Duncan J Maskell

List of Publications by Year
in descending order

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	HAM-ART: An optimised culture-free Hi-C metagenomics pipeline for tracking antimicrobial resistance genes in complex microbial communities. PLoS Genetics, 2022, 18, e1009776.	3.5	14
2	Mobility of antimicrobial resistance across serovars and disease presentations in non-typhoidal Salmonella from animals and humans in Vietnam. Microbial Genomics, 2022, 8, .	2.0	2
3	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
4	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
5	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
6	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
7	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
8	Generation and Evaluation of a Glaesserella (Haemophilus) parasuis Capsular Mutant. Infection and Immunity, 2020, 88, .	2.2	7
9	Identification of genes required for the fitness of Streptococcus equi subsp. equi in whole equine blood and hydrogen peroxide. Microbial Genomics, 2020, 6, .	2.0	3
10	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
11	Proposal of serovars 17 and 18 of Actinobacillus pleuropneumoniae based on serological and genotypic analysis. Veterinary Microbiology, 2018, 217, 1-6.	1.9	64
12	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
13	Streptococcus suis contains multiple phase-variable methyltransferases that show a discrete lineage distribution. Nucleic Acids Research, 2018, 46, 11466-11476.	14.5	31
14	New Variant of Multidrug-Resistant Salmonella enterica Serovar Typhimurium Associated with Invasive Disease in Immunocompromised Patients in Vietnam. MBio, 2018, 9, .	4.1	53
15	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
16	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
17	Phylogenetic analyses and antimicrobial resistance profiles of Campylobacter spp. from diarrhoeal patients and chickens in Botswana. PLoS ONE, 2018, 13, e0194481.	2.5	37
18	Identification and initial characterisation of a protein involved in Campylobacter jejuni cell shape. Microbial Pathogenesis, 2017, 104, 202-211.	2.9	12

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19	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
20	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
21	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
22	Overexpression of antibiotic resistance genes in hospital effluents over time. Journal of Antimicrobial Chemotherapy, 2017, 72, 1617-1623.	3.0	92
23	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
24	Defining the ABC of gene essentiality in streptococci. BMC Genomics, 2017, 18, 426.	2.8	25
25	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
26	A quantitative proteomic screen of the Campylobacter jejuni flagellar-dependent secretome. Journal of Proteomics, 2017, 152, 181-187.	2.4	10
27	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
28	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2017, 8, 311.	3.5	42
29	Investigation of the Fim1 putative pilus locus of Streptococcus equi subspecies equi. Microbiology (United Kingdom), 2017, 163, 1217-1228.	1.8	6
30	Transcriptome and proteome analysis of Salmonella enterica serovar Typhimurium systemic infection of wild type and immune-deficient mice. PLoS ONE, 2017, 12, e0181365.	2.5	6
31	ICEApl1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen Actinobacillus pleuropneumoniae. Frontiers in Microbiology, 2016, 7, 810.	3.5	20
32	Genomic variations leading to alterations in cell morphology of Campylobacter spp. Scientific Reports, 2016, 6, 38303.	3.3	25
33	The essential genome of Streptococcus agalactiae. BMC Genomics, 2016, 17, 406.	2.8	41
34	Phylogenomic exploration of the relationships between strains of Mycobacterium avium subspecies paratuberculosis. BMC Genomics, 2016, 17, 79.	2.8	71
35	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
36	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

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37	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of Actinobacillus pleuropneumoniae. Genome Announcements, 2016, 4, .	0.8	26
38	Single passage in mouse organs enhances the survival and spread of Salmonella enterica. Journal of the Royal Society Interface, 2015, 12, 20150702.	3.4	11
39	Metatranscriptomics reveals metabolic adaptation and induction of virulence factors by Haemophilus parasuis during lung infection. Veterinary Research, 2015, 46, 102.	3.0	13
40	Whole genome investigation of a divergent clade of the pathogen Streptococcus suis. Frontiers in Microbiology, 2015, 6, 1191.	3.5	27
41	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
42	Motility defects in Campylobacter jejuni defined gene deletion mutants caused by second-site mutations. Microbiology (United Kingdom), 2015, 161, 2316-2327.	1.8	29
43	Campylobacter jejuni PflB is required for motility and colonisation of the chicken gastrointestinal tract. Microbial Pathogenesis, 2015, 89, 93-99.	2.9	6
44	Vaccination with a live multi-gene deletion strain protects horses against virulent challenge with Streptococcus equi. Vaccine, 2015, 33, 1160-1167.	3.8	12
45	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
46	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in Actinobacillus pleuropneumoniae. Veterinary Microbiology, 2015, 178, 279-282.	1.9	34
47	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. Nature Communications, 2015, 6, 6740.	12.8	124
48	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of Haemophilus parasuis. Journal of Clinical Microbiology, 2015, 53, 3812-3821.	3.9	80
49	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. Nature Communications, 2015, 6, 6560.	12.8	105
50	Identification of dfrA14 in two distinct plasmids conferring trimethoprim resistance in Actinobacillus pleuropneumoniae. Journal of Antimicrobial Chemotherapy, 2015, 70, 2217-2222.	3.0	30
51	PinR mediates the generation of reversible population diversity in Streptococcus zooepidemicus. Microbiology (United Kingdom), 2015, 161, 1105-1112.	1.8	2
52	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
53	Latest developments on Streptococcus suis: an emerging zoonotic pathogen: part 2. Future Microbiology, 2014, 9, 587-591.	2.0	26
54	The Effects of Vaccination and Immunity on Bacterial Infection Dynamics In Vivo. PLoS Pathogens, 2014, 10, e1004359.	4.7	31

