Brendan W Wren

List of Publications by Year
in descending order

289 papers	17,884 citations	13865 67 h-index	18647 119 g-index
321 all docs	321 docs citations	321 times ranked	13801 citing authors

#	Article	IF	Citations
1	The multidrug-resistant human pathogen Clostridium difficile has a highly mobile, mosaic genome. Nature Genetics, 2006, 38, 779-786.	21.4	821
2	N-Linked Glycosylation in Campylobacter jejuni and Its Functional Transfer into E. coli. Science, 2002, 298, 1790-1793.	12.6	716
3	Emergence and global spread of epidemic healthcare-associated Clostridium difficile. Nature Genetics, 2013, 45, 109-113.	21.4	669
4	The complete genome sequence of Francisella tularensis, the causative agent of tularemia. Nature Genetics, 2005, 37, 153-159.	21.4	436
5	Comparative genome and phenotypic analysis of Clostridium difficile 027 strains provides insight into the evolution of a hypervirulent bacterium. Genome Biology, 2009, 10, R102.	9.6	431
6	Protein glycosylation in bacterial mucosal pathogens. Nature Reviews Microbiology, 2005, 3, 225-237.	28.6	380
7	Bacterial pathogenomics. Nature, 2007, 449, 835-842.	27.8	374
8	The HtrA family of serine proteases. Molecular Microbiology, 1997, 26, 209-221.	2.5	369
9	Evolutionary dynamics of Clostridium difficile over short and long time scales. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7527-7532.	7.1	346
10	The Clostridium difficile spo0A Gene Is a Persistence and Transmission Factor. Infection and Immunity, 2012, 80, 2704-2711.	2.2	324
11	The Yersiniae â€" a model genus to study the rapid evolution of bacterial pathogens. Nature Reviews Microbiology, 2003, 1, 55-64.	28.6	320
12	Antibiotic Treatment of Clostridium difficile Carrier Mice Triggers a Supershedder State, Spore-Mediated Transmission, and Severe Disease in Immunocompromised Hosts. Infection and Immunity, 2009, 77, 3661-3669.	2.2	315
13	Whole Genome Comparison of Campylobacter jejuni Human Isolates Using a Low-Cost Microarray Reveals Extensive Genetic Diversity. Genome Research, 2001, 11, 1706-1715.	5.5	278
14	Genetic and biochemical evidence of a Campylobacter jejuni capsular polysaccharide that accounts for Penner serotype specificity. Molecular Microbiology, 2002, 35, 529-541.	2.5	228
15	The Complete Genome Sequence and Comparative Genome Analysis of the High Pathogenicity Yersinia enterocolitica Strain 8081. PLoS Genetics, 2006, 2, e206.	3.5	227
16	The Response Regulator PhoP Is Important for Survival under Conditions of Macrophage-Induced Stress and Virulence in Yersinia pestis. Infection and Immunity, 2000, 68, 3419-3425.	2.2	210
17	Phase variation of a Î²-1,3 galactosyltransferase involved in generation of the ganglioside GM1-like lipo-oligosaccharide of Campylobacter jejuni. Molecular Microbiology, 2002, 37, 501-514.	2.5	206
18	Functional analysis of theCampylobacter jejuniN-linked protein glycosylation pathway. Molecular Microbiology, 2005, 55, 1695-1703.	2.5	193

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19	Re-annotation and re-analysis of the Campylobacter jejuni NCTC11168 genome sequence. BMC Genomics, 2007, 8, 162.	2.8	189
20	Molecular characterization of the surface layer proteins from Clostridium difficile. Molecular Microbiology, 2001, 40, 1187-1199.	2.5	177
21	Campylobacter â€“ a tale of two protein glycosylation systems. Trends in Microbiology, 2003, 11, 233-238.	7.7	166
22	Adaptation of Campylobacter jejuni NCTC11168 to High-Level Colonization of the Avian Gastrointestinal Tract. Infection and Immunity, 2004, 72, 3769-3776.	2.2	162
23	Analysis of Campylobacter jejuni capsular loci reveals multiple mechanisms for the generation of structural diversity and the ability to form complex heptoses. Molecular Microbiology, 2004, 55, 90-103.	2.5	162
24	Comparative phylogenomics of the food-borne pathogen Campylobacter jejuni reveals genetic markers predictive of infection source. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16043-16048.	7.1	158
25	Application of DNA Microarrays to Study the Evolutionary Genomics of Yersinia pestis and Yersinia pseudotuberculosis. Genome Research, 2003, 13, 2018-2029.	5.5	154
26	Parallel independent evolution of pathogenicity within the genus Yersinia. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	7.1	154
27	A novel paralogous gene family involved in phase-variable flagella-mediated motility in Campylobacter jejuni. Microbiology (United Kingdom), 2002, 148, 473-480.	1.8	149
28	Characterisation of Clostridium difficile Biofilm Formation, a Role for Spo0A. PLoS ONE, 2012, 7, e50527.	2.5	147
29	Helicobacter pylori Possesses Two CheY Response Regulators and a Histidine Kinase Sensor, CheA, Which Are Essential for Chemotaxis and Colonization of the Gastric Mucosa. Infection and Immunity, 2000, 68, 2016-2023.	2.2	140
30	Campylobacter jejuni Outer Membrane Vesicles Play an Important Role in Bacterial Interactions with Human Intestinal Epithelial Cells. Infection and Immunity, 2012, 80, 4089-4098.	2.2	138
31	'Add, stir and reduce': Yersinia spp. as model bacteria for pathogen evolution. Nature Reviews Microbiology, 2016, 14, 177-190.	28.6	130
32	Multiple N-acetyl neuraminic acid synthetase (neuB) genes in Campylobacter jejuni: identification and characterization of the gene involved in sialylation of lipo-oligosaccharide. Molecular Microbiology, 2000, 35, 1120-1134.	2.5	128
33	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. Nature Communications, 2015, 6, 6740.	12.8	124
34	Identification of N-acetylgalactosamine-containing glycoproteins PEB3 and CgpA in Campylobacter jejuni. Molecular Microbiology, 2002, 43, 497-508.	2.5	121
35	Campylobacter jejuni Glycosylation Island Important in Cell Charge, Legionaminic Acid Biosynthesis, and Colonization of Chickens. Infection and Immunity, 2009, 77, 2544-2556.	2.2	121
36	A Novel Campylobacter jejuni Two-Component Regulatory System Important for Temperature-Dependent Growth and Colonization. Journal of Bacteriology, 1999, 181, 3298-3302.	2.2	117

