

Steven P Djordjevic

List of Publications by Year in descending order

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Version: 2024-02-01

219
papers

8,127
citations

38742

50
h-index

82547

72
g-index

226
all docs

226
docs citations

226
times ranked

6559
citing authors

#	ARTICLE	IF	CITATIONS
1	Pesticide effects on nitrogen cycle related microbial functions and community composition. <i>Science of the Total Environment</i> , 2022, 807, 150734.	8.0	25
2	Close genetic linkage between human and companion animal extraintestinal pathogenic <i>Escherichia coli</i> ST127. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100106.	2.3	9
3	F Plasmid Lineages in <i>Escherichia coli</i> ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses. <i>MSystems</i> , 2022, 7, e0121221.	3.8	20
4	A role for ColV plasmids in the evolution of pathogenic <i>Escherichia coli</i> ST58. <i>Nature Communications</i> , 2022, 13, 683.	12.8	40
5	Complete Genome Sequence of <i>Pasteurella multocida</i> Sequence Type 394, Isolated from a Case of Bovine Respiratory Disease in Australia. <i>Microbiology Resource Announcements</i> , 2022, 11, e0089021.	0.6	3
6	Erratum for Cummins et al., "F Plasmid Lineages in <i>Escherichia coli</i> ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses" <i>MSystems</i> , 2022, 7, e0021022.	3.8	3
7	Urban Wildlife Crisis: Australian Silver Gull Is a Bystander Host to Widespread Clinical Antibiotic Resistance. <i>MSystems</i> , 2022, 7, e0015822.	3.8	21
8	Genomic Analysis of Carbapenem-Resistant <i>Comamonas</i> in Water Matrices: Implications for Public Health and Wastewater Treatments. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	10
9	Genomic and Temporal Trends in Canine ExPEC Reflect Those of Human ExPEC. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	11
10	Phylogenetic diversity analysis of shotgun metagenomic reads describes gut microbiome development and treatment effects in the post-weaned pig. <i>PLoS ONE</i> , 2022, 17, e0270372.	2.5	5
11	Complete Genomes of <i>Theileria orientalis</i> Chitose and Buffeli Genotypes Reveal within Species Translocations and Differences in ABC Transporter Content. <i>Pathogens</i> , 2022, 11, 801.	2.8	3
12	Interspecies Transmission of CMY-2-Producing <i>Escherichia coli</i> Sequence Type 963 Isolates between Humans and Gulls in Australia. <i>MSphere</i> , 2022, 7, .	2.9	6
13	Genomic Analysis of an I1 Plasmid Hosting a <i>sul3</i> -Class 1 Integron and <i>bla</i> SHV-12 within an Unusual <i>Escherichia coli</i> ST297 from Urban Wildlife. <i>Microorganisms</i> , 2022, 10, 1387.	3.6	3
14	Protein cleavage influences surface protein presentation in <i>Mycoplasma pneumoniae</i> . <i>Scientific Reports</i> , 2021, 11, 6743.	3.3	4
15	Epidemic HI2 Plasmids Mobilising the Carbapenemase Gene <i>bla</i> IMP-4 in Australian Clinical Samples Identified in Multiple Sublineages of <i>Escherichia coli</i> ST216 Colonising Silver Gulls. <i>Microorganisms</i> , 2021, 9, 567.	3.6	21
16	Antimicrobial Resistance Profile and ExPEC Virulence Potential in Commensal <i>Escherichia coli</i> of Multiple Sources. <i>Antibiotics</i> , 2021, 10, 351.	3.7	28
17	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021, 10, .	6.4	9
18	First Emergence of Resistance to Macrolides and Tetracycline Identified in <i>Mannheimia haemolytica</i> and <i>Pasteurella multocida</i> Isolates from Beef Feedlots in Australia. <i>Microorganisms</i> , 2021, 9, 1322.	3.6	11

