

Scott A Beatson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

161
papers

11,591
citations

47
h-index

106
g-index

186
ext. papers

15,035
ext. citations

6.4
avg, IF

6.16
L-index

#	Paper	IF	Citations
161	Differential Afa/Dr Fimbriae Expression in the Multidrug-Resistant Escherichia coli ST131 Clone.. <i>MBio</i> , 2022 , e0351921	7.8	2
160	Rescuing Tetracycline Class Antibiotics for the Treatment of Multidrug-Resistant Acinetobacter baumannii Pulmonary Infection.. <i>MBio</i> , 2022 , e0351721	7.8	1
159	Plasmid-mediated ciprofloxacin resistance imparts a selective advantage on ST131. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , AAC0214621	5.9	1
158	Fatal Respiratory Diphtheria Caused by β -Lactam-Resistant Corynebacterium diphtheriae. <i>Clinical Infectious Diseases</i> , 2021 , 73, e4531-e4538	11.6	2
157	Genomic surveillance, characterization and intervention of a polymicrobial multidrug-resistant outbreak in critical care. <i>Microbial Genomics</i> , 2021 , 7,	4.4	6
156	Molecular Epidemiology of Clinical and Colonizing Methicillin-Resistant Isolates in Companion Animals. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 620491	3.1	1
155	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	5.9	1
154	MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. <i>BMC Genomics</i> , 2021 , 22, 474	4.5	1
153	Outbreak of multi-drug-resistant (MDR) Shigella flexneri 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	5.3	0
152	Characterization of DtrJ as an IncC plasmid conjugative DNA transfer component. <i>Molecular Microbiology</i> , 2021 , 116, 154-167	4.1	0
151	Emergence and impact of oprD mutations in Pseudomonas aeruginosa strains in cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , 2021 ,	4.1	3
150	Antimicrobial Resistance in ESKAPE Pathogens. <i>Clinical Microbiology Reviews</i> , 2020 , 33,	34	290
149	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. <i>PLoS Pathogens</i> , 2020 , 16, e1008287	7.6	18
148	Phase variation in latB associated with a fatal Pasteurella multocida outbreak in captive squirrel gliders. <i>Veterinary Microbiology</i> , 2020 , 243, 108612	3.3	3
147	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing Enterobacter hormaechei. <i>Nature Communications</i> , 2020 , 11, 466	17.4	14
146	Predicting nitroimidazole antibiotic resistance mutations in Mycobacterium tuberculosis with protein engineering. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	
145	Genomic analysis of carbapenemase-producing in Queensland reveals widespread transmission of an IncHI2 plasmid. <i>Microbial Genomics</i> , 2020 , 6,	4.4	7

144	Using genomics to understand inter- and intra- outbreak diversity of isolates associated with fowl cholera in meat chickens. <i>Microbial Genomics</i> , 2020 , 6,	4.4	3
143	Companion Animals Are Spillover Hosts of the Multidrug-Resistant Human Extraintestinal Pandemic Clones ST131 and ST1193. <i>Frontiers in Microbiology</i> , 2020 , 11, 1968	5.7	19
142	Repurposing a neurodegenerative disease drug to treat Gram-negative antibiotic-resistant bacterial sepsis. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	13
141	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. <i>Nature Microbiology</i> , 2020 , 5, 1340-1348	26.6	6
140	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,	9.7	15
139	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
138	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
137	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
136	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering 2020 , 16, e1008287		
135	Whole-genome sequencing as an improved means of investigating <i>Neisseria gonorrhoeae</i> treatment failures. <i>Sexual Health</i> , 2019 , 16, 500-507	2	2
134	Control of Bacterial Sulfite Detoxification by Conserved and Species-Specific Regulatory Circuits. <i>Frontiers in Microbiology</i> , 2019 , 10, 960	5.7	4
133	Variation in hemolysin A expression between uropathogenic isolates determines NLRP3-dependent -independent macrophage cell death and host colonization. <i>FASEB Journal</i> , 2019 , 33, 7437-7450	0.9	9
132	Novel insights into pasteurellosis in captive pinnipeds. <i>Veterinary Microbiology</i> , 2019 , 231, 232-237	3.3	4
131	Detection of Epidemic Scarlet Fever Group A <i>Streptococcus</i> in Australia. <i>Clinical Infectious Diseases</i> , 2019 , 69, 1232-1234	11.6	10
130	Population dynamics of an <i>Escherichia coli</i> ST131 lineage during recurrent urinary tract infection. <i>Nature Communications</i> , 2019 , 10, 3643	17.4	36
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	4.9	6
128	Complex Multilevel Control of Hemolysin Production by Uropathogenic <i>Escherichia coli</i> . <i>MBio</i> , 2019 , 10,	7.8	6
127	SRA Down Under: Cache and Analysis Platform for Infectious Disease. <i>Studies in Health Technology and Informatics</i> , 2019 , 266, 76-82	0.5	