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37	Macro and Micro Diversity of Clostridium difficile Isolates from Diverse Sources and Geographical Locations. PLoS ONE, 2012, 7, e31559.	2.5	114
38	Campylobacter jejuniouter membrane vesicle-associated proteolytic activity promotes bacterial invasion by mediating cleavage of intestinal epithelial cell E-cadherin and occludin. Cellular Microbiology, 2016, 18, 561-572.	2.1	113
39	Microbial genome analysis: insights into virulence, host adaptation and evolution. Nature Reviews Genetics, 2000, 1, 30-39.	16.3	109
40	The agr Locus Regulates Virulence and Colonization Genes in Clostridium difficile 027. Journal of Bacteriology, 2013, 195, 3672-3681.	2.2	99
41	Para-cresol production by Clostridium difficile affects microbial diversity and membrane integrity of Gram-negative bacteria. PLoS Pathogens, 2018, 14, e1007191.	4.7	98
42	A major role for intestinal epithelial nucleotide oligomerization domain 1 (NOD1) in eliciting host bactericidal immune responses to Campylobacter jejuni. Cellular Microbiology, 2007, 9, 2404-2416.	2.1	95
43	Microarray analysis of the transcriptional responses of Clostridium difficile to environmental and antibiotic stress. Journal of Medical Microbiology, 2008, 57, 757-764.	1.8	94
44	Invertebrates as a source of emerging human pathogens. Nature Reviews Microbiology, 2004, 2, 833-841.	28.6	91
45	Galleria mellonella as an alternative infection model for Yersinia pseudotuberculosis. Microbiology (United Kingdom), 2009, 155, 1516-1522.	1.8	91
46	Single-Primer PCR Procedure for Rapid Identification of Transposon Insertion Sites. BioTechniques, 2000, 28, 1078-1082.	1.8	90
47	The glycome. FEMS Microbiology Reviews, 2005, 29, 377-390.	8.6	88
48	Revised nomenclature of Clostridium difficile toxins and associated genes. Journal of Medical Microbiology, 2005, 54, 113-117.	1.8	88
49	Commonality and Biosynthesis of the O-Methyl Phosphoramidate Capsule Modification in Campylobacter jejuni. Journal of Biological Chemistry, 2007, 282, 28566-28576.	3.4	86
50	Exploiting genome sequence: predictions for mechanisms of Campylobacter chemotaxis. Trends in Microbiology, 2002, 10, 155-159.	7.7	85
51	Explorative Multifactor Approach for Investigating Global Survival Mechanisms of Campylobacter jejuni under Environmental Conditions. Applied and Environmental Microbiology, 2005, 71, 2086-2094.	3.1	83
52	Neutrophil Extracellular Traps Exhibit Antibacterial Activity against Burkholderia pseudomallei and Are Influenced by Bacterial and Host Factors. Infection and Immunity, 2012, 80, 3921-3929.	2.2	83
53	Detection and Initial Characterization of Novel Capsular Polysaccharide among Diverse Campylobacter jejuni Strains Using Alcian Blue Dye. Journal of Clinical Microbiology, 2001, 39, 279-284.	3.9	81
54	Intestinal Innate Immunity to Campylobacter jejuni Results in Induction of Bactericidal Human Beta-Defensins 2 and 3. Infection and Immunity, 2005, 73, 7281-7289.	2.2	81

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55	Emergence of new PCR ribotypes from the hypervirulent Clostridium difficile 027 lineage. Journal of Medical Microbiology, 2012, 61, 49-56.	1.8	81
56	Structural characterization of lipo-oligosaccharide (LOS) from Yersinia pestis: regulation of LOS structure by the PhoPQ system. Molecular Microbiology, 2002, 44, 1637-1650.	2.5	80
57	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of Haemophilus parasuis. Journal of Clinical Microbiology, 2015, 53, 3812-3821.	3.9	80
58	Recent advances in the production of recombinant glycoconjugate vaccines. Npj Vaccines, 2019, 4, 16.	6.0	79
59	Application of Comparative Phylogenomics To Study the Evolution of Yersinia enterocolitica and To Identify Genetic Differences Relating to Pathogenicity. Journal of Bacteriology, 2006, 188, 3645-3653.	2.2	78
60	Demonstration of Polysaccharide Capsule in Campylobacter jejuni Using Electron Microscopy. Infection and Immunity, 2001, 69, 5921-5924.	2.2	76
61	Exploitation of bacterialN-linked glycosylation to develop a novel recombinant glycoconjugate vaccine againstFrancisella tularensis. Open Biology, 2013, 3, 130002.	3.6	76
62	Genome-Wide Saturation Mutagenesis of Burkholderia pseudomallei K96243 Predicts Essential Genes and Novel Targets for Antimicrobial Development. MBio, 2014, 5, e00926-13.	4.1	75
63	Cyclic diGMP Regulates Production of Sortase Substrates of Clostridium difficile and Their Surface Exposure through ZmpI Protease-mediated Cleavage. Journal of Biological Chemistry, 2015, 290, 24453-24469.	3.4	74
64	The importance of the glycosylation of antimicrobial peptides: natural and synthetic approaches. Drug Discovery Today, 2017, 22, 919-926.	6.4	73
65	Serotype Differences and Lack of Biofilm Formation Characterize Yersinia pseudotuberculosis Infection of the Xenopsylla cheopis Flea Vector of Yersinia pestis. Journal of Bacteriology, 2006, 188, 1113-1119.	2.2	72
66	The RovA regulons of Yersinia enterocolitica and Yersinia pestis are distinct: evidence that many RovA-regulated genes were acquired more recently than the core genome. Molecular Microbiology, 2007, 66, 189-205.	2.5	72
67	Insect Infection Model forCampylobacter jejuniReveals ThatOâ€methyl Phosphoramidate Has Insecticidal Activity. Journal of Infectious Diseases, 2010, 201, 100129142112076-000.	4.0	72
68	Bacterial epidemiology and biology - lessons from genome sequencing. Genome Biology, 2011, 12, 230.	9.6	72
69	Recent developments in bacterial protein glycan coupling technology and glycoconjugate vaccine design. Journal of Medical Microbiology, 2012, 61, 919-926.	1.8	71
70	Genome-Based Infection Tracking Reveals Dynamics ofClostridium difficileTransmission and Disease Recurrence. Clinical Infectious Diseases, 2016, 62, 746-752.	5.8	71
71	Pseudaminic Acid on Campylobacter jejuni Flagella Modulates Dendritic Cell IL-10 Expression via Siglec-10 Receptor: A Novel Flagellin-Host Interaction. Journal of Infectious Diseases, 2014, 210, 1487-1498.	4.0	70
72	Immunogenicity of aSalmonella typhimurium aroA aroDVaccine Expressing a Nontoxic Domain ofClostridium difficileToxin A. Infection and Immunity, 1999, 67, 2145-2152.	2.2	69

