Duncan J Maskell

List of Publications by Year
in descending order

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193 papers	13,285 citations	23567 58 h-index	27406 106 g-index

200 all docs	200 docs citations	200 times ranked	12541 citing authors

#	Article	IF	Citations
1	Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica. Nature Genetics, 2003, 35, 32-40.	21.4	898
2	Meticillin-resistant Staphylococcus aureus with a novel mecA homologue in human and bovine populations in the UK and Denmark: a descriptive study. Lancet Infectious Diseases, The, 2011, 11, 595-603.	9.1	751
3	Simultaneous assay of every Salmonella Typhi gene using one million transposon mutants. Genome Research, 2009, 19, 2308-2316.	5.5	544
4	Bacterial polysaccharide synthesis and gene nomenclature. Trends in Microbiology, 1996, 4, 495-503.	7.7	508
5	High-throughput sequencing provides insights into genome variation and evolution in Salmonella Typhi. Nature Genetics, 2008, 40, 987-993.	21.4	453
6	Comparative genome analysis of Salmonella Enteritidis PT4 and Salmonella Gallinarum 287/91 provides insights into evolutionary and host adaptation pathways. Genome Research, 2008, 18, 1624-1637.	5.5	394
7	Reverse Transcriptase-Mediated Tropism Switching in Bordetella Bacteriophage. Science, 2002, 295, 2091-2094.	12.6	247
8	Identification of host-specific colonization factors of Salmonella enterica serovar Typhimurium. Molecular Microbiology, 2004, 54, 994-1010.	2.5	244
9	Rapid Evolution of Virulence and Drug Resistance in the Emerging Zoonotic Pathogen Streptococcus suis. PLoS ONE, 2009, 4, e6072.	2.5	214
10	Patterns of genome evolution that have accompanied host adaptation in Salmonella. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 863-868.	7.1	213
11	Rapid Expression of Chemokines and Proinflammatory Cytokines in Newly Hatched Chickens Infected withSalmonella entericaSerovar Typhimurium. Infection and Immunity, 2004, 72, 2152-2159.	2.2	207
12	A Strand-Specific RNAâ€“Seq Analysis of the Transcriptome of the Typhoid Bacillus Salmonella Typhi. PLoS Genetics, 2009, 5, e1000569.	3.5	202
13	A lethal role for lipid A inSalmonellainfections. Molecular Microbiology, 1998, 29, 571-579.	2.5	201
14	Pilus-facilitated adherence of Neisseria meningitidis to human epithelial and endothelial cells: modulation of adherence phenotype occurs concurrently with changes in primary amino acid sequence and the glycosylation status of pilin. Molecular Microbiology, 1993, 10, 1013-1028.	2.5	198
15	Genomic Evidence for the Evolution of Streptococcus equi: Host Restriction, Increased Virulence, and Genetic Exchange with Human Pathogens. PLoS Pathogens, 2009, 5, e1000346.	4.7	197
16	Cytokine and Chemokine Responses Associated with Clearance of a Primary Salmonella enterica Serovar Typhimurium Infection in the Chicken and in Protective Immunity to Rechallenge. Infection and Immunity, 2005, 73, 5173-5182.	2.2	195
17	Modelling within-Host Spatiotemporal Dynamics of Invasive Bacterial Disease. PLoS Biology, 2008, 6, e74.	5.6	189
18	Comprehensive Assignment of Roles for Salmonella Typhimurium Genes in Intestinal Colonization of Food-Producing Animals. PLoS Genetics, 2013, 9, e1003456.	3.5	176

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19	Salmonella bongori Provides Insights into the Evolution of the Salmonellae. PLoS Pathogens, 2011, 7, e1002191.	4.7	171
20	Adaptation of Campylobacter jejuni NCTC11168 to High-Level Colonization of the Avian Gastrointestinal Tract. Infection and Immunity, 2004, 72, 3769-3776.	2.2	162