126	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> , 2018 , 73, 634-642	5.1	36
125	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	4.9	12
124	Genetic variation in IRF4 expression modulates growth characteristics, tyrosinase expression and interferon-gamma response in melanocytic cells. <i>Pigment Cell and Melanoma Research</i> , 2018 , 31, 51-63	4.5	13
123	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,	7.8	20
122	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,	4.8	17
121	Discovery of -Mediated Colistin Resistance in a Highly Virulent <i>Escherichia coli</i> Lineage. <i>MSphere</i> , 2018 , 3,	5	30
120	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> , 2018 , 19, 644	4.5	10
119	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: A Randomized Clinical Trial. <i>JAMA - Journal of the American Medical Association</i> , 2018 , 320, 984-994	27.4	339
118	Diving Deep Into Hospital-Acquired <i>Legionella pneumophila</i> With Whole-Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017 , 64, 1260-1262	11.6	4
117	Approaches to Study Uropathogenic <i>Escherichia coli</i> Virulence. <i>Trends in Microbiology</i> , 2017 , 25, 729-740	12.4	14
116	Genome-Wide Discovery of Genes Required for Capsule Production by Uropathogenic. <i>MBio</i> , 2017 , 8,	7.8	29
115	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	3.7	23
114	Complete Genome Sequence of Serotype III Sequence Type 17 Strain 874391. <i>Genome Announcements</i> , 2017 , 5,		6
113	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> , 2017 , 72, 2729-2736	5.1	28
112	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,	5.9	73
111	Novel genes associated with enhanced motility of <i>Escherichia coli</i> ST131. <i>PLoS ONE</i> , 2017 , 12, e0176290	3.7	20
110	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing β proteobacterium <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477(T)). <i>Standards in Genomic Sciences</i> , 2016 , 11, 38		5
109	Stability of active prophages in industrial <i>Lactococcus lactis</i> strains in the presence of heat, acid, osmotic, oxidative and antibiotic stressors. <i>International Journal of Food Microbiology</i> , 2016 , 220, 26-32	5.8	14