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73	Characterization of a haemolysin from Mycobacterium tuberculosis with homology to a virulence factor of Serpulina hyodysenteriae. Microbiology (United Kingdom), 1998, 144, 1205-1211.	1.8	68
74	Proposal of serovars 17 and 18 of Actinobacillus pleuropneumoniae based on serological and genotypic analysis. Veterinary Microbiology, 2018, 217, 1-6.	1.9	64
75	Characterization of N-Linked Protein Glycosylation in Helicobacter pullorum. Journal of Bacteriology, 2010, 192, 5228-5236.	2.2	63
76	The Campylobacter jejuni Transcriptional Regulator Cj1556 Plays a Role in the Oxidative and Aerobic Stress Response and Is Important for Bacterial SurvivalIn Vivo. Journal of Bacteriology, 2011, 193, 4238-4249.	2.2	63
77	Transcriptional Analysis of Temporal Gene Expression in Germinating Clostridium difficile 630 Endospores. PLoS ONE, 2013, 8, e64011.	2.5	63
78	Yersinia enterocolitica Provides the Link between Thyroid-Stimulating Antibodies and Their Germline Counterparts in Gravesâ€™ Disease. Journal of Immunology, 2013, 190, 5373-5381.	0.8	62
79	Construction and characterisation of aYersinia enterocoliticaO:8ompRmutant. FEMS Microbiology Letters, 1998, 165, 145-151.	1.8	61
80	Comparative analysis of BI/NAP1/027 hypervirulent strains reveals novel toxin B-encoding gene (tcdB) sequences. Journal of Medical Microbiology, 2008, 57, 771-775.	1.8	61
81	Delineation of the Innate and Adaptive T-Cell Immune Outcome in the Human Host in Response to Campylobacter jejuni Infection. PLoS ONE, 2010, 5, e15398.	2.5	61
82	Comprehensive Longitudinal Microbiome Analysis of the Chicken Cecum Reveals a Shift From Competitive to Environmental Drivers and a Window of Opportunity for Campylobacter. Frontiers in Microbiology, 2018, 9, 2452.	3.5	60
83	Clostridium difficile Modulates Host Innate Immunity via Toxin-Independent and Dependent Mechanism(s). PLoS ONE, 2013, 8, e69846.	2.5	59
84	Intracellular replication of the well-armed pathogen Burkholderia pseudomallei. Current Opinion in Microbiology, 2016, 29, 94-103.	5.1	59
85	Assessing the role of p-cresol tolerance in Clostridium difficile. Journal of Medical Microbiology, 2008, 57, 745-749.	1.8	59
86	A Phylogenetic and Phenotypic Analysis of Salmonella enterica Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. PLoS Neglected Tropical Diseases, 2016, 10, e0004446.	3.0	59
87	Understanding and Managing Zoonotic Risk in the New Livestock Industries. Environmental Health Perspectives, 2013, 121, 873-877.	6.0	58
88	Characterization of the Structurally Diverse N-Linked Glycans of Campylobacter Species. Journal of Bacteriology, 2012, 194, 2355-2362.	2.2	57
89	Yersinia pestis pFra Shows Biovar-Specific Differences and Recent Common Ancestry with a Salmonella enterica Serovar Typhi Plasmid. Journal of Bacteriology, 2001, 183, 2586-2594.	2.2	56
90	Characterization of the Burkholderia pseudomallei K96243 Capsular Polysaccharide I Coding Region. Infection and Immunity, 2012, 80, 1209-1221.	2.2	56

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91	The failure of different strains ofYersinia pestisto produce lipopolysaccharide O-antigen under different growth conditions is due to mutations in the O-antigen gene cluster. FEMS Microbiology Letters, 2001, 197, 229-233.	1.8	55
92	Comparative phylogenomics of pathogenic bacteria by microarray analysis. Current Opinion in Microbiology, 2005, 8, 620-626.	5.1	54
93	Hypervirulent Clostridium difficile PCR-Ribotypes Exhibit Resistance to Widely Used Disinfectants. PLoS ONE, 2011, 6, e25754.	2.5	54
94	Patterns of antimicrobial resistance in Streptococcus suis isolates from pigs with or without streptococcal disease in England between 2009 and 2014. Veterinary Microbiology, 2017, 207, 117-124.	1.9	53
95	Genomic variations define divergence of water/wildlifeâ€associated Campylobacter jejuni niche specialists from common clonal complexes. Environmental Microbiology, 2011, 13, 1549-1560.	3.8	52
96	Galleria mellonella is an effective model to study Actinobacillus pleuropneumoniae infection. Microbiology (United Kingdom), 2015, 161, 387-400.	1.8	52
97	Clostridium difficileâ€"A continually evolving and problematic pathogen. Infection, Genetics and Evolution, 2009, 9, 1410-1417.	2.3	50
98	Comparative Genome Analysis and Global Phylogeny of the Toxin Variant Clostridium difficile PCR Ribotype 017 Reveals the Evolution of Two Independent Sublineages. Journal of Clinical Microbiology, 2017, 55, 865-876.	3.9	50
99	Characterization of the lipopolysaccharide of Yersinia pestis. Microbial Pathogenesis, 2001, 30, 49-57.	2.9	49
100	Identification of Possible Virulence Marker fromCampylobacter jejuniIsolates. Emerging Infectious Diseases, 2014, 20, 1026-1029.	4.3	49
101	Role of Glycosyltransferases Modifying Type B Flagellin of Emerging Hypervirulent Clostridium difficile Lineages and Their Impact on Motility and Biofilm Formation. Journal of Biological Chemistry, 2016, 291, 25450-25461.	3.4	49
102	Comparative sequence analysis of the capsular polysaccharide loci of Actinobacillus pleuropneumoniae serovars 1â€"18, and development of two multiplex PCRs for comprehensive capsule typing. Veterinary Microbiology, 2018, 220, 83-89.	1.9	49
103	Sequencing of theFrancisella tularensisStrain Schu 4 Genome Reveals the Shikimate and Purine Metabolic Pathways, Targets for the Construction of a Rationally Attenuated Auxotrophic Vaccine. Microbial & Comparative Genomics, 2000, 5, 25-39.	0.4	48
104	The Sudden Dominance of blaCTXâ€"M Harbouring Plasmids in Shigella spp. Circulating in Southern Vietnam. PLoS Neglected Tropical Diseases, 2010, 4, e702.	3.0	48
105	Biological Roles of the O-Methyl Phosphoramidate Capsule Modification in Campylobacter jejuni. PLoS ONE, 2014, 9, e87051.	2.5	48
106	Characterization of the low-pH responses of Helicobacter pylori using genomic DNA arrays. Microbiology (United Kingdom), 2001, 147, 2285-2292.	1.8	48
107	Biofilm Development on Caenorhabditis elegans by Yersinia Is Facilitated by Quorum Sensing-Dependent Repression of Type III Secretion. PLoS Pathogens, 2011, 7, e1001250.	4.7	47
108	The postâ€translational modification of the <scp>C</scp>lostridium difficile flagellin affects motility, cell surface properties and virulence. Molecular Microbiology, 2014, 94, 272-289.	2.5	47