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19	Monitoring antibiotic resistance genes in wastewater treatment: Current strategies and future challenges. <i>Science of the Total Environment</i> , 2021, 783, 146964.	8.0	136
20	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
21	Multidrug-Resistant Lineage of Enterotoxigenic <i>Escherichia coli</i> ST182 With Serotype O169:H41 in Airline Waste. <i>Frontiers in Microbiology</i> , 2021, 12, 731050.	3.5	5
22	Genomic analysis of <i>Elizabethkingia</i> species from aquatic environments: evidence for potential clinical transmission. <i>Current Research in Microbial Sciences</i> , 2021, 3, 100083.	2.3	2
23	Progressing Antimicrobial Resistance Sensing Technologies across Human, Animal, and Environmental Health Domains. <i>ACS Sensors</i> , 2021, 6, 4283-4296.	7.8	5
24	Genomic comparisons of <i>Escherichia coli</i> ST131 from Australia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	22
25	<i>Escherichia coli</i> Sequence Type 457 Is an Emerging Extended-Spectrum- β -Lactam-Resistant Lineage with Reservoirs in Wildlife and Food-Producing Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	3.2	30
26	<i>Escherichia coli</i> ST8196 is a novel, locally evolved, and extensively drug resistant pathogenic lineage within the ST131 clonal complex. <i>Emerging Microbes and Infections</i> , 2020, 9, 1780-1792.	6.5	3
27	Snapshot Study of Whole Genome Sequences of <i>Escherichia coli</i> from Healthy Companion Animals, Livestock, Wildlife, Humans and Food in Italy. <i>Antibiotics</i> , 2020, 9, 782.	3.7	21
28	Genomic analysis of phylogenetic group B2 extraintestinal pathogenic <i>E. coli</i> causing infections in dogs in Australia. <i>Veterinary Microbiology</i> , 2020, 248, 108783.	1.9	20
29	Genomic Surveillance for One Health Antimicrobial Resistance: Understanding Human, Animal, and Environmental Reservoirs and Transmission. <i>Handbook of Environmental Chemistry</i> , 2020, , 71-100.	0.4	2
30	Whole-Genome Sequence Analysis of an Extensively Drug-Resistant <i>Salmonella enterica</i> Serovar Agona Isolate from an Australian Silver Gull (<i>Chroicocephalus novaehollandiae</i>) Reveals the Acquisition of Multidrug Resistance Plasmids. <i>MSphere</i> , 2020, 5, .	2.9	22
31	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	9
32	Genomic analysis of fluoroquinolone-susceptible phylogenetic group B2 extraintestinal pathogenic <i>Escherichia coli</i> causing infections in cats. <i>Veterinary Microbiology</i> , 2020, 245, 108685.	1.9	12
33	A comparison of virulence genes, antimicrobial resistance profiles and genetic diversity of avian pathogenic <i>Escherichia coli</i> (APEC) isolates from broilers and broiler breeders in Thailand and Australia. <i>Avian Pathology</i> , 2020, 49, 457-466.	2.0	13
34	Genomic Characterisation of a Multiple Drug Resistant IncHI2 ST4 Plasmid in <i>Escherichia coli</i> ST744 in Australia. <i>Microorganisms</i> , 2020, 8, 896.	3.6	15
35	Whole Genome Sequencing Analysis of Porcine Faecal Commensal <i>Escherichia coli</i> Carrying Class 1 Integrons from Sows and Their Offspring. <i>Microorganisms</i> , 2020, 8, 843.	3.6	22
36	<i>Escherichia coli</i> ST302: Genomic Analysis of Virulence Potential and Antimicrobial Resistance Mediated by Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2020, 10, 3098.	3.5	14

