

Lionel Guy

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1606947/publications.pdf>

Version: 2024-02-01

42
papers

3,440
citations

430874

18
h-index

265206

42
g-index

45
all docs

45
docs citations

45
times ranked

5142
citing authors

#	ARTICLE	IF	CITATIONS
1	Host Adaptation in <i>Legionellales</i> Is 1.9 Ga, Coincident with Eukaryogenesis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	15
2	Expression of the <i>qepA1</i> gene is induced under antibiotic exposure. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1433-1440.	3.0	5
3	Molecular Characterization of Multidrug-Resistant <i>Yersinia enterocolitica</i> From Foodborne Outbreaks in Sweden. <i>Frontiers in Microbiology</i> , 2021, 12, 664665.	3.5	22
4	Chromosomal Location Determines the Rate of Intrachromosomal Homologous Recombination in <i>Salmonella</i> . <i>MBio</i> , 2021, 12, e0115121.	4.1	2
5	Heimdallarchaea encodes profilin with eukaryotic-like actin regulation and polyproline binding. <i>Communications Biology</i> , 2021, 4, 1024.	4.4	11
6	miComplete: weighted quality evaluation of assembled microbial genomes. <i>Bioinformatics</i> , 2020, 36, 936-937.	4.1	26
7	<i>Chlamydia psittaci</i> in fulmars on the Faroe Islands: a causative link to South American psittacines eight decades after a severe epidemic. <i>Microbes and Infection</i> , 2020, 22, 356-359.	1.9	9
8	Paralogization and New Protein Architectures in Planctomycetes Bacteria with Complex Cell Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 1020-1040.	8.9	6
9	Deep mitochondrial origin outside the sampled alphaproteobacteria. <i>Nature</i> , 2018, 557, 101-105.	27.8	278
10	Origin and Evolution of the Bartonella Gene Transfer Agent. <i>Molecular Biology and Evolution</i> , 2018, 35, 451-464.	8.9	24
11	Experimental Determination and Prediction of the Fitness Effects of Random Point Mutations in the Biosynthetic Enzyme HisA. <i>Molecular Biology and Evolution</i> , 2018, 35, 704-718.	8.9	21
12	The all-intracellular order Legionellales is unexpectedly diverse, globally distributed and lowly abundant. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	18
13	Withdrawn as Duplicate: The all-intracellular order Legionellales is unexpectedly diverse, globally distributed and lowly abundant. <i>FEMS Microbiology Ecology</i> , 2018, , .	2.7	5
14	<i>Legionella pneumophila</i> recurrently isolated in a Spanish hospital: Two years of antimicrobial resistance surveillance. <i>Environmental Research</i> , 2018, 166, 638-646.	7.5	16
15	Genomes of two archaeal endosymbionts show convergent adaptations to an intracellular lifestyle. <i>ISME Journal</i> , 2018, 12, 2655-2667.	9.8	26
16	Asgard archaea are the closest prokaryotic relatives of eukaryotes. <i>PLoS Genetics</i> , 2018, 14, e1007080.	3.5	114
17	Resurrecting ancestral genes in bacteria to interpret ancient biosignatures. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2017, 375, 20160352.	3.4	19
18	phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics. <i>Bioinformatics</i> , 2017, 33, 1230-1232.	4.1	18

#	ARTICLE	IF	CITATIONS
19	The genome of Rhizobiales bacteria in predatory ants reveals urease gene functions but no genes for nitrogen fixation. <i>Scientific Reports</i> , 2016, 6, 39197.	3.3	55
20	<i>Coetzeea brasiliensis</i> gen. nov., sp. nov. isolated from larvae of <i>Anopheles darlingi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5211-5217.	1.7	10
21	Proposal of <i>Thorsellia kenyensis</i> sp. nov. and <i>Thorsellia kandunguensis</i> sp. nov., isolated from larvae of <i>Anopheles arabiensis</i> , as members of the family Thorselliaceae fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 444-451.	1.7	22
22	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	27.8	995
23	Single-cell genomics of a rare environmental alphaproteobacterium provides unique insights into Rickettsiaceae evolution. <i>ISME Journal</i> , 2015, 9, 2373-2385.	9.8	51
24	Exploring microbial dark matter to resolve the deep archaeal ancestry of eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140328.	4.0	40
25	â€˜Geoarchaeote NAC1â€™ is a deeply rooting lineage of the archaeal order Thermoproteales rather than a new phylum. <i>ISME Journal</i> , 2014, 8, 1353-1357.	9.8	19
26	The Archaeal Legacy of Eukaryotes: A Phylogenomic Perspective. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016022-a016022.	5.5	55
27	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , 2013, 7, 1173-1186.	9.8	124
28	A Gene Transfer Agent and a Dynamic Repertoire of Secretion Systems Hold the Keys to the Explosive Radiation of the Emerging Pathogen <i>Bartonella</i> . <i>PLoS Genetics</i> , 2013, 9, e1003393.	3.5	89
29	Close Encounters of the Third Domain: The Emerging Genomic View of Archaeal Diversity and Evolution. <i>Archaea</i> , 2013, 2013, 1-12.	2.3	24
30	Adaptive Mutations and Replacements of Virulence Traits in the <i>Escherichia coli</i> O104:H4 Outbreak Population. <i>PLoS ONE</i> , 2013, 8, e63027.	2.5	15
31	Genomic diversity of the 2011 European outbreaks of <i>Escherichia coli</i> O104:H4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3627-8.	7.1	8
32	A genome-wide study of recombination rate variation in <i>Bartonella henselae</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 65.	3.2	18
33	The archaeal â€˜TACKâ€™ superphylum and the origin of eukaryotes. <i>Trends in Microbiology</i> , 2011, 19, 580-587.	7.7	288
34	genoPlotR: comparative gene and genome visualization in R. <i>Bioinformatics</i> , 2010, 26, 2334-2335.	4.1	651
35	M-protein and other intrinsic virulence factors of <i>Streptococcus pyogenes</i> are encoded on an ancient pathogenicity island. <i>BMC Genomics</i> , 2009, 10, 198.	2.8	19
36	Solving ambiguities in contig assembly of <i>Idiomarina loihiensis</i> L2TR chromosome by in silico analyses. <i>FEMS Microbiology Letters</i> , 2007, 271, 187-192.	1.8	3

#	ARTICLE	IF	CITATIONS
37	Identification and characterization of pathogenicity and other genomic islands using base composition analyses. <i>Future Microbiology</i> , 2006, 1, 309-316.	2.0	11
38	Describing ancient horizontal gene transfers at the nucleotide and gene levels by comparative pathogenicity island genomics. <i>Bioinformatics</i> , 2006, 22, 1072-1079.	4.1	18
39	Genomics as an essential tool for the assembly of whole genome sequences: the example of the chromosome of <i>Bifidobacterium longum</i> NCC2705. <i>BMC Microbiology</i> , 2005, 5, 60.	3.3	12
40	Quorum-Sensing-Negative (<i>lasR</i>) Mutants of <i>Pseudomonas aeruginosa</i> Avoid Cell Lysis and Death. <i>Journal of Bacteriology</i> , 2005, 187, 4875-4883.	2.2	160
41	A genomic island present along the bacterial chromosome of the Parachlamydiaceae UWE25, an obligate amoebal endosymbiont, encodes a potentially functional F-like conjugative DNA transfer system. <i>BMC Microbiology</i> , 2004, 4, 48.	3.3	69
42	Genomic analyses of the organization of circular chromosomes: a universal pressure determines the direction of ribosomal RNA genes transcription relative to chromosome replication. <i>Gene</i> , 2004, 340, 45-52.	2.2	42