Steven P Djordjevic

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

210
papers

6,012
citations

h-index

63
g-index

7,299
ext. papers

4.8
avg, IF

L-index

#	Paper	IF	Citations
210	Close genetic linkage between human and companion animal extraintestinal pathogenic ST127 <i>Current Research in Microbial Sciences</i> , 2022 , 3, 100106	3.3	3
209	F Plasmid Lineages in Escherichia coli ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses <i>MSystems</i> , 2022 , e0121221	7.6	4
208	A role for ColV plasmids in the evolution of pathogenic Escherichia coli ST58 <i>Nature Communications</i> , 2022 , 13, 683	17.4	3
207	Genomic analysis of species from aquatic environments: Evidence for potential clinical transmission <i>Current Research in Microbial Sciences</i> , 2022 , 3, 100083	3.3	1
206	Pesticide effects on nitrogen cycle related microbial functions and community composition. <i>Science of the Total Environment</i> , 2022 , 807, 150734	10.2	3
205	Complete Genome Sequence of Pasteurella multocida Sequence Type 394, Isolated from a Case of Bovine Respiratory Disease in Australia <i>Microbiology Resource Announcements</i> , 2022 , e0089021	1.3	0
204	Erratum for Cummins et al., "F Plasmid Lineages in Escherichia coli ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses" <i>MSystems</i> , 2022 , e0021022	7.6	O
203	Urban Wildlife Crisis: Australian Silver Gull Is a Bystander Host to Widespread Clinical Antibiotic Resistance <i>MSystems</i> , 2022 , e0015822	7.6	2
202	Epidemic HI2 Plasmids Mobilising the Carbapenemase Gene in Australian Clinical Samples Identified in Multiple Sublineages of ST216 Colonising Silver Gulls. <i>Microorganisms</i> , 2021 , 9,	4.9	3
201	Antimicrobial Resistance Profile and ExPEC Virulence Potential in Commensal of Multiple Sources. <i>Antibiotics</i> , 2021 , 10,	4.9	9
200	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021 , 10,	7.6	2
199	First Emergence of Resistance to Macrolides and Tetracycline Identified in and Isolates from Beef Feedlots in Australia. <i>Microorganisms</i> , 2021 , 9,	4.9	2
198	Protein cleavage influences surface protein presentation in Mycoplasma pneumoniae. <i>Scientific Reports</i> , 2021 , 11, 6743	4.9	3
197	Monitoring antibiotic resistance genes in wastewater treatment: Current strategies and future challenges. <i>Science of the Total Environment</i> , 2021 , 783, 146964	10.2	27
196	Post-weaning shifts in microbiome composition and metabolism revealed by over 25 000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
195	Multidrug-Resistant Lineage of Enterotoxigenic ST182 With Serotype O169:H41 in Airline Waste. <i>Frontiers in Microbiology</i> , 2021 , 12, 731050	5.7	O
194	Genomic comparisons of ST131 from Australia <i>Microbial Genomics</i> , 2021 , 7,	4.4	5