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109	Genomic Epidemiology of a Protracted Hospital Outbreak Caused by a Toxin A-Negative Clostridium difficile Sublineage PCR Ribotype 017 Strain in London, England. Journal of Clinical Microbiology, 2015, 53, 3141-3147.	3.9	46
110	Role of the Cj1371 periplasmic protein and the Cj0355c two-component regulator in the Campylobacter jejuni NCTC 11168 response to oxidative stress caused by paraquat. Research in Microbiology, 2008, 159, 718-726.	2.1	44
111	Deciphering Campylobacter jejuni cell surface interactions from the genome sequence. Current Opinion in Microbiology, 2001, 4, 35-40.	5.1	43
112	Hijacking bacterial glycosylation for the production of glycoconjugates, from vaccines to humanised glycoproteins. Journal of Pharmacy and Pharmacology, 2015, 67, 338-350.	2.4	43
113	Degenerate PCR primers for the amplification of fragments from genes encoding response regulators from a range of pathogenic bacteria. FEMS Microbiology Letters, 1992, 99, 287-291.	1.8	42
114	Helicobacter pylori Pore-Forming Cytolysin Orthologue TlyA Possesses In Vitro Hemolytic Activity and Has a Role in Colonization of the Gastric Mucosa. Infection and Immunity, 2001, 69, 1697-1703.	2.2	42
115	The In Vitro and In Vivo Effect of Carvacrol in Preventing Campylobacter Infection, Colonization and in Improving Productivity of Chicken Broilers. Foodborne Pathogens and Disease, 2017, 14, 341-349.	1.8	42
116	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2017, 8, 311.	3.5	42
117	Yersinia pseudotuberculosis mntH functions in intracellular manganese accumulation, which is essential for virulence and survival in cells expressing functional Nramp1. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	42
118	Virulence characteristics of hcp + Campylobacter jejuni and Campylobacter coli isolates from retail chicken. Gut Pathogens, 2015, 7, 20.	3.4	41
119	Characterization of New Virulence Factors Involved in the Intracellular Growth and Survival of Burkholderia pseudomallei. Infection and Immunity, 2016, 84, 701-710.	2.2	41
120	Adaptation of host transmission cycle during Clostridium difficile speciation. Nature Genetics, 2019, 51, 1315-1320.	21.4	41
121	Are bacterial exotoxins cytokine network regulators?. Trends in Microbiology, 1997, 5, 454-458.	7.7	40
122	The importance of the Rcs phosphorelay in the survival and pathogenesis of the enteropathogenic yersiniae. Microbiology (United Kingdom), 2008, 154, 1117-1131.	1.8	40
123	Altered Innate Defenses in the Neonatal Gastrointestinal Tract in Response to Colonization by Neuropathogenic Escherichia coli. Infection and Immunity, 2013, 81, 3264-3275.	2.2	40
124	Campylobacter jejuni Lipooligosaccharide Sialylation, Phosphorylation, and Amide/Ester Linkage Modifications Fine-tune Human Toll-like Receptor 4 Activation. Journal of Biological Chemistry, 2013, 288, 19661-19672.	3.4	40
125	LsaA, an Antigen Involved in Cell Attachment and Invasion, Is Expressed by Lawsonia intracellularis during Infection In Vitro and In Vivo. Infection and Immunity, 2002, 70, 2899-2907.	2.2	39
126	A recombinant conjugated pneumococcal vaccine that protects against murine infections with a similar efficacy to Prevnar-13. Npj Vaccines, 2018, 3, 53.	6.0	39

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127	Quantitative Analyses Reveal Novel Roles for N- Glycosylation in a Major Enteric Bacterial Pathogen. MBio, 2019, 10, .	4.1	39
128	The Campylobacter jejuni Type VI Secretion System Enhances the Oxidative Stress Response and Host Colonization. Frontiers in Microbiology, 2019, 10, 2864.	3.5	39
129	Local and Systemic Neutralizing Antibody Responses Induced by Intranasal Immunization with the Nontoxic Binding Domain of Toxin A from Clostridium difficile. Infection and Immunity, 1999, 67, 5124-5132.	2.2	39
130	Investigation into the role of the serine protease HtrA in Yersinia pestis pathogenesis. FEMS Microbiology Letters, 2000, 186, 281-286.	1.8	38
131	Helicobacter pylori adherence to gastric epithelial cells: a role for non-adhesin virulence genes. Journal of Medical Microbiology, 2002, 51, 495-502.	1.8	38
132	Impact of industrial production system parameters on chicken microbiomes: mechanisms to improve performance and reduce Campylobacter. Microbiome, 2020, 8, 128.	11.1	38
133	Gene Content and Diversity of the Loci Encoding Biosynthesis of Capsular Polysaccharides of the 15 Serovar Reference Strains of Haemophilus parasuis. Journal of Bacteriology, 2013, 195, 4264-4273.	2.2	37
134	Genomic Epidemiology ofVibrio choleraeO1 Associated with Floods, Pakistan, 2010. Emerging Infectious Diseases, 2014, 20, 13-20.	4.3	37
135	Multiplex PCR Assay for Unequivocal Differentiation of Actinobacillus pleuropneumoniae Serovars 1 to 3, 5 to 8, 10, and 12. Journal of Clinical Microbiology, 2014, 52, 2380-2385.	3.9	36
136	The recent emergence of a highly related virulent Clostridium difficile clade with unique characteristics. Clinical Microbiology and Infection, 2020, 26, 492-498.	6.0	36
137	Revisiting Campylobacter jejuni Virulence and Fitness Factors: Role in Sensing, Adapting, and Competing. Frontiers in Cellular and Infection Microbiology, 2020, 10, 607704.	3.9	36
138	Recombinant expression ofStreptococcus pneumoniaecapsular polysaccharides inEscherichia coli. Open Biology, 2016, 6, 150243.	3.6	35
139	Nucleotide sequence of a chloramphenicol acetyl transferase gene fromClostridium difficile. Nucleic Acids Research, 1989, 17, 4877-4877.	14.5	34
140	Increase in Campylobacter jejuni Invasion of Intestinal Epithelial Cells under Low-Oxygen Coculture Conditions That Reflect the In Vivo Environment. Infection and Immunity, 2012, 80, 1690-1698.	2.2	34
141	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in Haemophilus parasuis. BMC Genomics, 2014, 15, 1179.	2.8	34
142	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in Actinobacillus pleuropneumoniae. Veterinary Microbiology, 2015, 178, 279-282.	1.9	34
143	Extracellular DNA, cell surface proteins and c-di-GMP promote biofilm formation in Clostridioides difficile. Scientific Reports, 2021, 11, 3244.	3.3	34
144	The second century of Campylobacter research: recent advances, new opportunities and old problems. Current Opinion in Infectious Diseases, 2007, 20, 514-518.	3.1	33

