

Chris Creevey

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1044803/publications.pdf>

Version: 2024-02-01

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	STRING 8—a global view on proteins and their functional interactions in 630 organisms. <i>Nucleic Acids Research</i> , 2009, 37, D412-D416.	14.5	2,195
2	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. <i>Science</i> , 2006, 311, 1283-1287.	12.6	1,435
3	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. <i>BMC Evolutionary Biology</i> , 2006, 6, 29.	3.2	977
4	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	14.5	526
5	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
6	Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer. <i>Science</i> , 2007, 318, 1449-1452.	12.6	383
7	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	3.5	255
8	Clann: investigating phylogenetic information through supertree analyses. <i>Bioinformatics</i> , 2005, 21, 390-392.	4.1	196
9	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. <i>Molecular Biology and Evolution</i> , 2005, 22, 1175-1184.	8.9	171
10	Determining the culturability of the rumen bacterial microbiome. <i>Microbial Biotechnology</i> , 2014, 7, 467-479.	4.2	159
11	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. <i>Microbiome</i> , 2019, 7, 6.	11.1	150
12	Genome Phylogenies Indicate a Meaningful $\hat{\pm}$ -Proteobacterial Phylogeny and Support a Grouping of the Mitochondria with the Rickettsiales. <i>Molecular Biology and Evolution</i> , 2006, 23, 74-85.	8.9	133
13	CowPI: A Rumen Microbiome Focussed Version of the PICRUSt Functional Inference Software. <i>Frontiers in Microbiology</i> , 2018, 9, 1095.	3.5	132
14	Fatty acid biosynthesis in <i>Mycobacterium tuberculosis</i> : Lateral gene transfer, adaptive evolution, and gene duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10320-10325.	7.1	119
15	Does a tree-like phylogeny only exist at the tips in the prokaryotes?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 2551-2558.	2.6	114
16	Temporal dynamics of the metabolically active rumen bacteria colonizing fresh perennial ryegrass. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv137.	2.7	108
17	Universally Distributed Single-Copy Genes Indicate a Constant Rate of Horizontal Transfer. <i>PLoS ONE</i> , 2011, 6, e22099.	2.5	99
18	RNA-seq analysis of differential gene expression in liver from lactating dairy cows divergent in negative energy balance. <i>BMC Genomics</i> , 2012, 13, 193.	2.8	98

#	ARTICLE	IF	CITATIONS
19	The Shape of Supertrees to Come: Tree Shape Related Properties of Fourteen Supertree Methods. <i>Systematic Biology</i> , 2005, 54, 419-431.	5.6	88
20	Rumen Methanogenic Genotypes Differ in Abundance According to Host Residual Feed Intake Phenotype and Diet Type. <i>Applied and Environmental Microbiology</i> , 2014, 80, 586-594.	3.1	75
21	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010, 7, S16-S25.	19.0	73
22	Divergent functional isoforms drive niche specialisation for nutrient acquisition and use in rumen microbiome. <i>ISME Journal</i> , 2017, 11, 932-944.	9.8	70
23	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
24	Meta-proteomics of rumen microbiota indicates niche compartmentalisation and functional dominance in a limited number of metabolic pathways between abundant bacteria. <i>Scientific Reports</i> , 2018, 8, 10504.	3.3	59
25	Fecal Microbiota Transplantation in Gestating Sows and Neonatal Offspring Alters Lifetime Intestinal Microbiota and Growth in Offspring. <i>MSystems</i> , 2018, 3, .	3.8	57
26	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2019, 36, 1344-1356.	8.9	56
27	Differential gene expression in the endometrium reveals cytoskeletal and immunological genes in lactating dairy cows genetically divergent for fertility traits. <i>Reproduction, Fertility and Development</i> , 2017, 29, 274.	0.4	55
28	AQUA: automated quality improvement for multiple sequence alignments. <i>Bioinformatics</i> , 2010, 26, 263-265.	4.1	53
29	The rumen microbiome: an underexplored resource for novel antimicrobial discovery. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 33.	6.4	51
30	Implementing and testing Bayesian and maximum-likelihood supertree methods in phylogenetics. <i>Royal Society Open Science</i> , 2015, 2, 140436.	2.4	49
31	An algorithm for detecting directional and non-directional positive selection, neutrality and negative selection in protein coding DNA sequences. <i>Gene</i> , 2002, 300, 43-51.	2.2	47
32	Snpsdat: Easy and rapid annotation of results from de novo snp discovery projects for model and non-model organisms. <i>BMC Bioinformatics</i> , 2013, 14, 45.	2.6	43
33	Can rumen bacteria communicate to each other?. <i>Microbiome</i> , 2020, 8, 23.	11.1	43
34	A Computational Screen for Type I Polyketide Synthases in Metagenomics Shotgun Data. <i>PLoS ONE</i> , 2008, 3, e3515.	2.5	39
35	Whole genome association study identifies regions of the bovine genome and biological pathways involved in carcass trait performance in Holstein-Friesian cattle. <i>BMC Genomics</i> , 2014, 15, 837.	2.8	38
36	Concatabominations: Identifying Unstable Taxa in Morphological Phylogenetics using a Heuristic Extension to Safe Taxonomic Reduction. <i>Systematic Biology</i> , 2015, 64, 137-143.	5.6	37

