Brendan W Wren

List of Publications by Year in descending order

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289 papers 17,884 citations

67 h-index 119 g-index

321 all docs

321 docs citations

times ranked

321

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.	9.4	821
2	N-Linked Glycosylation in Campylobacter jejuni and Its Functional Transfer into E. coli. Science, 2002, 298, 1790-1793.	6.0	716
3	Emergence and global spread of epidemic healthcare-associated Clostridium difficile. Nature Genetics, 2013, 45, 109-113.	9.4	669
4	The complete genome sequence of Francisella tularensis, the causative agent of tularemia. Nature Genetics, 2005, 37, 153-159.	9.4	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.	13.9	431
6	Protein glycosylation in bacterial mucosal pathogens. Nature Reviews Microbiology, 2005, 3, 225-237.	13.6	380
7	Bacterial pathogenomics. Nature, 2007, 449, 835-842.	13.7	374
8	The HtrA family of serine proteases. Molecular Microbiology, 1997, 26, 209-221.	1.2	369
9	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7527-7532.	3.3	346
10	The <i>Clostridium difficile spo0A</i> Gene Is a Persistence and Transmission Factor. Infection and Immunity, 2012, 80, 2704-2711.	1.0	324
11	The Yersiniae $\hat{a}\in$ " a model genus to study the rapid evolution of bacterial pathogens. Nature Reviews Microbiology, 2003, 1, 55-64.	13.6	320
12	Antibiotic Treatment of <i>Clostridium difficile</i> Carrier Mice Triggers a Supershedder State, Spore-Mediated Transmission, and Severe Disease in Immunocompromised Hosts. Infection and Immunity, 2009, 77, 3661-3669.	1.0	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.	2.4	278
14	Genetic and biochemical evidence of a Campylobacter jejuni capsular polysaccharide that accounts for Penner serotype specificity. Molecular Microbiology, 2002, 35, 529-541.	1.2	228
15	The Complete Genome Sequence and Comparative Genome Analysis of the High Pathogenicity Yersinia enterocolitica Strain 8081. PLoS Genetics, 2006, 2, e206.	1.5	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.	1.0	210
17	Phase variation of a \hat{l}^2 -1,3 galactosyltransferase involved in generation of the ganglioside GM1-like lipo-oligosaccharide of Campylobacter jejuni. Molecular Microbiology, 2002, 37, 501-514.	1.2	206
18	Functional analysis of theCampylobacter jejuniN-linked protein glycosylation pathway. Molecular Microbiology, 2005, 55, 1695-1703.	1.2	193