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145	Mutational Analysis of Genes Encoding the Early Flagellar Components of Helicobacter pylori: Evidence for Transcriptional Regulation of Flagellin A Biosynthesis. Journal of Bacteriology, 2000, 182, 5274-5277.	2.2	32
146	A flagellar-specific ATPase (FliI) is necessary for flagellar export in Helicobacter pylori. FEMS Microbiology Letters, 2006, 152, 205-211.	1.8	32
147	Administration of capsule-selective endosialidase E minimizes upregulation of organ gene expression induced by experimental systemic infection with Escherichia coli K1. Microbiology (United Kingdom), 2010, 156, 2205-2215.	1.8	32
148	Improved Bacterial Mutagenesis by High-Frequency Allele Exchange, Demonstrated in Clostridium difficile and Streptococcus suis. Applied and Environmental Microbiology, 2013, 79, 4768-4771.	3.1	32
149	The Campylobacter jejuni Oxidative Stress Regulator RrpB Is Associated with a Genomic Hypervariable Region and Altered Oxidative Stress Resistance. Frontiers in Microbiology, 2016, 07, 2117.	3.5	32
150	Reviving Phage Therapy for the Treatment of Cholera. Journal of Infectious Diseases, 2019, 219, 786-794.	4.0	32
151	Molecular cloning and expression ofClostridium difficiletoxin A inEscherichia coliK 12. FEBS Letters, 1987, 225, 82-86.	2.8	31
152	Genomic Epidemiology ofVibrio choleraeO1 Associated with Floods, Pakistan, 2010. Emerging Infectious Diseases, 2014, 20, 13-20.	4.3	31
153	The continually evolving Clostridium difficile species. Future Microbiology, 2012, 7, 945-957.	2.0	30
154	Identification of dfrA14 in two distinct plasmids conferring trimethoprim resistance in Actinobacillus pleuropneumoniae. Journal of Antimicrobial Chemotherapy, 2015, 70, 2217-2222.	3.0	30
155	Functional analysis of N-linking oligosaccharyl transferase enzymes encoded by deep-sea vent proteobacteria. Glycobiology, 2016, 26, 398-409.	2.5	30
156	Functional analysis of the roles of FliQ and FlhB in flagellar expression inHelicobacter pylori. FEMS Microbiology Letters, 1999, 174, 33-39.	1.8	29
157	Mucosal Immunization with a Urease B DNA Vaccine Induces Innate and Cellular Immune Responses Against Helicobacter pylori. Helicobacter, 2006, 11, 113-122.	3.5	29
158	N-linked glycosylation in bacteria: an unexpected application. Future Microbiology, 2009, 4, 401-412.	2.0	29
159	Global transcriptional profiling of Burkholderia pseudomallei under salt stress reveals differential effects on the Bsa type III secretion system. BMC Microbiology, 2010, 10, 171.	3.3	29
160	In-depth genetic analysis ofClostridiumdifficilePCR-ribotype 027 strains reveals high genome fluidity including point mutations and inversions. Gut Microbes, 2010, 1, 269-276.	9.8	29
161	The N -linking glycosylation system from Actinobacillus pleuropneumoniae is required for adhesion and has potential use in glycoengineering. Open Biology, 2017, 7, 160212.	3.6	29
162	Pathotyping the Zoonotic Pathogen Streptococcus suis: Novel Genetic Markers To Differentiate Invasive Disease-Associated Isolates from Non-Disease-Associated Isolates from England and Wales. Journal of Clinical Microbiology, 2019, 57, .	3.9	29

#	Article	IF	Citations
163	Nucleotide sequence ofClostridium difficiletoxin A gene fragment and detection of toxigenic strains by polymerase chain reaction. FEMS Microbiology Letters, 1990, 70, 1-6.	1.8	28
164	Production and efficacy of a low-cost recombinant pneumococcal protein polysaccharide conjugate vaccine. Vaccine, 2018, 36, 3809-3819.	3.8	28
165	The Campylobacter jejuni NCTC11168 capsule prevents excessive cytokine production by dendritic cells. Medical Microbiology and Immunology, 2012, 201, 137-144.	4.8	27
166	The Campylobacter jejuni MarR-like transcriptional regulators RrpA and RrpB both influence bacterial responses to oxidative and aerobic stresses. Frontiers in Microbiology, 2015, 6, 724.	3.5	27
167	Whole genome investigation of a divergent clade of the pathogen Streptococcus suis. Frontiers in Microbiology, 2015, 6, 1191.	3.5	27
168	The bile salt sodium taurocholate inducesCampylobacter jejuniouter membrane vesicle production and increases OMV-associated proteolytic activity. Cellular Microbiology, 2018, 20, e12814.	2.1	27
169	Deletion of a previously uncharacterized flagellar-hook-length control gene fliK modulates the Ïf 54-dependent regulon in Campylobacter jejuni. Microbiology (United Kingdom), 2007, 153, 3099-3111.	1.8	26
170	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of Actinobacillus pleuropneumoniae. Genome Announcements, 2016, 4, .	0.8	26
171	Sodium Taurocholate Stimulates Campylobacter jejuni Outer Membrane Vesicle Production via Down-Regulation of the Maintenance of Lipid Asymmetry Pathway. Frontiers in Cellular and Infection Microbiology, 2019, 9, 177.	3.9	26
172	Domestication of Campylobacter jejuni NCTC 11168. Microbial Genomics, 2019, 5, .	2.0	26
173	Identification, cloning and initial characterisation of FeuPQ inBrucella suis: a new sub-family of two-component regulatory systems. FEMS Microbiology Letters, 1998, 162, 143-150.	1.8	24
174	TheCampylobacter jejuniglycome. FEMS Microbiology Reviews, 2005, 29, 377-390.	8.6	24
175	Clostridium difficilehas a single sortase, SrtB, that can be inhibited by small-molecule inhibitors. BMC Microbiology, 2014, 14, 219.	3.3	24
176	Phenotypic and Genotypic Characterizations of Campylobacter jejuni Isolated from the Broiler Meat Production Process. Current Microbiology, 2012, 65, 398-406.	2.2	23
177	The Generation of Successive Unmarked Mutations and Chromosomal Insertion of Heterologous Genes in Actinobacillus pleuropneumoniae Using Natural Transformation. PLoS ONE, 2014, 9, e111252.	2.5	23
178	Numerical analysis of DNA microarray data of Campylobacter jejuni strains correlated with survival, cytolethal distending toxin and haemolysin analyses. International Journal of Medical Microbiology, 2006, 296, 353-363.	3.6	22
179	Glycoproteomics: a powerful tool for characterizing the diverse glycoforms of bacterial pilins and flagellins. Biochemical Society Transactions, 2010, 38, 1307-1313.	3.4	22
180	All Yersinia enterocolitica are pathogenic: virulence of phylogroup 1 Y. enterocolitica in a Galleria mellonella infection model. Microbiology (United Kingdom), 2016, 162, 1379-1387.	1.8	22