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193	Whole-Genome Sequence Analysis of an Extensively Drug-Resistant Salmonella enterica Serovar Agona Isolate from an Australian Silver Gull () Reveals the Acquisition of Multidrug Resistance Plasmids. <i>MSphere</i> , 2020 , 5,	5	8
192	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	4
191	Genomic analysis of fluoroquinolone-susceptible phylogenetic group B2 extraintestinal pathogenic Escherichia coli causing infections in cats. <i>Veterinary Microbiology</i> , 2020 , 245, 108685	3.3	7
190	A comparison of virulence genes, antimicrobial resistance profiles and genetic diversity of avian pathogenic (APEC) isolates from broilers and broiler breeders in Thailand and Australia. <i>Avian Pathology</i> , 2020 , 49, 457-466	2.4	9
189	Genomic Characterisation of a Multiple Drug Resistant IncHI2 ST4 Plasmid in ST744 in Australia. <i>Microorganisms</i> , 2020 , 8,	4.9	8
188	Whole Genome Sequencing Analysis of Porcine Faecal Commensal Carrying Class 1 Integrons from Sows and Their Offspring. <i>Microorganisms</i> , 2020 , 8,	4.9	11
187	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	2.9	4
186	Genomic Island 1 is Broadly Disseminated within Gammaproteobacteriaceae. <i>Microorganisms</i> , 2020 , 8,	4.9	13
185	Osteoarticular Infection in Three Young Thoroughbred Horses Caused by a Novel Gram Negative Cocco-Bacillus. <i>Case Reports in Veterinary Medicine</i> , 2020 , 2020, 9785861	0.3	
184	Whole genome sequence comparison of avian pathogenic Escherichia coli from acute and chronic salpingitis of egg laying hens. <i>BMC Veterinary Research</i> , 2020 , 16, 148	2.7	5
183	Whole-genome analysis of extraintestinal sequence type 73 from a single hospital over a 2 year period identified different circulating clonal groups. <i>Microbial Genomics</i> , 2020 , 6,	4.4	9
182	Genomic profiling of isolates from bacteraemia patients: a 3-year cohort study of isolates collected at a Sydney teaching hospital. <i>Microbial Genomics</i> , 2020 , 6,	4.4	16
181	Whole-genome sequence analysis of environmental from the faeces of straw-necked ibis () nesting on inland wetlands. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
180	Duplication and diversification of a unique chromosomal virulence island hosting the subtilase cytotoxin in ST58. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
179	Genomic analysis of trimethoprim-resistant extraintestinal pathogenic and recurrent urinary tract infections. <i>Microbial Genomics</i> , 2020 , 6,	4.4	10
178	Escherichia coli Sequence Type 457 Is an Emerging Extended-Spectrum-Lactam-Resistant Lineage with Reservoirs in Wildlife and Food-Producing Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 65,	5.9	10
177	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	18.9	2
176	Snapshot Study of Whole Genome Sequences of from Healthy Companion Animals, Livestock, Wildlife, Humans and Food in Italy. <i>Antibiotics</i> , 2020 , 9,	4.9	8

175	Genomic analysis of phylogenetic group B2 extraintestinal pathogenic E. coli causing infections in dogs in Australia. <i>Veterinary Microbiology</i> , 2020 , 248, 108783	3.3	9
174	Genomic Surveillance for One Health Antimicrobial Resistance: Understanding Human, Animal, and Environmental Reservoirs and Transmission. <i>Handbook of Environmental Chemistry</i> , 2020 , 71-100	0.8	О
173	Cell surface processing of the P1 adhesin of Mycoplasma pneumoniae identifies novel domains that bind host molecules. <i>Scientific Reports</i> , 2020 , 10, 6384	4.9	6
172	Z/I1 Hybrid Virulence Plasmids Carrying Antimicrobial Resistance genes in Typhimurium from Australian Food Animal Production. <i>Microorganisms</i> , 2019 , 7,	4.9	4
171	Terminomics Methodologies and the Completeness of Reductive Dimethylation: A Meta-Analysis of Publicly Available Datasets. <i>Proteomes</i> , 2019 , 7,	4.6	3
170	Genomic Island 1B Variant Found in a Sequence Type 117 Avian Pathogenic Escherichia coli Isolate. <i>MSphere</i> , 2019 , 4,	5	12
169	Formylated N-terminal methionine is absent from the Mycoplasma hyopneumoniae proteome: Implications for translation initiation. <i>International Journal of Medical Microbiology</i> , 2019 , 309, 288-298	3.7	1
168	Identification of a novel lineage of plasmids within phylogenetically diverse subclades of IncHI2-ST1 plasmids. <i>Plasmid</i> , 2019 , 102, 56-61	3.3	4
167	High contiguity genome sequence of a multidrug-resistant hospital isolate of. <i>Gut Pathogens</i> , 2019 , 11, 3	5.4	16
166	Whole Genome Sequencing of From Store-Bought Produce. <i>Frontiers in Microbiology</i> , 2019 , 10, 3050	5.7	19
165	ST302: Genomic Analysis of Virulence Potential and Antimicrobial Resistance Mediated by Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2019 , 10, 3098	5.7	10
164	Mycoplasma hyopneumoniae surface-associated proteases cleave bradykinin, substance P, neurokinin A and neuropeptide Y. <i>Scientific Reports</i> , 2019 , 9, 14585	4.9	7
163	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	5.6	5
162	Australian porcine clonal complex 10 (CC10) Escherichia coli belong to multiple sublineages of a highly diverse global CC10 phylogeny. <i>Microbial Genomics</i> , 2019 , 5,	4.4	16
161	Whole genome sequence analysis of Australian avian pathogenic Escherichia coli that carry the class 1 integrase gene. <i>Microbial Genomics</i> , 2019 , 5,	4.4	31
160	Clonal ST131-22 strains from a healthy pig and a human urinary tract infection carry highly similar resistance and virulence plasmids. <i>Microbial Genomics</i> , 2019 , 5,	4.4	18
159	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	0.8	4
158	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in Escherichia coli of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019 , 3,	4.8	16