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19	Re-annotation and re-analysis of the Campylobacter jejuni NCTC11168 genome sequence. BMC Genomics, 2007, 8, 162.	1.2	189
20	Molecular characterization of the surface layer proteins from Clostridium difficile. Molecular Microbiology, 2001, 40, 1187-1199.	1.2	177
21	Campylobacter – a tale of two protein glycosylation systems. Trends in Microbiology, 2003, 11, 233-238.	3.5	166
22	Adaptation of Campylobacter jejuni NCTC11168 to High-Level Colonization of the Avian Gastrointestinal Tract. Infection and Immunity, 2004, 72, 3769-3776.	1.0	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.	1.2	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.	3.3	158
25	Application of DNA Microarrays to Study the Evolutionary Genomics of Yersinia pestis and Yersinia pseudotuberculosis. Genome Research, 2003, 13, 2018-2029.	2.4	154
26	Parallel independent evolution of pathogenicity within the genus $\langle i \rangle$ Yersinia $\langle i \rangle$. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	3.3	154
27	A novel paralogous gene family involved in phase-variable flagella-mediated motility in Campylobacter jejuni. Microbiology (United Kingdom), 2002, 148, 473-480.	0.7	149
28	Characterisation of Clostridium difficile Biofilm Formation, a Role for SpoOA. PLoS ONE, 2012, 7, e50527.	1.1	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.	1.0	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.	1.0	138
31	'Add, stir and reduce': Yersinia spp. as model bacteria for pathogen evolution. Nature Reviews Microbiology, 2016, 14, 177-190.	13.6	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.	1.2	128
33	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. Nature Communications, 2015, 6, 6740.	5.8	124
34	Identification of N-acetylgalactosamine-containing glycoproteins PEB3 and CgpA in Campylobacter jejuni. Molecular Microbiology, 2002, 43, 497-508.	1.2	121
35	<i>Campylobacter jejuni</i> Glycosylation Island Important in Cell Charge, Legionaminic Acid Biosynthesis, and Colonization of Chickens. Infection and Immunity, 2009, 77, 2544-2556.	1.0	121
36	A Novel Campylobacter jejuni Two-Component Regulatory System Important for Temperature-Dependent Growth and Colonization. Journal of Bacteriology, 1999, 181, 3298-3302.	1.0	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.	1.1	114
38	<i>Campylobacter jejuni</i> outer 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.	1.1	113
39	Microbial genome analysis: insights into virulence, host adaptation and evolution. Nature Reviews Genetics, 2000, 1, 30-39.	7.7	109
40	The <i>agr</i> Locus Regulates Virulence and Colonization Genes in Clostridium difficile 027. Journal of Bacteriology, 2013, 195, 3672-3681.	1.0	99
41	Para-cresol production by Clostridium difficile affects microbial diversity and membrane integrity of Gram-negative bacteria. PLoS Pathogens, 2018, 14, e1007191.	2.1	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.	1.1	95
43	Microarray analysis of the transcriptional responses of Clostridium difficile to environmental and antibiotic stress. Journal of Medical Microbiology, 2008, 57, 757-764.	0.7	94
44	Invertebrates as a source of emerging human pathogens. Nature Reviews Microbiology, 2004, 2, 833-841.	13.6	91
45	Galleria mellonella as an alternative infection model for Yersinia pseudotuberculosis. Microbiology (United Kingdom), 2009, 155, 1516-1522.	0.7	91
46	Single-Primer PCR Procedure for Rapid Identification of Transposon Insertion Sites. BioTechniques, 2000, 28, 1078-1082.	0.8	90
47	The glycome. FEMS Microbiology Reviews, 2005, 29, 377-390.	3.9	88
48	Revised nomenclature of Clostridium difficile toxins and associated genes. Journal of Medical Microbiology, 2005, 54, 113-117.	0.7	88
49	Commonality and Biosynthesis of the O-Methyl Phosphoramidate Capsule Modification in Campylobacter jejuni. Journal of Biological Chemistry, 2007, 282, 28566-28576.	1.6	86
50	Exploiting genome sequence: predictions for mechanisms of Campylobacter chemotaxis. Trends in Microbiology, 2002, 10, 155-159.	3.5	85
51	Explorative Multifactor Approach for Investigating Global Survival Mechanisms of Campylobacter jejuni under Environmental Conditions. Applied and Environmental Microbiology, 2005, 71, 2086-2094.	1.4	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.	1.0	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.	1.8	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.	1.0	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.	0.7	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.	1.2	80
