Steven P Djordjevic

List of Publications by Year in descending order

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219 papers

8,127 citations

50 h-index 72 g-index

226 all docs

226 docs citations

times ranked

226

6559 citing authors

#	Article	IF	CITATIONS
1	Simultaneous Glycan-Peptide Characterization Using Hydrophilic Interaction Chromatography and Parallel Fragmentation by CID, Higher Energy Collisional Dissociation, and Electron Transfer Dissociation MS Applied to the N-Linked Glycoproteome of Campylobacter jejuni. Molecular and Cellular Proteomics, 2011, 10, S1-S18.	3.8	265
	Detection of Shiga-Like Toxin (<i> stx ₁ </i> and <i> stx ₂ </i>), Intimin () Tj ETQq0 0	_	
2	Genes in Animal Feces by Multiplex PCR. Applied and Environmental Microbiology, 1999, 65, 868-872.	3.1	217
3	Nitrogen fixation ability of exopolysaccharide synthesis mutants of Rhizobium sp. strain NGR234 and Rhizobium trifolii is restored by the addition of homologous exopolysaccharides. Journal of Bacteriology, 1987, 169, 53-60.	2.2	173
4	The Genomic Island SGI1, Containing the Multiple Antibiotic Resistance Region of Salmonella enterica Serovar Typhimurium DT104 or Variants of It, Is Widely Distributed in Other S. enterica Serovars. Journal of Bacteriology, 2005, 187, 4401-4409.	2.2	161
5	Monitoring antibiotic resistance genes in wastewater treatment: Current strategies and future challenges. Science of the Total Environment, 2021, 783, 146964.	8.0	136
6	Distribution of Intimin Subtypes among Escherichia coli Isolates from Ruminant and Human Sources. Journal of Clinical Microbiology, 2003, 41, 5022-5032.	3.9	131
7	Mycoplasma leachii sp. nov. as a new species designation for Mycoplasma sp. bovine group 7 of Leach, and reclassification of Mycoplasma mycoides subsp. mycoides LC as a serovar of Mycoplasma mycoides subsp. capri. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 1353-1358.	1.7	121
8	The Diverse Functional Roles of Elongation Factor Tu (EF-Tu) in Microbial Pathogenesis. Frontiers in Microbiology, 2019, 10, 2351.	3.5	118
9	Identification and detection of Actinobacillus pleuropneumoniae by PCR based on the gene apxIVA. Veterinary Microbiology, 2001, 79, 47-62.	1.9	114
10	Distribution of Class 1 Integrons with IS26-Mediated Deletions in Their 3′-Conserved Segments in Escherichia coli of Human and Animal Origin. PLoS ONE, 2010, 5, e12754.	2.5	108
11	Mobile elements, zoonotic pathogens and commensal bacteria: conduits for the delivery of resistance genes into humans, production animals and soil microbiota. Frontiers in Microbiology, 2013, 4, 86.	3.5	103
12	Transposons Related to Tn <i>1696</i> in IncHI2 Plasmids in Multiply Antibiotic Resistant <i>Salmonella enterica</i> Serovar Typhimurium from Australian Animals. Microbial Drug Resistance, 2010, 16, 197-202.	2.0	102
13	Proteolytic Processing of the Mycoplasma hyopneumoniae Cilium Adhesin. Infection and Immunity, 2004, 72, 2791-2802.	2.2	101
14	Surface Analyses and Immune Reactivities of Major Cell Wall-Associated Proteins of Group A Streptococcus. Infection and Immunity, 2005, 73, 3137-3146.	2.2	99
15	stx 1c Is the Most Common Shiga Toxin 1 Subtype among Shiga Toxin-Producing Escherichia coli Isolates from Sheep but Not among Isolates from Cattle. Journal of Clinical Microbiology, 2003, 41, 926-936.	3.9	96
16	P159 is a proteolytically processed, surface adhesin of Mycoplasma hyopneumoniae: defined domains of P159 bind heparin and promote adherence to eukaryote cells. Molecular Microbiology, 2006, 60, 669-686.	2.5	89
17	Porcine commensal Escherichia coli: a reservoir for class 1 integrons associated with IS26. Microbial Genomics, 2017, 3, .	2.0	89
18	Identification of membraneâ€associated proteins from <i>Campylobacter jejuni</i> strains using complementary proteomics technologies. Proteomics, 2008, 8, 122-139.	2.2	87