#	Article	IF	Citations
181	Investigation into the role of the response regulator NtrC in the metabolism and virulence ofBrucella suis. Microbial Pathogenesis, 1999, 27, 1-11.	2.9	21
182	Population Biology of Streptococcus pneumoniae in West Africa: Multilocus Sequence Typing of Serotypes That Exhibit Different Predisposition to Invasive Disease and Carriage. PLoS ONE, 2013, 8, e53925.	2.5	21
183	An O-Antigen Glycoconjugate Vaccine Produced Using Protein Glycan Coupling Technology Is Protective in an Inhalational Rat Model of Tularemia. Journal of Immunology Research, 2018, 2018, 1-12.	2.2	21
184	Improving protein glycan coupling technology (PGCT) for glycoconjugate vaccine production. Expert Review of Vaccines, 2020, 19, 507-527.	4.4	21
185	Gene Function Hypotheses for the Campylobacter jejuni Glycome Generated by a Logic-Based Approach. Journal of Molecular Biology, 2013, 425, 186-197.	4.2	20
186	ICEApl1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2016, 7, 810.	3.5	20
187	Characterization of Posttranslationally Modified Multidrug Efflux Pumps Reveals an Unexpected Link between Glycosylation and Antimicrobial Resistance. MBio, 2020, 11, .	4.1	20
188	An improved physical and genetic map of Campylobacter jejuni NCTC 11168 (UA580). Microbiology (United Kingdom), 1998, 144, 503-508.	1.8	19
189	The importance of the magnesium transporter MgtB for virulence of Yersinia pseudotuberculosis and Yersinia pestis. Microbiology (United Kingdom), 2014, 160, 2710-2717.	1.8	19
190	Genome-Wide Evaluation of the Interplay between Caenorhabditis elegans and Yersinia pseudotuberculosis duringIn VivoBiofilm Formation. Infection and Immunity, 2015, 83, 17-27.	2.2	19
191	In vitro and in vivo characterisation of Listeria monocytogenes outbreak isolates. Food Control, 2020, 107, 106784.	5.5	19
192	Use of Precision-Cut Tissue Slices as a Translational Model to Study Host-Pathogen Interaction. Frontiers in Veterinary Science, 2021, 8, 686088.	2.2	19
193	â€œPathotypingâ€•Multiplex PCR Assay for Haemophilus parasuis: a Tool for Prediction of Virulence. Journal of Clinical Microbiology, 2017, 55, 2617-2628.	3.9	18
194	'Going wrong with confidence': misleading sequence analyses of CiaB and ClpX. Molecular Microbiology, 1999, 34, 195-195.	2.5	17
195	Growth Inhibition of Pathogenic Bacteria by Sulfonylurea Herbicides. Antimicrobial Agents and Chemotherapy, 2013, 57, 1513-1517.	3.2	17
196	Functional analysis of the Helicobacter pullorum N-linked protein glycosylation system. Glycobiology, 2018, 28, 233-244.	2.5	17
197	Type III secretion system confers enhanced virulence in clinical non-O1/non-O139 Vibrio cholerae. Microbial Pathogenesis, 2019, 135, 103645.	2.9	17
198	Identification and characterisation of a novel adhesin Ifp in Yersinia pseudotuberculosis. BMC Microbiology, 2011, 11, 85.	3.3	16

#	Article	IF	Citations
199	Escherichia coli Pathotypes in Pakistan from Consecutive Floods in 2010 and 2011. American Journal of Tropical Medicine and Hygiene, 2013, 88, 519-525.	1.4	16
200	Characterization of water and wildlife strains as a subgroup of <scp>C</scp>ampylobacter jejuni using <scp>DNA</scp> microarrays. Environmental Microbiology, 2013, 15, 2371-2383.	3.8	16
201	The Type B Flagellin of Hypervirulent Clostridium difficile Is Modified with Novel Sulfonated Peptidylamido-glycans. Journal of Biological Chemistry, 2016, 291, 25439-25449.	3.4	16
202	Microbe Profile: Campylobacter jejuni â€“ survival instincts. Microbiology (United Kingdom), 2020, 166, 230-232.	1.8	16
203	Use of Proteins Identified through a Functional Genomic Screen To Develop a Protein Subunit Vaccine That Provides Significant Protection against Virulent Streptococcus suis in Pigs. Infection and Immunity, 2018, 86, .	2.2	16
204	Identification of Immunogenic and Virulence-Associated Campylobacter jejuni Proteins. Vaccine Journal, 2012, 19, 113-119.	3.1	15
205	Generation of a Tn5 transposon library in Haemophilus parasuis and analysis by transposon-directed insertion-site sequencing (TraDIS). Veterinary Microbiology, 2013, 166, 558-566.	1.9	15
206	Simple sequence repeats in Helicobacter canadensis and their role in phase variable expression and C-terminal sequence switching. BMC Genomics, 2010, 11, 67.	2.8	14
207	Exploring the oxidative, antimicrobial and genomic properties of Campylobacter jejuni strains isolated from poultry. Research in Veterinary Science, 2018, 119, 170-175.	1.9	14
208	The Twin Arginine Translocation System Is Essential for Aerobic Growth and Full Virulence of Burkholderia thailandensis. Journal of Bacteriology, 2014, 196, 407-416.	2.2	13
209	Chromosomal integration vectors allowing flexible expression of foreign genes in Campylobacter jejuni. BMC Microbiology, 2015, 15, 230.	3.3	13
210	Galleria mellonella is low cost and suitable surrogate host for studying virulence of human pathogenic Vibrio cholerae. Gene, 2017, 628, 1-7.	2.2	13
211	The S-layer protein of a Clostridium difficile SLCT-11 strain displays a complex glycan required for normal cell growth and morphology. Journal of Biological Chemistry, 2018, 293, 18123-18137.	3.4	13
212	High-throughput analysis of Yersinia pseudotuberculosis gene essentiality in optimised in vitro conditions, and implications for the speciation of Yersinia pestis. BMC Microbiology, 2018, 18, 46.	3.3	13
213	Vibrio cholerae accessory colonisation factor AcfC: a chemotactic protein with a role in hyperinfectivity. Scientific Reports, 2018, 8, 8390.	3.3	13
214	Transmission of multidrug-resistant Campylobacter jejuni to children from different sources in Pakistan. Journal of Global Antimicrobial Resistance, 2020, 20, 219-224.	2.2	13
215	Evaluation of Glycosylated FlpA and SodB as Subunit Vaccines Against Campylobacter jejuni Colonisation in Chickens. Vaccines, 2020, 8, 520.	4.4	13
216	Systems analysis of bacterial glycomes. Biochemical Society Transactions, 2010, 38, 1290-1293.	3.4	12

