

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	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	13.7	770
2	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
3	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018, 9, 870.	5.8	405
4	Comparative genome analysis of <i>Salmonella</i> Enteritidis PT4 and <i>Salmonella</i> Gallinarum 287/91 provides insights into evolutionary and host adaptation pathways. <i>Genome Research</i> , 2008, 18, 1624-1637.	2.4	394
5	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
6	The rumen microbial metagenome associated with high methane production in cattle. <i>BMC Genomics</i> , 2015, 16, 839.	1.2	306
7	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
8	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
9	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
10	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	3.3	187
11	Errors in long-read assemblies can critically affect protein prediction. <i>Nature Biotechnology</i> , 2019, 37, 124-126.	9.4	185
12	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
13	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 65-88.	3.6	172
14	Exome Sequencing: Current and Future Perspectives. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1543-1550.	0.8	165
15	Errors in RNA-Seq quantification affect genes of relevance to human disease. <i>Genome Biology</i> , 2015, 16, 177.	3.8	153
16	CoXpress: differential co-expression in gene expression data. <i>BMC Bioinformatics</i> , 2006, 7, 509.	1.2	145
17	A Review of Bioinformatics Tools for Bio-Prospecting from Metagenomic Sequence Data. <i>Frontiers in Genetics</i> , 2017, 8, 23.	1.1	137
18	MicroRNA Profile of Marek's Disease Virus-Transformed T-Cell Line MSB-1: Predominance of Virus-Encoded MicroRNAs. <i>Journal of Virology</i> , 2008, 82, 4007-4015.	1.5	130

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19	Successful test launch for nanopore sequencing. <i>Nature Methods</i> , 2015, 12, 303-304.	9.0	129
20	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
21	The automatic annotation of bacterial genomes. <i>Briefings in Bioinformatics</i> , 2013, 14, 1-12.	3.2	122
22	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
23	Livestock 2.0 – genome editing for fitter, healthier, and more productive farmed animals. <i>Genome Biology</i> , 2018, 19, 204.	3.8	114
24	Assembly of hundreds of novel bacterial genomes from the chicken caecum. <i>Genome Biology</i> , 2020, 21, 34.	3.8	112
25	MinION, nanopore sequencing of environmental metagenomes: a synthetic approach. <i>GigaScience</i> , 2017, 6, 1-10.	3.3	111
26	<i>Aedes aegypti</i> Piwi4 Is a Noncanonical PIWI Protein Involved in Antiviral Responses. <i>MSphere</i> , 2017, 2, .	1.3	92
27	poRe: an R package for the visualization and analysis of nanopore sequencing data. <i>Bioinformatics</i> , 2015, 31, 114-115.	1.8	85
28	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
29	RNA Interference Targets Arbovirus Replication in <i>Culicoides</i> Cells. <i>Journal of Virology</i> , 2013, 87, 2441-2454.	1.5	75
30	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	3.8	74
31	<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
32	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
33	<sc>GO</sc> – FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
34	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
35	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
36	When will “open science” become simply “science”? <i>Genome Biology</i> , 2015, 16, 101.	3.8	62