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19	Multiple antibiotic resistance gene recruitment onto the enterohemorrhagic <i>Escherichia coli</i> virulence plasmid. FASEB Journal, 2010, 24, 1160-1166.	0.5	85
20	RSF1010-Like Plasmids in AustralianSalmonella entericaSerovar Typhimurium and Origin of Theirsul2-strA-strBAntibiotic Resistance Gene Cluster. Microbial Drug Resistance, 2010, 16, 249-252.	2.0	83
21	Elongation factor Tu is a multifunctional and processed moonlighting protein. Scientific Reports, 2017, 7, 11227.	3.3	82
22	Serum and mucosal antibody responses and protection in pigs vaccinated against Mycoplasma hyopneumoniae with vaccines containing a denatured membrane antigen pool and adjuvant. Australian Veterinary Journal, 1997, 75, 504-511.	1.1	81
23	Defined chromosome structure in the genome-reduced bacterium Mycoplasma pneumoniae. Nature Communications, 2017, 8, 14665.	12.8	81
24	Virulence Properties and Serotypes of Shiga Toxin-Producing Escherichia coli from Healthy Australian Slaughter-Age Sheep. Journal of Clinical Microbiology, 2001, 39, 2017-2021.	3.9	80
25	Sequences of Two Related Multiple Antibiotic Resistance Virulence Plasmids Sharing a Unique IS26-Related Molecular Signature Isolated from Different Escherichia coli Pathotypes from Different Hosts. PLoS ONE, 2013, 8, e78862.	2.5	80
26	A Processed Multidomain Mycoplasma hyopneumoniae Adhesin Binds Fibronectin, Plasminogen, and Swine Respiratory Cilia. Journal of Biological Chemistry, 2010, 285, 33971-33978.	3.4	77
27	Mhp182 (P102) binds fibronectin and contributes to the recruitment of plasmin(ogen) to the Mycoplasma hyopneumoniae cell surface. Cellular Microbiology, 2012, 14, 81-94.	2.1	76
28	Repeat regions R1 and R2 in the P97 paralogue Mhp271 of <i>Mycoplasma hyopneumoniae</i> bind heparin, fibronectin and porcine cilia. Molecular Microbiology, 2010, 78, 444-458.	2.5	74
29	SGI1-K, a Variant of the SGI1 Genomic Island Carrying a Mercury Resistance Region, in Salmonella enterica Serovar Kentucky. Antimicrobial Agents and Chemotherapy, 2007, 51, 317-323.	3.2	69
30	The Common Ovine Shiga Toxin 2-Containing Escherichia coli Serotypes and Human Isolates of the Same Serotypes Possess a Stx2d Toxin Type. Journal of Clinical Microbiology, 2001, 39, 1932-1937.	3.9	68
31	SGI2, a Relative of <i>Salmonella </i> Genomic Island SGI1 with an Independent Origin. Antimicrobial Agents and Chemotherapy, 2008, 52, 2529-2537.	3.2	68
32	Virulence Properties and Serotypes of Shiga Toxin-Producing Escherichia coli from Healthy Australian Cattle. Applied and Environmental Microbiology, 2002, 68, 6439-6445.	3.1	65
33	Bovine Non-O157 Shiga Toxin 2-Containing Escherichia coli Isolates Commonly Possess stx 2-EDL933 and/or stx 2vhb Subtypes. Journal of Clinical Microbiology, 2003, 41, 2716-2722.	3.9	63
34	Modification of the Campylobacter jejuni N-Linked Glycan by EptC Protein-mediated Addition of Phosphoethanolamine. Journal of Biological Chemistry, 2012, 287, 29384-29396.	3.4	63
35	Environmental dimensions of antibiotic resistance: assessment of basic science gaps. FEMS Microbiology Ecology, 2018, 94, .	2.7	63
36	Mhp493 (P216) is a proteolytically processed, cilium and heparin binding protein of <i>Mycoplasma hyopneumoniae</i> . Molecular Microbiology, 2009, 71, 566-582.	2.5	62