21	Identification and Functional Characterization of Chicken Toll-Like Receptor 5 Reveals a Fundamental Role in the Biology of Infection with Salmonella enterica Serovar Typhimurium. Infection and Immunity, 2005, 73, 2344-2350.	2.2	159
22	Salmonella typhimuriumaroA mutants as carriers of the Escherichia coli heat-labile enterotoxin B subunit to the murine secretory and systemic immune systems. Microbial Pathogenesis, 1987, 2, 211-221.	2.9	144
23	Two msbB Genes Encoding Maximal Acylation of Lipid A Are Required for Invasive Shigella flexneri to Mediate Inflammatory Rupture and Destruction of the Intestinal Epithelium. Journal of Immunology, 2002, 168, 5240-5251.	0.8	143
24	Elucidation of the MD-2/TLR4 Interface Required for Signaling by Lipid IVa. Journal of Immunology, 2008, 181, 1245-1254.	0.8	134
25	Dynamics of bacterial growth and distribution within the liver duringSalmonellainfection. Cellular Microbiology, 2003, 5, 593-600.	2.1	126
26	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. Nature Communications, 2015, 6, 6740.	12.8	124
27	The identification, cloning and mutagenesis of a genetic locus required for lipopolysaccharide biosynthesis in Bordetella pertussis. Molecular Microbiology, 1996, 19, 37-52.	2.5	121
28	Multiple Roles for Bordetella Lipopolysaccharide Molecules during Respiratory Tract Infection. Infection and Immunity, 2000, 68, 6720-6728.	2.2	113
29	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. Nature Communications, 2015, 6, 6560.	12.8	105
30	A dynamic view of the spread and intracellular distribution of Salmonella enterica. Nature Reviews Microbiology, 2009, 7, 73-80.	28.6	103
31	The Bordetellae: lessons from genomics. Nature Reviews Microbiology, 2004, 2, 379-390.	28.6	96
32	Bordetella bronchiseptica PagP is a Bvg-regulated lipid A palmitoyl transferase that is required for persistent colonization of the mouse respiratory tract. Molecular Microbiology, 2003, 48, 725-736.	2.5	95
33	Toward a Structural Understanding of the Dehydratase Mechanism. Structure, 2002, 10, 81-92.	3.3	94
34	Overexpression of antibiotic resistance genes in hospital effluents over time. Journal of Antimicrobial Chemotherapy, 2017, 72, 1617-1623.	3.0	92
35	Phase-Variable Surface Structures Are Required for Infection of Campylobacter jejuni by Bacteriophages. Applied and Environmental Microbiology, 2006, 72, 4638-4647.	3.1	88
36	Metabolite and transcriptome analysis of Campylobacter jejuni in vitro growth reveals a stationary-phase physiological switch. Microbiology (United Kingdom), 2009, 155, 80-94.	1.8	88

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37	Genomeâ€wide association of functional traits linked with <scp>C</scp>ampylobacter jejuni survival from farm to fork. Environmental Microbiology, 2017, 19, 361-380.	3.8	88
38	Stable expression of foreign antigens from the chromosome of Salmonella typhimurium vaccine strains. Gene, 1990, 88, 57-63.	2.2	85
39	Genomic and Genetic Analysis of Bordetella Bacteriophages Encoding Reverse Transcriptase-Mediated Tropism-Switching Cassettes. Journal of Bacteriology, 2004, 186, 1503-1517.	2.2	81
40	Resistance to the Antimicrobial Peptide Polymyxin Requires Myristoylation of Escherichia coli and Salmonella typhimurium Lipid A. Journal of Biological Chemistry, 2005, 280, 28186-28194.	3.4	80
41	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of Haemophilus parasuis. Journal of Clinical Microbiology, 2015, 53, 3812-3821.	3.9	80
42	SadA, a Trimeric Autotransporter from Salmonella enterica Serovar Typhimurium, Can Promote Biofilm Formation and Provides Limited Protection against Infection. Infection and Immunity, 2011, 79, 4342-4352.	2.2	79