#	ARTICLE	IF	CITATIONS
37	Changes in the Total Fecal Bacterial Population in Individual Horses Maintained on a Restricted Diet Over 6 Weeks. <i>Frontiers in Microbiology</i> , 2017, 8, 1502.	3.5	37
38	CRANN: detecting adaptive evolution in protein-coding DNA sequences. <i>Bioinformatics</i> , 2003, 19, 1726-1726.	4.1	36
39	Improvement of Feed Efficiency in Pigs through Microbial Modulation via Fecal Microbiota Transplantation in Sows and Dietary Supplementation of Inulin in Offspring. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	33
40	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.	2.5	32
41	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. <i>Annals of Botany</i> , 2016, 118, 71-87.	2.9	31
42	Analysis of the Rumen Microbiome and Metabolome to Study the Effect of an Antimethanogenic Treatment Applied in Early Life of Kid Goats. <i>Frontiers in Microbiology</i> , 2018, 9, 2227.	3.5	31
43	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. <i>IScience</i> , 2019, 21, 587-602.	4.1	27
44	Global endometrial transcriptomic profiling: transient immune activation precedes tissue proliferation and repair in healthy beef cows. <i>BMC Genomics</i> , 2012, 13, 489.	2.8	26
45	Deep sequence analysis reveals the ovine rumen as a reservoir of antibiotic resistance genes. <i>Environmental Pollution</i> , 2018, 235, 571-575.	7.5	26
46	Identifying Single Copy Orthologs in Metazoa. <i>PLoS Computational Biology</i> , 2011, 7, e1002269.	3.2	23
47	Genome sequence of <i>Ensifer adhaerens</i> OV14 provides insights into its ability as a novel vector for the genetic transformation of plant genomes. <i>BMC Genomics</i> , 2014, 15, 268.	2.8	23
48	Horizontal gene flow from Eubacteria to Archaeobacteria and what it means for our understanding of eukaryogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140337.	4.0	23
49	Trees from Trees: Construction of Phylogenetic Supertrees Using Clann. <i>Methods in Molecular Biology</i> , 2009, 537, 139-161.	0.9	23
50	Rumen Virus Populations: Technological Advances Enhancing Current Understanding. <i>Frontiers in Microbiology</i> , 2020, 11, 450.	3.5	22
51	The integration of omic™ disciplines and systems biology in cattle breeding. <i>Animal</i> , 2011, 5, 493-505.	3.3	21
52	Rumen Protozoa Play a Significant Role in Fungal Predation and Plant Carbohydrate Breakdown. <i>Frontiers in Microbiology</i> , 2020, 11, 720.	3.5	21
53	No one tool to rule them all: prokaryotic gene prediction tool annotations are highly dependent on the organism of study. <i>Bioinformatics</i> , 2022, 38, 1198-1207.	4.1	20
54	Buwchitin: A Ruminal Peptide with Antimicrobial Potential against <i>Enterococcus faecalis</i> . <i>Frontiers in Chemistry</i> , 2017, 5, 51.	3.6	19

