

# Mark J Pallen

## 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.

182  
papers

13,690  
citations

62  
h-index

115  
g-index

201  
ext. papers

15,686  
ext. citations

9.2  
avg, IF

6.34  
L-index

#	Paper	IF	Citations
182	The microbial ecology of <i>Escherichia coli</i> in the vertebrate gut.. <i>FEMS Microbiology Reviews</i> , <b>2022</b> ,	15.1	2
181	Archaeal and Bacterial Metagenome-Assembled Genome Sequences Derived from Pig Feces.. <i>Microbiology Resource Announcements</i> , <b>2022</b> , 11, e0114221	1.3	0
180	Remarkable genomic diversity among isolates recovered from healthy chickens.. <i>PeerJ</i> , <b>2022</b> , 10, e12935,1	3.1	1
179	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity.. <i>PeerJ</i> , <b>2022</b> , 10, e13084	3.1	1
178	: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	3
177	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , <b>2021</b> , 9, e10941	3.1	21
176	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , <b>2021</b> , 6, 821-823	26.6	91
175	The Next Million Names for Archaea and Bacteria. <i>Trends in Microbiology</i> , <b>2021</b> , 29, 289-298	12.4	15
174	The status for uncultured taxa of and : SWOT analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2021</b> , 71,	2.2	5
173	Bacterial nomenclature in the era of genomics. <i>New Microbes and New Infections</i> , <b>2021</b> , 44, 100942	4.1	2
172	Genomic diversity of from healthy children in rural Gambia. <i>PeerJ</i> , <b>2021</b> , 9, e10572	3.1	4
171	Genomic diversity of isolates from backyard chickens and guinea fowl in the Gambia. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	6
170	Restoration of wild-type motility to flagellin-knockout by varying promoter, copy number and induction strength in plasmid-based expression of flagellin. <i>Current Research in Biotechnology</i> , <b>2020</b> , 2, 45-52	4.8	1
169	Assembly of hundreds of novel bacterial genomes from the chicken caecum. <i>Genome Biology</i> , <b>2020</b> , 21, 34	18.3	42
168	Evolution of <i>Mycobacterium tuberculosis</i> complex lineages and their role in an emerging threat of multidrug resistant tuberculosis in Bamako, Mali. <i>Scientific Reports</i> , <b>2020</b> , 10, 327	4.9	10
167	Genomic diversity of isolates from non-human primates in the Gambia. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	7
166	Creation of Golden Gate constructs for gene doctoring. <i>BMC Biotechnology</i> , <b>2020</b> , 20, 54	3.5	2

165	Towards standardisation of naming novel prokaryotic taxa in the age of high-throughput microbiology. <i>Gut</i> , <b>2020</b> , 69, 1358-1359	19.2	2
164	Loss of microbial diversity and pathogen domination of the gut microbiota in critically ill patients. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	31
163	Metagenomic profiling of ticks: Identification of novel rickettsial genomes and detection of tick-borne canine parvovirus. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0006805	4.8	14
162	Organization and architecture of AggR-dependent promoters from enteroaggregative <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , <b>2019</b> , 111, 534-551	4.1	6
161	A prehistoric Egyptian mummy: Evidence for an embalming recipe and the evolution of early formative funerary treatments. <i>Journal of Archaeological Science</i> , <b>2018</b> , 100, 191-200	2.9	23
160	Bacterial Flagellins: Does Size Matter?. <i>Trends in Microbiology</i> , <b>2018</b> , 26, 575-581	12.4	5
159	Giant flagellins form thick flagellar filaments in two species of marine $\epsilon$ proteobacteria. <i>PLoS ONE</i> , <b>2018</b> , 13, e0206544	3.7	6
158	The gut-adherent microbiota of PSC-IBD is distinct to that of IBD. <i>Gut</i> , <b>2017</b> , 66, 386-388	19.2	91
157	Identification of the anti-mycobacterial functional properties of piperidinol derivatives. <i>British Journal of Pharmacology</i> , <b>2017</b> , 174, 2183-2193	8.6	7
156	The Gut Microbiota and the Hepatologist: Will Our Bugs Prove to be the Missing Link?. <i>Digestive Diseases</i> , <b>2017</b> , 35, 377-383	3.2	1
155	Doggerland and the Lost Frontiers Project (2015-2020). <i>Coastal Research Library</i> , <b>2017</b> , 305-319	0.4	10
154	Whole-genome sequencing illuminates the evolution and spread of multidrug-resistant tuberculosis in Southwest Nigeria. <i>PLoS ONE</i> , <b>2017</b> , 12, e0184510	3.7	19
153	An Chicken Gut Model Demonstrates Transfer of a Multidrug Resistance Plasmid from to Commensal. <i>MBio</i> , <b>2017</b> , 8,	7.8	40
152	The Enigmatic Esx Proteins: Looking Beyond Mycobacteria. <i>Trends in Microbiology</i> , <b>2017</b> , 25, 192-204	12.4	63
151	Forensic Analysis Reveals Acute Decompensation of Chronic Heart Failure in a 3500-Year-Old Egyptian Dignitary. <i>Journal of Forensic Sciences</i> , <b>2016</b> , 61, 1378-81	1.8	8
150	The emerging threat of pre-extensively drug-resistant tuberculosis in West Africa: preparing for large-scale tuberculosis research and drug resistance surveillance. <i>BMC Medicine</i> , <b>2016</b> , 14, 160	11.4	25
149	An outbreak of pneumococcal meningitis among older children (5 years) and adults after the implementation of an infant vaccination programme with the 13-valent pneumococcal conjugate vaccine in Ghana. <i>BMC Infectious Diseases</i> , <b>2016</b> , 16, 575	4	52
148	Draft Genome Sequences of Six Novel Bacterial Isolates from Chicken Ceca. <i>Genome Announcements</i> , <b>2016</b> , 4,		4