43	Stimulation of Toll-Like Receptor 4 by Lipopolysaccharide During Cellular Invasion by Live Salmonella typhimurium Is a Critical But Not Exclusive Event Leading to Macrophage Responses. Journal of Immunology, 2003, 170, 5445-5454.	0.8	78
44	Comparison of the Genome Sequence of the Poultry Pathogen Bordetella avium with Those of B. bronchiseptica , B. pertussis , and B. parapertussis Reveals Extensive Diversity in Surface Structures Associated with Host Interaction. Journal of Bacteriology, 2006, 188, 6002-6015.	2.2	75
45	Comprehensive Identification of Salmonella enterica Serovar Typhimurium Genes Required for Infection of BALB/c Mice. PLoS Pathogens, 2009, 5, e1000529.	4.7	75
46	Structural studies of the saccharide part of the cell envelope lipopolysaccharide from Haemophilus influenzae strain AH1-3 (lic3 +). Carbohydrate Research, 1993, 246, 319-330.	2.3	74
47	Role in virulence and protective efficacy in pigs of Salmonella enterica serovar Typhimurium secreted components identified by signature-tagged mutagenesis. Microbiology (United Kingdom), 2007, 153, 1940-1952.	1.8	74
48	Genetic Basis for Lipopolysaccharide O-Antigen Biosynthesis in Bordetellae. Infection and Immunity, 1999, 67, 3763-3767.	2.2	74
49	Generation and Characterization of a Defined Mutant of Streptococcus suis Lacking Suilysin. Infection and Immunity, 2001, 69, 2732-2735.	2.2	72
50	Induction of Proinflammatory Responses in the Human Monocytic Cell Line THP-1 by Campylobacter jejuni. Infection and Immunity, 2003, 71, 2626-2633.	2.2	72
51	IFN-Î³ Enhances Production of Nitric Oxide from Macrophages via a Mechanism That Depends on Nucleotide Oligomerization Domain-2. Journal of Immunology, 2006, 176, 4804-4810.	0.8	72
52	Phylogenomic exploration of the relationships between strains of Mycobacterium avium subspecies paratuberculosis. BMC Genomics, 2016, 17, 79.	2.8	71
53	Dynamics of Salmonella infection of macrophages at the single cell level. Journal of the Royal Society Interface, 2012, 9, 2696-2707.	3.4	70
54	Intracellular Demography and the Dynamics of Salmonella enterica Infections. PLoS Biology, 2006, 4, e349.	5.6	68

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55	The initial suppression of bacterial growth in a salmonella infection is mediated by a localized rather than a systemic response. Microbial Pathogenesis, 1987, 2, 295-305.	2.9	67
56	Shortened Hydroxyacyl Chains on Lipid A of Escherichia coli Cells Expressing a Foreign UDP-N-Acetylglucosamine O-Acyltransferase. Journal of Biological Chemistry, 1997, 272, 19688-19696.	3.4	66
57	Genome-wide fitness analyses of the foodborne pathogen Campylobacter jejuni in in vitro and in vivo models. Scientific Reports, 2017, 7, 1251.	3.3	64
58	Proposal of serovars 17 and 18 of Actinobacillus pleuropneumoniae based on serological and genotypic analysis. Veterinary Microbiology, 2018, 217, 1-6.	1.9	64
59	An Oral Recombinant Vaccine in Dogs against Echinococcus granulosus, the Causative Agent of Human Hydatid Disease: A Pilot Study. PLoS Neglected Tropical Diseases, 2008, 2, e125.	3.0	62
60	Search Engine for Antimicrobial Resistance: A Cloud Compatible Pipeline and Web Interface for Rapidly Detecting Antimicrobial Resistance Genes Directly from Sequence Data. PLoS ONE, 2015, 10, e0133492.	2.5	62
61	Molecular and functional analysis of the lipopolysaccharide biosynthesis locuswlbfromBordetella pertussis,Bordetella parapertussisandBordetella bronchiseptica. Molecular Microbiology, 1998, 29, 27-38.	2.5	60
62	Role of Bordetella O Antigen in Respiratory Tract Infection. Infection and Immunity, 2003, 71, 86-94.	2.2	60