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37	Molecular Analysis of an IncF ColV-Like Plasmid Lineage That Carries a Complex Resistance Locus with a Trackable Genetic Signature. <i>Microbial Drug Resistance</i> , 2020, 26, 787-793.	2.0	6
38	Salmonella Genomic Island 1 is Broadly Disseminated within Gammaproteobacteriaceae. <i>Microorganisms</i> , 2020, 8, 161.	3.6	25
39	Osteoarticular Infection in Three Young Thoroughbred Horses Caused by a Novel Gram Negative Cocco-Bacillus. <i>Case Reports in Veterinary Medicine</i> , 2020, 2020, 1-8.	0.2	0
40	Cell surface processing of the P1 adhesin of <i>Mycoplasma pneumoniae</i> identifies novel domains that bind host molecules. <i>Scientific Reports</i> , 2020, 10, 6384.	3.3	16
41	Whole-genome analysis of extraintestinal <i>Escherichia coli</i> sequence type 73 from a single hospital over a 2 year period identified different circulating clonal groups. <i>Microbial Genomics</i> , 2020, 6, .	2.0	14
42	Genomic profiling of <i>Escherichia coli</i> isolates from bacteraemia patients: a 3-year cohort study of isolates collected at a Sydney teaching hospital. <i>Microbial Genomics</i> , 2020, 6, .	2.0	25
43	Whole-genome sequence analysis of environmental <i>Escherichia coli</i> from the faeces of straw-necked ibis (<i>Threskiornis spinicollis</i>) nesting on inland wetlands. <i>Microbial Genomics</i> , 2020, 6, .	2.0	5
44	Duplication and diversification of a unique chromosomal virulence island hosting the subtilase cytotoxin in <i>Escherichia coli</i> ST58. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
45	Genomic analysis of trimethoprim-resistant extraintestinal pathogenic <i>Escherichia coli</i> and recurrent urinary tract infections. <i>Microbial Genomics</i> , 2020, 6, .	2.0	17
46	Whole genome sequence comparison of avian pathogenic <i>Escherichia coli</i> from acute and chronic salpingitis of egg laying hens. <i>BMC Veterinary Research</i> , 2020, 16, 148.	1.9	13
47	<i>Mycoplasma hyopneumoniae</i> surface-associated proteases cleave bradykinin, substance P, neurokinin A and neuropeptide Y. <i>Scientific Reports</i> , 2019, 9, 14585.	3.3	11
48	L-DOPA causes mitochondrial dysfunction in vitro: A novel mechanism of L-DOPA toxicity uncovered. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 117, 105624.	2.8	10
49	Z/11 Hybrid Virulence Plasmids Carrying Antimicrobial Resistance genes in <i>S. Typhimurium</i> from Australian Food Animal Production. <i>Microorganisms</i> , 2019, 7, 299.	3.6	7
50	Terminomics Methodologies and the Completeness of Reductive Dimethylation: A Meta-Analysis of Publicly Available Datasets. <i>Proteomes</i> , 2019, 7, 11.	3.5	3
51	<i>Salmonella</i> Genomic Island 1B Variant Found in a Sequence Type 117 Avian Pathogenic <i>Escherichia coli</i> Isolate. <i>MSphere</i> , 2019, 4, .	2.9	18
52	Formylated N-terminal methionine is absent from the <i>Mycoplasma hyopneumoniae</i> proteome: Implications for translation initiation. <i>International Journal of Medical Microbiology</i> , 2019, 309, 288-298.	3.6	2
53	Identification of a novel lineage of plasmids within phylogenetically diverse subclades of IncHI2-ST1 plasmids. <i>Plasmid</i> , 2019, 102, 56-61.	1.4	6
54	High contiguity genome sequence of a multidrug-resistant hospital isolate of <i>Enterobacter hormaechei</i> . <i>Gut Pathogens</i> , 2019, 11, 3.	3.4	26

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55	A One Health genomic approach to antimicrobial resistance is essential for generating relevant data for a holistic assessment of the biggest threat to public health. <i>Microbiology Australia</i> , 2019, 40, 73.	0.4	8
56	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in <i>Escherichia coli</i> of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	3.9	31
57	Genetic Features of <i>mcr-1</i> Mediated Colistin Resistance in CMY-2-Producing <i>Escherichia coli</i> From Romanian Poultry. <i>Frontiers in Microbiology</i> , 2019, 10, 2267.	3.5	29
58	The Diverse Functional Roles of Elongation Factor Tu (EF-Tu) in Microbial Pathogenesis. <i>Frontiers in Microbiology</i> , 2019, 10, 2351.	3.5	118
59	Diversity of P1 phage-like elements in multidrug resistant <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019, 9, 18861.	3.3	43
60	<i>Vibrio cholerae</i> residing in food vacuoles expelled by protozoa are more infectious in vivo. <i>Nature Microbiology</i> , 2019, 4, 2466-2474.	13.3	27
61	Whole Genome Sequencing of <i>Escherichia coli</i> From Store-Bought Produce. <i>Frontiers in Microbiology</i> , 2019, 10, 3050.	3.5	33
62	Australian porcine clonal complex 10 (CC10) <i>Escherichia coli</i> belong to multiple sublineages of a highly diverse global CC10 phylogeny. <i>Microbial Genomics</i> , 2019, 5, .	2.0	25
63	Whole genome sequence analysis of Australian avian pathogenic <i>Escherichia coli</i> that carry the class 1 integrase gene. <i>Microbial Genomics</i> , 2019, 5, .	2.0	51
64	Clonal ST131-H22 <i>Escherichia coli</i> strains from a healthy pig and a human urinary tract infection carry highly similar resistance and virulence plasmids. <i>Microbial Genomics</i> , 2019, 5, .	2.0	33
65	The Effect of Collimating Lens Focusing on Laser Beam Shape in Matrix Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-MS). <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 512-515.	2.8	0
66	Analysis of <i>Theileria orientalis</i> draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. <i>BMC Genomics</i> , 2018, 19, 298.	2.8	24
67	The quest for improved reproducibility in MALDI mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2018, 37, 217-228.	5.4	54
68	Proteomic Analysis of Extracellular HMGB1 Identifies Binding Partners and Exposes Its Potential Role in Airway Epithelial Cell Homeostasis. <i>Journal of Proteome Research</i> , 2018, 17, 33-45.	3.7	14
69	<i>Mycoplasma hyopneumoniae</i> resides intracellularly within porcine epithelial cells. <i>Scientific Reports</i> , 2018, 8, 17697.	3.3	36
70	Environmental dimensions of antibiotic resistance: assessment of basic science gaps. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	63
71	Genomic analysis of multidrug-resistant <i>Escherichia coli</i> ST58 causing urosepsis. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 430-435.	2.5	62
72	Extracellular DNA release from the genome-reduced pathogen <i>Mycoplasma hyopneumoniae</i> is essential for biofilm formation on abiotic surfaces. <i>Scientific Reports</i> , 2018, 8, 10373.	3.3	24