108	Molecular Characterization of the Vacuolating Autotransporter Toxin in Uropathogenic Escherichia coli. <i>Journal of Bacteriology</i> , 2016 , 198, 1487-98	3.5	21
107	Genomic Comparison of Two O111:H- Enterohemorrhagic Escherichia coli Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. <i>Infection and Immunity</i> , 2016 , 84, 775-81	3.7	11
106	Discovery and Characterization of Human-Urine Utilization by Asymptomatic-Bacteriuria-Causing Streptococcus agalactiae. <i>Infection and Immunity</i> , 2016 , 84, 307-19	3.7	15
105	Hospital-wide Eradication of a Nosocomial Legionella pneumophila Serogroup 1 Outbreak. <i>Clinical Infectious Diseases</i> , 2016 , 62, 273-279	11.6	37
104	Differential Regulation of the Surface-Exposed and Secreted SsIE Lipoprotein in Extraintestinal Pathogenic Escherichia coli. <i>PLoS ONE</i> , 2016 , 11, e0162391	3.7	8
103	Comprehensive analysis of type 1 fimbriae regulation in fimB-null strains from the multidrug resistant Escherichia coli ST131 clone. <i>Molecular Microbiology</i> , 2016 , 101, 1069-87	4.1	13
102	Molecular and Structural Characterization of a Novel Escherichia coli Interleukin Receptor Mimic Protein. <i>MBio</i> , 2016 , 7, e02046	7.8	11
101	A Novel Protective Vaccine Antigen from the Core Genome. <i>MSphere</i> , 2016 , 1,	5	26
100	Mechanisms Involved in Acquisition of blaNDM Genes by IncA/C2 and IncFIY Plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 4082-8	5.9	34
99	Sequential Acquisition of Virulence and Fluoroquinolone Resistance Has Shaped the Evolution of Escherichia coli ST131. <i>MBio</i> , 2016 , 7, e00347-16	7.8	121
98	The host metabolite D-serine contributes to bacterial niche specificity through gene selection. <i>ISME Journal</i> , 2015 , 9, 1039-51	11.9	28
97	Third-generation cephalosporin resistance conferred by a chromosomally encoded blaCMY-23 gene in the Escherichia coli ST131 reference strain EC958. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 1969-72	5.1	9
96	The co-transcriptome of uropathogenic Escherichia coli-infected mouse macrophages reveals new insights into host-pathogen interactions. <i>Cellular Microbiology</i> , 2015 , 17, 730-46	3.9	55
95	Stepwise evolution of pandrug-resistance in Klebsiella pneumoniae. <i>Scientific Reports</i> , 2015 , 5, 15082	4.9	87
94	Transfer of scarlet fever-associated elements into the group A Streptococcus M1T1 clone. <i>Scientific Reports</i> , 2015 , 5, 15877	4.9	41
93	The role of H4 flagella in Escherichia coli ST131 virulence. <i>Scientific Reports</i> , 2015 , 5, 16149	4.9	24
92	Deep sequence characterisation of a divergent HPIV-4a from an adult with prolonged influenza-like illness. <i>Virology Reports</i> , 2015 , 5, 19-28		
91	Lineage-Specific Methyltransferases Define the Methylome of the Globally Disseminated Escherichia coli ST131 Clone. <i>MBio</i> , 2015 , 6, e01602-15	7.8	21

