Chris Creevey

List of Publications by Year
in descending order

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84 papers	9,443 citations	101543 36 h-index	53230 85 g-index
100 all docs	100 docs citations	100 times ranked	15422 citing authors

#	Article	IF	Citations
1	Adult schistosomes have an epithelial bacterial population distinct from the surrounding mammalian host blood. PLoS ONE, 2022, 17, e0263188.	2.5	5
2	Using the forces of hydrodynamic countercurrent chromatography for the study of bacteriophages. Access Microbiology, 2022, 4, 000310.	0.5	1
3	Forage grass growth under future climate change scenarios affects fermentation and ruminant efficiency. Scientific Reports, 2022, 12, 4454.	3.3	3
4	Whole-Genome Sequencing and Comparative Genomic Analysis of Antimicrobial Producing Streptococcus lutetiensis from the Rumen. Microorganisms, 2022, 10, 551.	3.6	2
5	No one tool to rule them all: prokaryotic gene prediction tool annotations are highly dependent on the organism of study. Bioinformatics, 2022, 38, 1198-1207.	4.1	20
6	In silico identification of two peptides with antibacterial activity against multidrug-resistant Staphylococcus aureus. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	11
7	On the complexity of haplotyping a microbial community. Bioinformatics, 2021, 37, 1360-1366.	4.1	17
8	The rumen eukaryotome is a source of novel antimicrobial peptides with therapeutic potential. BMC Microbiology, 2021, 21, 105.	3.3	11
9	Long-Term Effects of Dietary Supplementation with Olive Oil and Hydrogenated Vegetable Oil on the Rumen Microbiome of Dairy Cows. Microorganisms, 2021, 9, 1121.	3.6	7
10	Microbiomes attached to fresh perennial ryegrass are temporally resilient and adapt to changing ecological niches. Microbiome, 2021, 9, 143.	11.1	9
11	Characterization of an Ex Vivo Equine Endometrial Tissue Culture Model Using Next-Generation RNA-Sequencing Technology. Animals, 2021, 11, 1995.	2.3	0
12	Phylogenetic systematics of Butyrivibrio and Pseudobutyrivibrio genomes illustrate vast taxonomic diversity, open genomes and an abundance of carbohydrate-active enzyme family isoforms. Microbial Genomics, 2021, 7, .	2.0	9
13	Genomic and gene expression evidence of nonribosomal peptide and polyketide production among ruminal bacteria: a potential role in niche colonization?. FEMS Microbiology Ecology, 2020, 96, .	2.7	9
14	The Isolation and Genome Sequencing of Five Novel Bacteriophages From the Rumen Active Against Butyrivibrio fibrisolvens. Frontiers in Microbiology, 2020, 11, 1588.	3.5	5
15	Insights into the skin of caecilian amphibians from gene expression profiles. BMC Genomics, 2020, 21, 515.	2.8	4
16	Rumen Protozoa Play a Significant Role in Fungal Predation and Plant Carbohydrate Breakdown. Frontiers in Microbiology, 2020, 11, 720.	3.5	21
17	Can rumen bacteria communicate to each other?. Microbiome, 2020, 8, 23.	11.1	43
18	Rumen Virus Populations: Technological Advances Enhancing Current Understanding. Frontiers in Microbiology, 2020, 11, 450.	3.5	22