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37	Genomic analysis of multidrug-resistant Escherichia coli ST58 causing urosepsis. International Journal of Antimicrobial Agents, 2018, 52, 430-435.	2.5	62
38	Bovine Feces from Animals with Gastrointestinal Infections Are a Source of Serologically Diverse Atypical Enteropathogenic Escherichia coli and Shiga Toxin-Producing E. coli Strains That Commonly Possess Intimin. Applied and Environmental Microbiology, 2005, 71, 3405-3412.	3.1	61
39	Tn6026 and Tn6029 are found in complex resistance regions mobilised by diverse plasmids and chromosomal islands in multiple antibiotic resistant Enterobacteriaceae. Plasmid, 2015, 80, 127-137.	1.4	61
40	Low-Level Fluoroquinolone Resistance among Campylobacter jejuni Isolates in Australia. Clinical Infectious Diseases, 2006, 42, 1368-1374.	5.8	60
41	MHJ_0461 is a multifunctional leucine aminopeptidase on the surface of <i>Mycoplasma hyopneumoniae</i> . Open Biology, 2015, 5, 140175.	3.6	59
42	MHJ_0125 is an M42 glutamyl aminopeptidase that moonlights as a multifunctional adhesin on the surface of <i>Mycoplasma hyopneumoniae</i>). Open Biology, 2013, 3, 130017.	3.6	58
43	Two Domains within the Mycoplasma hyopneumoniae Cilium Adhesin Bind Heparin. Infection and Immunity, 2006, 74, 481-487.	2.2	56
44	The structure of the exopolysaccharide from Rhizobium sp. strain ANU280 (NGR234). Carbohydrate Research, 1986, 148, 87-99.	2.3	55
45	Reiterated repeat region variability in the ciliary adhesin gene of Mycoplasma hyopneumoniae. Microbiology (United Kingdom), 1998, 144, 1931-1943.	1.8	55
46	Identification of Lipoprotein MsIA as a Neoteric Virulence Factor of <i>Mycoplasma gallisepticum</i> Infection and Immunity, 2010, 78, 3475-3483.	2.2	54
47	Characterization of Cleavage Events in the Multifunctional Cilium Adhesin Mhp684 (P146) Reveals a Mechanism by Which Mycoplasma hyopneumoniae Regulates Surface Topography. MBio, 2012, 3, .	4.1	54
48	The quest for improved reproducibility in MALDI mass spectrometry. Mass Spectrometry Reviews, 2018, 37, 217-228.	5.4	54
49	Genomic Microbial Epidemiology Is Needed to Comprehend the Global Problem of Antibiotic Resistance and to Improve Pathogen Diagnosis. Frontiers in Microbiology, 2016, 7, 843.	3.5	53
50	Post-translational processing targets functionally diverse proteins in <i>Mycoplasma hyopneumoniae</i> . Open Biology, 2016, 6, 150210.	3.6	53
51	<i>Mycoplasma hyopneumoniae</i> Surface Proteins Mhp385 and Mhp384 Bind Host Cilia and Glycosaminoglycans and Are Endoproteolytically Processed by Proteases That Recognize Different Cleavage Motifs. Journal of Proteome Research, 2012, 11, 1924-1936.	3.7	52
52	Whole genome sequence analysis of Australian avian pathogenic Escherichia coli that carry the class 1 integrase gene. Microbial Genomics, 2019, 5, .	2.0	51
53	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. Journal of Molecular Medicine, 2012, 90, 1197-1207.	3.9	49
54	P159 from <i>Mycoplasma hyopneumoniae</i> Binds Porcine Cilia and Heparin and Is Cleaved in a Manner Akin to Ectodomain Shedding. Journal of Proteome Research, 2013, 12, 5891-5903.	3.7	49