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157	Genetic Features of Mediated Colistin Resistance in CMY-2-Producing From Romanian Poultry. <i>Frontiers in Microbiology</i> , 2019 , 10, 2267	5.7	20	
156	The Diverse Functional Roles of Elongation Factor Tu (EF-Tu) in Microbial Pathogenesis. <i>Frontiers in Microbiology</i> , 2019 , 10, 2351	5.7	39	
155	Diversity of P1 phage-like elements in multidrug resistant Escherichia coli. <i>Scientific Reports</i> , 2019 , 9, 18861	4.9	20	
154	Vibrio cholerae residing in food vacuoles expelled by protozoa are more infectious in vivo. <i>Nature Microbiology</i> , 2019 , 4, 2466-2474	26.6	12	
153	Multidrug Resistant Uropathogenic ST405 With a Novel, Composite IS Transposon in a Unique Chromosomal Location. <i>Frontiers in Microbiology</i> , 2018 , 9, 3212	5.7	17	
152	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	3.5		
151	Analysis of Theileria orientalis draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. <i>BMC Genomics</i> , 2018 , 19, 298	4.5	14	
150	The quest for improved reproducibility in MALDI mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2018 , 37, 217-228	11	36	
149	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	5.6	10	
148	Extracellular DNA release from the genome-reduced pathogen Mycoplasma hyopneumoniae is essential for biofilm formation on abiotic surfaces. <i>Scientific Reports</i> , 2018 , 8, 10373	4.9	16	
147	Extracellular Actin Is a Receptor for. Frontiers in Cellular and Infection Microbiology, 2018, 8, 54	5.9	20	
146	Mycoplasma hyopneumoniae resides intracellularly within porcine epithelial cells. <i>Scientific Reports</i> , 2018 , 8, 17697	4.9	25	
145	Environmental dimensions of antibiotic resistance: assessment of basic science gaps. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	40	
144	Genomic analysis of multidrug-resistant Escherichia coli ST58 causing urosepsis. <i>International Journal of Antimicrobial Agents</i> , 2018 , 52, 430-435	14.3	40	
143	Defined chromosome structure in the genome-reduced bacterium Mycoplasma pneumoniae. <i>Nature Communications</i> , 2017 , 8, 14665	17.4	59	
142	Genomic islands 1 and 2 carry multiple antibiotic resistance genes in Pseudomonas aeruginosa ST235, ST253, ST111 and ST175 and are globally dispersed. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 620-622	5.1	17	
141	Elongation factor Tu is a multifunctional and processed moonlighting protein. <i>Scientific Reports</i> , 2017 , 7, 11227	4.9	57	
140	N-terminomics identifies widespread endoproteolysis and novel methionine excision in a genome-reduced bacterial pathogen. <i>Scientific Reports</i> , 2017 , 7, 11063	4.9	27	