63	Signature-Tagged Transposon Mutagenesis Studies Demonstrate the Dynamic Nature of Cecal Colonization of 2-Week-Old Chickens by Campylobacter jejuni. Applied and Environmental Microbiology, 2005, 71, 8031-8041.	3.1	60
64	<scp>ChIP</scp>â€seq and transcriptome analysis of the <scp><scp>OmpR</scp></scp> regulon of <scp>S</scp>almonella enterica serovars <scp>T</scp>yphi and <scp>T</scp>yphimurium reveals accessory genes implicated in host colonization. Molecular Microbiology, 2013, 87, 526-538.	2.5	60
65	Evaluation ofSalmonella typhimuriumMutants in a Model of Experimental Gastroenteritis. Infection and Immunity, 1999, 67, 2815-2821.	2.2	58
66	Tollâ€like receptor 4 signalling through MyD88 is essential to control Salmonella enterica serovar Typhimurium infection, but not for the initiation of bacterial clearance. Immunology, 2009, 128, 472-483.	4.4	56
67	Mutation of the Maturase Lipoprotein Attenuates the Virulence of Streptococcus equi to a Greater Extent than Does Loss of General Lipoprotein Lipidation. Infection and Immunity, 2006, 74, 6907-6919.	2.2	55
68	pagP Is Required for Resistance to Antibody-Mediated Complement Lysis during Bordetella bronchiseptica Respiratory Infection. Infection and Immunity, 2004, 72, 2837-2842.	2.2	54
69	Attenuated Salmonella Typhimurium Lacking the Pathogenicity Island-2 Type 3 Secretion System Grow to High Bacterial Numbers inside Phagocytes in Mice. PLoS Pathogens, 2012, 8, e1003070.	4.7	54
70	Proteus mirabilis fimbriae (PMF) are important for both bladder and kidney colonization in mice. Microbiology (United Kingdom), 2003, 149, 3231-3237.	1.8	53
71	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
72	New Variant of Multidrug-Resistant Salmonella enterica Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. MBio, 2018, 9, .	4.1	53

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73	Isolation of stable aroA mutants of Salmonella typhi Ty2: Properties and preliminary characterisation in mice. Molecular Genetics and Genomics, 1987, 207, 402-405.	2.4	51
74	Single, double and triple mutants of Salmonella enterica serovar Typhimurium degP (htrA), degQ (hhoA) and degS (hhoB) have diverse phenotypes on exposure to elevated temperature and their growth in vivo is attenuated to different extents. Microbial Pathogenesis, 2006, 41, 174-182.	2.9	51
75	Toll-Like Receptor Expression in C3H/HeN and C3H/HeJ Mice duringSalmonella entericaSerovar Typhimurium Infection. Infection and Immunity, 2003, 71, 6653-6657.	2.2	50
76	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
77	Ciliostasis is a key early event during colonization of canine tracheal tissue by Bordetella bronchiseptica. Microbiology (United Kingdom), 2004, 150, 2843-2855.	1.8	47
78	PDZ Domains Facilitate Binding of High Temperature Requirement Protease A (HtrA) and Tail-specific Protease (Tsp) to Heterologous Substrates through Recognition of the Small Stable RNA A (ssrA)-encoded Peptide. Journal of Biological Chemistry, 2002, 277, 39443-39449.	3.4	46
79	Competing Isogenic Campylobacter Strains Exhibit Variable Population Structures In Vivo. Applied and Environmental Microbiology, 2008, 74, 3857-3867.	3.1	46
80	Comparative metagenomics reveals a diverse range of antimicrobial resistance genes in effluents entering a river catchment. Water Science and Technology, 2016, 73, 1541-1549.	2.5	46
81	Cloning and characterisation of the serC and aroA genes of Yersinia enterocolitica, and construction of an aroA mutant. Gene, 1989, 84, 23-30.	2.2	44
82	Quantitative RNA-seq analysis of the Campylobacter jejuni transcriptome. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.8	44