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55	Comparative Proteomics and Glycoproteomics Reveal Increased N-Linked Glycosylation and Relaxed Sequon Specificity in Campylobacter jejuni NCTC11168 O. Journal of Proteome Research, 2014, 13, 5136-5150.	3.7	48
56	Serotypes and Virulence Gene Profiles of Shiga Toxin-Producing Escherichia coli Strains Isolated from Feces of Pasture-Fed and Lot-Fed Sheep. Applied and Environmental Microbiology, 2004, 70, 3910-3917.	3.1	47
57	Sequence TTKF↓QE Defines the Site of Proteolytic Cleavage in Mhp683 Protein, a Novel Glycosaminoglycan and Cilium Adhesin of Mycoplasma hyopneumoniae. Journal of Biological Chemistry, 2011, 286, 41217-41229.	3.4	47
58	Evaluation of clinical, histological and immunological changes and qPCR detection of Mycoplasma hyopneumoniae in tissues during the early stages of mycoplasmal pneumonia in pigs after experimental challenge with two field isolates. Veterinary Microbiology, 2012, 161, 186-195.	1.9	47
59	Genomic islands 1 and 2 play key roles in the evolution of extensively drug-resistant ST235 isolates of <i>Pseudomonas aeruginosa</i> . Open Biology, 2016, 6, 150175.	3.6	47
60	Rapid identification of some Leptospira isolates from cattle by random amplified polymorphic DNA fingerprinting. Journal of Clinical Microbiology, 1993, 31, 2927-2932.	3.9	47
61	Mhp107 Is a Member of the Multifunctional Adhesin Family of Mycoplasma hyopneumoniae. Journal of Biological Chemistry, 2011, 286, 10097-10104.	3.4	46
62	Exploitation of plasmin(ogen) by bacterial pathogens of veterinary significance. Veterinary Microbiology, 2015, 178, 1-13.	1.9	46
63	Proteome analysis of multidrugâ€resistant, breast cancer–derived microparticles. Journal of Extracellular Vesicles, 2014, 3, .	12.2	45
64	The Role of CD44 and ERM Proteins in Expression and Functionality of P-glycoprotein in Breast Cancer Cells. Molecules, 2016, 21, 290.	3.8	45
65	Diversity of P1 phage-like elements in multidrug resistant Escherichia coli. Scientific Reports, 2019, 9, 18861.	3.3	43
66	A Role for Tn6029 in the Evolution of the Complex Antibiotic Resistance Gene Loci in Genomic Island 3 in Enteroaggregative Hemorrhagic Escherichia coli O104:H4. PLoS ONE, 2015, 10, e0115781.	2.5	43
67	Development of a hemi-nested PCR assay for the specific detection of <i>Melissococcus pluton </i> Journal of Apicultural Research, 1998, 37, 165-174.	1.5	42
68	Role of group A <i>Streptococcus</i> HtrA in the maturation of SpeB protease. Proteomics, 2007, 7, 4488-4498.	2.2	42
69	Multilocus sequence typing of Campylobacter jejuni isolates from New South Wales, Australia. Journal of Applied Microbiology, 2007, 102, 144-152.	3.1	42
70	Mass Spectrometric Characterization of the Surface-Associated 42 kDa Lipoprotein JlpA as a Glycosylated Antigen in Strains of <i>Campylobacter jejuni</i> Journal of Proteome Research, 2009, 8, 4654-4664.	3.7	41
71	Multidrug Resistant Uropathogenic Escherichia coli ST405 With a Novel, Composite IS26 Transposon in a Unique Chromosomal Location. Frontiers in Microbiology, 2018, 9, 3212.	3.5	41
72	A role for ColV plasmids in the evolution of pathogenic Escherichia coli ST58. Nature Communications, 2022, 13, 683.	12.8	40