90	Molecular Characterization of the Multidrug Resistant Escherichia coli ST131 Clone. <i>Pathogens</i> , 2015 , 4, 422-30	4.5	28
89	Draft Genome Sequence of Pseudomonas fluorescens SRM1, an Isolate from Spoiled Raw Milk. <i>Genome Announcements</i> , 2015 , 3,		3
88	Molecular analysis of asymptomatic bacteriuria Escherichia coli strain VR50 reveals adaptation to the urinary tract by gene acquisition. <i>Infection and Immunity</i> , 2015 , 83, 1749-64	3.7	20
87	Molecular characterization of a multidrug resistance IncF plasmid from the globally disseminated Escherichia coli ST131 clone. <i>PLoS ONE</i> , 2015 , 10, e0122369	3.7	32
86	uPEPperoni: an online tool for upstream open reading frame location and analysis of transcript conservation. <i>BMC Bioinformatics</i> , 2014 , 15, 36	3.6	22
85	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing Escherichia coli (STEC) in global food production systems. <i>International Journal of Food Microbiology</i> , 2014 , 187, 57-72	5.8	58
84	Genome analysis and CRISPR typing of Salmonella enterica serovar Virchow. <i>BMC Genomics</i> , 2014 , 15, 389	4.5	21
83	The complete genome sequence of Escherichia coli EC958: a high quality reference sequence for the globally disseminated multidrug resistant E. coli O25b:H4-ST131 clone. <i>PLoS ONE</i> , 2014 , 9, e104400	3.7	75
82	Global dissemination of a multidrug resistant Escherichia coli clone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5694-9	11.5	354
81	Mutual exclusivity of hyaluronan and hyaluronidase in invasive group A Streptococcus. <i>Journal of Biological Chemistry</i> , 2014 , 289, 32303-32315	5.4	23
80	The metabolic enzyme AdhE controls the virulence of Escherichia coli O157:H7. <i>Molecular Microbiology</i> , 2014 , 93, 199-211	4.1	40
79	Microbiology. Tracking antibiotic resistance. <i>Science</i> , 2014 , 345, 1454-5	33.3	23
78	The Intimin-Like Protein FdeC Is Regulated by H-NS and Temperature in Enterohemorrhagic Escherichia coli. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 7337-47	4.8	15
77	Galleria mellonella infection model demonstrates high lethality of ST69 and ST127 uropathogenic E. coli. <i>PLoS ONE</i> , 2014 , 9, e101547	3.7	45
76	Draft genome sequence of the male-killing Wolbachia strain wBol1 reveals recent horizontal gene transfers from diverse sources. <i>BMC Genomics</i> , 2013 , 14, 20	4.5	49
75	Streptococcal collagen-like protein A and general stress protein 24 are immunomodulating virulence factors of group A Streptococcus. <i>FASEB Journal</i> , 2013 , 27, 2633-43	0.9	10
74	Molecular analysis of the Acinetobacter baumannii biofilm-associated protein. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6535-43	4.8	49
73	Genome Sequence of Hydrothermal Arsenic-Respiring Bacterium Marinobacter santoriniensis NKSG1T. <i>Genome Announcements</i> , 2013 , 1,		5

72	The serum resistome of a globally disseminated multidrug resistant uropathogenic Escherichia coli clone. <i>PLoS Genetics</i> , 2013 , 9, e1003834	6	106
71	Genomic evolution of the pathogenic Wolbachia strain, wMelPop. <i>Genome Biology and Evolution</i> , 2013 , 5, 2189-204	3.9	77
70	A FimH inhibitor prevents acute bladder infection and treats chronic cystitis caused by multidrug-resistant uropathogenic Escherichia coli ST131. <i>Journal of Infectious Diseases</i> , 2013 , 208, 921-8	3.7	96
69	Acquisition of the Sda1-encoding bacteriophage does not enhance virulence of the serotype M1 Streptococcus pyogenes strain SF370. <i>Infection and Immunity</i> , 2013 , 81, 2062-9	3.7	17
68	Chaperone-usher fimbriae of Escherichia coli. <i>PLoS ONE</i> , 2013 , 8, e52835	3.7	111
67	Identification of novel vaccine candidates against multidrug-resistant Acinetobacter baumannii. <i>PLoS ONE</i> , 2013 , 8, e77631	3.7	56
66	A distinct and divergent lineage of genomic island-associated Type IV Secretion Systems in Legionella. <i>PLoS ONE</i> , 2013 , 8, e82221	3.7	17
65	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> , 2013 , 8, e68386	3.7	24
64	Extragenic suppressor mutations that restore twitching motility to fimL mutants of Pseudomonas aeruginosa are associated with elevated intracellular cyclic AMP levels. <i>MicrobiologyOpen</i> , 2012 , 1, 490-501	3.4	10
63	Analysis of a Streptococcus pyogenes puerperal sepsis cluster by use of whole-genome sequencing. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 2224-8	9.7	47
62	Tracing the evolutionary history of the pandemic group A streptococcal M1T1 clone. <i>FASEB Journal</i> , 2012 , 26, 4675-84	0.9	41
61	Characterisation of a cell wall-anchored protein of Staphylococcus saprophyticus associated with linoleic acid resistance. <i>BMC Microbiology</i> , 2012 , 12, 8	4.5	15
60	Origin of the diversity in DNA recognition domains in phasevarion associated modA genes of pathogenic Neisseria and Haemophilus influenzae. <i>PLoS ONE</i> , 2012 , 7, e32337	3.7	32
59	Comparative genomics of the Staphylococcus intermedius group of animal pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 44	5.9	33
58	Epidemiology. Outsmarting outbreaks. <i>Science</i> , 2012 , 338, 1161-2	33.3	11
57	Physical and Linkage Maps for Drosophila serrata, a Model Species for Studies of Clinal Adaptation and Sexual Selection. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 287-97	3.2	10
56	Lysogeny with Shiga toxin 2-encoding bacteriophages represses type III secretion in enterohemorrhagic Escherichia coli. <i>PLoS Pathogens</i> , 2012 , 8, e1002672	7.6	46
55	Heat resistance and salt hypersensitivity in Lactococcus lactis due to spontaneous mutation of lmg_1816 (gdpP) induced by high-temperature growth. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7753-9	4.8	61