57	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of Haemophilus parasuis. Journal of Clinical Microbiology, 2015, 53, 3812-3821.	1.8	80
58	Recent advances in the production of recombinant glycoconjugate vaccines. Npj Vaccines, 2019, 4, 16.	2.9	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.	1.0	78
60	Demonstration of Polysaccharide Capsule in Campylobacter jejuni Using Electron Microscopy. Infection and Immunity, 2001, 69, 5921-5924.	1.0	76
61	Exploitation of bacterial <i>N</i> -linked glycosylation to develop a novel recombinant glycoconjugate vaccine against <i>Francisella tularensis</i> . Open Biology, 2013, 3, 130002.	1.5	76
62	Genome-Wide Saturation Mutagenesis of Burkholderia pseudomallei K96243 Predicts Essential Genes and Novel Targets for Antimicrobial Development. MBio, 2014, 5, e00926-13.	1.8	75
63	Cyclic diGMP Regulates Production of Sortase Substrates of Clostridium difficile and Their Surface Exposure through Zmpl Protease-mediated Cleavage. Journal of Biological Chemistry, 2015, 290, 24453-24469.	1.6	74
64	The importance of the glycosylation of antimicrobial peptides: natural and synthetic approaches. Drug Discovery Today, 2017, 22, 919-926.	3.2	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.	1.0	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.	1.2	72
67	Insect Infection Model for <i>Campylobacter jejuni</i> Reveals That <i>O</i> â€methyl Phosphoramidate Has Insecticidal Activity. Journal of Infectious Diseases, 2010, 201, 100129142112076-000.	1.9	72
68	Bacterial epidemiology and biology - lessons from genome sequencing. Genome Biology, 2011, 12, 230.	13.9	72
69	Recent developments in bacterial protein glycan coupling technology and glycoconjugate vaccine design. Journal of Medical Microbiology, 2012, 61, 919-926.	0.7	71
70	Genome-Based Infection Tracking Reveals Dynamics of <i>Clostridium difficile </i> Transmission and Disease Recurrence. Clinical Infectious Diseases, 2016, 62, 746-752.	2.9	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.	1.9	70
72	Immunogenicity of a <i> Salmonella typhimurium aroA aroD < /i > Vaccine Expressing a Nontoxic Domain of <i> Clostridium difficile < /i > Toxin A. Infection and Immunity, 1999, 67, 2145-2152.</i></i>	1.0	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.	0.7	68
74	Proposal of serovars 17 and 18 of Actinobacillus pleuropneumoniae based on serological and genotypic analysis. Veterinary Microbiology, 2018, 217, 1-6.	0.8	64
75	Characterization of N-Linked Protein Glycosylation in <i>Helicobacter pullorum</i> Bacteriology, 2010, 192, 5228-5236.	1.0	63
76	The Campylobacter jejuni Transcriptional Regulator Cj1556 Plays a Role in the Oxidative and Aerobic Stress Response and Is Important for Bacterial Survival <i>In Vivo</i> . Journal of Bacteriology, 2011, 193, 4238-4249.	1.0	63
77	Transcriptional Analysis of Temporal Gene Expression in Germinating Clostridium difficile 630 Endospores. PLoS ONE, 2013, 8, e64011.	1.1	63
78	<i>Yersinia enterocolitica</i> Provides the Link between Thyroid-Stimulating Antibodies and Their Germline Counterparts in Graves' Disease. Journal of Immunology, 2013, 190, 5373-5381.	0.4	62
79	Construction and characterisation of aYersinia enterocoliticaO:8ompRmutant. FEMS Microbiology Letters, 1998, 165, 145-151.	0.7	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.	0.7	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.	1.1	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.	1.5	60
83	Clostridium difficile Modulates Host Innate Immunity via Toxin-Independent and Dependent Mechanism(s). PLoS ONE, 2013, 8, e69846.	1.1	59
84	Intracellular replication of the well-armed pathogen Burkholderia pseudomallei. Current Opinion in Microbiology, 2016, 29, 94-103.	2.3	59
85	Assessing the role of p-cresol tolerance in Clostridium difficile. Journal of Medical Microbiology, 2008, 57, 745-749.	0.7	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.	1.3	59
87	Understanding and Managing Zoonotic Risk in the New Livestock Industries. Environmental Health Perspectives, 2013, 121, 873-877.	2.8	58
88	Characterization of the Structurally Diverse N-Linked Glycans of Campylobacter Species. Journal of Bacteriology, 2012, 194, 2355-2362.	1.0	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.	1.0	56
90	Characterization of the Burkholderia pseudomallei K96243 Capsular Polysaccharide I Coding Region. Infection and Immunity, 2012, 80, 1209-1221.	1.0	56