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73	Identification of novel species-specific antigens of Mycoplasma hyopneumoniae by preparative SDS-PAGE ELISA profiling. Microbiology (United Kingdom), 1997, 143, 663-673.	1.8	39
74	Mastitis, polyarthritis and abortion caused by Mycoplasma species bovine group 7 in dairy cattle. Australian Veterinary Journal, 2000, 78, 744-750.	1.1	39
75	Clonal Complexes of Campylobacter jejuni Identified by Multilocus Sequence Typing Are Reliably Predicted by Restriction Fragment Length Polymorphism Analyses of the flaA Gene. Journal of Clinical Microbiology, 2007, 45, 102-108.	3.9	39
76	SpeciatingCampylobacter jejuniandCampylobacter coliisolates from poultry and humans using six PCR-based assays. FEMS Microbiology Letters, 2002, 216, 201-209.	1.8	38
77	Antibiotic resistance among verocytotoxigenic Escherichia coli (VTEC) and non-VTEC isolated from domestic animals and humans. Journal of Medical Microbiology, 2003, 52, 155-162.	1.8	38
78	The detection of Melissococcus pluton in honey bees (Apis mellifera) and their products using a hemi-nested PCR. Apidologie, 2003, 34, 19-27.	2.0	38
79	New Integron-Associated Gene Cassette Encoding a 3- N -Aminoglycoside Acetyltransferase. Antimicrobial Agents and Chemotherapy, 2005, 49, 1238-1241.	3.2	38
80	Diverse Mobilized Class 1 Integrons Are Common in the Chromosomes of Pathogenic Pseudomonas aeruginosa Clinical Isolates. Antimicrobial Agents and Chemotherapy, 2012, 56, 2169-2172.	3.2	38
81	Aquariums as Reservoirs for Multidrug-resistant <i>Salmonella</i> Paratyphi B. Emerging Infectious Diseases, 2006, 12, 507-510.	4.3	37
82	Structural and Functional Characterization of an Organic Hydroperoxide Resistance Protein from Mycoplasma gallisepticum. Journal of Bacteriology, 2008, 190, 2206-2216.	2.2	37
83	Proteolytic processing of the cilium adhesin MHJ_0194 (P123 _J) in <i>M</i> ycoplasma hyopneumoniaegenerates a functionally diverse array of cleavage fragments that bind multiple host molecules. Cellular Microbiology, 2015, 17, 425-444.	2.1	37
84	Induction of pathogenic-like responses in the legume Macroptilium atropurpureum by a transposon-induced mutant of the fast-growing, broad-host-range Rhizobium strain NGR234. Journal of Bacteriology, 1988, 170, 1848-1857.	2.2	36
85	Cilium Adhesin P216 (MHJ_0493) Is a Target of Ectodomain Shedding and Aminopeptidase Activity on the Surface of <i>Mycoplasma hyopneumoniae</i>). Journal of Proteome Research, 2014, 13, 2920-2930.	3.7	36
86	A Comprehensive Guide for Performing Sample Preparation and Top-Down Protein Analysis. Proteomes, 2017, 5, 11.	3.5	36
87	Mycoplasma hyopneumoniae resides intracellularly within porcine epithelial cells. Scientific Reports, 2018, 8, 17697.	3.3	36
88	Characterisation of Erysipelothrix rhusiopathiae isolates from pigs associated with vaccine breakdowns. Veterinary Microbiology, 2006, 115, 329-338.	1.9	35
89	Indigenous <i>Vibrio cholerae</i> strains from a non-endemic region are pathogenic. Open Biology, 2013, 3, 120181.	3.6	35
90	N-terminomics identifies widespread endoproteolysis and novel methionine excision in a genome-reduced bacterial pathogen. Scientific Reports, 2017, 7, 11063.	3.3	35