139	Identification of a novel qnrA allele, qnrA8, in environmental Shewanella algae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 2949-2952	5.1	4
138	A Comprehensive Guide for Performing Sample Preparation and Top-Down Protein Analysis. <i>Proteomes</i> , 2017 , 5,	4.6	26
137	, an Evolutionary Dead-End Pathogen. Frontiers in Microbiology, 2017 , 8, 1054	5.7	21
136	Evaluation of ddRADseq for reduced representation metagenome sequencing. <i>PeerJ</i> , 2017 , 5, e3837	3.1	8
135	Porcine commensal Escherichia coli: a reservoir for class 1 integrons associated with IS26. <i>Microbial Genomics</i> , 2017 , 3,	4.4	43
134	Cross reactivity among the swine mycoplasmas as identified by protein microarray. <i>Veterinary Microbiology</i> , 2016 , 192, 204-212	3.3	13
133	Post-translational processing targets functionally diverse proteins in Mycoplasma hyopneumoniae. <i>Open Biology</i> , 2016 , 6, 150210	7	42
132	The application of terminomics for the identification of protein start sites and proteoforms in bacteria. <i>Proteomics</i> , 2016 , 16, 257-72	4.8	24
131	Comparative genomic analysis of toxin-negative strains of Clostridium difficile from humans and animals with symptoms of gastrointestinal disease. <i>BMC Microbiology</i> , 2016 , 16, 41	4.5	9
130	Genomic islands 1 and 2 play key roles in the evolution of extensively drug-resistant ST235 isolates of Pseudomonas aeruginosa. <i>Open Biology</i> , 2016 , 6,	7	33
129	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,		1
128	The Role of CD44 and ERM Proteins in Expression and Functionality of P-glycoprotein in Breast Cancer Cells. <i>Molecules</i> , 2016 , 21, 290	4.8	38
127	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	5.7	28
126	MHJ_0461 is a multifunctional leucine aminopeptidase on the surface of Mycoplasma hyopneumoniae. <i>Open Biology</i> , 2015 , 5, 140175	7	43
125	Temporal dynamics and subpopulation analysis of Theileria orientalis genotypes in cattle. <i>Infection, Genetics and Evolution</i> , 2015 , 32, 199-207	4.5	21
124	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic E. coli O157 lineage from Australian pigs. <i>BMC Genomics</i> , 2015 , 16, 165	4.5	21
123	Tn6026 and Tn6029 are found in complex resistance regions mobilised by diverse plasmids and chromosomal islands in multiple antibiotic resistant Enterobacteriaceae. <i>Plasmid</i> , 2015 , 80, 127-37	3.3	34
122	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, 637-44	2.2	17