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91	The failure of different strains of Yersinia 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.	0.7	55
92	Comparative phylogenomics of pathogenic bacteria by microarray analysis. Current Opinion in Microbiology, 2005, 8, 620-626.	2.3	54
93	Hypervirulent Clostridium difficile PCR-Ribotypes Exhibit Resistance to Widely Used Disinfectants. PLoS ONE, 2011, 6, e25754.	1.1	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.	0.8	53
95	Genomic variations define divergence of water/wildlifeâ€associated <i>Campylobacter jejuni</i> niche specialists from common clonal complexes. Environmental Microbiology, 2011, 13, 1549-1560.	1.8	52
96	Galleria mellonella is an effective model to study Actinobacillus pleuropneumoniae infection. Microbiology (United Kingdom), 2015, 161, 387-400.	0.7	52
97	Clostridium difficile—A continually evolving and problematic pathogen. Infection, Genetics and Evolution, 2009, 9, 1410-1417.	1.0	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.	1.8	50
99	Characterization of the lipopolysaccharide of Yersinia pestis. Microbial Pathogenesis, 2001, 30, 49-57.	1.3	49
100	Identification of Possible Virulence Marker from Campylobacter jejunilsolates. Emerging Infectious Diseases, 2014, 20, 1026-1029.	2.0	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.	1.6	49
102	Comparative sequence analysis of the capsular polysaccharide loci of Actinobacillus pleuropneumoniae serovars 1–18, and development of two multiplex PCRs for comprehensive capsule typing. Veterinary Microbiology, 2018, 220, 83-89.	0.8	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.	0.6	48
104	The Sudden Dominance of blaCTX–M Harbouring Plasmids in Shigella spp. Circulating in Southern Vietnam. PLoS Neglected Tropical Diseases, 2010, 4, e702.	1.3	48
105	Biological Roles of the O-Methyl Phosphoramidate Capsule Modification in Campylobacter jejuni. PLoS ONE, 2014, 9, e87051.	1.1	48
106	Characterization of the low-pH responses of Helicobacter pylori using genomic DNA arrays. Microbiology (United Kingdom), 2001, 147, 2285-2292.	0.7	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.	2.1	47
108	The postâ€translational modification of the <scp><i>C</i></scp> <i>lostridium difficile</i> flagellin affects motility, cell surface properties and virulence. Molecular Microbiology, 2014, 94, 272-289.	1.2	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.	1.8	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.	1.0	44
111	Deciphering Campylobacter jejuni cell surface interactions from the genome sequence. Current Opinion in Microbiology, 2001, 4, 35-40.	2.3	43
112	Hijacking bacterial glycosylation for the production of glycoconjugates, from vaccines to humanised glycoproteins. Journal of Pharmacy and Pharmacology, 2015, 67, 338-350.	1.2	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.	0.7	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.	1.0	42
115	The <i>In Vitro</i> and <i>In Vivo</i> Effect of Carvacrol in Preventing <i>Campylobacter</i> Infection, Colonization and in Improving Productivity of Chicken Broilers. Foodborne Pathogens and Disease, 2017, 14, 341-349.	0.8	42
116	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2017, 8, 311.	1.5	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 0.78	43 ₫ ærgBT	'/Ommerlock 10
118	Virulence characteristics of hcp + Campylobacter jejuni and Campylobacter coli isolates from retail chicken. Gut Pathogens, 2015, 7, 20.	1.6	41
119	Characterization of New Virulence Factors Involved in the Intracellular Growth and Survival of Burkholderia pseudomallei. Infection and Immunity, 2016, 84, 701-710.	1.0	41
120	Adaptation of host transmission cycle during Clostridium difficile speciation. Nature Genetics, 2019, 51, 1315-1320.	9.4	41
121	Are bacterial exotoxins cytokine network regulators?. Trends in Microbiology, 1997, 5, 454-458.	3.5	40
122	The importance of the Rcs phosphorelay in the survival and pathogenesis of the enteropathogenic yersiniae. Microbiology (United Kingdom), 2008, 154, 1117-1131.	0.7	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.	1.0	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.	1.6	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.	1.0	39
126	A recombinant conjugated pneumococcal vaccine that protects against murine infections with a similar efficacy to Prevnar-13. Npj Vaccines, 2018, 3, 53.	2.9	39