83	Campylobacter jejuni colonization and transmission in broiler chickens: a modelling perspective. Journal of the Royal Society Interface, 2007, 4, 819-829.	3.4	42
84	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2017, 8, 311.	3.5	42
85	The essential genome of Streptococcus agalactiae. BMC Genomics, 2016, 17, 406.	2.8	41
86	Unique Features and Distribution of the Chicken CD83+ Cell. Journal of Immunology, 2007, 179, 5117-5125.	0.8	40
87	Retrospective Application of Transposon-Directed Insertion Site Sequencing to a Library of Signature-Tagged Mini-Tn 5 Km2 Mutants of Escherichia coli O157:H7 Screened in Cattle. Journal of Bacteriology, 2011, 193, 1771-1776.	2.2	40
88	Differential Phenotypic Diversity among Epidemic-Spanning Salmonella enterica Serovar Enteritidis Isolates from Humans or Animals. Applied and Environmental Microbiology, 2010, 76, 6812-6820.	3.1	38
89	High-Resolution Structures of RmlC from Streptococcus suis in Complex with Substrate Analogs Locate the Active Site of This Class of Enzyme. Structure, 2003, 11, 715-723.	3.3	37
90	Proteus mirabilisuroepithelial cell adhesin (UCA) fimbria plays a role in the colonization of the urinary tract. Pathogens and Disease, 2013, 67, 104-107.	2.0	37

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91	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
92	Effects of Environmental and Management-Associated Factors on Prevalence and Diversity of Streptococcus suis in Clinically Healthy Pig Herds in China and the United Kingdom. Applied and Environmental Microbiology, 2018, 84, .	3.1	37
93	Phylogenetic analyses and antimicrobial resistance profiles of Campylobacter spp. from diarrhoeal patients and chickens in Botswana. PLoS ONE, 2018, 13, e0194481.	2.5	37
94	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
95	Unexpected Similarities between Bordetella avium and Other Pathogenic Bordetellae. Infection and Immunity, 2003, 71, 2591-2597.	2.2	34
96	New putative virulence factors of Streptococcus suis involved in invasion of porcine brain microvascular endothelial cells. Microbial Pathogenesis, 2009, 46, 13-20.	2.9	34
97	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
98	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in Actinobacillus pleuropneumoniae. Veterinary Microbiology, 2015, 178, 279-282.	1.9	34
99	Relaxed Acyl Chain Specificity of Bordetella UDP-N-acetylglucosamine Acyltransferases. Journal of Biological Chemistry, 2002, 277, 18281-18290.	3.4	33
100	Activation of murine dendritic cells and macrophages induced by Salmonella enterica serovar Typhimurium. Immunology, 2005, 115, 462-472.	4.4	33
101	Caspaseâ€3â€dependent phagocyte death during systemic Salmonella enterica serovar Typhimurium infection of mice. Immunology, 2008, 125, 28-37.	4.4	33
102	Bordetella pertussis waaAEncodes a Monofunctional 2-Keto-3-Deoxy-<scp>d</scp>-manno-Octulosonic Acid Transferase That Can Complement anEscherichia coli waaAMutation. Journal of Bacteriology, 1999, 181, 2648-2651.	2.2	33
103	Salmonella typhimurium aroBmutants are attentuated in BALB/cmice. Microbial Pathogenesis, 1997, 23, 311-316.	2.9	32
104	Oligosaccharide conjugates of Bordetella pertussis and bronchiseptica induce bactericidal antibodies, an addition to pertussis vaccine. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4087-4092.	7.1	32
105	Identification and Cloning of waaF (rfaF) from Bordetella pertussis and Use To Generate Mutants of Bordetella spp. with Deep Rough Lipopolysaccharide. Journal of Bacteriology, 1998, 180, 35-40.	2.2	32
106	The Effects of Vaccination and Immunity on Bacterial Infection Dynamics In Vivo. PLoS Pathogens, 2014, 10, e1004359.	4.7	31