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generates a functionally diverse array of cleavage fragments that bind multiple host molecules. <i>Cellular Microbiology</i> , 2015 , 17, 425-44	3.9	29	
Non-proteolytic functions of microbial proteases increase pathological complexity. <i>Proteomics</i> , 2015 , 15, 1075-88	4.8	11	
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, 1836-40	2.2	13	
P40 and P90 from Mpn142 are Targets of Multiple Processing Events on the Surface of. <i>Proteomes</i> , 2015 , 3, 512-537	4.6	14	
Exploitation of plasmin(ogen) by bacterial pathogens of veterinary significance. <i>Veterinary Microbiology</i> , 2015 , 178, 1-13	3.3	30	
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. <i>PLoS ONE</i> , 2015 , 10, e0115781	3.7	21	
Comparative proteomics and glycoproteomics reveal increased N-linked glycosylation and relaxed sequon specificity in Campylobacter jejuni NCTC11168 O. <i>Journal of Proteome Research</i> , 2014 , 13, 5136	- 50 6	37	
Evaluation of recombinant Mycoplasma hyopneumoniae P97/P102 paralogs formulated with selected adjuvants as vaccines against mycoplasmal pneumonia in pigs. <i>Vaccine</i> , 2014 , 32, 4333-41	4.1	20	
Cilium adhesin P216 (MHJ_0493) is a target of ectodomain shedding and aminopeptidase activity on the surface of Mycoplasma hyopneumoniae. <i>Journal of Proteome Research</i> , 2014 , 13, 2920-30	5.6	31	
Proteogenomic mapping of Mycoplasma hyopneumoniae virulent strain 232. <i>BMC Genomics</i> , 2014 , 15, 576	4.5	18	
Proteome analysis of multidrug-resistant, breast cancer-derived microparticles. <i>Journal of Extracellular Vesicles</i> , 2014 , 3,	16.4	38	
Genomic interplay in bacterial communities: implications for growth promoting practices in animal husbandry. <i>Frontiers in Microbiology</i> , 2014 , 5, 394	5.7	17	
A draft genome of Escherichia coli sequence type 127 strain 2009-46. Gut Pathogens, 2014 , 6, 32	5.4	7	
The genome of Clostridium difficile 5.3. <i>Gut Pathogens</i> , 2014 , 6, 4	5.4	13	
Formation of assemblies on cell membranes by secreted proteins: molecular studies of free light chain aggregates found on the surface of myeloma cells. <i>Biochemical Journal</i> , 2013 , 454, 479-89	3.8	10	
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. <i>Veterinary Microbiology</i> , 2013 , 164, 60-6	3.3	20	
Indigenous Vibrio cholerae strains from a non-endemic region are pathogenic. <i>Open Biology</i> , 2013 , 3, 120181	7	23	
P159 from Mycoplasma hyopneumoniae binds porcine cilia and heparin and is cleaved in a manner akin to ectodomain shedding. <i>Journal of Proteome Research</i> , 2013 , 12, 5891-903	5.6	36	
	Cellular Microbiology, 2015, 17, 425-44 Non-proteolytic functions of microbial proteases increase pathological complexity. Proteomics, 2015, 15, 1075-88 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. Rapid Communications in Mass Spectrometry, 2015, 29, 1836-40 P40 and P90 from Mpn142 are Targets of Multiple Processing Events on the Surface of. Proteomes, 2015, 3, 512-537 Exploitation of plasmin(ogen) by bacterial pathogens of veterinary significance. Veterinary Microbiology, 2015, 178, 1-13 A role for Tn6029 in the evolution of the complex antibiotic resistance gene loci in genomic Island 3 in enteroaggregative hemorrhagic Escherichia coli 0104:H4. PLoS ONE, 2015, 10, e0115781 Comparative proteomics and glycoproteomics reveal increased N-linked glycosylation and relaxed sequen specificity in Campylobacter jejuni NCTC11168 0. Journal of Proteome Research, 2014, 13, 5136 Evaluation of recombinant Mycoplasma hyopneumoniae P97/P102 paralogs formulated with selected adjuvants as vaccines against mycoplasmal pneumonia in pigs. Vaccine, 2014, 32, 4333-41 Clilium adhesin P216 (MHJ_0493) is a target of ectodomain shedding and aminopeptidase activity on the surface of Mycoplasma hyopneumoniae. Journal of Proteome Research, 2014, 13, 2920-30 Proteogenomic mapping of Mycoplasma hyopneumoniae virulent strain 232. BMC Genomics, 2014, 15, 576 Proteome analysis of multidrug-resistant, breast cancer-derived microparticles. Journal of Extracellular Vesicles, 2014, 3, Genomic interplay in bacterial communities: implications for growth promoting practices in animal husbandry. Frontiers in Microbiology, 2014, 5, 394 A draft genome of Escherichia coli sequence type 127 strain 2009-46. Gut Pathogens, 2014, 6, 32 The genome of Clostridium difficile 5.3. 