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55	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
56	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
57	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
58	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
59	<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
60	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
61	Comprehensive Assignment of Roles for Salmonella Typhimurium Genes in Intestinal Colonization of Food-Producing Animals. PLoS Genetics, 2013, 9, e1003456.	3.5	176
62	Don't forget the science. Veterinary Record, 2013, 172, 293-294.	0.3	1
63	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
64	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
65	Dynamics of Salmonella infection of macrophages at the single cell level. Journal of the Royal Society Interface, 2012, 9, 2696-2707.	3.4	70
66	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
67	Investigation into the role of fiveSalmonella entericaserovar Enteritidis genomic islands in colonization of the chicken reproductive tract and other organs following oral challenge. FEMS Microbiology Letters, 2012, 336, 73-78.	1.8	8
68	Genomic Comparison of the Closely Related Salmonella enterica Serovars Enteritidis and Dublin. Open Microbiology Journal, 2012, 6, 5-13.	0.7	30
69	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
70	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
71	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
72	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

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73	Enhanced Virulence of Salmonella enterica Serovar Typhimurium after Passage through Mice. Infection and Immunity, 2011, 79, 636-643.	2.2	28
74	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
75	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
76	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
77	Salmonella bongori Provides Insights into the Evolution of the Salmonellae. PLoS Pathogens, 2011, 7, e1002191.	4.7	171
78	Quantitative RNA-seq analysis of the Campylobacter jejuni transcriptome. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	1.8	44
79	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
80	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
81	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
82	Recent advances in the field ofSalmonella Typhivaccines. Hum Vaccin, 2010, 6, 379-384.	2.4	14
83	Simultaneous assay of every Salmonella Typhi gene using one million transposon mutants. Genome Research, 2009, 19, 2308-2316.	5.5	544
84	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
85	Post-assembly Modification of Bordetella bronchiseptica O Polysaccharide by a Novel Periplasmic Enzyme Encoded by wbmE. Journal of Biological Chemistry, 2009, 284, 1474-1483.	3.4	8
86	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
87	Comprehensive Identification of Salmonella enterica Serovar Typhimurium Genes Required for Infection of BALB/c Mice. PLoS Pathogens, 2009, 5, e1000529.	4.7	75
88	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
89	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
90	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

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91	A dynamic view of the spread and intracellular distribution of Salmonella enterica. Nature Reviews Microbiology, 2009, 7, 73-80.	28.6	103
92	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
93	A Strand-Specific RNAâ€"Seq Analysis of the Transcriptome of the Typhoid Bacillus Salmonella Typhi. PLoS Genetics, 2009, 5, e1000569.	3.5	202
94	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
95	Chemical synthesis of UDP-Glc-2,3-diNAcA, a key intermediate in cell surface polysaccharide biosynthesis in the human respiratory pathogens B. pertussis and P. aeruginosa. Organic and Biomolecular Chemistry, 2009, 7, 1203.	2.8	14
96	Rapid Evolution of Virulence and Drug Resistance in the Emerging Zoonotic Pathogen Streptococcus suis. PLoS ONE, 2009, 4, e6072.	2.5	214
97	High-throughput sequencing provides insights into genome variation and evolution in Salmonella Typhi. Nature Genetics, 2008, 40, 987-993.	21.4	453
98	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
99	Caspaseâ€3â€dependent phagocyte death during systemic Salmonella enterica serovar Typhimurium infection of mice. Immunology, 2008, 125, 28-37.	4.4	33
100	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
101	Competing Isogenic Campylobacter Strains Exhibit Variable Population Structures In Vivo. Applied and Environmental Microbiology, 2008, 74, 3857-3867.	3.1	46
102	Elucidation of the MD-2/TLR4 Interface Required for Signaling by Lipid IVa. Journal of Immunology, 2008, 181, 1245-1254.	0.8	134
103	Modelling within-Host Spatiotemporal Dynamics of Invasive Bacterial Disease. PLoS Biology, 2008, 6, e74.	5.6	189
104	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
105	Unique Features and Distribution of the Chicken CD83+ Cell. Journal of Immunology, 2007, 179, 5117-5125.	0.8	40
106	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
107	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
108	Campylobacter jejuni colonization and transmission in broiler chickens: a modelling perspective. Journal of the Royal Society Interface, 2007, 4, 819-829.	3.4	42

