

Mark J Pallen

List of Publications by Year in descending order

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183
papers

16,886
citations

15466

65
h-index

16605

123
g-index

201
all docs

201
docs citations

201
times ranked

19450
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences. <i>Nature</i> , 2000, 403, 665-668.	13.7	1,869
2	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 434-439.	9.4	1,226
3	A novel EspA-associated surface organelle of enteropathogenic <i>Escherichia coli</i> involved in protein translocation into epithelial cells. <i>EMBO Journal</i> , 1998, 17, 2166-2176.	3.5	543
4	Type VI secretion: a beginner's guide. <i>Current Opinion in Microbiology</i> , 2008, 11, 3-8.	2.3	535
5	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
6	Open-Source Genomic Analysis of Shiga-Toxin-Producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011, 365, 718-724.	13.9	392
7	Bacterial pathogenomics. <i>Nature</i> , 2007, 449, 835-842.	13.7	374
8	The HtrA family of serine proteases. <i>Molecular Microbiology</i> , 1997, 26, 209-221.	1.2	369
9	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <i>Nature Reviews Microbiology</i> , 2012, 10, 599-606.	13.6	367
10	Extensive Microbial and Functional Diversity within the Chicken Cecal Microbiome. <i>PLoS ONE</i> , 2014, 9, e91941.	1.1	359
11	The ESAT-6/WXG100 superfamily and a new Gram-positive secretion system?. <i>Trends in Microbiology</i> , 2002, 10, 209-212.	3.5	321
12	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> , 2013, 309, 1502.	3.8	290
13	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. <i>Nucleic Acids Research</i> , 2003, 31, 6516-6523.	6.5	285
14	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , 2015, 13, 787-794.	13.6	246
15	Sequencing and analysis of the genome of the Whipple's disease bacterium <i>Tropheryma whippeli</i> . <i>Lancet</i> , The, 2003, 361, 637-644.	6.3	232
16	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	5.9	221
17	An embarrassment of sortases and a richness of substrates?. <i>Trends in Microbiology</i> , 2001, 9, 97-101.	3.5	219
18	Defining bacterial species in the genomic era: insights from the genus <i>Acinetobacter</i> . <i>BMC Microbiology</i> , 2012, 12, 302.	1.3	188

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19	Characterization of novel LPXTG-containing proteins of <i>Staphylococcus aureus</i> identified from genome sequences. <i>Microbiology (United Kingdom)</i> , 2003, 149, 643-654.	0.7	184
20	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , 2016, 2, e000086.	1.0	176
21	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
22	Complete Genome Sequence and Comparative Metabolic Profiling of the Prototypical Enteroaggregative <i>Escherichia coli</i> Strain O42. <i>PLoS ONE</i> , 2010, 5, e8801.	1.1	165
23	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , 2015, 6, 6717.	5.8	165
24	Identification of Novel Imidazo[1,2-a]pyridine Inhibitors Targeting <i>M. tuberculosis</i> QcrB. <i>PLoS ONE</i> , 2012, 7, e52951.	1.1	162
25	Genomic analysis of secretion systems. <i>Current Opinion in Microbiology</i> , 2003, 6, 519-527.	2.3	150
26	From The Origin of Species to the origin of bacterial flagella. <i>Nature Reviews Microbiology</i> , 2006, 4, 784-790.	13.6	143
27	Gene doctoring: a method for recombineering in laboratory and pathogenic <i>Escherichia coli</i> strains. <i>BMC Microbiology</i> , 2009, 9, 252.	1.3	143
28	Nucleotide sequence of two genes from <i>Helicobacter pylori</i> encoding for urease subunits. <i>Nucleic Acids Research</i> , 1990, 18, 362-362.	6.5	142
29	Bacterial copper- and zinc-cofactored superoxide dismutase contributes to the pathogenesis of systemic salmonellosis. <i>Molecular Microbiology</i> , 1997, 25, 785-796.	1.2	137
30	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> , 2010, 75, 37-41.	1.4	136
31	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
32	High-throughput sequencing and clinical microbiology: progress, opportunities and challenges. <i>Current Opinion in Microbiology</i> , 2010, 13, 625-631.	2.3	135
33	The gut-adherent microbiota of PSC-IBD is distinct to that of IBD. <i>Gut</i> , 2017, 66, 386.1-388.	6.1	132
34	Variation in bacterial flagellins: from sequence to structure. <i>Trends in Microbiology</i> , 2006, 14, 151-155.	3.5	129
35	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> , 2013, 8, e60933.	1.1	123
36	xBASE2: a comprehensive resource for comparative bacterial genomics. <i>Nucleic Acids Research</i> , 2007, 36, D543-D546.	6.5	119