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19	Interaction of preimplantation factor with the global bovine endometrial transcriptome. PLoS ONE, 2020, 15, e0242874.	2.5	4
20	Gene Fusions Derived by Transcriptional Readthrough are Driven by Segmental Duplication in Human. Genome Biology and Evolution, 2019, 11, 2678-2690.	2.5	7
21	Improvement of Feed Efficiency in Pigs through Microbial Modulation via Fecal Microbiota Transplantation in Sows and Dietary Supplementation of Inulin in Offspring. Applied and Environmental Microbiology, 2019, 85, .	3.1	33
22	What lies beneath? Molecular evolution during the radiation of caecilian amphibians. BMC Genomics, 2019, 20, 354.	2.8	7
23	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. Molecular Biology and Evolution, 2019, 36, 1344-1356.	8.9	56
24	From treetops to tabletops: a preliminary investigation of how plants are represented in popular modern board games. Plants People Planet, 2019, 1, 290-300.	3.3	3
25	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. IScience, 2019, 21, 587-602.	4.1	27
26	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. Microbiome, 2019, 7, 6.	11.1	150
27	Multi-tissue transcriptomes of caecilian amphibians highlight incomplete knowledge of vertebrate gene families. DNA Research, 2019, 26, 13-20.	3.4	19
28	Deep sequence analysis reveals the ovine rumen as a reservoir of antibiotic resistance genes. Environmental Pollution, 2018, 235, 571-575.	7.5	26
29	Fecal Microbiota Transplantation in Gestating Sows and Neonatal Offspring Alters Lifetime Intestinal Microbiota and Growth in Offspring. MSystems, 2018, 3, .	3.8	57
30	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	17.5	414
31	Analysis of the Rumen Microbiome and Metabolome to Study the Effect of an Antimethanogenic Treatment Applied in Early Life of Kid Goats. Frontiers in Microbiology, 2018, 9, 2227.	3.5	31
32	CowPI: A Rumen Microbiome Focussed Version of the PICRUSt Functional Inference Software. Frontiers in Microbiology, 2018, 9, 1095.	3.5	132
33	Meta-proteomics of rumen microbiota indicates niche compartmentalisation and functional dominance in a limited number of metabolic pathways between abundant bacteria. Scientific Reports, 2018, 8, 10504.	3.3	59
34	Spherical: an iterative workflow for assembling metagenomic datasets. BMC Bioinformatics, 2018, 19, 20.	2.6	9
35	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. Frontiers in Microbiology, 2018, 9, 2161.	3.5	255
36	Divergent functional isoforms drive niche specialisation for nutrient acquisition and use in rumen microbiome. ISME Journal, 2017, 11, 932-944.	9.8	70

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37	Differential gene expression in the endometrium reveals cytoskeletal and immunological genes in lactating dairy cows genetically divergent for fertility traits. Reproduction, Fertility and Development, 2017, 29, 274.	0.4	55
38	The rumen microbiome: an underexplored resource for novel antimicrobial discovery. Npj Biofilms and Microbiomes, 2017, 3, 33.	6.4	51
39	Buwchitin: A Ruminal Peptide with Antimicrobial Potential against Enterococcus faecalis. Frontiers in Chemistry, 2017, 5, 51.	3.6	19
40	Changes in the Total Fecal Bacterial Population in Individual Horses Maintained on a Restricted Diet Over 6 Weeks. Frontiers in Microbiology, 2017, 8, 1502.	3.5	37
41	Effect of short term diet restriction on gene expression in the bovine hypothalamus using next generation RNA sequencing technology. BMC Genomics, 2017, 18, 857.	2.8	7
42	Transcriptomics of liver and muscle in Holstein cows genetically divergent for fertility highlight differences in nutrient partitioning and inflammation processes. BMC Genomics, 2016, 17, 603.	2.8	18
43	Fertility and genomics: comparison of gene expression in contrasting reproductive tissues of female cattle. Reproduction, Fertility and Development, 2016, 28, 11.	0.4	11
44	An ultra-high density genetic linkage map of perennial ryegrass (<i>Lolium perenne</i>) using genotyping by sequencing (GBS) based on a reference shotgun genome assembly. Annals of Botany, 2016, 118, 71-87.	2.9	31
45	Temporal dynamics of the metabolically active rumen bacteria colonizing fresh perennial ryegrass. FEMS Microbiology Ecology, 2016, 92, fiv137.	2.7	108
46	Implementing and testing Bayesian and maximum-likelihood supertree methods in phylogenetics. Royal Society Open Science, 2015, 2, 140436.	2.4	49
47	Concatabominations: Identifying Unstable Taxa in Morphological Phylogenetics using a Heuristic Extension to Safe Taxonomic Reduction. Systematic Biology, 2015, 64, 137-143.	5.6	37
48	Horizontal gene flow from Eubacteria to Archaebacteria and what it means for our understanding of eukaryogenesis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140337.	4.0	23
49	Diversity and Community Composition of Methanogenic Archaea in the Rumen of Scottish Upland Sheep Assessed by Different Methods. PLoS ONE, 2014, 9, e106491.	2.5	32
50	Whole genome association study identifies regions of the bovine genome and biological pathways involved in carcass trait performance in Holstein-Friesian cattle. BMC Genomics, 2014, 15, 837.	2.8	38
51	Mitochondrial data are not suitable for resolving placental mammal phylogeny. Mammalian Genome, 2014, 25, 636-647.	2.2	18
52	Determining the culturability of the rumen bacterial microbiome. Microbial Biotechnology, 2014, 7, 467-479.	4.2	159
53	Rumen Methanogenic Genotypes Differ in Abundance According to Host Residual Feed Intake Phenotype and Diet Type. Applied and Environmental Microbiology, 2014, 80, 586-594.	3.1	75
54	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	14.5	526