107	Streptococcus suis contains multiple phase-variable methyltransferases that show a discrete lineage distribution. Nucleic Acids Research, 2018, 46, 11466-11476.	14.5	31
108	Defined mutants ofProteus mirabilislacking flagella cause ascending urinary tract infection in mice. Microbial Pathogenesis, 1996, 21, 395-405.	2.9	30

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109	Identification of dfrA14 in two distinct plasmids conferring trimethoprim resistance in Actinobacillus pleuropneumoniae. Journal of Antimicrobial Chemotherapy, 2015, 70, 2217-2222.	3.0	30
110	Genomic Comparison of the Closely Related Salmonella enterica Serovars Enteritidis and Dublin. Open Microbiology Journal, 2012, 6, 5-13.	0.7	30
111	An ex vivo swine tracheal organ culture for the study of influenza infection. Influenza and Other Respiratory Viruses, 2010, 4, 7-15.	3.4	29
112	Identification of Cj1051c as a Major Determinant for the Restriction Barrier of Campylobacter jejuni Strain NCTC11168. Applied and Environmental Microbiology, 2012, 78, 7841-7848.	3.1	29
113	Motility defects in Campylobacter jejuni defined gene deletion mutants caused by second-site mutations. Microbiology (United Kingdom), 2015, 161, 2316-2327.	1.8	29
114	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
115	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
116	Identification and characterisation of hyaluronate lyase from Streptococcus suis. Microbial Pathogenesis, 2004, 36, 327-335.	2.9	28
117	Enhanced Virulence of Salmonella enterica Serovar Typhimurium after Passage through Mice. Infection and Immunity, 2011, 79, 636-643.	2.2	28
118	O-antigen repeat number inSalmonella entericaserovar Enteritidis is important for egg contamination, colonisation of the chicken reproductive tract and survival in egg albumen. FEMS Microbiology Letters, 2013, 343, 169-176.	1.8	28
119	Sublethal Infection of C57BL/6 Mice with Salmonella enterica Serovar Typhimurium Leads to an Increase in Levels of Toll-Like Receptor 1 (TLR1), TLR2, and TLR9 mRNA as Well as a Decrease in Levels of TLR6 mRNA in Infected Organs. Infection and Immunity, 2005, 73, 1873-1878.	2.2	27
120	Transposon mutagenesis in a hyper-invasive clinical isolate of Campylobacter jejuni reveals a number of genes with potential roles in invasion. Microbiology (United Kingdom), 2010, 156, 1134-1143.	1.8	27
121	Whole genome investigation of a divergent clade of the pathogen Streptococcus suis. Frontiers in Microbiology, 2015, 6, 1191.	3.5	27
122	DNA Analysis of Pneumocystis Infecting a Cavalier King Charles Spaniel. Journal of Eukaryotic Microbiology, 2001, 48, 106s-106s.	1.7	26
123	Latest developments on Streptococcus suis: an emerging zoonotic pathogen: part 2. Future Microbiology, 2014, 9, 587-591.	2.0	26
124	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of Actinobacillus pleuropneumoniae. Genome Announcements, 2016, 4, .	0.8	26
125	Early responses to Salmonella typhimurium infection in mice occur at focal lesions in infected organs. Microbial Pathogenesis, 2001, 30, 29-38.	2.9	25
126	Genomic variations leading to alterations in cell morphology of Campylobacter spp. Scientific Reports, 2016, 6, 38303.	3.3	25

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127	Defining the ABC of gene essentiality in streptococci. BMC Genomics, 2017, 18, 426.	2.8	25
128	Transmission and doseâ€“response experiments for social animals: a reappraisal of the colonization biology of Campylobacter jejuni in chickens. Journal of the Royal Society Interface, 2011, 8, 1720-1735.	3.4	24
129	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