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91	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic E. coli O157 lineage from Australian pigs. BMC Genomics, 2015, 16, 165.	2.8	34
92	Clostridium chauvoei, an Evolutionary Dead-End Pathogen. Frontiers in Microbiology, 2017, 8, 1054.	3.5	33
93	Whole Genome Sequencing of Escherichia coli From Store-Bought Produce. Frontiers in Microbiology, 2019, 10, 3050.	3 . 5	33
94	CORRESPONDENCE. Journal of Medical Microbiology, 2002, 51, 713-714.	1.8	33
95	Clonal ST131-H22 Escherichia coli strains from a healthy pig and a human urinary tract infection carry highly similar resistance and virulence plasmids. Microbial Genomics, 2019, 5, .	2.0	33
96	The Mycoplasma gallisepticum OsmC-like protein MG1142 resides on the cell surface and binds heparin. Microbiology (United Kingdom), 2007, 153, 1455-1463.	1.8	32
97	Temporal dynamics and subpopulation analysis of Theileria orientalis genotypes in cattle. Infection, Genetics and Evolution, 2015, 32, 199-207.	2.3	31
98	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in Escherichia coli of Porcine Origin in Australia. Frontiers in Sustainable Food Systems, 2019, 3, .	3.9	31
99	Oral immunization of swine with attenuated Salmonella typhimurium aro A SL3261 expressing a recombinant antigen of Mycoplasma hyopneumoniae (NrdF) primes the immune system for a NrdF specific secretory IgA response in the lungs. Microbial Pathogenesis, 2001, 30, 101-110.	2.9	30
100	Mass spectrometric characterization of the <i>Campylobacter jejuni </i> adherence factor CadF reveals post-translational processing that removes immunogenicity while retaining fibronectin binding. Proteomics, 2010, 10, 277-288.	2.2	30
101	Extracellular Actin Is a Receptor for Mycoplasma hyopneumoniae. Frontiers in Cellular and Infection Microbiology, 2018, 8, 54.	3.9	30
102	Escherichia coli Sequence Type 457 Is an Emerging Extended-Spectrum-β-Lactam-Resistant Lineage with Reservoirs in Wildlife and Food-Producing Animals. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	30
103	DNA restriction endonuclease profiles and typing of geographically diverse isolates ofBacillus larvae. Journal of Apicultural Research, 1994, 33, 95-103.	1.5	29
104	Emergence and Evolution of Multiply Antibiotic-Resistant <i>Salmonella enterica </i> Serovar Paratyphi B <scp>d</scp> -Tartrate-Utilizing Strains Containing SGI1. Antimicrobial Agents and Chemotherapy, 2009, 53, 2319-2326.	3.2	29
105	Genetic Features of mcr-1 Mediated Colistin Resistance in CMY-2-Producing Escherichia coli From Romanian Poultry. Frontiers in Microbiology, 2019, 10, 2267.	3.5	29
106	Molecular characterization of a ribonucleotide reductase (nrdF) gene fragment of Mycoplasma hyopneumoniae and assessment of the recombinant product as an experimental vaccine for enzootic pneumonia. Infection and Immunity, 1996, 64, 1060-1064.	2.2	29
107	Genetic diversity among Mycoplasma species bovine group 7: Clonal isolates from an outbreak of polyarthritis, mastitis, and abortion in dairy cattle. Electrophoresis, 2001, 22, 3551-3561.	2.4	28
108	Genomic interplay in bacterial communities: implications for growth promoting practices in animal husbandry. Frontiers in Microbiology, 2014, 5, 394.	3.5	28