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37	Genome Sequences of Salmonella enterica Serovar Typhimurium, Choleraesuis, Dublin, and Gallinarum Strains of Well- Defined Virulence in Food-Producing Animals. Journal of Bacteriology, 2011, 193, 3162-3163.	1.0	61
38	Differential expression of microRNAs in Marek's disease virus-transformed T-lymphoma cell lines. Journal of General Virology, 2009, 90, 1551-1559.	1.3	59
39	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
40	Regional and global changes in TCR β T cell repertoires in the gut are dependent upon the complexity of the enteric microflora. Developmental and Comparative Immunology, 2010, 34, 406-417.	1.0	53
41	Complete Genome Sequences of Elephant Endotheliotropic Herpesviruses 1A and 1B Determined Directly from Fatal Cases. Journal of Virology, 2013, 87, 6700-6712.	1.5	52
42	RNA Interference Restricts Rift Valley Fever Virus in Multiple Insect Systems. MSphere, 2017, 2, .	1.3	52
43	Characterisation of the British honey bee metagenome. Nature Communications, 2018, 9, 4995.	5.8	51
44	Identification of Complex Rumen Microbiome Interaction Within Diverse Functional Niches as Mechanisms Affecting the Variation of Methane Emissions in Bovine. Frontiers in Microbiology, 2020, 11, 659.	1.5	51
45	Ability of the Encephalitic Arbovirus Semliki Forest Virus To Cross the Blood-Brain Barrier Is Determined by the Charge of the E2 Glycoprotein. Journal of Virology, 2015, 89, 7536-7549.	1.5	46
46	Song exposure regulates known and novel microRNAs in the zebra finch auditory forebrain. BMC Genomics, 2011, 12, 277.	1.2	45
47	The Antiviral RNAi Response in Vector and Non-vector Cells against Orthobunyaviruses. PLoS Neglected Tropical Diseases, 2017, 11, e0005272.	1.3	43
48	Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. Frontiers in Genetics, 2019, 10, 701.	1.1	43
49	viRome: an R package for the visualization and analysis of viral small RNA sequence datasets. Bioinformatics, 2013, 29, 1902-1903.	1.8	41
50	An Avian Retrovirus Uses Canonical Expression and Processing Mechanisms To Generate Viral MicroRNA. Journal of Virology, 2014, 88, 2-9.	1.5	40
51	Development of the duodenal, ileal, jejunal and caecal microbiota in chickens. Animal Microbiome, 2019, 1, 17.	1.5	40
52	Illuminating the future of DNA sequencing. Genome Biology, 2014, 15, 108.	13.9	39
53	1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. Genome Biology, 2020, 21, 229.	3.8	38
54	Granulocyte chemotactic properties of M. tuberculosis versus M. bovis-infected bovine alveolar macrophages. Molecular Immunology, 2008, 45, 740-749.	1.0	36

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55	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. <i>Bioinformatics</i> , 2015, 31, 140-142.	1.8	34
56	MAGpy: a reproducible pipeline for the downstream analysis of metagenome-assembled genomes (MAGs). <i>Bioinformatics</i> , 2019, 35, 2150-2152.	1.8	33
57	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
58	Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. <i>Scientific Reports</i> , 2021, 11, 1990.	1.6	32
59	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
60	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
61	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
62	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
63	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
64	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
65	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
66	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
67	Bovine host genome acts on rumen microbiome function linked to methane emissions. <i>Communications Biology</i> , 2022, 5, 350.	2.0	25
68	So you want to be a computational biologist?. <i>Nature Biotechnology</i> , 2013, 31, 996-998.	9.4	24
69	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
70	DetectiV: visualization, normalization and significance testing for pathogen-detection microarray data. <i>Genome Biology</i> , 2007, 8, R190.	13.9	23
71	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. <i>BMC Genomics</i> , 2015, 16, 970.	1.2	22
72	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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73	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	20
74	Tandem Amplification of the Staphylococcal Cassette Chromosome <i>mec</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
75	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
76	Novel microRNAs encoded by duck enteritis virus. <i>Journal of General Virology</i> , 2012, 93, 1530-1536.	1.3	17
77	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
78	MicroRNA expression profiles in avian haemopoietic cells. <i>Frontiers in Genetics</i> , 2013, 4, 153.	1.1	14
79	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
80	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. <i>PLoS Genetics</i> , 2019, 15, e1008102.	1.5	14
81	The bovine chemokine receptors and their mRNA abundance in mononuclear phagocytes. <i>BMC Genomics</i> , 2010, 11, 439.	1.2	12
82	Transcriptional Response of Ovine Lung to Infection with Jaagsiekte Sheep Retrovirus. <i>Journal of Virology</i> , 2019, 93, .	1.5	12
83	Low coverage sequencing of two Asian elephant (<i>Elephas maximus</i>) genomes. <i>GigaScience</i> , 2014, 3, 12.	3.3	11
84	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
85	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
86	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
87	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
88	Differential protein profiling as a potential multi-marker approach for TSE diagnosis. <i>BMC Infectious Diseases</i> , 2009, 9, 188.	1.3	9
89	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
90	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

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91	Quality assessment and control of high-throughput sequencing data. <i>Frontiers in Genetics</i> , 2014, 5, 235.	1.1	8
92	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
93	poRe GUIs for parallel and real-time processing of MinION sequence data. <i>Bioinformatics</i> , 2017, 33, 2207-2208.	1.8	7
94	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
95	ProGenExpress: visualization of quantitative data on prokaryotic genomes. <i>BMC Bioinformatics</i> , 2005, 6, 98.	1.2	5
96	The incredible complexity of RNA splicing. <i>Genome Biology</i> , 2016, 17, 265.	3.8	5
97	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019, 47, 7262-7275.	6.5	4
98	Analysis of the real EADGENE data set: Multivariate approaches and post analysis (Open Access) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	1
99	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