial Genomics, 2020, 6, .	1.0	19
112	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium Starkeya novella type strain (ATCC 8093T). Standards in Genomic Sciences, 2012, 7, 44-58.	1.5	19
113	A Minimal Tiling Path Cosmid Library for Functional Analysis of the<i>Pseudomonas aeruginosa</i> PAO1 Genome. Microbial & Comparative Genomics, 2000, 5, 189-203.	0.6	18
114	Streptococcal collagenâ€šlike protein A and general stress protein 24 are immunomodulating virulence factors of group A Streptococcus. FASEB Journal, 2013, 27, 2633-2643.	0.2	18
115	Stability of active prophages in industrial Lactococcus lactis strains in the presence of heat, acid, osmotic, oxidative and antibiotic stressors. International Journal of Food Microbiology, 2016, 220, 26-32.	2.1	18
116	Fatal Respiratory Diphtheria Caused by ã€š-Lactamâ€šResistant Corynebacterium diphtheriae. Clinical Infectious Diseases, 2020, 73, e4531-e4538.	2.9	18
117	Molecular and Structural Characterization of a Novel Escherichia coli Interleukin Receptor Mimic Protein. MBio, 2016, 7, e02046.	1.8	17
118	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium Starkeya novella type strain (ATCC 8093T). Standards in Genomic Sciences, 2012, 7, 44-58.	1.5	16
119	Whole genome sequencing reveals the emergence of a Pseudomonas aeruginosa shared strain sub-lineage among patients treated within a single cystic fibrosis centre. BMC Genomics, 2018, 19, 644.	1.2	16
120	Variation in hemolysin A expression between uropathogenic Escherichia coli isolates determines NLRP3â€šdependent vs . â€š-independent macrophage cell death and host colonization. FASEB Journal, 2019, 33, 7437-7450.	0.2	16
121	Complex Multilevel Control of Hemolysin Production by Uropathogenic Escherichia coli. MBio, 2019, 10, .	1.8	15
122	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. Journal of Antimicrobial Chemotherapy, 2015, 70, 1969-1972.	1.3	14
123	Genomic Comparison of Two O111:Hã€šEnterohemorrhagic Escherichia coli Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. Infection and Immunity, 2016, 84, 775-781.	1.0	14
124	Plasmid-Mediated Ciprofloxacin Resistance Imparts a Selective Advantage on Escherichia coli ST131. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0214621.	1.4	14
125	Outsmarting Outbreaks. Science, 2012, 338, 1161-1162.	6.0	13
126	Extragenic suppressor mutations that restore twitching motility to <sc>i>fimL</sc> mutants of <i>Pseudomonas aeruginosa</i> are associated with elevated intracellular cyclic <sc>AMP</sc> levels. MicrobiologyOpen, 2012, 1, 490-501.	1.2	13

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127	Complete Genome Sequence of Serotype III <i>Streptococcus agalactiae</i> Sequence Type 17 Strain 874391. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
128	Rescuing Tetracycline Class Antibiotics for the Treatment of Multidrug-Resistant <i>Acinetobacter baumannii</i> Pulmonary Infection. <i>MBio</i> , 2022, 13, e0351721.	1.8	11
129	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> , 2019, 9, 9436.	1.6	10
130	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> , 2021, 40, 279-286.	1.3	10
131	Optimising Treatment Outcomes for Children and Adults Through Rapid Genome Sequencing of Sepsis Pathogens. A Study Protocol for a Prospective, Multi-Centre Trial (DIRECT). <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 667680.	1.8	10
132	Differential Regulation of the Surface-Exposed and Secreted SslE Lipoprotein in Extraintestinal Pathogenic <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2016, 11, e0162391.	1.1	9
133	Molecular Epidemiology of Clinical and Colonizing Methicillin-Resistant <i>Staphylococcus</i> Isolates in Companion Animals. <i>Frontiers in Veterinary Science</i> , 2021, 8, 620491.	0.9	9
134	Differential Afa/Dr Fimbriae Expression in the Multidrug-Resistant <i>Escherichia coli</i> ST131 Clone. <i>MBio</i> , 2022, 13, e0351921.	1.8	9
135	Emergence and impact of <i>oprD</i> mutations in <i>Pseudomonas aeruginosa</i> strains in cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , 2022, 21, e35-e43.	0.3	8
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