

Mick Watson

List of Publications by Year in descending order

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Version: 2024-02-01

99
papers

8,242
citations

66315

42
h-index

56687

83
g-index

129
all docs

129
docs citations

129
times ranked

11662
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of cecal microbiota transplantation between different broiler breeds on the chick flora in the first week of life. <i>Poultry Science</i> , 2022, 101, 101624.	1.5	10
2	Bovine host genome acts on rumen microbiome function linked to methane emissions. <i>Communications Biology</i> , 2022, 5, 350.	2.0	25
3	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	20
4	Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. <i>Scientific Reports</i> , 2021, 11, 1990.	1.6	32
5	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
6	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	3.8	74
7	Single-cell RNA-seq reveals CD16 ⁺ monocytes as key regulators of human monocyte transcriptional response to <i>Toxoplasma</i> . <i>Scientific Reports</i> , 2020, 10, 21047.	1.6	8
8	1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. <i>Genome Biology</i> , 2020, 21, 229.	3.8	38
9	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	3.3	187
10	Identification of Microbial Genetic Capacities and Potential Mechanisms Within the Rumen Microbiome Explaining Differences in Beef Cattle Feed Efficiency. <i>Frontiers in Microbiology</i> , 2020, 11, 1229.	1.5	28
11	Assembly of hundreds of novel bacterial genomes from the chicken caecum. <i>Genome Biology</i> , 2020, 21, 34.	3.8	112
12	Role of Cecal Microbiota in the Differential Resistance of Inbred Chicken Lines to Colonization by <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	19
13	Identification of Complex Rumen Microbiome Interaction Within Diverse Functional Niches as Mechanisms Affecting the Variation of Methane Emissions in Bovine. <i>Frontiers in Microbiology</i> , 2020, 11, 659.	1.5	51
14	Unravelling the Role of Rumen Microbial Communities, Genes, and Activities on Milk Fatty Acid Profile Using a Combination of Omics Approaches. <i>Frontiers in Microbiology</i> , 2020, 11, 590441.	1.5	11
15	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. <i>Nature Biotechnology</i> , 2019, 37, 953-961.	9.4	353
16	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	3.8	66
17	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019, 47, 7262-7275.	6.5	4
18	Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 701.	1.1	43

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19	Transcriptional Response of Ovine Lung to Infection with Jaagsiekte Sheep Retrovirus. <i>Journal of Virology</i> , 2019, 93, .	1.5	12
20	Errors in long-read assemblies can critically affect protein prediction. <i>Nature Biotechnology</i> , 2019, 37, 124-126.	9.4	185
21	Marek's Disease Virus-Encoded MicroRNA 155 Ortholog Critical for the Induction of Lymphomas Is Not Essential for the Proliferation of Transformed Cell Lines. <i>Journal of Virology</i> , 2019, 93, .	1.5	29
22	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. <i>PLoS Genetics</i> , 2019, 15, e1008102.	1.5	14
23	Temporal stability of the rumen microbiota in beef cattle, and response to diet and supplements. <i>Animal Microbiome</i> , 2019, 1, 16.	1.5	29
24	Development of the duodenal, ileal, jejunal and caecal microbiota in chickens. <i>Animal Microbiome</i> , 2019, 1, 17.	1.5	40
25	MAGpy: a reproducible pipeline for the downstream analysis of metagenome-assembled genomes (MAGs). <i>Bioinformatics</i> , 2019, 35, 2150-2152.	1.8	33
26	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 65-88.	3.6	172
27	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018, 9, 870.	5.8	405
28	Fat accretion measurements strengthen the relationship between feed conversion efficiency and Nitrogen isotopic discrimination while rumen microbial genes contribute little. <i>Scientific Reports</i> , 2018, 8, 3854.	1.6	7
29	The Madness of Microbiome: Attempting To Find Consensus "Best Practice" for 16S Microbiome Studies. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	422
30	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	5.8	51
31	Livestock 2.0 " genome editing for fitter, healthier, and more productive farmed animals. <i>Genome Biology</i> , 2018, 19, 204.	3.8	114
32	Chromosome Level Genome Assembly and Comparative Genomics between Three Falcon Species Reveals an Unusual Pattern of Genome Organisation. <i>Diversity</i> , 2018, 10, 113.	0.7	31
33	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	1.5	255
34	<i>Aedes aegypti</i> Piwi4 Is a Noncanonical PIWI Protein Involved in Antiviral Responses. <i>MSphere</i> , 2017, 2, .	1.3	92
35	Tandem Amplification of the Staphylococcal Cassette Chromosome <i>mecA</i> Element Can Drive High-Level Methicillin Resistance in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	19
36	MinION, nanopore sequencing of environmental metagenomes: a synthetic approach. <i>GigaScience</i> , 2017, 6, 1-10.	3.3	111