#	Article	IF	Citations
217	Structure-activity relationships in a new class of non-substrate-like covalent inhibitors of the bacterial glycosyltransferase LgtC. Bioorganic and Medicinal Chemistry, 2018, 26, 2973-2983.	3.0	12
218	Inactivation of bpsl1039-1040 ATP-binding cassette transporter reduces intracellular survival in macrophages, biofilm formation and virulence in the murine model of Burkholderia pseudomallei infection. PLoS ONE, 2018, 13, e0196202.	2.5	12
219	Clostridioides difficile para -Cresol Production Is Induced by the Precursor para -Hydroxyphenylacetate. Journal of Bacteriology, 2020, 202, .	2.2	12
220	Hostâ€“bacterial interactions and the pathogenesis of Helicobacter pylori infection. Trends in Microbiology, 1998, 6, 379-380.	7.7	11
221	Procedure for the Investigation of Bacterial Genomes: Random Shot-Gun Cloning, Sample Sequencing and Mutagenesis of Campylobacter jejuni. BioTechniques, 1999, 26, 50-56.	1.8	11
222	A major role for intestinal epithelial nucleotide oligomerization domain 1 (NOD1) in eliciting host bactericidal immune responses to Campylobacter jejuni. Cellular Microbiology, 2007, 9, 2541-2541.	2.1	11
223	YtxR Acts as an Overriding Transcriptional Off Switch for the Yersinia enterocolitica Ysc-Yop Type 3 Secretion System. Journal of Bacteriology, 2009, 191, 514-524.	2.2	11
224	Phenotypic and genotypic characterization of enteroaggregative Escherichia coli isolates from pediatric population in Pakistan. Apmis, 2016, 124, 872-880.	2.0	11
225	Comparative Genomic Analysis and In Vivo Modeling of Streptococcus pneumoniae ST3081 and ST618 Isolates Reveal Key Genetic and Phenotypic Differences Contributing to Clonal Replacement of Serotype 1 in The Gambia. Journal of Infectious Diseases, 2017, 216, 1318-1327.	4.0	11
226	Cytoplasmic glycoengineering of Apx toxin fragments in the development of Actinobacillus pleuropneumoniae glycoconjugate vaccines. BMC Veterinary Research, 2019, 15, 6.	1.9	11
227	Epidemiology and typing of Clostridium difficile. European Journal of Gastroenterology and Hepatology, 1996, 8, 1035-1040.	1.6	10
228	Genes to genetic immunization: identification of bacterial vaccine candidates. Methods, 2003, 31, 193-198.	3.8	10
229	Recent advances in systems microbiology. Current Opinion in Microbiology, 2009, 12, 577-581.	5.1	10
230	Shared characteristics between Mycobacterium tuberculosis and fungi contribute to virulence. Future Microbiology, 2014, 9, 657-668.	2.0	10
231	Characterization of enteropathogenicEscherichia coliof clinical origin from the pediatric population in Pakistan. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2016, 110, 414-420.	1.8	10
232	Host Immunity to Clostridium difficile PCR Ribotype 017 Strains. Infection and Immunity, 2014, 82, 4989-4996.	2.2	9
233	Serovar-dependent differences in Hfq-regulated phenotypes inActinobacillus pleuropneumoniae. Pathogens and Disease, 2020, 78, .	2.0	9
234	Pancreatic Amylase Is an Environmental Signal for Regulation of Biofilm Formation and Host Interaction in Campylobacter jejuni. Infection and Immunity, 2015, 83, 4884-4895.	2.2	8

#	Article	IF	Citations
235	Infection Susceptibility in Gastric Intrinsic Factor (Vitamin B ₁₂)-Defective Mice Is Subject to Maternal Influences. MBio, 2016, 7, .	4.1	8
236	Clostridium perfringens epsilon toxin vaccine candidate lacking toxicity to cells expressing myelin and lymphocyte protein. Npj Vaccines, 2019, 4, 32.	6.0	8
237	Virulence of the emerging pathogen, Burkholderia pseudomallei, depends upon the O-linked oligosaccharyltransferase, PglL. Future Microbiology, 2020, 15, 241-257.	2.0	8
238	Comparative Genome Analyses of the Pathogenic Yersiniae Based on the Genome Sequence of Yersinia enterocolitica Strain 8081. Advances in Experimental Medicine and Biology, 2007, 603, 2-16.	1.6	8
239	Temporal changes in nasopharyngeal carriage ofStreptococcus pneumoniaeserotype 1 genotypes in healthy Gambians before and after the 7-valent pneumococcal conjugate vaccine. PeerJ, 2015, 3, e903.	2.0	8
240	Development and application of the active surveillance of pathogens microarray to monitor bacterial gene flux.. BMC Microbiology, 2008, 8, 177.	3.3	7
241	Generation and Evaluation of a Glaesserella (Haemophilus) parasuis Capsular Mutant. Infection and Immunity, 2020, 88, .	2.2	7
242	The Streptococcos suis sortases SrtB and SrtF are essential for disease in pigs. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	7
243	Multivalent poultry vaccine development using Protein Glycan Coupling Technology. Microbial Cell Factories, 2021, 20, 193.	4.0	7
244	Production of p-cresol by Decarboxylation of p-HPA by All Five Lineages of Clostridioides difficile Provides a Growth Advantage. Frontiers in Cellular and Infection Microbiology, 2021, 11, 757599.	3.9	7
245	Bacteria like sharing their sweets. Molecular Microbiology, 2013, 89, 811-815.	2.5	6
246	Construction of a pneumolysin deficient mutant in streptococcus pneumoniae serotype 1 strain 519/43 and phenotypic characterisation. Microbial Pathogenesis, 2020, 141, 103999.	2.9	6
247	Genome-wide assessment of antimicrobial tolerance in Yersinia pseudotuberculosis under ciprofloxacin stress. Microbial Genomics, 2019, 5, .	2.0	6
248	Probing Differences in Gene Essentiality Between the Human and Animal Adapted Lineages of the Mycobacterium tuberculosis Complex Using TnSeq. Frontiers in Veterinary Science, 2021, 8, 760717.	2.2	6
249	Delivery of non-toxic fragments of Clostridium difficile toxin A to the mucosal immune system. Reviews in Medical Microbiology, 1997, 8, S37.	0.9	5
250	Deciphering tsetse's secret partner. Nature Genetics, 2002, 32, 335-336.	21.4	5
251	Cellular Response of Campylobacter jejuni to Trisodium Phosphate. Applied and Environmental Microbiology, 2012, 78, 1411-1415.	3.1	5
252	Disparate subcellular location of putative sortase substrates in Clostridium difficile. Scientific Reports, 2017, 7, 9204.	3.3	5