147	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000086	4.4	105
146	Draft Genome Sequences of Nine Clinical Isolates of Vancomycin-Resistant Enterococci. <i>Genome Announcements</i> , <b>2016</b> , 4,		1
145	Transmission of <i>Staphylococcus aureus</i> from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 5910-7	4.8	22
144	Microbial bioinformatics 2020. <i>Microbial Biotechnology</i> , <b>2016</b> , 9, 681-6	6.3	8
143	Archaeology. Sedimentary DNA from a submerged site reveals wheat in the British Isles 8000 years ago. <i>Science</i> , <b>2015</b> , 347, 998-1001	33.3	73
142	Response to Comment on Sedimentary DNA from a submerged site reveals wheat in the British Isles 8000 years ago. <i>Science</i> , <b>2015</b> , 349, 247.3-247	33.3	4
141	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , <b>2015</b> , 6, 6717	17.4	122
140	Complete genome sequence of Pig-tailed macaque rhadinovirus 2 and its evolutionary relationship with rhesus macaque rhadinovirus and human herpesvirus 8/Kaposi's sarcoma-associated herpesvirus. <i>Journal of Virology</i> , <b>2015</b> , 89, 3888-909	6.6	13
139	Parallel evolutionary pathways to antibiotic resistance selected by biocide exposure. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 2241-8	5.1	85
138	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 787-94	22.2	181
137	The <i>pla</i> gene, encoding plasminogen activator, is not specific to <i>Yersinia pestis</i> . <i>BMC Research Notes</i> , <b>2015</b> , 8, 535	2.3	21
136	Differences in the Faecal Microbiome in <i>Schistosoma haematobium</i> Infected Children vs. Uninfected Children. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003861	4.8	56
135	What Genomics Has Taught Us about Gram-Positive Protein Secretion and Targeting <b>2014</b> , 301-326		2
134	Microarray analysis of the <i>Ler</i> regulon in enteropathogenic and enterohaemorrhagic <i>Escherichia coli</i> strains. <i>PLoS ONE</i> , <b>2014</b> , 9, e80160	3.7	20
133	Impact of Phages on Evolution of Bacterial Pathogenicity <b>2014</b> , 267-300		4
132	Genomic epidemiology of a protracted hospital outbreak caused by multidrug-resistant <i>Acinetobacter baumannii</i> in Birmingham, England. <i>Genome Medicine</i> , <b>2014</b> , 6, 70	14.4	52
131	Draft Genome Sequence of <i>Elizabethkingia meningoseptica</i> Isolated from a Traumatic Wound. <i>Genome Announcements</i> , <b>2014</b> , 2,		8
130	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. <i>BMJ Open</i> , <b>2014</b> , 4, e006278	3	69