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37	poRe GUIs for parallel and real-time processing of MinION sequence data. <i>Bioinformatics</i> , 2017, 33, 2207-2208.	1.8	7
38	RNA Interference Restricts Rift Valley Fever Virus in Multiple Insect Systems. <i>MSphere</i> , 2017, 2, .	1.3	52
39	A Review of Bioinformatics Tools for Bio-Propecting from Metagenomic Sequence Data. <i>Frontiers in Genetics</i> , 2017, 8, 23.	1.1	137
40	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>). <i>PLoS Genetics</i> , 2017, 13, e1006997.	1.5	210
41	The Antiviral RNAi Response in Vector and Non-vector Cells against Orthobunyaviruses. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005272.	1.3	43
42	The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle. <i>Microbiome</i> , 2017, 5, 159.	4.9	128
43	Identification, Comparison, and Validation of Robust Rumen Microbial Biomarkers for Methane Emissions Using Diverse <i>Bos Taurus</i> Breeds and Basal Diets. <i>Frontiers in Microbiology</i> , 2017, 8, 2642.	1.5	64
44	Activation of gga-miR-155 by reticuloendotheliosis virus T strain and its contribution to transformation. <i>Journal of General Virology</i> , 2017, 98, 810-820.	1.3	11
45	Differentially expressed genes during spontaneous lytic switch of Marek's disease virus in lymphoblastoid cell lines determined by global gene expression profiling. <i>Journal of General Virology</i> , 2017, 98, 779-790.	1.3	10
46	Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance. <i>PLoS Genetics</i> , 2016, 12, e1005846.	1.5	267
47	Rapid identification of bovine MHCII haplotypes in genetically divergent cattle populations using next-generation sequencing. <i>Immunogenetics</i> , 2016, 68, 765-781.	1.2	14
48	<sc>GO</sc>â€œ<sc>FAANG</sc> meeting: a Gathering On Functional Annotation of <sc>Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
49	The incredible complexity of RNA splicing. <i>Genome Biology</i> , 2016, 17, 265.	3.8	5
50	The rumen microbial metagenome associated with high methane production in cattle. <i>BMC Genomics</i> , 2015, 16, 839.	1.2	306
51	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. <i>BMC Genomics</i> , 2015, 16, 970.	1.2	22
52	<i>Ixodes scapularis</i> and <i>Ixodes ricinus</i> tick cell lines respond to infection with tick-borne encephalitis virus: transcriptomic and proteomic analysis. <i>Parasites and Vectors</i> , 2015, 8, 599.	1.0	71
53	Identification of Low-Confidence Regions in the Pig Reference Genome (<i>Sscrofa10.2</i>). <i>Frontiers in Genetics</i> , 2015, 6, 338.	1.1	28
54	When will â€œopen scienceâ€™ become simply â€œscienceâ€™?. <i>Genome Biology</i> , 2015, 16, 101.	3.8	62

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55	A single chromosome assembly of <i>Bacteroides fragilis</i> strain BE1 from Illumina and MinION nanopore sequencing data. <i>GigaScience</i> , 2015, 4, 60.	3.3	64
56	Ability of the Encephalitic Arbovirus Semliki Forest Virus To Cross the Blood-Brain Barrier Is Determined by the Charge of the E2 Glycoprotein. <i>Journal of Virology</i> , 2015, 89, 7536-7549.	1.5	46
57	Exome Sequencing: Current and Future Perspectives. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1543-1550.	0.8	165
58	poRe: an R package for the visualization and analysis of nanopore sequencing data. <i>Bioinformatics</i> , 2015, 31, 114-115.	1.8	85
59	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. <i>Bioinformatics</i> , 2015, 31, 140-142.	1.8	34
60	Successful test launch for nanopore sequencing. <i>Nature Methods</i> , 2015, 12, 303-304.	9.0	129
61	Errors in RNA-Seq quantification affect genes of relevance to human disease. <i>Genome Biology</i> , 2015, 16, 177.	3.8	153
62	Global Gene Expression Profiling of Myeloid Immune Cell Subsets in Response to In Vitro Challenge with Porcine Circovirus 2b. <i>PLoS ONE</i> , 2014, 9, e91081.	1.1	9
63	Diversity and Community Composition of Methanogenic Archaea in the Rumen of Scottish Upland Sheep Assessed by Different Methods. <i>PLoS ONE</i> , 2014, 9, e106491.	1.1	32
64	Definition of the Cattle Killer Cell Ig-like Receptor Gene Family: Comparison with Aurochs and Human Counterparts. <i>Journal of Immunology</i> , 2014, 193, 6016-6030.	0.4	29
65	An Avian Retrovirus Uses Canonical Expression and Processing Mechanisms To Generate Viral MicroRNA. <i>Journal of Virology</i> , 2014, 88, 2-9.	1.5	40
66	Quality assessment and control of high-throughput sequencing data. <i>Frontiers in Genetics</i> , 2014, 5, 235.	1.1	8
67	Induction and suppression of tick cell antiviral RNAi responses by tick-borne flaviviruses. <i>Nucleic Acids Research</i> , 2014, 42, 9436-9446.	6.5	118
68	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Elephantidae). <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 222-232.	1.0	31
69	Illuminating the future of DNA sequencing. <i>Genome Biology</i> , 2014, 15, 108.	13.9	39
70	Design and development of exome capture sequencing for the domestic pig (<i>Sus scrofa</i>). <i>BMC Genomics</i> , 2014, 15, 550.	1.2	24
71	Low coverage sequencing of two Asian elephant (<i>Elephas maximus</i>) genomes. <i>GigaScience</i> , 2014, 3, 12.	3.3	11
72	Knockdown of piRNA pathway proteins results in enhanced Semliki Forest virus production in mosquito cells. <i>Journal of General Virology</i> , 2014, 95, 244-244.	1.3	0

