

# Mark J Pallen

## List of Publications by Citations

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182  
papers

13,690  
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62  
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115  
g-index

201  
ext. papers

15,686  
ext. citations

9.2  
avg, IF

6.34  
L-index

#	Paper	IF	Citations
182	The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences. <i>Nature</i> , <b>2000</b> , 403, 665-8	50.4	1628
181	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 434-9	44.5	1035
180	A novel EspA-associated surface organelle of enteropathogenic <i>Escherichia coli</i> involved in protein translocation into epithelial cells. <i>EMBO Journal</i> , <b>1998</b> , 17, 2166-76	13	464
179	Type VI secretion: a beginner's guide. <i>Current Opinion in Microbiology</i> , <b>2008</b> , 11, 3-8	7.9	418
178	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> , <b>2006</b> , 103, 14941-6	11.5	370
177	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
176	The HtrA family of serine proteases. <i>Molecular Microbiology</i> , <b>1997</b> , 26, 209-21	4.1	329
175	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
174	Bacterial pathogenomics. <i>Nature</i> , <b>2007</b> , 449, 835-42	50.4	301
173	The ESAT-6/WXG100 superfamily -- and a new Gram-positive secretion system?. <i>Trends in Microbiology</i> , <b>2002</b> , 10, 209-12	12.4	275
172	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 6516-23	20.1	255
171	Extensive microbial and functional diversity within the chicken cecal microbiome. <i>PLoS ONE</i> , <b>2014</b> , 9, e91941	3.7	239
170	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
169	An embarrassment of sortases - a richness of substrates?. <i>Trends in Microbiology</i> , <b>2001</b> , 9, 97-102	12.4	209
168	Sequencing and analysis of the genome of the Whipple's disease bacterium <i>Tropheryma whippelii</i> . <i>Lancet, The</i> , <b>2003</b> , 361, 637-44	40	204
167	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 787-94	22.2	181
166	Characterization of novel LPXTG-containing proteins of <i>Staphylococcus aureus</i> identified from genome sequences. <i>Microbiology (United Kingdom)</i> , <b>2003</b> , 149, 643-654	2.9	161

165	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
164	Genomic analysis of secretion systems. <i>Current Opinion in Microbiology</i> , <b>2003</b> , 6, 519-27	7.9	139
163	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
162	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
161	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
160	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
159	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
158	Bacterial copper- and zinc-cofactored superoxide dismutase contributes to the pathogenesis of systemic salmonellosis. <i>Molecular Microbiology</i> , <b>1997</b> , 25, 785-96	4.1	117
157	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
156	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D543-6	20.1	113
155	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
154	Nucleotide sequence of two genes from <i>Helicobacter pylori</i> encoding for urease subunits. <i>Nucleic Acids Research</i> , <b>1990</b> , 18, 362	20.1	108
153	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
152	Variation in bacterial flagellins: from sequence to structure. <i>Trends in Microbiology</i> , <b>2006</b> , 14, 151-5	12.4	106
151	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
150	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
149	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
148	Bacterial FHA domains: neglected players in the phospho-threonine signalling game?. <i>Trends in Microbiology</i> , <b>2002</b> , 10, 556-63	12.4	94

147	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
146	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
145	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
144	Mutations affecting the Rossman fold of isoleucyl-tRNA synthetase are correlated with low-level mupirocin resistance in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2002</b> , 46, 438-42	5.9	89
143	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
142	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
141	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
140	Bacterial flagellar diversity in the post-genomic era. <i>Trends in Microbiology</i> , <b>2005</b> , 13, 143-9	12.4	85
139	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
138	Metagenomic analysis of tuberculosis in a mummy. <i>New England Journal of Medicine</i> , <b>2013</b> , 369, 289-90	59.2	82
137	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
136	Down-regulation of key virulence factors makes the <i>Salmonella enterica</i> serovar Typhimurium rfaH mutant a promising live-attenuated vaccine candidate. <i>Infection and Immunity</i> , <b>2006</b> , 74, 5914-25	3.7	82
135	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
134	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
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	A group II intron in a conjugative transposon from the gram-positive bacterium, <i>Clostridium difficile</i> . <i>Gene</i> , <b>1996</b> , 174, 145-50	3.8	75
131	Coiled-coil domains in proteins secreted by type III secretion systems. <i>Molecular Microbiology</i> , <b>1997</b> , 25, 423-5	4.1	74
130	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