129	Recovery of a medieval <i>Brucella melitensis</i> genome using shotgun metagenomics. <i>MBio</i> , <b>2014</b> , 5, e013377-14		54
128	Extensive microbial and functional diversity within the chicken cecal microbiome. <i>PLoS ONE</i> , <b>2014</b> , 9, e91941	3.7	239
127	Culture-independent detection and characterisation of <i>Mycobacterium tuberculosis</i> and <i>M. africanum</i> in sputum samples using shotgun metagenomics on a benchtop sequencer. <i>PeerJ</i> , <b>2014</b> , 2, e585	3.1	84
126	A culture-independent sequence-based metagenomics approach to the investigation of an outbreak of Shiga-toxigenic <i>Escherichia coli</i> O104:H4. <i>JAMA - Journal of the American Medical Association</i> , <b>2013</b> , 309, 1502-10	27.4	226
125	Genomics and outbreak investigation: from sequence to consequence. <i>Genome Medicine</i> , <b>2013</b> , 5, 36	14.4	50
124	Metagenomic analysis of tuberculosis in a mummy. <i>New England Journal of Medicine</i> , <b>2013</b> , 369, 289-90	59.2	82
123	Clonal expansion within pneumococcal serotype 6C after use of seven-valent vaccine. <i>PLoS ONE</i> , <b>2013</b> , 8, e64731	3.7	20
122	Bridging the gap between the technological singularity and mainstream medicine: highlighting a course on technology and the future of medicine. <i>Global Journal of Health Science</i> , <b>2013</b> , 5, 112-25	1.3	7
121	Tetrahydropyrazolo[1,5-a]pyrimidine-3-carboxamide and N-benzyl-6',7'-dihydrospiro[piperidine-4,4'-thieno[3,2-c]pyran] analogues with bactericidal efficacy against <i>Mycobacterium tuberculosis</i> targeting MmpL3. <i>PLoS ONE</i> , <b>2013</b> , 8, e60933	3.7	103
120	Translation of a minigene in the 5' leader sequence of the enterohaemorrhagic <i>Escherichia coli</i> LEE1 transcription unit affects expression of the neighbouring downstream gene. <i>Biochemical Journal</i> , <b>2012</b> , 441, 247-53	3.8	9
119	Defining bacterial species in the genomic era: insights from the genus <i>Acinetobacter</i> . <i>BMC Microbiology</i> , <b>2012</b> , 12, 302	4.5	138
118	The "Annie hypothesis": did the death of his daughter cause Darwin to "give up Christianity"? <i>Centaurus</i> , <b>2012</b> , 54, 105-23	1.1	1
117	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <i>Nature Reviews Microbiology</i> , <b>2012</b> , 10, 599-606	22.2	326
116	Genome analysis of a highly virulent serotype 1 strain of <i>Streptococcus pneumoniae</i> from West Africa. <i>PLoS ONE</i> , <b>2012</b> , 7, e26742	3.7	14
115	High-throughput sequencing of 16S rRNA gene amplicons: effects of extraction procedure, primer length and annealing temperature. <i>PLoS ONE</i> , <b>2012</b> , 7, e38094	3.7	56
114	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 434-9	44.5	1035
113	Identification of novel imidazo[1,2-a]pyridine inhibitors targeting <i>M. tuberculosis</i> QcrB. <i>PLoS ONE</i> , <b>2012</b> , 7, e52951	3.7	135
112	Deletion of TnAbaR23 results in both expected and unexpected antibiogram changes in a multidrug-resistant <i>Acinetobacter baumannii</i> strain. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2012</b> , 56, 1845-53	5.9	19

111	Whole-genome sequence of the emerging pathogen <i>Mycobacterium abscessus</i> strain 47J26. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 549	3.5	15
110	The TCA cycle is not required for selection or survival of multidrug-resistant <i>Salmonella</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2012</b> , 67, 589-99	5.1	11
109	Open-source genomic analysis of Shiga-toxin-producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , <b>2011</b> , 365, 718-24	59.2	340
108	Time to recognise that mitochondria are bacteria?. <i>Trends in Microbiology</i> , <b>2011</b> , 19, 58-64	12.4	37
107	Flagella mediate attachment of enterotoxigenic <i>Escherichia coli</i> to fresh salad leaves. <i>Environmental Microbiology Reports</i> , <b>2011</b> , 3, 112-7	3.7	22
106	Cellulose mediates attachment of <i>Salmonella enterica</i> Serovar Typhimurium to tomatoes. <i>Environmental Microbiology Reports</i> , <b>2011</b> , 3, 569-73	3.7	18
105	The Human Microbiome and Host-Pathogen Interactions <b>2011</b> , 43-61		4
104	Calculating orthologs in bacteria and Archaea: a divide and conquer approach. <i>PLoS ONE</i> , <b>2011</b> , 6, e28388	3.7	9
103	A cryptic promoter in the LEE1 regulatory region of enterohaemorrhagic <i>Escherichia coli</i> : promoter specificity in AT-rich gene regulatory regions. <i>Biochemical Journal</i> , <b>2011</b> , 436, 681-6	3.8	4
102	Organization of the LEE1 operon regulatory region of enterohaemorrhagic <i>Escherichia coli</i> O157:H7 and activation by GrlA. <i>Molecular Microbiology</i> , <b>2011</b> , 79, 468-83	4.1	32
101	Are diagnostic and public health bacteriology ready to become branches of genomic medicine?. <i>Genome Medicine</i> , <b>2011</b> , 3, 53	14.4	17
100	Whole-genome comparison of two <i>Acinetobacter baumannii</i> isolates from a single patient, where resistance developed during tigecycline therapy. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2011</b> , 66, 1499-503	5.1	79
99	Genome sequences of three <i>Acinetobacter baumannii</i> strains assigned to the multilocus sequence typing genotypes ST2, ST25, and ST78. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2359-60	3.5	16
98	Complete genome sequence of the Crohn's disease-associated adherent-invasive <i>Escherichia coli</i> strain HM605. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4540	3.5	34
97	Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative <i>Escherichia coli</i> strain 042. <i>PLoS ONE</i> , <b>2010</b> , 5, e8801	3.7	134
96	SepL resembles an aberrant effector in binding to a class 1 type III secretion chaperone and carrying an N-terminal secretion signal. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 6093-8	3.5	22
95	High-throughput sequencing and clinical microbiology: progress, opportunities and challenges. <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 625-31	7.9	106
94	A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic <i>Escherichia coli</i> strain H10407. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 5822-31	3.5	141