54	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> , 2012 , 7, 44-58		12
53	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , 2012 , 7, 44-58		15
52	Characterization of EhaJ, a New Autotransporter Protein from Enterohemorrhagic and Enteropathogenic <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2011 , 2, 120	5.7	22
51	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	3.7	149
50	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, 1349-65	4.1	38
49	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> , 2011 , 62, 273-82		4
48	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. <i>BMC Genomics</i> , 2011 , 12, 402	4.5	1617
47	Easyfig: a genome comparison visualizer. <i>Bioinformatics</i> , 2011 , 27, 1009-10	7.2	1590
46	Genome sequence of the emerging pathogen <i>Aeromonas caviae</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 1286-7		30
45	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	2.9	29
44	New plasmids and putative virulence factors from the draft genome of an Australian clinical isolate of <i>Photobacterium damela</i> . <i>FEMS Microbiology Letters</i> , 2010 , 309, 136-43	2.9	19
43	<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, 6001-16	3.5	95
42	Multiple antibiotic resistance gene recruitment onto the enterohemorrhagic <i>Escherichia coli</i> virulence plasmid. <i>FASEB Journal</i> , 2010 , 24, 1160-6	0.9	60
41	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> , 2010 , 78, 1659-69	3.7	70
40	A commensal gene bad: complete genome sequence of the prototypical enterotoxigenic <i>Escherichia coli</i> strain H10407. <i>Journal of Bacteriology</i> , 2010 , 192, 5822-31	3.5	141
39	Molecular analysis of type 3 fimbrial genes from <i>Escherichia coli</i> , <i>Klebsiella</i> and <i>Citrobacter</i> species. <i>BMC Microbiology</i> , 2010 , 10, 183	4.5	39
38	Accelerated evolution of the Prdm9 speciation gene across diverse metazoan taxa. <i>PLoS Genetics</i> , 2009 , 5, e1000753	6	203
37	Conjugative plasmid transfer and adhesion dynamics in an <i>Escherichia coli</i> biofilm. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6783-91	4.8	48

