Stephen J Bent

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7929515/publications.pdf

Version: 2024-02-01

218677 214800 3,428 46 26 47 h-index citations g-index papers 50 50 50 5533 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Morphological changes and genome evolution in <i>Raphidiopsis raciborskii</i> CS-506 after 23 years in living culture. Applied Phycology, 2022, 3, 189-198.	1.3	6
2	Assessing <scp>DNA</scp> for fish identifications from reference collections: the good, bad and ugly shed light on formalin fixation and sequencing approaches. Journal of Fish Biology, 2021, 98, 1421-1432.	1.6	8
3	Genome sequencing in persistently unsolved white matter disorders. Annals of Clinical and Translational Neurology, 2020, 7, 144-152.	3.7	26
4	Heterozygous Variants in the Mechanosensitive Ion Channel TMEM63A Result in Transient Hypomyelination during Infancy. American Journal of Human Genetics, 2019, 105, 996-1004.	6.2	52
5	Leukoencephalopathy due to variants in <i>GFPT1-</i> associated congenital myasthenic syndrome. Neurology, 2019, 92, e587-e593.	1.1	14
6	Pathogenic copy number variants that affect gene expression contribute to genomic burden in cerebral palsy. Npj Genomic Medicine, 2018, 3, 33.	3.8	31
7	A novel embryo culture media supplement that improves pregnancy rates in mice. Reproduction, 2017, 153, 327-340.	2.6	7
8	Placental transcriptome co-expression analysis reveals conserved regulatory programs across gestation. BMC Genomics, 2017, 18, 10.	2.8	26
9	Mural lymphatic endothelial cells regulate meningeal angiogenesis in the zebrafish. Nature Neuroscience, 2017, 20, 774-783.	14.8	91
10	X-linked hypomyelination with spondylometaphyseal dysplasia (H-SMD) associated with mutations in AIFM1. Neurogenetics, 2017, 18, 185-194.	1.4	38
11	Closely-related Borrelia burgdorferi (sensu stricto) strains exhibit similar fitness in single infections and asymmetric competition in multiple infections. Parasites and Vectors, 2017, 10, 64.	2.5	21
12	A recurrent de novo mutation in TMEM106B causes hypomyelinating leukodystrophy. Brain, 2017, 140, 3105-3111.	7.6	64
13	Effects of long-term tenofovir-based combination antiretroviral therapy in HIV-hepatitis B virus coinfection on persistent hepatitis B virus viremia and the role of hepatitis B virus quasispecies diversity. Aids, 2016, 30, 1597-1606.	2.2	15
14	Genomic Comparison of Two O111:Hâ^'Enterohemorrhagic Escherichia coli Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. Infection and Immunity, 2016, 84, 775-781.	2.2	14
15	A discrete role for FNR in the transcriptional response to moderate changes in oxygen by Haemophilus influenzae Rd KW20. Research in Microbiology, 2016, 167, 103-113.	2.1	1
16	Generation of a Chimeric Hepatitis C Replicon Encoding a Genotype-6a NS3 Protease and Assessment of Boceprevir (SCH503034) Sensitivity and Drug-Associated Mutations. Antiviral Therapy, 2015, 20, 271-280.	1.0	4
17	Inducible and Reversible Lentiviral and Recombination Mediated Cassette Exchange (RMCE) Systems for Controlling Gene Expression. PLoS ONE, 2015, 10, e0116373.	2.5	4
18	A genetic screen reveals a periplasmic copper chaperone required for nitrite reductase activity in pathogenic <i>Neisseria </i> . FASEB Journal, 2015, 29, 3828-3838.	0.5	16