93	High-throughput whole-genome sequencing to dissect the epidemiology of <i>Acinetobacter baumannii</i> isolates from a hospital outbreak. <i>Journal of Hospital Infection</i> , <b>2010</b> , 75, 37-41	6.9	116
92	Simple sequence repeats in <i>Helicobacter canadensis</i> and their role in phase variable expression and C-terminal sequence switching. <i>BMC Genomics</i> , <b>2010</b> , 11, 67	4.5	12
91	The homodimeric GBS1074 from <i>Streptococcus agalactiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2010</b> , 66, 1421-5		13
90	EntrezAJAX: direct web browser access to the Entrez Programming Utilities. <i>Source Code for Biology and Medicine</i> , <b>2010</b> , 5, 6	1.9	0
89	The complete genome and proteome of <i>Laribacter hongkongensis</i> reveal potential mechanisms for adaptations to different temperatures and habitats. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000416	6	45
88	Comparative analysis of two <i>Neisseria gonorrhoeae</i> genome sequences reveals evidence of mobilization of Corraia Repeat Enclosed Elements and their role in regulation. <i>BMC Genomics</i> , <b>2009</b> , 10, 70	4.5	24
87	Gene doctoring: a method for recombineering in laboratory and pathogenic <i>Escherichia coli</i> strains. <i>BMC Microbiology</i> , <b>2009</b> , 9, 252	4.5	108
86	Next-generation sequencing--the promise and perils of charting the great microbial unknown. <i>Microbial Ecology</i> , <b>2009</b> , 57, 1-3	4.4	27
85	Interaction of <i>Salmonella enterica</i> with basil and other salad leaves. <i>ISME Journal</i> , <b>2009</b> , 3, 261-5	11.9	82
84	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. <i>Trends in Microbiology</i> , <b>2009</b> , 17, 1-5	12.4	28
83	Microbial TIR domains: not necessarily agents of subversion?. <i>Trends in Microbiology</i> , <b>2009</b> , 17, 393-8	12.4	45
82	Interaction of enteroaggregative <i>Escherichia coli</i> with salad leaves. <i>Environmental Microbiology Reports</i> , <b>2009</b> , 1, 234-9	3.7	33
81	Subversion of actin dynamics by EspM effectors of attaching and effacing bacterial pathogens. <i>Cellular Microbiology</i> , <b>2008</b> , 10, 1429-41	3.9	63
80	Type VI secretion: a beginner's guide. <i>Current Opinion in Microbiology</i> , <b>2008</b> , 11, 3-8	7.9	418
79	Identification of amino acid residues within the N-terminal domain of EspA that play a role in EspA filament biogenesis and function. <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 2221-6	3.5	7
78	Enterohemorrhagic <i>Escherichia coli</i> exploits EspA filaments for attachment to salad leaves. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 2908-14	4.8	85
77	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D543-6	20.1	113
76	Bacterial pathogenomics. <i>Nature</i> , <b>2007</b> , 449, 835-42	50.4	301