36	Secretion of flagellin by the LEE-encoded type III secretion system of enteropathogenic Escherichia coli. <i>BMC Microbiology</i> , 2009 , 9, 30	4.5	21
35	EhaA is a novel autotransporter protein of enterohemorrhagic Escherichia coli O157:H7 that contributes to adhesion and biofilm formation. <i>Environmental Microbiology</i> , 2008 , 10, 589-604	5.2	101
34	Regulatory interplay between pap operons in uropathogenic Escherichia coli. <i>Molecular Microbiology</i> , 2008 , 67, 996-1011	4.1	29
33	Identification of type 3 fimbriae in uropathogenic Escherichia coli reveals a role in biofilm formation. <i>Journal of Bacteriology</i> , 2008 , 190, 1054-63	3.5	78
32	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> , 2006 , 103, 14941-6	11.5	370
31	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, 935-41	6.3	76
30	Variation in bacterial flagellins: from sequence to structure. <i>Trends in Microbiology</i> , 2006 , 14, 151-5	12.4	106
29	Prevalence of pathogenicity island IICFT073 genes among extraintestinal clinical isolates of Escherichia coli. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 2425-34	9.7	39
28	Protein secretion systems in Fusobacterium nucleatum: 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> , 2005 , 1713, 92-112	3.8	49
27	Bioinformatics, genomics and evolution of non-flagellar type-III secretion systems: a Darwinian perspective. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 201-29	15.1	124
26	Pseudomonas aeruginosa fimL regulates multiple virulence functions by intersecting with Vfr-modulated pathways. <i>Molecular Microbiology</i> , 2005 , 55, 1357-78	4.1	79
25	Bioinformatics analysis of the locus for enterocyte effacement provides novel insights into type-III secretion. <i>BMC Microbiology</i> , 2005 , 5, 9	4.5	95
24	The Flag-2 locus, an ancestral gene cluster, is potentially associated with a novel flagellar system from Escherichia coli. <i>Journal of Bacteriology</i> , 2005 , 187, 1430-40	3.5	69
23	FpvB, an alternative type I ferripyoverdine receptor of Pseudomonas aeruginosa. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 1671-1680	2.9	129
22	Evolution and comparative genomics of odorant- and pheromone-associated genes in rodents. <i>Genome Research</i> , 2004 , 14, 591-602	9.7	72
21	Characterization of a complex chemosensory signal transduction system which controls twitching motility in Pseudomonas aeruginosa. <i>Molecular Microbiology</i> , 2004 , 52, 873-93	4.1	167
20	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
19	GIFT domains: linking eukaryotic intraflagellar transport and glycosylation to bacterial gliding. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 396-9	10.3	18

18	Sub-inhibitory concentrations of ceftazidime and tobramycin reduce the quorum sensing signals of <i>Pseudomonas aeruginosa</i> . <i>Pathology</i> , 2004 , 36, 571-5	1.6	27
17	Identification of type II and type III pyoverdine receptors from <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2003 , 149, 821-831	2.9	75
16	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	2.9	111
15	Cadherin-like domains in alpha-dystroglycan, alpha/epsilon-sarcoglycan and yeast and bacterial proteins. <i>Current Biology</i> , 2002 , 12, R197-9	6.3	50
14	Quorum sensing is not required for twitching motility in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002 , 184, 3598-604	3.5	115
13	Differential regulation of twitching motility and elastase production by Vfr in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002 , 184, 3605-13	3.5	148
12	A minimal tiling path cosmid library for functional analysis of the <i>Pseudomonas aeruginosa</i> PAO1 genome. <i>Microbial & Comparative Genomics</i> , 2000 , 5, 189-203		18
11	An interactive web-based <i>Pseudomonas aeruginosa</i> genome database: discovery of new genes, pathways and structures. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 10), 2351-2364	2.9	56
10	Zoocin A immunity factor: a femA-like gene found in a group C streptococcus. <i>FEMS Microbiology Letters</i> , 1998 , 163, 73-7	2.9	23
9	The comparative in-vitro activity of roxithromycin and other antibiotics against <i>Bordetella pertussis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 1998 , 41 Suppl B, 23-7	5.1	15
8	Contiguity: Contig adjacency graph construction and visualisation		4
7	Contiguity: Contig adjacency graph construction and visualisation		9
6	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
5	Sequential acquisition of virulence and fluoroquinolone resistance has shaped the evolution of <i>Escherichia coli</i> ST131		3
4	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing <i>Enterobacter hormaechei</i>		2
3	Strain and lineage-level methylome heterogeneity in the multi-drug resistant pathogenic <i>Escherichia coli</i> ST101 clone		1
2	Multiple evolutionary trajectories for non-O157 Shiga toxigenic <i>Escherichia coli</i>		2
1	Genomic characterisation and context of the bla _{NDM-1} carbapenemase in <i>Escherichia coli</i> ST101		2