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37	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> , 2004, 186, 3547-3560.	1.0	117
38	Parallel evolutionary pathways to antibiotic resistance selected by biocide exposure. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2241-2248.	1.3	116
39	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> , 2014, 2, e585.	0.9	113
40	Assembly of hundreds of novel bacterial genomes from the chicken caecum. <i>Genome Biology</i> , 2020, 21, 34.	3.8	112
41	The Enigmatic Esx Proteins: Looking Beyond Mycobacteria. <i>Trends in Microbiology</i> , 2017, 25, 192-204.	3.5	109
42	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> , 2014, 4, e006278.	0.8	104
43	Bacterial flagellar diversity in the post-genomic era. <i>Trends in Microbiology</i> , 2005, 13, 143-149.	3.5	103
44	Bacterial FHA domains: neglected players in the phospho-threonine signalling game?. <i>Trends in Microbiology</i> , 2002, 10, 556-563.	3.5	102
45	Metagenomic Analysis of Tuberculosis in a Mummy. <i>New England Journal of Medicine</i> , 2013, 369, 289-290.	13.9	101
46	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
47	Interaction of <i>Salmonella enterica</i> with basil and other salad leaves. <i>ISME Journal</i> , 2009, 3, 261-265.	4.4	100
48	Comparative cell wall core biosynthesis in the mycolated pathogens, <i>Mycobacterium tuberculosis</i> and <i>Corynebacterium diphtheriae</i> . <i>FEMS Microbiology Reviews</i> , 2004, 28, 225-250.	3.9	99
49	Sedimentary DNA from a submerged site reveals wheat in the British Isles 8000 years ago. <i>Science</i> , 2015, 347, 998-1001.	6.0	99
50	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> , 2011, 66, 1499-1503.	1.3	96
51	Differences in the Faecal Microbiome in <i>Schistosoma haematobium</i> Infected Children vs. Uninfected Children. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003861.	1.3	94
52	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> , 2002, 46, 438-442.	1.4	93
53	Enterohemorrhagic <i>Escherichia coli</i> Exploits EspA Filaments for Attachment to Salad Leaves. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2908-2914.	1.4	93
54	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> , 2004, 72, 7282-7293.	1.0	89

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55	Down-Regulation of Key Virulence Factors Makes the Salmonella enterica Serovar Typhimurium rfaH Mutant a Promising Live-Attenuated Vaccine Candidate. <i>Infection and Immunity</i> , 2006, 74, 5914-5925.	1.0	88
56	Coiled-coil domains in proteins secreted by type III secretion systems. <i>Molecular Microbiology</i> , 1997, 25, 423-425.	1.2	84
57	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
58	A group II intron in a conjugative transposon from the gram-positive bacterium, <i>Clostridium difficile</i> . <i>Gene</i> , 1996, 174, 145-150.	1.0	80
59	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
60	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> , 2005, 187, 1430-1440.	1.0	78
61	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> , 2006, 44, 4528-4536.	1.8	74
62	The rpoS-dependent starvation-stress response locus stiA encodes a nitrate reductase (narZYWW) required for carbon-starvation-inducible thermotolerance and acid tolerance in <i>Salmonella typhimurium</i> . <i>Microbiology (United Kingdom)</i> , 1999, 145, 3035-3045.	0.7	74
63	Genomic epidemiology of a protracted hospital outbreak caused by multidrug-resistant <i>Acinetobacter baumannii</i> in Birmingham, England. <i>Genome Medicine</i> , 2014, 6, 70.	3.6	72
64	Subversion of actin dynamics by EspM effectors of attaching and effacing bacterial pathogens. <i>Cellular Microbiology</i> , 2008, 10, 1429-1441.	1.1	70
65	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> , 2001, 69, 4055-4064.	1.0	69
66	Tetratricopeptide-like repeats in type-III-secretion chaperones and regulators. <i>FEMS Microbiology Letters</i> , 2003, 223, 53-60.	0.7	69
67	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> , 2006, 34, e3-e3.	6.5	67
68	Recovery of a Medieval <i>Brucella melitensis</i> Genome Using Shotgun Metagenomics. <i>MBio</i> , 2014, 5, e01337-14.	1.8	67
69	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> , 2016, 16, 575.	1.3	67
70	RpoN-dependent transcription of rpoH?. <i>Molecular Microbiology</i> , 1999, 31, 393-393.	1.2	65
71	coliBASE: an online database for <i>Escherichia coli</i> , <i>Shigella</i> and <i>Salmonella</i> comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, 296D-299.	6.5	65
72	High-Throughput Sequencing of 16S rRNA Gene Amplicons: Effects of Extraction Procedure, Primer Length and Annealing Temperature. <i>PLoS ONE</i> , 2012, 7, e38094.	1.1	65