#	Article	IF	Citations
253	CSF Levels of Elongation Factor Tu Is Associated With Increased Mortality in Malawian Adults With Streptococcus pneumoniae Meningitis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 603623.	3.9	5
254	Revisiting aminocoumarins for the treatment of melioidosis. International Journal of Antimicrobial Agents, 2020, 56, 106002.	2.5	5
255	Evaluation of the recombinant proteins RlpB and VacJ as a vaccine for protection against Glaesserella parasuis in pigs. BMC Veterinary Research, 2020, 16, 167.	1.9	5
256	Development of an automated platform for the optimal production of glycoconjugate vaccines expressed in Escherichia coli. Microbial Cell Factories, 2021, 20, 104.	4.0	5
257	The Three Bears and Virulence-Associated Plasmids in the Genus Yersinia. Microbiology Monographs, 2009, , 171-186.	0.6	5
258	Transient internalization of Campylobacter jejuni in Amoebae enhances subsequent invasion of human cells. Microbiology (United Kingdom), 2022, 168, .	1.8	5
259	Engineering a suite of E. coli strains for enhanced expression of bacterial polysaccharides and glycoconjugate vaccines. Microbial Cell Factories, 2022, 21, 66.	4.0	5
260	Ferric Citrate Regulator FecR Is Translocated across the Bacterial Inner Membrane via a Unique Twin-Arginine Transport-Dependent Mechanism. Journal of Bacteriology, 2020, 202, .	2.2	4
261	Sequential Vaccination With Heterologous Acinetobacter baumannii Strains Induces Broadly Reactive Antibody Responses. Frontiers in Immunology, 2021, 12, 705533.	4.8	4
262	BÂG@Sbase--a microbial gene expression and comparative genomic database. Nucleic Acids Research, 2012, 40, D605-D609.	14.5	3
263	Comparative Genomics of Campylobacter jejuni. , 2014, , 63-71.		3
264	Campylobacter jejuni Capsular Polysaccharide. , 0, , 505-521.		3
265	Draft Genome Sequence of Campylobacter jejuni 11168H. Genome Announcements, 2017, 5, .	0.8	3
266	Clostridium difficile clade 3 (RT023) have a modified cell surface and contain a large transposable island with novel cargo. Scientific Reports, 2019, 9, 15330.	3.3	3
267	Environmental interactions are regulated by temperature in Burkholderia seminalis TC3.4.2R3. Scientific Reports, 2019, 9, 5486.	3.3	3
268	MdaB and NfrA, Two Novel Reductases Important in the Survival and Persistence of the Major Enteropathogen Campylobacter jejuni. Journal of Bacteriology, 2022, 204, JB0042121.	2.2	3
269	Evaluation of a Campylobacter jejuni N-glycan-ExoA glycoconjugate vaccine to reduce C. jejuni colonisation in chickens. Vaccine, 2021, , .	3.8	3
270	PglB function and glycosylation efficiency is temperature dependent when the pgl locus is integrated in the Escherichia coli chromosome. Microbial Cell Factories, 2022, 21, 6.	4.0	3

#	Article	IF	Citations
271	Defining the Genes Required for Survival of Mycobacterium bovis in the Bovine Host Offers Novel Insights into the Genetic Basis of Survival of Pathogenic Mycobacteria. MBio, 2022, 13, .	4.1	3
272	Draft Genome Sequences of the Type Strains of Actinobacillus indolicus (46K2C) and Actinobacillus porcinus (NM319), Two NAD-Dependent Bacterial Species Found in the Respiratory Tract of Pigs. Microbiology Resource Announcements, 2020, 9, .	0.6	2
273	Campylobacter jejuni Infection in Intestinal Lymphoma: A Strong Association with Immunoproliferative Small Intestinal Disease.. Blood, 2004, 104, 1369-1369.	1.4	2
274	Clostridium difficile â€“ A Pathogen on the Move. , 2015, , 1031-1040.		1
275	Draft Genome Sequence of Robinsoniella peoriensis 6600698, a Confounder of Clostridium difficile Diagnosis. Genome Announcements, 2016, 4, .	0.8	1
276	YPTB3816 of Yersinia pseudotuberculosis strain IP32953 is a virulence-related metallo-oligopeptidase. BMC Microbiology, 2016, 16, 282.	3.3	1
277	The X-ray structure of<scp>L</scp>-threonine dehydrogenase from the common hospital pathogenClostridium difficile. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 269-274.	0.8	1
278	Plague The mysterious past and terrifying future of the worldâ€™s most deadly disease. Journal of Clinical Investigation, 2005, 115, 4-4.	8.2	1
279	Constructing Mutants in Serotype 1 Streptococcus pneumoniae strain 519/43. Journal of Visualized Experiments, 2020, , .	0.3	1
280	Complete genome for Actinobacillus pleuropneumoniae serovar 8 reference strain 405: comparative analysis with draft genomes for different laboratory stock cultures indicates little genetic variation. Microbial Genomics, 2021, 7, .	2.0	1
281	Rationally designed mariner vectors for functional genomic analysis of Actinobacillus pleuropneumoniae and other Pasteurellaceae species by transposon-directed insertion-site sequencing (TraDIS). Animal Diseases, 2021, 1, 29.	1.4	1
282	Further strategies for signature-tagged mutagenesis and the application of oligonucleotide microarrays for the quantification of DNA-tagged strains. Methods in Microbiology, 2002, 33, 167-184.	0.8	0
283	Microarrays for Bacterial Pathogens â€” Hope or Hype?. Comparative and Functional Genomics, 2002, 3, 330-332.	2.0	0
284	Microarray Analysis ofCampylobacter jejuni: To the Guts of the Problem!. Comparative and Functional Genomics, 2002, 3, 338-341.	2.0	0
285	Innate immunity: past, present and future. Molecular Immunology, 2005, 42, 925-926.	2.2	0
286	Post-genome Analysis of the Foodborne Pathogen Campylobacter jejuni. , 2011, , 55-94.		0
287	Profiling of Haemophilus influenzae strain R2866 with carbohydrate-based covalent probes. Organic and Biomolecular Chemistry, 2021, 19, 476-485.	2.8	0
288	Evolution of Pathogenic Yersinia. , 0, , 385-396.		0

#	Article	IF	Citations
289	Genomics of the Enteropathogenic Yersiniae. , 0, , 101-111.		0