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73	So you want to be a computational biologist?. <i>Nature Biotechnology</i> , 2013, 31, 996-998.	9.4	24
74	Knockdown of piRNA pathway proteins results in enhanced Semliki Forest virus production in mosquito cells. <i>Journal of General Virology</i> , 2013, 94, 1680-1689.	1.3	184
75	The automatic annotation of bacterial genomes. <i>Briefings in Bioinformatics</i> , 2013, 14, 1-12.	3.2	122
76	RNA Interference Targets Arbovirus Replication in Culicoides Cells. <i>Journal of Virology</i> , 2013, 87, 2441-2454.	1.5	75
77	viRome: an R package for the visualization and analysis of viral small RNA sequence datasets. <i>Bioinformatics</i> , 2013, 29, 1902-1903.	1.8	41
78	Complete Genome Sequences of Elephant Endotheliotropic Herpesviruses 1A and 1B Determined Directly from Fatal Cases. <i>Journal of Virology</i> , 2013, 87, 6700-6712.	1.5	52
79	MicroRNA expression profiles in avian haemopoietic cells. <i>Frontiers in Genetics</i> , 2013, 4, 153.	1.1	14
80	Meta4: a web application for sharing and annotating metagenomic gene predictions using web services. <i>Frontiers in Genetics</i> , 2013, 4, 168.	1.1	8
81	Novel microRNAs encoded by duck enteritis virus. <i>Journal of General Virology</i> , 2012, 93, 1530-1536.	1.3	17
82	Early response of bovine alveolar macrophages to infection with live and heat-killed <i>Mycobacterium bovis</i> . <i>Developmental and Comparative Immunology</i> , 2011, 35, 580-591.	1.0	16
83	Song exposure regulates known and novel microRNAs in the zebra finch auditory forebrain. <i>BMC Genomics</i> , 2011, 12, 277.	1.2	45
84	Genome Sequences of <i>Salmonella enterica</i> Serovar Typhimurium, Choleraesuis, Dublin, and Gallinarum Strains of Well- Defined Virulence in Food-Producing Animals. <i>Journal of Bacteriology</i> , 2011, 193, 3162-3163.	1.0	61
85	The bovine chemokine receptors and their mRNA abundance in mononuclear phagocytes. <i>BMC Genomics</i> , 2010, 11, 439.	1.2	12
86	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	13.7	770
87	Regional and global changes in TCR α T cell repertoires in the gut are dependent upon the complexity of the enteric microflora. <i>Developmental and Comparative Immunology</i> , 2010, 34, 406-417.	1.0	53
88	Differential expression of microRNAs in Marek's disease virus-transformed T-lymphoma cell lines. <i>Journal of General Virology</i> , 2009, 90, 1551-1559.	1.3	59
89	Novel MicroRNAs (miRNAs) Encoded by Herpesvirus of Turkeys: Evidence of miRNA Evolution by Duplication. <i>Journal of Virology</i> , 2009, 83, 6969-6973.	1.5	28
90	Correlation between lymph node pathology and chemokine expression during bovine tuberculosis. <i>Tuberculosis</i> , 2009, 89, 417-422.	0.8	20

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91	Differential protein profiling as a potential multi-marker approach for TSE diagnosis. BMC Infectious Diseases, 2009, 9, 188.	1.3	9
92	Analysis of the role of 13 major fimbrial subunits in colonisation of the chicken intestines by Salmonella enterica serovar Enteritidis reveals a role for a novel locus. BMC Microbiology, 2008, 8, 228.	1.3	54
93	Granulocyte chemotactic properties of M. tuberculosis versus M. bovis-infected bovine alveolar macrophages. Molecular Immunology, 2008, 45, 740-749.	1.0	36
94	Comparative genome analysis of <i>Salmonella</i> Enteritidis PT4 and <i>Salmonella</i> Gallinarum 287/91 provides insights into evolutionary and host adaptation pathways. Genome Research, 2008, 18, 1624-1637.	2.4	394
95	MicroRNA Profile of Marek's Disease Virus-Transformed T-Cell Line MSB-1: Predominance of Virus-Encoded MicroRNAs. Journal of Virology, 2008, 82, 4007-4015.	1.5	130
96	DetectiV: visualization, normalization and significance testing for pathogen-detection microarray data. Genome Biology, 2007, 8, R190.	13.9	23
97	Analysis of the real EADGENE data set: Multivariate approaches and post analysis (Open Access) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	1
98	CoXpress: differential co-expression in gene expression data. BMC Bioinformatics, 2006, 7, 509.	1.2	145
99	ProGenExpress: visualization of quantitative data on prokaryotic genomes. BMC Bioinformatics, 2005, 6, 98.	1.2	5