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55	L.U.St: a tool for approximated maximum likelihood supertree reconstruction. BMC Bioinformatics, 2014, 15, 183.	2.6	14
56	Genome sequence of Ensifer adhaerens OV14 provides insights into its ability as a novel vector for the genetic transformation of plant genomes. BMC Genomics, 2014, 15, 268.	2.8	23
57	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. BMC Genomics, 2014, 15, 356.	2.8	13
58	Snpdat: Easy and rapid annotation of results from de novo snp discovery projects for model and non-model organisms. BMC Bioinformatics, 2013, 14, 45.	2.6	43
59	Consistent mutational paths predict eukaryotic thermostability. BMC Evolutionary Biology, 2013, 13, 7.	3.2	60
60	RNA-seq analysis of differential gene expression in liver from lactating dairy cows divergent in negative energy balance. BMC Genomics, 2012, 13, 193.	2.8	98
61	Global endometrial transcriptomic profiling: transient immune activation precedes tissue proliferation and repair in healthy beef cows. BMC Genomics, 2012, 13, 489.	2.8	26
62	Polymorphism discovery and allele frequency estimation using high-throughput DNA sequencing of target-enriched pooled DNA samples. BMC Genomics, 2012, 13, 16.	2.8	18
63	The integration of â€˜omicâ€™ disciplines and systems biology in cattle breeding. Animal, 2011, 5, 493-505.	3.3	21
64	Identifying Single Copy Orthologs in Metazoa. PLoS Computational Biology, 2011, 7, e1002269.	3.2	23
65	Universally Distributed Single-Copy Genes Indicate a Constant Rate of Horizontal Transfer. PLoS ONE, 2011, 6, e22099.	2.5	99
66	Visualization of multiple alignments, phylogenies and gene family evolution. Nature Methods, 2010, 7, S16-S25.	19.0	73
67	Duplicate retention in signalling proteins and constraints from network dynamics. Journal of Evolutionary Biology, 2010, 23, 2410-2421.	1.7	8
68	AQUA: automated quality improvement for multiple sequence alignments. Bioinformatics, 2010, 26, 263-265.	4.1	53
69	STRING 8--a global view on proteins and their functional interactions in 630 organisms. Nucleic Acids Research, 2009, 37, D412-D416.	14.5	2,195
70	Trees from Trees: Construction of Phylogenetic Supertrees Using Clann. Methods in Molecular Biology, 2009, 537, 139-161.	0.9	23
71	A Computational Screen for Type I Polyketide Synthases in Metagenomics Shotgun Data. PLoS ONE, 2008, 3, e3515.	2.5	39
72	Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer. Science, 2007, 318, 1449-1452.	12.6	383

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73	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. Science, 2006, 311, 1283-1287.	12.6	1,435
74	Assessment of methods for amino acid matrix selection and their use on empirical data shows that ad hoc assumptions for choice of matrix are not justified. BMC Evolutionary Biology, 2006, 6, 29.	3.2	977
75	Genome Phylogenies Indicate a Meaningful Î±-Proteobacterial Phylogeny and Support a Grouping of the Mitochondria with the Rickettsiales. Molecular Biology and Evolution, 2006, 23, 74-85.	8.9	133
76	Evidence of Positive Darwinian Selection in Putative Meningococcal Vaccine Antigens. Journal of Molecular Evolution, 2005, 61, 90-98.	1.8	9
77	The Shape of Supertrees to Come: Tree Shape Related Properties of Fourteen Supertree Methods. Systematic Biology, 2005, 54, 419-431.	5.6	88
78	Clann: investigating phylogenetic information through supertree analyses. Bioinformatics, 2005, 21, 390-392.	4.1	196
79	The Opisthokonta and the Ecdysozoa May Not Be Clades: Stronger Support for the Grouping of Plant and Animal than for Animal and Fungi and Stronger Support for the Coelomata than Ecdysozoa. Molecular Biology and Evolution, 2005, 22, 1175-1184.	8.9	171
80	Does a treeâ€“like phylogeny only exist at the tips in the prokaryotes?. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 2551-2558.	2.6	114
81	Detecting Adaptive Molecular Evolution: Additional Tools for the Parasitologist. Advances in Parasitology, 2003, 54, 359-379.	3.2	4
82	Fatty acid biosynthesis in Mycobacterium tuberculosis: Lateral gene transfer, adaptive evolution, and gene duplication. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10320-10325.	7.1	119
83	CRANN: detecting adaptive evolution in protein-coding DNA sequences. Bioinformatics, 2003, 19, 1726-1726.	4.1	36
84	An algorithm for detecting directional and non-directional positive selection, neutrality and negative selection in protein coding DNA sequences. Gene, 2002, 300, 43-51.	2.2	47