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PLoS ONE, 2015, 10, e0115781 Comparative proteomics and glycoproteomics reveal increased N-linked glycosylation and relaxed sequen specificity in Campylobacter jejuni NCTC11168 O. Journal of Proteome Research, 2014, 13, 5136-50 Evaluation of recombinant Mycoplasma hyooneumoniae P97/P102 paralogs formulated with selected adjuvants as vaccines against mycoplasmal pneumonia in pigs. Vaccine, 2014, 32, 4333-41 Cilium adhesin P216 (MHJ_0493) is a target of ectodomain shedding and aminopeptidase activity on the surface of Mycoplasma hyopneumoniae. Journal of Proteome Research, 2014, 13, 2920-30 Proteogenomic mapping of Mycoplasma hyopneumoniae virulent strain 232. BMC Genomics, 2014, 15, 576 Proteome analysis of multidrug-resistant, breast cancer-derived microparticles. Journal of Extracellular Vesicles, 2014, 3, Genomic interplay in bacterial communities: implications for growth promoting practices in animal husbandry. Frontiers in Microbiology, 2014, 5, 394 The genome of Clostridium difficile 5.3. Gut Pathogens, 2014, 6, 4 Formation of assemblies on cell membranes by secreted proteins: molecular studies of free llight chain aggregates found on the surface of myeloma cells. Biochemical Journal, 2013, 454, 479-89 Alsmin activity in	Cellular Microbiology, 2015, 17, 425-44 Non-proteolytic Functions of microbial proteases increase pathological complexity. Proteomics, 2015, 15, 1075-88 A non-instrument-based method for the analysis of formallin-fixed paraffin-embedded human spinal cord via matrix-assisted laser desorption/foinsiation imaging mass spectrometry. Rapid 2.2 13 Communications in Mass Spectrometry, 2015, 29, 1836-40 P40 and P90 from Mpn142 are Targets of Multiple Processing Events on the Surface of. Proteomes, 2015, 3, 512-537 Exploitation of plasmin(ogen) by bacterial pathogens of veterinary significance. Veterinary Microbiology, 2015, 178, 1-13 A role for Tin6029 in the evolution of the complex antibiotic resistance gene loci in genomic island 3 in enteroaggregative hemorrhagic Escherichia coli 0104:H4. PLoS ONE, 2015, 10, e0115781 Comparative proteomics and glycoproteomics reveal increased N-linked glycosylation and relaxed sequen specificity in Campylobacter jejuni NCTC11168 0. Journal of Proteome Research, 2014, 13, 5136-50 Evaluation of recombinant Mycoplasma hyoponeumoniae P97/P102 paralogs formulated with selected adjuvants as vaccines against mycoplasmal pneumonia in pigs. Vaccine, 2014, 32, 4333-41 Cillium adhesin P216 (MHJ_0493) is a target of ectodomain shedding and aminopeptidase activity on the surface of Mycoplasma hyopneumoniae. Journal of Proteome Research, 2014, 13, 290-30 Froteogenomic mapping of Mycoplasma hyopneumoniae virulent strain 232. BMC Genomics, 2014, 15, 576 Proteome analysis of multidrug-resistant, breast cancer-derived microparticles. Journal of Extracellular Vesicles, 2014, 3, 38 Genomic interplay in bacterial communities: implications for growth promoting practices in animal hybabandly. Frontiers in Microbiology, 2014, 5, 394 A draft genome of Escherichia coli sequence type 127 strain 2009-46. Gut Pathogens, 2014, 6, 32 The genome of Clostridium difficile 5.3. Gut Pathogens, 2014, 6, 4 Formation of assemblies on cell membranes by secreted proteins: molecular studies of free light chai