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73	Extracellular Actin Is a Receptor for <i>Mycoplasma hyopneumoniae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 54.	3.9	30
74	Multidrug Resistant Uropathogenic <i>Escherichia coli</i> ST405 With a Novel, Composite IS26 Transposon in a Unique Chromosomal Location. <i>Frontiers in Microbiology</i> , 2018, 9, 3212.	3.5	41
75	Defined chromosome structure in the genome-reduced bacterium <i>Mycoplasma pneumoniae</i> . <i>Nature Communications</i> , 2017, 8, 14665.	12.8	81
76	Genomic islands 1 and 2 carry multiple antibiotic resistance genes in <i>Pseudomonas aeruginosa</i> ST235, ST253, ST111 and ST175 and are globally dispersed. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 620-622.	3.0	22
77	Elongation factor Tu is a multifunctional and processed moonlighting protein. <i>Scientific Reports</i> , 2017, 7, 11227.	3.3	82
78	N-terminomics identifies widespread endoproteolysis and novel methionine excision in a genome-reduced bacterial pathogen. <i>Scientific Reports</i> , 2017, 7, 11063.	3.3	35
79	Identification of a novel <i>qnrA</i> allele, <i>qnrA8</i> , in environmental <i>Shewanella</i> algae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2949-2952.	3.0	4
80	A Comprehensive Guide for Performing Sample Preparation and Top-Down Protein Analysis. <i>Proteomes</i> , 2017, 5, 11.	3.5	36
81	<i>Clostridium chauvoei</i> , an Evolutionary Dead-End Pathogen. <i>Frontiers in Microbiology</i> , 2017, 8, 1054.	3.5	33
82	Porcine commensal <i>Escherichia coli</i> : a reservoir for class 1 integrons associated with IS26. <i>Microbial Genomics</i> , 2017, 3, .	2.0	89
83	Evaluation of ddRADseq for reduced representation metagenome sequencing. <i>PeerJ</i> , 2017, 5, e3837.	2.0	11
84	The Renaissance of Microbiology: The Necessary Future for Matrix Assisted Laser Desorption Ionisation Mass Spectrometry Based Bio Typing. <i>Journal of Microbial & Biochemical Technology</i> , 2016, 8, .	0.2	1
85	The Role of CD44 and ERM Proteins in Expression and Functionality of P-glycoprotein in Breast Cancer Cells. <i>Molecules</i> , 2016, 21, 290.	3.8	45
86	Genomic Microbial Epidemiology Is Needed to Comprehend the Global Problem of Antibiotic Resistance and to Improve Pathogen Diagnosis. <i>Frontiers in Microbiology</i> , 2016, 7, 843.	3.5	53
87	Cross reactivity among the swine mycoplasmas as identified by protein microarray. <i>Veterinary Microbiology</i> , 2016, 192, 204-212.	1.9	15
88	Post-translational processing targets functionally diverse proteins in <i>Mycoplasma hyopneumoniae</i> . <i>Open Biology</i> , 2016, 6, 150210.	3.6	53
89	The application of terminomics for the identification of protein start sites and proteoforms in bacteria. <i>Proteomics</i> , 2016, 16, 257-272.	2.2	28
90	Comparative genomic analysis of toxin-negative strains of <i>Clostridium difficile</i> from humans and animals with symptoms of gastrointestinal disease. <i>BMC Microbiology</i> , 2016, 16, 41.	3.3	13