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109	The application of terminomics for the identification of protein start sites and proteoforms in bacteria. Proteomics, 2016, 16, 257-272.	2.2	28
110	Antimicrobial Resistance Profile and ExPEC Virulence Potential in Commensal Escherichia coli of Multiple Sources. Antibiotics, 2021, 10, 351.	3.7	28
111	Geographically diverse Australian isolates of Melissococcus plutonexhibit minimal genotypic diversity by restriction endonuclease analysis. FEMS Microbiology Letters, 1999, 173, 311-318.	1.8	27
112	The genome of Clostridium difficile 5.3. Gut Pathogens, 2014, 6, 4.	3.4	27
113	Vibrio cholerae residing in food vacuoles expelled by protozoa are more infectious in vivo. Nature Microbiology, 2019, 4, 2466-2474.	13.3	27
114	Demonstration that Australian Pasteurella multocida isolates from sporadic outbreaks of porcine pneumonia are non-toxigenic (toxA-) and display heterogeneous DNA restriction endonuclease profiles compared with toxigenic isolates from herds with progressive atrophic rhinitis. Journal of Medical Microbiology, 1998, 47, 679-688.	1.8	26
115	The detection of Shiga toxin-producingEscherichia coliin diagnostic bovine faecal samples using vancomycin-cefixime-cefsulodin blood agar and PCR. FEMS Microbiology Letters, 2001, 198, 17-22.	1.8	26
116	Australian multicentre comparison of subtyping methods for the investigation of Campylobacter infection. Epidemiology and Infection, 2006, 134, 768-779.	2.1	26
117	High contiguity genome sequence of a multidrug-resistant hospital isolate of Enterobacter hormaechei. Gut Pathogens, 2019, 11, 3.	3.4	26
118	Plasmin activity in the porcine airways is enhanced during experimental infection with Mycoplasma hyopneumoniae, is positively correlated with proinflammatory cytokine levels and is ameliorated by vaccination. Veterinary Microbiology, 2013, 164, 60-66.	1.9	25
119	Evaluation of recombinant Mycoplasma hyopneumoniae P97/P102 paralogs formulated with selected adjuvants as vaccines against mycoplasmal pneumonia in pigs. Vaccine, 2014, 32, 4333-4341.	3.8	25
120	Salmonella Genomic Island 1 is Broadly Disseminated within Gammaproteobacteriaceae. Microorganisms, 2020, 8 , 161 .	3.6	25
121	Australian porcine clonal complex 10 (CC10) Escherichia coli belong to multiple sublineages of a highly diverse global CC10 phylogeny. Microbial Genomics, 2019, 5, .	2.0	25
122	Genomic profiling of Escherichia coli isolates from bacteraemia patients: a 3-year cohort study of isolates collected at a Sydney teaching hospital. Microbial Genomics, 2020, 6, .	2.0	25
123	Pesticide effects on nitrogen cycle related microbial functions and community composition. Science of the Total Environment, 2022, 807, 150734.	8.0	25
124	Genetic and Biochemical Diversity among Isolates of Paenibacillus alvei Cultured from Australian Honeybee (Apis mellifera) Colonies. Applied and Environmental Microbiology, 2000, 66, 1098-1106.	3.1	24
125	Analysis of Theileria orientalis draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. BMC Genomics, 2018, 19, 298.	2.8	24
126	Extracellular DNA release from the genome-reduced pathogen Mycoplasma hyopneumoniae is essential for biofilm formation on abiotic surfaces. Scientific Reports, 2018, 8, 10373.	3.3	24