103	MHJ_0125 is an M42 glutamyl aminopeptidase that moonlights as a multifunctional adhesin on the surface of Mycoplasma hyopneumoniae. <i>Open Biology</i> , 2013 , 3, 130017	7	46
102	Mobile elements, zoonotic pathogens and commensal bacteria: conduits for the delivery of resistance genes into humans, production animals and soil microbiota. <i>Frontiers in Microbiology</i> , 2013 , 4, 86	5.7	78
101	Deletion of integron-associated gene cassettes impact on the surface properties of Vibrio rotiferianus DAT722. <i>PLoS ONE</i> , 2013 , 8, e58430	3.7	6
100	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. <i>PLoS ONE</i> , 2013 , 8, e78862	3.7	37
99	Mobilized Integrons: Team Players in the Spread of Antibiotic Resistance Genes 2013 , 79-103		2
98	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. <i>Veterinary Microbiology</i> , 2012 , 161, 186-95	3.3	41
97	Class 1 integron-associated spread of resistance regions in Pseudomonas aeruginosa: plasmid or chromosomal platforms?. <i>Journal of Antimicrobial Chemotherapy</i> , 2012 , 67, 1799-800	5.1	10
96	Mycoplasma hyopneumoniae Surface proteins Mhp385 and Mhp384 bind host cilia and glycosaminoglycans and are endoproteolytically processed by proteases that recognize different cleavage motifs. <i>Journal of Proteome Research</i> , 2012 , 11, 1924-36	5.6	44
95	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. <i>Journal of Molecular Medicine</i> , 2012 , 90, 1197-207	5.5	40
94	Mhp182 (P102) binds fibronectin and contributes to the recruitment of plasmin(ogen) to the Mycoplasma hyopneumoniae cell surface. <i>Cellular Microbiology</i> , 2012 , 14, 81-94	3.9	63
93	Diverse mobilized class 1 integrons are common in the chromosomes of pathogenic Pseudomonas aeruginosa clinical isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 2169-72	5.9	33
92	Modification of the Campylobacter jejuni N-linked glycan by EptC protein-mediated addition of phosphoethanolamine. <i>Journal of Biological Chemistry</i> , 2012 , 287, 29384-96	5.4	53
91	Characterization of cleavage events in the multifunctional cilium adhesin Mhp684 (P146) reveals a mechanism by which Mycoplasma hyopneumoniae regulates surface topography. <i>MBio</i> , 2012 , 3,	7.8	44
90	Molecular characterization of a 21.4 kilobase antibiotic resistance plasmid from an Ehemolytic Escherichia coli O108:H- human clinical isolate. <i>PLoS ONE</i> , 2012 , 7, e34718	3.7	
89	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. <i>Molecular and</i>	7.6	233
88	Cellular Proteomics, 2011 , 10, M000031-MCP201 Mhp107 is a member of the multifunctional adhesin family of Mycoplasma hyopneumoniae. <i>Journal of Biological Chemistry</i> , 2011 , 286, 10097-104	5.4	40
87	Sequence TTKF? QE defines the site of proteolytic cleavage in Mhp683 protein, a novel glycosaminoglycan and cilium adhesin of Mycoplasma hyopneumoniae. <i>Journal of Biological Chemistry</i> , 2011 , 286, 41217-41229	5.4	40
86	Repeat regions R1 and R2 in the P97 paralogue Mhp271 of Mycoplasma hyopneumoniae bind heparin, fibronectin and porcine cilia. <i>Molecular Microbiology</i> , 2010 , 78, 444-58	4.1	60

(2008-2010)

85	Distribution of class 1 integrons with IS26-mediated deletions in their 3Rconserved segments in Escherichia coli of human and animal origin. <i>PLoS ONE</i> , 2010 , 5, e12754	3.7	72
84	Multiple antibiotic resistance gene recruitment onto the enterohemorrhagic Escherichia coli virulence plasmid. <i>FASEB Journal</i> , 2010 , 24, 1160-6	0.9	60
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