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73	An abundance of bacterial ADP-ribosyltransferases – implications for the origin of exotoxins and their human homologues. <i>Trends in Microbiology</i> , 2001, 9, 302-307.	3.5	64
74	Laboratory strains of <i>Escherichia coli</i> : model citizens or deceitful delinquents growing old disgracefully?. <i>Molecular Microbiology</i> , 2007, 64, 881-885.	1.2	64
75	Genomics and outbreak investigation: from sequence to consequence. <i>Genome Medicine</i> , 2013, 5, 36.	3.6	64
76	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> , 1999, 274, 35969-35974.	1.6	63
77	Tetratricopeptide repeats in the type III secretion chaperone, LcrH: their role in substrate binding and secretion. <i>Molecular Microbiology</i> , 2006, 59, 31-44.	1.2	63
78	The medium-/long-chain fatty acyl-CoA dehydrogenase (<i>fadF</i>) gene of <i>Salmonella typhimurium</i> is a phase 1 starvation-stress response (SSR) locus. <i>Microbiology (United Kingdom)</i> , 1999, 145, 15-31.	0.7	62
79	A Degenerate Type III Secretion System from Septicemic <i>Escherichia coli</i> Contributes to Pathogenesis. <i>Journal of Bacteriology</i> , 2005, 187, 8164-8171.	1.0	62
80	xBASE, a collection of online databases for bacterial comparative genomics. <i>Nucleic Acids Research</i> , 2006, 34, D335-D337.	6.5	62
81	An <i>In Vitro</i> Chicken Gut Model Demonstrates Transfer of a Multidrug Resistance Plasmid from <i>Salmonella</i> to Commensal <i>Escherichia coli</i> . <i>MBio</i> , 2017, 8, .	1.8	60
82	Loss of microbial diversity and pathogen domination of the gut microbiota in critically ill patients. <i>Microbial Genomics</i> , 2019, 5, .	1.0	59
83	Type III secretion: what's in a name?. <i>Trends in Microbiology</i> , 2006, 14, 157-160.	3.5	57
84	The Complete Genome and Proteome of <i>Laribacter hongkongensis</i> Reveal Potential Mechanisms for Adaptations to Different Temperatures and Habitats. <i>PLoS Genetics</i> , 2009, 5, e1000416.	1.5	52
85	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> , 2007, 2, e352.	1.1	51
86	Complete Genome Sequence of the Crohn's Disease-Associated Adherent-Invasive <i>Escherichia coli</i> Strain HM605. <i>Journal of Bacteriology</i> , 2011, 193, 4540-4540.	1.0	50
87	Microbial TIR domains: not necessarily agents of subversion?. <i>Trends in Microbiology</i> , 2009, 17, 393-398.	3.5	49
88	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 & Comparative Genomics</i> , 2000, 5, 25-39.	0.6	48
89	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 (<i>ssrA</i>)-encoded Peptide. <i>Journal of Biological Chemistry</i> , 2002, 277, 39443-39449.	1.6	46
90	Time to recognise that mitochondria are bacteria?. <i>Trends in Microbiology</i> , 2011, 19, 58-64.	3.5	45