75	Laboratory strains of <i>Escherichia coli</i> : model citizens or deceitful delinquents growing old disgracefully?. <i>Molecular Microbiology</i> , <b>2007</b> , 64, 881-5	4.1	54
74	Bacterial flagella and Type III secretion: case studies in the evolution of complexity. <i>Genome Dynamics</i> , <b>2007</b> , 3, 30-47		21
73	Genome sequencing shows that European isolates of <i>Francisella tularensis</i> subspecies <i>tularensis</i> are almost identical to US laboratory strain Schu S4. <i>PLoS ONE</i> , <b>2007</b> , 2, e352	3.7	41
72	Sigma(s)-Dependent carbon-starvation induction of <i>pbpG</i> (PBP 7) is required for the starvation-stress response in <i>Salmonella enterica</i> serovar Typhimurium. <i>Microbiology (United Kingdom)</i> , <b>2007</b> , 153, 2148-2158	2.9	11
71	An extensive repertoire of type III secretion effectors in <i>Escherichia coli</i> O157 and the role of lambdaoid 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
70	Phylogenetic comparisons reveal multiple acquisitions of the toxin genes by enterotoxigenic <i>Escherichia coli</i> strains of different evolutionary lineages. <i>Journal of Clinical Microbiology</i> , <b>2006</b> , 44, 4528-36	9.7	61
69	Down-regulation of key virulence factors makes the <i>Salmonella enterica</i> serovar Typhimurium <i>rfaH</i> mutant a promising live-attenuated vaccine candidate. <i>Infection and Immunity</i> , <b>2006</b> , 74, 5914-25	3.7	82
68	A novel strategy for the identification of genomic islands by comparative analysis of the contents and contexts of tRNA sites in closely related bacteria. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, e3	20.1	62
67	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
66	xBASE, a collection of online databases for bacterial comparative genomics. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D335-7	20.1	60
65	Variation in bacterial flagellins: from sequence to structure. <i>Trends in Microbiology</i> , <b>2006</b> , 14, 151-5	12.4	106
64	Type III secretion: what's in a name?. <i>Trends in Microbiology</i> , <b>2006</b> , 14, 157-60	12.4	45
63	<i>Escherichia Coli</i> : From Genome Sequences to Consequences (or "Ceci n'est pas un Elephant..."). <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , <b>2006</b> , 17, 114-6	2.6	3
62	Tetratricopeptide repeats in the type III secretion chaperone, LcrH: their role in substrate binding and secretion. <i>Molecular Microbiology</i> , <b>2006</b> , 59, 31-44	4.1	55
61	Analysis of host response to bacterial infection using error model based gene expression microarray experiments. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, e53	20.1	5
60	A degenerate type III secretion system from septicemic <i>Escherichia coli</i> contributes to pathogenesis. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 8164-71	3.5	56
59	Bacterial flagellar diversity in the post-genomic era. <i>Trends in Microbiology</i> , <b>2005</b> , 13, 143-9	12.4	85
58	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



57	Genomic analysis of the protein secretion systems in <i>Clostridium acetobutylicum</i> ATCC 824. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2005</b> , 1745, 223-53	4.9	38
56	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
55	Point mutations in the DNA- and cNMP-binding domains of the homologue of the cAMP receptor protein (CRP) in <i>Mycobacterium bovis</i> BCG: implications for the inactivation of a global regulator and strain attenuation. <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 547-556	2.9	43
54	Shifts from glucose to certain secondary carbon-sources result in activation of the extracytoplasmic function sigma factor sigmaE in <i>Salmonella enterica</i> serovar Typhimurium. <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 2373-2383	2.9	13
53	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
52	Regulators encoded in the <i>Escherichia coli</i> type III secretion system 2 gene cluster influence expression of genes within the locus for enterocyte effacement in enterohemorrhagic <i>E. coli</i> O157:H7. <i>Infection and Immunity</i> , <b>2004</b> , 72, 7282-93	3.7	82
51	The ETT2 gene cluster, encoding a second type III secretion system from <i>Escherichia coli</i> , is present in the majority of strains but has undergone widespread mutational attrition. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 3547-60	3.5	93
50	coliBASE: an online database for <i>Escherichia coli</i> , <i>Shigella</i> and <i>Salmonella</i> comparative genomics. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D296-9	20.1	63
49	Comparative cell wall core biosynthesis in the mycolated pathogens, <i>Mycobacterium tuberculosis</i> and <i>Corynebacterium diphtheriae</i> . <i>FEMS Microbiology Reviews</i> , <b>2004</b> , 28, 225-50	15.1	88
48	An analysis of type-III secretion gene clusters in <i>Chromobacterium violaceum</i> . <i>Trends in Microbiology</i> , <b>2004</b> , 12, 476-82	12.4	23
47	Bacterial genomes for the masses: relevance to the clinical laboratory. <i>Methods in Molecular Biology</i> , <b>2004</b> , 266, 3-15	1.4	1
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