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127	An aromatic amino acid auxotrophic mutant ofBordetella bronchisepticais attenuated and immunogenic in a mouse model of infection. FEMS Microbiology Letters, 2003, 221, 7-16.	1.8	23
128	Unusual Class 1 Integron-Associated Gene Cassette Configuration Found in IncA/C Plasmids from <i>Salmonella enterica </i> . Antimicrobial Agents and Chemotherapy, 2009, 53, 2640-2642.	3.2	22
129	Genomic islands 1 and 2 carry multiple antibiotic resistance genes in <i>Pseudomonas aeruginosa</i> ST235, ST253, ST111 and ST175 and are globally dispersed. Journal of Antimicrobial Chemotherapy, 2017, 72, 620-622.	3.0	22
130	Whole-Genome Sequence Analysis of an Extensively Drug-Resistant Salmonella enterica Serovar Agona Isolate from an Australian Silver Gull (<i>Chroicocephalus novaehollandiae</i>) Reveals the Acquisition of Multidrug Resistance Plasmids. MSphere, 2020, 5, .	2.9	22
131	Whole Genome Sequencing Analysis of Porcine Faecal Commensal Escherichia coli Carrying Class 1 Integrons from Sows and Their Offspring. Microorganisms, 2020, 8, 843.	3.6	22
132	Genomic comparisons of Escherichia coli ST131 from Australia. Microbial Genomics, 2021, 7, .	2.0	22
133	Manipulating systemic and mucosal immune responses with skin-deliverable adjuvants. Journal of Biotechnology, 1996, 44, 13-19.	3.8	21
134	Snapshot Study of Whole Genome Sequences of Escherichia coli from Healthy Companion Animals, Livestock, Wildlife, Humans and Food in Italy. Antibiotics, 2020, 9, 782.	3.7	21
135	Epidemic HI2 Plasmids Mobilising the Carbapenemase Gene blaIMP-4 in Australian Clinical Samples Identified in Multiple Sublineages of Escherichia coli ST216 Colonising Silver Gulls. Microorganisms, 2021, 9, 567.	3.6	21
136	Urban Wildlife Crisis: Australian Silver Gull Is a Bystander Host to Widespread Clinical Antibiotic Resistance. MSystems, 2022, 7, e0015822.	3.8	21
137	Proteogenomic mapping of Mycoplasma hyopneumoniae virulent strain 232. BMC Genomics, 2014, 15, 576.	2.8	20
138	A versatile cost-effective method for the analysis of fresh frozen tissue sections via matrix-assisted laser desorption/ionisation imaging mass spectrometry. Rapid Communications in Mass Spectrometry, 2015, 29, 637-644.	1.5	20
139	Genomic analysis of phylogenetic group B2 extraintestinal pathogenic E. coli causing infections in dogs in Australia. Veterinary Microbiology, 2020, 248, 108783.	1.9	20
140	F Plasmid Lineages in Escherichia coli ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses. MSystems, 2022, 7, e0121221.	3.8	20
141	An improved enzyme linked immunosorbent assay (ELISA) for the detection of porcine serum antibodies against Mycoplasma hyopneumoniae. Veterinary Microbiology, 1994, 39, 261-273.	1.9	19
142	New Integron-Associated Gene Cassette Encoding a Trimethoprim-Resistant DfrB-Type Dihydrofolate Reductase. Antimicrobial Agents and Chemotherapy, 2006, 50, 2863-2865.	3.2	19
143	Development of Non-Antibiotic-Resistant, Chromosomally Based, Constitutive and Inducible Expression Systems for <i>aroA</i> Attenuated <i>Salmonella enterica</i> Infection and Immunity, 2009, 77, 1817-1826.	2.2	19
144	The pyruvate dehydrogenase complex of Mycoplasma hyopneumoniae contains a novel lipoyl domain arrangement. Gene, 2003, 319, 99-106.	2.2	18

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145	Cell Surface Antigens of Mycoplasma Species Bovine Group 7 Bind to and Activate Plasminogen. Infection and Immunity, 2003, 71, 4823-4827.	2.2	18
146	Isolation and Solubilization of Gram-Positive Bacterial Cell Wall-Associated Proteins. Methods in Molecular Biology, 2008, 425, 295-311.	0.9	18
147	<i>Salmonella</i> Genomic Island 1B Variant Found in a Sequence Type 117 Avian Pathogenic Escherichia coli Isolate. MSphere, 2019, 4, .	2.9	18
148	Preparative gel chromatography of acidic oligosaccharides using a volatile buffer. Journal of Chromatography A, 1986, 354, 507-510.	3.7	17
149	Isolation of Escherichia coli O5 : H \hat{a}° , possessing genes for Shiga toxin 1, intimin- \hat{l}^2 and enterohaemolysin, from an intestinal biopsy from an adult case of bloody diarrhoea: evidence for two distinct O5 : H \hat{a}° pathotypes. Journal of Medical Microbiology, 2005, 54, 605-607.	1.8	17
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