130	Distribution, Genetic Diversity, and Variable Expression of the Gene Encoding Hyaluronate Lyase within the Streptococcus suis Population. Journal of Bacteriology, 2004, 186, 4740-4747.	2.2	22
131	Nasal immunization with attenuated Salmonella Typhimurium expressing an MrpAâ€“TetC fusion protein significantly reduces Proteus mirabilis colonization in the mouse urinary tract. Journal of Medical Microbiology, 2011, 60, 899-904.	1.8	22
132	Predicting Protein Function from Structureâ€”The Roles of Short-chain Dehydrogenase/Reductase Enzymes in Bordetella O-antigen Biosynthesis. Journal of Molecular Biology, 2007, 374, 749-763.	4.2	21
133	Analysis of Campylobacter jejuni infection in the gnotobiotic piglet and genome-wide identification of bacterial factors required for infection. Scientific Reports, 2017, 7, 44283.	3.3	21
134	Modifying bacterial flagellin to evade Nod-like Receptor CARD 4 recognition enhances protective immunity against Salmonella. Nature Microbiology, 2020, 5, 1588-1597.	13.3	21
135	Mutation of waaN Reduces Salmonella enterica Serovar Typhimurium-Induced Enteritis and Net Secretion of Type III Secretion System 1-Dependent Proteins. Infection and Immunity, 2000, 68, 3768-3771.	2.2	20
136	Bordetella pertussis risA, but Not risS, Is Required for Maximal Expression of Bvg-Repressed Genes. Infection and Immunity, 2005, 73, 5995-6004.	2.2	20
137	ICEApl1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2016, 7, 810.	3.5	20
138	Genes Required for the Fitness of Salmonella enterica Serovar Typhimurium during Infection of Immunodeficient gp91 ^{â^'/â^'} phox Mice. Infection and Immunity, 2016, 84, 989-997.	2.2	20
139	Salmonella-induced SipB-independent cell death requires Toll-like receptor-4 signalling via the adapter proteins Tram and Trif. Immunology, 2007, 122, 222-229.	4.4	19
140	Naturally Occurring Motility-Defective Mutants of Salmonella enterica Serovar Enteritidis Isolated Preferentially from Nonhuman Rather than Human Sources. Applied and Environmental Microbiology, 2011, 77, 7740-7748.	3.1	19
141	Multiple redundant stress resistance mechanisms are induced in Salmonella enterica serovar Typhimurium in response to alteration of the intracellular environment via TLR4 signalling. Microbiology (United Kingdom), 2009, 155, 2919-2929.	1.8	18
142	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
143	Deletion of the gene encoding the glycolytic enzyme triosephosphate isomerase (tpi) alters morphology ofSalmonella entericaserovar Typhimurium and decreases fitness in mice. FEMS Microbiology Letters, 2009, 294, 45-51.	1.8	17
144	Salmonella enterica Serovar Typhimurium Expressing Mutant Lipid A with Decreased Endotoxicity Causes Maturation of Murine Dendritic Cells. Infection and Immunity, 2003, 71, 6132-6140.	2.2	16

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145	Bacterial Growth Rate and Host Factors as Determinants of Intracellular Bacterial Distributions in SystemicSalmonella entericaInfections. Infection and Immunity, 2009, 77, 5608-5611.	2.2	16
146	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
147	Mutational analysis of the Bordetella pertussis wlb LPS biosynthesis locus. Microbial Pathogenesis, 2002, 33, 91-95.	2.9	15
148	Virulent Salmonella enterica infections can be exacerbated by concomitant infection of the host with a live attenuated S.â€ƒenterica vaccine via Tollâ€like receptor 4â€dependent interleukinâ€10 production with the involvement of both TRIF and MyD88. Immunology, 2008, 124, 469-479.	4.4	15
149	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
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