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109	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
110	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
111	Development of anex vivoorgan culture model using human gastro-intestinal tissue andCampylobacter jejuni. FEMS Microbiology Letters, 2006, 263, 240-243.	1.8	10
112	Differential modulatory effects of Annexin 1 on nitric oxide synthase induction by lipopolysaccharide in macrophages. Immunology, 2006, 117, 340-349.	4.4	12
113	Intracellular Demography and the Dynamics of Salmonella enterica Infections. PLoS Biology, 2006, 4, e349.	5.6	68
114	Practitioners' views. Veterinary Record, 2006, 159, 500-500.	0.3	0
115	Phase-Variable Surface Structures Are Required for Infection of Campylobacter jejuni by Bacteriophages. Applied and Environmental Microbiology, 2006, 72, 4638-4647.	3.1	88
116	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
117	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
118	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
119	Activation of murine dendritic cells and macrophages induced by Salmonella enterica serovar Typhimurium. Immunology, 2005, 115, 462-472.	4.4	33
120	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
121	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
122	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
123	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
124	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
125	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
126	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

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127	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
128	Adaptation of Campylobacter jejuni NCTC11168 to High-Level Colonization of the Avian Gastrointestinal Tract. Infection and Immunity, 2004, 72, 3769-3776.	2.2	162
129	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
130	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
131	Genomic and Genetic Analysis of Bordetella Bacteriophages Encoding Reverse Transcriptase-Mediated Tropism-Switching Cassettes. Journal of Bacteriology, 2004, 186, 1503-1517.	2.2	81
132	Identification of host-specific colonization factors of Salmonella enterica serovar Typhimurium. Molecular Microbiology, 2004, 54, 994-1010.	2.5	244
133	Development of an in vivoHimar1transposon mutagenesis system for use inStreptococcus equisubsp.equi. FEMS Microbiology Letters, 2004, 238, 401-409.	1.8	10
134	The Bordetellae: lessons from genomics. Nature Reviews Microbiology, 2004, 2, 379-390.	28.6	96
135	Development of an in vivo transposon mutagenesis system for use in subsp.. FEMS Microbiology Letters, 2004, 238, 401-409.	1.8	12
136	Identification and characterisation of hyaluronate lyase from Streptococcus suis. Microbial Pathogenesis, 2004, 36, 327-335.	2.9	28
137	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
138	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
139	Dynamics of bacterial growth and distribution within the liver duringSalmonellainfection. Cellular Microbiology, 2003, 5, 593-600.	2.1	126
140	Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica. Nature Genetics, 2003, 35, 32-40.	21.4	898
141	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
142	Proteus mirabilis fimbriae (PMF) are important for both bladder and kidney colonization in mice. Microbiology (United Kingdom), 2003, 149, 3231-3237.	1.8	53
143	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
144	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

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145	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
146	Role of Bordetella O Antigen in Respiratory Tract Infection. Infection and Immunity, 2003, 71, 86-94.	2.2	60
147	Unexpected Similarities between Bordetella avium and Other Pathogenic Bordetellae. Infection and Immunity, 2003, 71, 2591-2597.	2.2	34
148	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
149	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
150	Relaxed Acyl Chain Specificity of Bordetella UDP-N-acetylglucosamine Acyltransferases. Journal of Biological Chemistry, 2002, 277, 18281-18290.	3.4	33
151	Mutational analysis of the Bordetella pertussis wlb LPS biosynthesis locus. Microbial Pathogenesis, 2002, 33, 91-95.	2.9	15
152	Molecular genetics and role in infection of environmentally regulated lipopolysaccharide expression. International Journal of Medical Microbiology, 2002, 292, 7-15.	3.6	8
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