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127	Quantitative Analyses Reveal Novel Roles for $\langle i \rangle N \cdot \langle i \rangle$ Glycosylation in a Major Enteric Bacterial Pathogen. MBio, 2019, 10, .	1.8	39
128	The Campylobacter jejuni Type VI Secretion System Enhances the Oxidative Stress Response and Host Colonization. Frontiers in Microbiology, 2019, 10, 2864.	1.5	39
129	Local and Systemic Neutralizing Antibody Responses Induced by Intranasal Immunization with the Nontoxic Binding Domain of Toxin A from <i>Clostridium difficile</i> . Infection and Immunity, 1999, 67, 5124-5132.	1.0	39
130	Investigation into the role of the serine protease HtrA in Yersinia pestis pathogenesis. FEMS Microbiology Letters, 2000, 186, 281-286.	0.7	38
131	Helicobacter pylori adherence to gastric epithelial cells: a role for non-adhesin virulence genes. Journal of Medical Microbiology, 2002, 51, 495-502.	0.7	38
132	Impact of industrial production system parameters on chicken microbiomes: mechanisms to improve performance and reduce Campylobacter. Microbiome, 2020, 8, 128.	4.9	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.	1.0	37
134	Genomic Epidemiology of <i>Vibrio cholerae </i> O1 Associated with Floods, Pakistan, 2010. Emerging Infectious Diseases, 2014, 20, 13-20.	2.0	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.	1.8	36
136	The recent emergence of a highly related virulent Clostridium difficile clade with unique characteristics. Clinical Microbiology and Infection, 2020, 26, 492-498.	2.8	36
137	Revisiting Campylobacter jejuni Virulence and Fitness Factors: Role in Sensing, Adapting, and Competing. Frontiers in Cellular and Infection Microbiology, 2020, 10, 607704.	1.8	36
138	Recombinant expression of <i>Streptococcus pneumoniae </i> capsular polysaccharides in <i>Escherichia coli </i> . Open Biology, 2016, 6, 150243.	1.5	35
139	Nucleotide sequence of a chloramphenicol acetyl transferase gene fromClostridium difficile. Nucleic Acids Research, 1989, 17, 4877-4877.	6.5	34
140	Increase in Campylobacter jejuni Invasion of Intestinal Epithelial Cells under Low-Oxygen Coculture Conditions That Reflect the <i>In Vivo</i> Environment. Infection and Immunity, 2012, 80, 1690-1698.	1.0	34
141	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in Haemophilus parasuis. BMC Genomics, 2014, 15, 1179.	1.2	34
142	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in Actinobacillus pleuropneumoniae. Veterinary Microbiology, 2015, 178, 279-282.	0.8	34
143	Extracellular DNA, cell surface proteins and c-di-GMP promote biofilm formation in Clostridioides difficile. Scientific Reports, 2021, 11, 3244.	1.6	34
144	The second century of Campylobacter research: recent advances, new opportunities and old problems. Current Opinion in Infectious Diseases, 2007, 20, 514-518.	1.3	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.	1.0	32
146	A flagellar-specific ATPase (FliI) is necessary for flagellar export in Helicobacter pylori. FEMS Microbiology Letters, 2006, 152, 205-211.	0.7	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.	0.7	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.	1.4	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.	1.5	32
150	Reviving Phage Therapy for the Treatment of Cholera. Journal of Infectious Diseases, 2019, 219, 786-794.	1.9	32
151	Molecular cloning and expression of Clostridium difficiletoxin A in Escherichia coliK 12. FEBS Letters, 1987, 225, 82-86.	1.3	31
152	Genomic Epidemiology of <i>Vibrio cholerae </i> O1 Associated with Floods, Pakistan, 2010. Emerging Infectious Diseases, 2014, 20, 13-20.	2.0	31
153	The continually evolving <i>Clostridium difficile</i> species. Future Microbiology, 2012, 7, 945-957.	1.0	30
154	Identification of <i>dfrA14</i> in two distinct plasmids conferring trimethoprim resistance in <i>Actinobacillus pleuropneumoniae</i> Journal of Antimicrobial Chemotherapy, 2015, 70, 2217-2222.	1.3	30
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