129	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
128	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
127	Coiled-coil domain of enteropathogenic <i>Escherichia coli</i> type III secreted protein EspD is involved in EspA filament-mediated cell attachment and hemolysis. <i>Infection and Immunity</i> , <b>2001</b> , 69, 4055-64	3.7	64
126	The rpoS-dependent starvation-stress response locus stiA encodes a nitrate reductase (narZYWV) required for carbon-starvation-inducible thermotolerance and acid tolerance in <i>Salmonella typhimurium</i> . <i>Microbiology (United Kingdom)</i> , <b>1999</b> , 145 ( Pt 11), 3035-3045	2.9	64
125	The Enigmatic Esx Proteins: Looking Beyond Mycobacteria. <i>Trends in Microbiology</i> , <b>2017</b> , 25, 192-204	12.4	63
124	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
123	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
122	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
121	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
120	RpoN-dependent transcription of rpoH?. <i>Molecular Microbiology</i> , <b>1999</b> , 31, 393	4.1	61
119	xBASE, a collection of online databases for bacterial comparative genomics. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D335-7	20.1	60
118	An abundance of bacterial ADP-ribosyltransferases--implications for the origin of exotoxins and their human homologues. <i>Trends in Microbiology</i> , <b>2001</b> , 9, 302-7; discussion 308	12.4	60
117	The coiled-coil domain of EspA is essential for the assembly of the type III secretion translocon on the surface of enteropathogenic <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 35969-74	5.4	58
116	Tetratricopeptide-like repeats in type-III-secretion chaperones and regulators. <i>FEMS Microbiology Letters</i> , <b>2003</b> , 223, 53-60	2.9	57
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	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
113	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
112	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

111	The medium-/long-chain fatty acyl-CoA dehydrogenase (fadF) gene of <i>Salmonella typhimurium</i> is a phase 1 starvation-stress response (SSR) locus. <i>Microbiology (United Kingdom)</i> , <b>1999</b> , 145 ( Pt 1), 15-31	2.9	55
110	Recovery of a medieval <i>Brucella melitensis</i> genome using shotgun metagenomics. <i>MBio</i> , <b>2014</b> , 5, e01337-14	7.84	54
109	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
108	An outbreak of pneumococcal meningitis among older children (8 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
107	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
106	Genomics and outbreak investigation: from sequence to consequence. <i>Genome Medicine</i> , <b>2013</b> , 5, 36	14.4	50
105	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
104	Microbial TIR domains: not necessarily agents of subversion?. <i>Trends in Microbiology</i> , <b>2009</b> , 17, 393-8	12.4	45
103	Type III secretion: what's in a name?. <i>Trends in Microbiology</i> , <b>2006</b> , 14, 157-60	12.4	45
102	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
101	Assembly of hundreds of novel bacterial genomes from the chicken caecum. <i>Genome Biology</i> , <b>2020</b> , 21, 34	18.3	42
100	Degenerate PCR primers for the amplification of fragments from genes encoding response regulators from a range of pathogenic bacteria. <i>FEMS Microbiology Letters</i> , <b>1992</b> , 99, 287-291	2.9	41
99	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
98	An Chicken Gut Model Demonstrates Transfer of a Multidrug Resistance Plasmid from to Commensal. <i>MBio</i> , <b>2017</b> , 8,	7.8	40
97	PDZ domains facilitate binding of high temperature requirement protease A (HtrA) and tail-specific protease (Tsp) to heterologous substrates through recognition of the small stable RNA A (ssrA)-encoded peptide. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 39443-9	5.4	39
96	Sequencing of the <i>Francisella tularensis</i> strain Schu 4 genome reveals the shikimate and purine metabolic pathways, targets for the construction of a rationally attenuated auxotrophic vaccine. <i>Microbial &amp; Comparative Genomics</i> , <b>2000</b> , 5, 25-39		39
95	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
94	Time to recognise that mitochondria are bacteria?. <i>Trends in Microbiology</i> , <b>2011</b> , 19, 58-64	12.4	37