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91	Genomic islands 1 and 2 play key roles in the evolution of extensively drug-resistant ST235 isolates of <i>Pseudomonas aeruginosa</i> . <i>Open Biology</i> , 2016, 6, 150175.	3.6	47
92	A non-instrument-based method for the analysis of formalin-fixed paraffin-embedded human spinal cord via matrix-assisted laser desorption/ionisation imaging mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 1836-1840.	1.5	16
93	P40 and P90 from Mpn142 are Targets of Multiple Processing Events on the Surface of <i>Mycoplasma pneumoniae</i> . <i>Proteomes</i> , 2015, 3, 512-537.	3.5	17
94	Exploitation of plasmin(ogen) by bacterial pathogens of veterinary significance. <i>Veterinary Microbiology</i> , 2015, 178, 1-13.	1.9	46
95	MHJ_0461 is a multifunctional leucine aminopeptidase on the surface of <i>Mycoplasma hyopneumoniae</i> . <i>Open Biology</i> , 2015, 5, 140175.	3.6	59
96	Temporal dynamics and subpopulation analysis of <i>Theileria orientalis</i> genotypes in cattle. <i>Infection, Genetics and Evolution</i> , 2015, 32, 199-207.	2.3	31
97	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic <i>E. coli</i> O157 lineage from Australian pigs. <i>BMC Genomics</i> , 2015, 16, 165.	2.8	34
98	Tn6026 and Tn6029 are found in complex resistance regions mobilised by diverse plasmids and chromosomal islands in multiple antibiotic resistant <i>Enterobacteriaceae</i> . <i>Plasmid</i> , 2015, 80, 127-137.	1.4	61
99	A versatile cost-effective method for the analysis of fresh frozen tissue sections via matrix-assisted laser desorption/ionisation imaging mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 637-644.	1.5	20
100	Proteolytic processing of the cilium adhesin MHJ_0194 (P123 _J) in <i>Mycoplasma hyopneumoniae</i> generates a functionally diverse array of cleavage fragments that bind multiple host molecules. <i>Cellular Microbiology</i> , 2015, 17, 425-444.	2.1	37
101	Non-proteolytic functions of microbial proteases increase pathological complexity. <i>Proteomics</i> , 2015, 15, 1075-1088.	2.2	16
102	A Role for Tn6029 in the Evolution of the Complex Antibiotic Resistance Gene Loci in Genomic Island 3 in Enterotoxigenic Hemorrhagic <i>Escherichia coli</i> O104:H4. <i>PLoS ONE</i> , 2015, 10, e0115781.	2.5	43
103	Genomic interplay in bacterial communities: implications for growth promoting practices in animal husbandry. <i>Frontiers in Microbiology</i> , 2014, 5, 394.	3.5	28
104	A draft genome of <i>Escherichia coli</i> sequence type 127 strain 2009-46. <i>Gut Pathogens</i> , 2014, 6, 32.	3.4	8
105	The genome of <i>Clostridium difficile</i> 5.3. <i>Gut Pathogens</i> , 2014, 6, 4.	3.4	27
106	Comparative Proteomics and Glycoproteomics Reveal Increased N-Linked Glycosylation and Relaxed Sequon Specificity in <i>Campylobacter jejuni</i> NCTC11168 O. <i>Journal of Proteome Research</i> , 2014, 13, 5136-5150.	3.7	48
107	Evaluation of recombinant <i>Mycoplasma hyopneumoniae</i> P97/P102 paralogs formulated with selected adjuvants as vaccines against mycoplasmal pneumonia in pigs. <i>Vaccine</i> , 2014, 32, 4333-4341.	3.8	25
108	Cilium Adhesin P216 (MHJ_0493) Is a Target of Ectodomain Shedding and Aminopeptidase Activity on the Surface of <i>Mycoplasma hyopneumoniae</i> . <i>Journal of Proteome Research</i> , 2014, 13, 2920-2930.	3.7	36