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91	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> , 2005, 151, 547-556.	0.7	44
92	Degenerate PCR primers for the amplification of fragments from genes encoding response regulators from a range of pathogenic bacteria. <i>FEMS Microbiology Letters</i> , 1992, 99, 287-291.	0.7	42
93	Genomic analysis of the protein secretion systems in <i>Clostridium acetobutylicum</i> ATCC 824. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2005, 1745, 223-253.	1.9	40
94	The Next Million Names for Archaea and Bacteria. <i>Trends in Microbiology</i> , 2021, 29, 289-298.	3.5	39
95	Organization of the <i>LEE1</i> operon regulatory region of enterohaemorrhagic <i>Escherichia coli</i> O157:H7 and activation by GrlA. <i>Molecular Microbiology</i> , 2011, 79, 468-483.	1.2	37
96	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> , 2012, 56, 1845-1853.	1.4	37
97	Genome sequencing in clinical microbiology. <i>Nature Biotechnology</i> , 2012, 30, 1068-1071.	9.4	37
98	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> , 2016, 14, 160.	2.3	37
99	PDZ domains in bacterial proteins. <i>Molecular Microbiology</i> , 1997, 26, 411-413.	1.2	36
100	Interaction of enteroaggregative <i>Escherichia coli</i> with salad leaves. <i>Environmental Microbiology Reports</i> , 2009, 1, 234-239.	1.0	36
101	Next-Generation Sequencing—the Promise and Perils of Charting the Great Microbial Unknown. <i>Microbial Ecology</i> , 2009, 57, 1-3.	1.4	35
102	Bacterial flagellar diversity and evolution: seek simplicity and distrust it?. <i>Trends in Microbiology</i> , 2009, 17, 1-5.	3.5	34
103	The microbial ecology of <i>Escherichia coli</i> in the vertebrate gut. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	34
104	A prehistoric Egyptian mummy: Evidence for an “embalming recipe” and the evolution of early formative funerary treatments. <i>Journal of Archaeological Science</i> , 2018, 100, 191-200.	1.2	33
105	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> , 2016, 82, 5910-5917.	1.4	30
106	Bacterial Flagella and Type III Secretion: Case Studies in the Evolution of Complexity. , 2007, 3, 30-47.		29
107	Comparative analysis of two <i>Neisseria gonorrhoeae</i> genome sequences reveals evidence of mobilization of Correia Repeat Enclosed Elements and their role in regulation. <i>BMC Genomics</i> , 2009, 10, 70.	1.2	29
108	Flagella mediate attachment of enterotoxigenic <i>Escherichia coli</i> to fresh salad leaves. <i>Environmental Microbiology Reports</i> , 2011, 3, 112-117.	1.0	29