93	Complete genome sequence of the Crohn's disease-associated adherent-invasive Escherichia coli strain HM605. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4540	3.5	34
92	Interaction of enteroaggregative Escherichia coli with salad leaves. <i>Environmental Microbiology Reports</i> , <b>2009</b> , 1, 234-9	3.7	33
91	PDZ domains in bacterial proteins. <i>Molecular Microbiology</i> , <b>1997</b> , 26, 411-3	4.1	33
90	Organization of the LEE1 operon regulatory region of enterohaemorrhagic Escherichia coli O157:H7 and activation by GrlA. <i>Molecular Microbiology</i> , <b>2011</b> , 79, 468-83	4.1	32
89	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
88	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. <i>Trends in Microbiology</i> , <b>2009</b> , 17, 1-5	12.4	28
87	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
86	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
85	Comparative analysis of two Neisseria gonorrhoeae genome sequences reveals evidence of mobilization of Correia Repeat Enclosed Elements and their role in regulation. <i>BMC Genomics</i> , <b>2009</b> , 10, 70	4.5	24
84	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
83	An analysis of type-III secretion gene clusters in Chromobacterium violaceum. <i>Trends in Microbiology</i> , <b>2004</b> , 12, 476-82	12.4	23
82	Flagella mediate attachment of enterotoxigenic Escherichia coli to fresh salad leaves. <i>Environmental Microbiology Reports</i> , <b>2011</b> , 3, 112-7	3.7	22
81	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
80	Transmission of Staphylococcus aureus 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
79	The pla gene, encoding plasminogen activator, is not specific to Yersinia pestis. <i>BMC Research Notes</i> , <b>2015</b> , 8, 535	2.3	21
78	Bacterial flagella and Type III secretion: case studies in the evolution of complexity. <i>Genome Dynamics</i> , <b>2007</b> , 3, 30-47		21
77	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , <b>2021</b> , 9, e10941	3.1	21
76	Microarray analysis of the Ler regulon in enteropathogenic and enterohaemorrhagic Escherichia coli strains. <i>PLoS ONE</i> , <b>2014</b> , 9, e80160	3.7	20

75	Clonal expansion within pneumococcal serotype 6C after use of seven-valent vaccine. <i>PLoS ONE</i> , <b>2013</b> , 8, e64731	3.7	20
74	A beta-propeller domain within TolB. <i>Molecular Microbiology</i> , <b>1999</b> , 31, 739-40	4.1	20
73	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
72	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
71	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
70	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
69	Glucoamylase-like domains in the alpha- and beta-subunits of phosphorylase kinase. <i>Protein Science</i> , <b>2003</b> , 12, 1804-7	6.3	17
68	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
67	'Going wrong with confidence': misleading sequence analyses of CiaB and clpX. <i>Molecular Microbiology</i> , <b>1999</b> , 34, 195	4.1	16
66	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
65	beta-propeller repeats and a PDZ domain in the tricorn protease: predicted self-compartmentalisation and C-terminal polypeptide-binding strategies of substrate selection. <i>FEMS Microbiology Letters</i> , <b>1999</b> , 179, 447-51	2.9	15
64	The Next Million Names for Archaea and Bacteria. <i>Trends in Microbiology</i> , <b>2021</b> , 29, 289-298	12.4	15
63	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
62	New strategies in microbiological diagnosis. <i>Journal of Hospital Infection</i> , <b>1991</b> , 18 Suppl A, 147-58	6.9	14
61	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
60	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
59	The homodimeric GBS1074 from <i>Streptococcus agalactiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2010</b> , 66, 1421-5		13
58	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



57	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
56	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
55	Sigma(s)-Dependent carbon-starvation induction of pbpG (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
54	Doggerland and the Lost Frontiers Project (2015-2020). <i>Coastal Research Library</i> , <b>2017</b> , 305-319	0.4	10
53	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
52	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
51	Calculating orthologs in bacteria and Archaea: a divide and conquer approach. <i>PLoS ONE</i> , <b>2011</b> , 6, e28388	3.7	9
50	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
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