#	ARTICLE	IF	CITATIONS
55	Multi-tissue transcriptomes of caecilian amphibians highlight incomplete knowledge of vertebrate gene families. <i>DNA Research</i> , 2019, 26, 13-20.	3.4	19
56	Polymorphism discovery and allele frequency estimation using high-throughput DNA sequencing of target-enriched pooled DNA samples. <i>BMC Genomics</i> , 2012, 13, 16.	2.8	18
57	Mitochondrial data are not suitable for resolving placental mammal phylogeny. <i>Mammalian Genome</i> , 2014, 25, 636-647.	2.2	18
58	Transcriptomics of liver and muscle in Holstein cows genetically divergent for fertility highlight differences in nutrient partitioning and inflammation processes. <i>BMC Genomics</i> , 2016, 17, 603.	2.8	18
59	On the complexity of haplotyping a microbial community. <i>Bioinformatics</i> , 2021, 37, 1360-1366.	4.1	17
60	L.U.St: a tool for approximated maximum likelihood supertree reconstruction. <i>BMC Bioinformatics</i> , 2014, 15, 183.	2.6	14
61	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. <i>BMC Genomics</i> , 2014, 15, 356.	2.8	13
62	Fertility and genomics: comparison of gene expression in contrasting reproductive tissues of female cattle. <i>Reproduction, Fertility and Development</i> , 2016, 28, 11.	0.4	11
63	The rumen eukaryotome is a source of novel antimicrobial peptides with therapeutic potential. <i>BMC Microbiology</i> , 2021, 21, 105.	3.3	11
64	In silico identification of two peptides with antibacterial activity against multidrug-resistant <i>Staphylococcus aureus</i> . <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	11
65	Evidence of Positive Darwinian Selection in Putative Meningococcal Vaccine Antigens. <i>Journal of Molecular Evolution</i> , 2005, 61, 90-98.	1.8	9
66	Spherical: an iterative workflow for assembling metagenomic datasets. <i>BMC Bioinformatics</i> , 2018, 19, 20.	2.6	9
67	Genomic and gene expression evidence of nonribosomal peptide and polyketide production among ruminal bacteria: a potential role in niche colonization?. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	9
68	Microbiomes attached to fresh perennial ryegrass are temporally resilient and adapt to changing ecological niches. <i>Microbiome</i> , 2021, 9, 143.	11.1	9
69	Phylogenetic systematics of <i>Butyrivibrio</i> and <i>Pseudobutyrvibrio</i> genomes illustrate vast taxonomic diversity, open genomes and an abundance of carbohydrate-active enzyme family isoforms. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
70	Duplicate retention in signalling proteins and constraints from network dynamics. <i>Journal of Evolutionary Biology</i> , 2010, 23, 2410-2421.	1.7	8
71	Effect of short term diet restriction on gene expression in the bovine hypothalamus using next generation RNA sequencing technology. <i>BMC Genomics</i> , 2017, 18, 857.	2.8	7
72	Gene Fusions Derived by Transcriptional Readthrough are Driven by Segmental Duplication in Human. <i>Genome Biology and Evolution</i> , 2019, 11, 2678-2690.	2.5	7

#	ARTICLE	IF	CITATIONS
73	What lies beneath? Molecular evolution during the radiation of caecilian amphibians. BMC Genomics, 2019, 20, 354.	2.8	7
74	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
75	The Isolation and Genome Sequencing of Five Novel Bacteriophages From the Rumen Active Against <i>Butyrivibrio fibrisolvens</i> . Frontiers in Microbiology, 2020, 11, 1588.	3.5	5
76	Adult schistosomes have an epithelial bacterial population distinct from the surrounding mammalian host blood. PLoS ONE, 2022, 17, e0263188.	2.5	5
77	Detecting Adaptive Molecular Evolution: Additional Tools for the Parasitologist. Advances in Parasitology, 2003, 54, 359-379.	3.2	4
78	Insights into the skin of caecilian amphibians from gene expression profiles. BMC Genomics, 2020, 21, 515.	2.8	4
79	Interaction of preimplantation factor with the global bovine endometrial transcriptome. PLoS ONE, 2020, 15, e0242874.	2.5	4
80	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
81	Forage grass growth under future climate change scenarios affects fermentation and ruminant efficiency. Scientific Reports, 2022, 12, 4454.	3.3	3
82	Whole-Genome Sequencing and Comparative Genomic Analysis of Antimicrobial Producing <i>Streptococcus lutetiensis</i> from the Rumen. Microorganisms, 2022, 10, 551.	3.6	2
83	Using the forces of hydrodynamic countercurrent chromatography for the study of bacteriophages. Access Microbiology, 2022, 4, 000310.	0.5	1
84	Characterization of an Ex Vivo Equine Endometrial Tissue Culture Model Using Next-Generation RNA-Sequencing Technology. Animals, 2021, 11, 1995.	2.3	0