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109	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> , 2011, 193, 2359-2360.	1.0	28
110	Whole-genome sequencing illuminates the evolution and spread of multidrug-resistant tuberculosis in Southwest Nigeria. <i>PLoS ONE</i> , 2017, 12, e0184510.	1.1	27
111	Metagenomic profiling of ticks: Identification of novel rickettsial genomes and detection of tick-borne canine parvovirus. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0006805.	1.3	27
112	Microarray Analysis of the Ler Regulon in Enteropathogenic and Enterohaemorrhagic <i>Escherichia coli</i> Strains. <i>PLoS ONE</i> , 2014, 9, e80160.	1.1	26
113	An analysis of type-III secretion gene clusters in <i>Chromobacterium violaceum</i> . <i>Trends in Microbiology</i> , 2004, 12, 476-482.	3.5	24
114	Cellulose mediates attachment of <i>Salmonella enterica</i> Serovar Typhimurium to tomatoes. <i>Environmental Microbiology Reports</i> , 2011, 3, 569-573.	1.0	24
115	Calculating Orthologs in Bacteria and Archaea: A Divide and Conquer Approach. <i>PLoS ONE</i> , 2011, 6, e28388.	1.1	24
116	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> , 2010, 192, 6093-6098.	1.0	23
117	The <i>pla</i> gene, encoding plasminogen activator, is not specific to <i>Yersinia pestis</i> . <i>BMC Research Notes</i> , 2015, 8, 535.	0.6	23
118	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> , 2020, 10, 327.	1.6	23
119	Clonal Expansion within Pneumococcal Serotype 6C after Use of Seven-Valent Vaccine. <i>PLoS ONE</i> , 2013, 8, e64731.	1.1	21
120	A beta-propeller domain within TolB. <i>Molecular Microbiology</i> , 1999, 31, 739-740.	1.2	20
121	Are diagnostic and public health bacteriology ready to become branches of genomic medicine?. <i>Genome Medicine</i> , 2011, 3, 53.	3.6	20
122	Glucoamylase-like domains in the $\hat{1}\pm$ - and $\hat{1}^2$ -subunits of phosphorylase kinase. <i>Protein Science</i> , 2003, 12, 1804-1807.	3.1	18
123	XDR-TB genome sequencing: a glimpse of the microbiology of the future. <i>Future Microbiology</i> , 2008, 3, 111-113.	1.0	18
124	Whole-Genome Sequence of the Emerging Pathogen <i>Mycobacterium abscessus</i> Strain 47J26. <i>Journal of Bacteriology</i> , 2012, 194, 549-549.	1.0	18
125	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. <i>Microbial Genomics</i> , 2021, 7, .	1.0	18
126	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity. <i>PeerJ</i> , 2022, 10, e13084.	0.9	18

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127	New strategies in microbiological diagnosis. <i>Journal of Hospital Infection</i> , 1991, 18, 147-158.	1.4	17
128	'Going wrong with confidence': misleading sequence analyses of CiaB and ClpX. <i>Molecular Microbiology</i> , 1999, 34, 195-195.	1.2	17
129	ÅŽÅ²-Propeller repeats and a PDZ domain in the tricorner protease: predicted self-compartmentalisation and C-terminal polypeptide-binding strategies of substrate selection. <i>FEMS Microbiology Letters</i> , 1999, 179, 447-451.	0.7	17
130	Shifts from glucose to certain secondary carbon-sources result in activation of the extracytoplasmic function sigma factor Ĭf E in <i>Salmonella enterica</i> serovar Typhimurium. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2373-2383.	0.7	17
131	Genome Analysis of a Highly Virulent Serotype 1 Strain of <i>Streptococcus pneumoniae</i> from West Africa. <i>PLoS ONE</i> , 2012, 7, e26742.	1.1	17
132	The homodimeric GBS1074 from <i>Streptococcus agalactiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1421-1425.	0.7	16
133	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> , 2015, 89, 3888-3909.	1.5	16
134	Microbial bioinformatics 2020. <i>Microbial Biotechnology</i> , 2016, 9, 681-686.	2.0	16
135	Forensic Analysis Reveals Acute Decompensation of Chronic Heart Failure in a 3500â€Yearâ€Old Egyptian Dignitary. <i>Journal of Forensic Sciences</i> , 2016, 61, 1378-1381.	0.9	16
136	Simple sequence repeats in <i>Helicobacter canadensis</i> and their role in phase variable expression and C-terminal sequence switching. <i>BMC Genomics</i> , 2010, 11, 67.	1.2	14
137	The TCA cycle is not required for selection or survival of multidrug-resistant <i>Salmonella</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 589-599.	1.3	14
138	Towards standardisation of naming novel prokaryotic taxa in the age of high-throughput microbiology. <i>Gut</i> , 2020, 69, 1358.1-1359.	6.1	14
139	The status Candidatus for uncultured taxa of Bacteria and Archaea: SWOT analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
140	The â€Annie Hypothesis': Did the Death of His Daughter Cause Darwin to â€Give up Christianityâ€™?. <i>Centaurus</i> , 2012, 54, 105-123.	0.2	13
141	Doggerland and the Lost Frontiers Project (2015â€2020). <i>Coastal Research Library</i> , 2017, , 305-319.	0.2	13
142	Bacterial Flagellins: Does Size Matter?. <i>Trends in Microbiology</i> , 2018, 26, 575-581.	3.5	13
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