#	Article	IF	Citations
19	Whole genome capture of vector-borne pathogens from mixed DNA samples: a case study of Borrelia burgdorferi. BMC Genomics, 2015, 16, 434.	2.8	38
20	Borrelia burgdorferi sensu stricto and Borrelia afzelii: Population structure and differential pathogenicity. International Journal of Medical Microbiology, 2015, 305, 673-681.	3.6	40
21	Monitoring Human Babesiosis Emergence through Vector Surveillance New England, USA. Emerging Infectious Diseases, 2014, 20, 225-231.	4.3	8
22	Integrative transcriptome meta-analysis reveals widespread sex-biased gene expression at the human fetal-maternal interface. Molecular Human Reproduction, 2014, 20, 810-819.	2.8	139
23	<i>massiR</i> : a method for predicting the sex of samples in gene expression microarray datasets. Bioinformatics, 2014, 30, 2084-2085.	4.1	26
24	Monitoring Human Babesiosis Emergence through Vector Surveillance New England, USA. Emerging Infectious Diseases, 2014, 20, 225-231.	4.3	64
25	There is a specific response to pH by isolates of Haemophilus influenzae and this has a direct influence on biofilm formation. BMC Microbiology, 2014, 14, 47.	3.3	11
26	Phylogeny of beak and feather disease virus in cockatoos demonstrates host generalism and multiple-variant infections within Psittaciformes. Virology, 2014, 460-461, 72-82.	2.4	55
27	Quantitative PCR for Detection of <i> Babesia microti < /i > in <i> lxodes scapularis < /i > Ticks and in Human Blood. Vector-Borne and Zoonotic Diseases, 2013, 13, 784-790.</i></i>	1.5	40
28	Identification of Borrelia burgdorferi ospC Genotypes in Host Tissue and Feeding Ticks by Terminal Restriction Fragment Length Polymorphisms. Applied and Environmental Microbiology, 2013, 79, 958-964.	3.1	8
29	<i>Colpodella</i> spp.–like Parasite Infection in Woman, China. Emerging Infectious Diseases, 2012, 18, 125-127.	4.3	40
30	Loop analysis for pathogens: niche partitioning in the transmission graph for pathogens of the North American tick Ixodes scapularis. Journal of Theoretical Biology, 2011, 269, 96-103.	1.7	27
31	Regional Variation in Immature Ixodes scapularis Parasitism on North American Songbirds: Implications for Transmission of the Lyme Pathogen, Borrelia burgdorferi. Journal of Medical Entomology, 2011, 48, 422-428.	1.8	23
32	Genotypic Diversity of <i>Borrelia burgdorferi</i> Strains Detected in <i>Ixodes scapularis</i> Larvae Collected from North American Songbirds. Applied and Environmental Microbiology, 2010, 76, 8265-8268.	3.1	24
33	One Health approach to identify research needs in bovine and human babesioses: workshop report. Parasites and Vectors, 2010, 3, 36.	2.5	61
34	Phylogeography of <i>Borrelia burgdorferi</i> in the eastern United States reflects multiple independent Lyme disease emergence events. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15013-15018.	7.1	148
35	Bacterial succession in a glacier foreland of the High Arctic. ISME Journal, 2009, 3, 1258-1268.	9.8	102
36	Advances in the use of terminal restriction fragment length polymorphism (T-RFLP) analysis of 16S rRNA genes to characterize microbial communities. Applied Microbiology and Biotechnology, 2008, 80, 365-380.	3.6	318

#	Article	IF	CITATIONS
37	The tragedy of the uncommon: understanding limitations in the analysis of microbial diversity. ISME Journal, 2008, 2, 689-695.	9.8	244
38	Measuring Species Richness Based on Microbial Community Fingerprints: the Emperor Has No Clothes. Applied and Environmental Microbiology, 2007, 73, 2399-2401.	3.1	100
39	MiCA: A Web-Based Tool for the Analysis of Microbial Communities Based on Terminal-Restriction Fragment Length Polymorphisms of 16S and 18S rRNA Genes. Microbial Ecology, 2007, 53, 562-570.	2.8	215
40	Statistical methods for characterizing diversity of microbial communities by analysis of terminal restriction fragment length polymorphisms of 16S rRNA genes. Environmental Microbiology, 2006, 8, 929-938.	3.8	369
41	Characterization of vaginal microbial communities in adult healthy women using cultivation-independent methods. Microbiology (United Kingdom), 2004, 150, 2565-2573.	1.8	438
42	Spatial Distribution of Rhodopseudomonas palustris Ecotypes on a Local Scale. Applied and Environmental Microbiology, 2003, 69, 5192-5197.	3.1	37
43	Parathyroid hormone-related peptide and Indian hedgehog expression patterns in naturally acquired equine osteochondrosis. Journal of Orthopaedic Research, 2002, 20, 1290-1297.	2.3	30
44	Chondrocytic differentiation of mesenchymal stem cells sequentially exposed to transforming growth factorâ€Î¹1 in monolayer and insulinâ€like growth factorâ€Î in a threeâ€dimensional matrix. Journal of Orthopaedic Research, 2001, 19, 738-749.	2.3	242
45	Gene mediated insulin-like growth factor-I delivery to the synovium. Journal of Orthopaedic Research, 2001, 19, 759-767.	2.3	31
46	Insulinlike Growth Factor-I Gene Therapy Applications for Cartilage Repair. Clinical Orthopaedics and Related Research, 2000, 379, S201-S213.	1.5	100