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109	Proteogenomic mapping of <i>Mycoplasma hyopneumoniae</i> virulent strain 232. BMC Genomics, 2014, 15, 576.	2.8	20
110	Proteome analysis of multidrug-resistant, breast cancer-derived microparticles. Journal of Extracellular Vesicles, 2014, 3, .	12.2	45
111	Formation of assemblies on cell membranes by secreted proteins: molecular studies of free light chain aggregates found on the surface of myeloma cells. Biochemical Journal, 2013, 454, 479-489.	3.7	10
112	Plasmin activity in the porcine airways is enhanced during experimental infection with <i>Mycoplasma hyopneumoniae</i> , is positively correlated with proinflammatory cytokine levels and is ameliorated by vaccination. Veterinary Microbiology, 2013, 164, 60-66.	1.9	25
113	Indigenous <i>Vibrio cholerae</i> strains from a non-endemic region are pathogenic. Open Biology, 2013, 3, 120181.	3.6	35
114	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
115	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
116	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
117	Mobilized Integrons: Team Players in the Spread of Antibiotic Resistance Genes. , 2013, , 79-103.		2
118	Deletion of Integron-Associated Gene Cassettes Impact on the Surface Properties of <i>Vibrio rotiferianus</i> DAT722. PLoS ONE, 2013, 8, e58430.	2.5	7
119	Sequences of Two Related Multiple Antibiotic Resistance Virulence Plasmids Sharing a Unique IS26-Related Molecular Signature Isolated from Different <i>Escherichia coli</i> Pathotypes from Different Hosts. PLoS ONE, 2013, 8, e78862.	2.5	80
120	Diverse Mobilized Class 1 Integrons Are Common in the Chromosomes of Pathogenic <i>Pseudomonas aeruginosa</i> Clinical Isolates. Antimicrobial Agents and Chemotherapy, 2012, 56, 2169-2172.	3.2	38
121	Modification of the <i>Campylobacter jejuni</i> N-Linked Glycan by EptC Protein-mediated Addition of Phosphoethanolamine. Journal of Biological Chemistry, 2012, 287, 29384-29396.	3.4	63
122	Characterization of Cleavage Events in the Multifunctional Cilium Adhesin Mhp684 (P146) Reveals a Mechanism by Which <i>Mycoplasma hyopneumoniae</i> Regulates Surface Topography. MBio, 2012, 3, .	4.1	54
123	Evaluation of clinical, histological and immunological changes and qPCR detection of <i>Mycoplasma hyopneumoniae</i> 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
124	Class 1 integron-associated spread of resistance regions in <i>Pseudomonas aeruginosa</i> : plasmid or chromosomal platforms?. Journal of Antimicrobial Chemotherapy, 2012, 67, 1799-1800.	3.0	13
125	<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
126	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. Journal of Molecular Medicine, 2012, 90, 1197-1207.	3.9	49

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127	Mhp182 (P102) binds fibronectin and contributes to the recruitment of plasmin(ogen) to the <i>Mycoplasma hyopneumoniae</i> cell surface. <i>Cellular Microbiology</i> , 2012, 14, 81-94.	2.1	76
128	Molecular Characterization of a 21.4 Kilobase Antibiotic Resistance Plasmid from an $\hat{\pm}$ -Hemolytic <i>Escherichia coli</i> O108:H- Human Clinical Isolate. <i>PLoS ONE</i> , 2012, 7, e34718.	2.5	0
129	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 <i>Campylobacter jejuni</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S18.	3.8	265
130	Mhp107 Is a Member of the Multifunctional Adhesin Family of <i>Mycoplasma hyopneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 10097-10104.	3.4	46
131	Sequence TTKFâ†“QE Defines the Site of Proteolytic Cleavage in Mhp683 Protein, a Novel Glycosaminoglycan and Cilium Adhesin of <i>Mycoplasma hyopneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 41217-41229.	3.4	47
132	Mass spectrometric characterization of the <i>Campylobacter jejuni</i> adherence factor CadF reveals post-translational processing that removes immunogenicity while retaining fibronectin binding. <i>Proteomics</i> , 2010, 10, 277-288.	2.2	30
133	Repeat regions R1 and R2 in the P97 paralogue Mhp271 of <i>Mycoplasma hyopneumoniae</i> bind heparin, fibronectin and porcine cilia. <i>Molecular Microbiology</i> , 2010, 78, 444-458.	2.5	74
134	Distribution of Class 1 Integrons with IS26-Mediated Deletions in Their 3â€²-Conserved Segments in <i>Escherichia coli</i> of Human and Animal Origin. <i>PLoS ONE</i> , 2010, 5, e12754.	2.5	108
135	Multiple antibiotic resistance gene recruitment onto the enterohemorrhagic <i>Escherichia coli</i> virulence plasmid. <i>FASEB Journal</i> , 2010, 24, 1160-1166.	0.5	85
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