

Lionel Guy

List of Publications by Year in descending order

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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	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	27.8	995
2	genoPlotR: comparative gene and genome visualization in R. <i>Bioinformatics</i> , 2010, 26, 2334-2335.	4.1	651
3	The archaeal "TACK" superphylum and the origin of eukaryotes. <i>Trends in Microbiology</i> , 2011, 19, 580-587.	7.7	288
4	Deep mitochondrial origin outside the sampled alphaproteobacteria. <i>Nature</i> , 2018, 557, 101-105.	27.8	278
5	Quorum-Sensing-Negative (lasR) Mutants of <i>Pseudomonas aeruginosa</i> Avoid Cell Lysis and Death. <i>Journal of Bacteriology</i> , 2005, 187, 4875-4883.	2.2	160
6	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , 2013, 7, 1173-1186.	9.8	124
7	Asgard archaea are the closest prokaryotic relatives of eukaryotes. <i>PLoS Genetics</i> , 2018, 14, e1007080.	3.5	114
8	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
9	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
10	The Archaeal Legacy of Eukaryotes: A Phylogenomic Perspective. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016022-a016022.	5.5	55
11	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
12	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
13	Genometric 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
14	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
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	miComplete: weighted quality evaluation of assembled microbial genomes. <i>Bioinformatics</i> , 2020, 36, 936-937.	4.1	26
17	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
18	Origin and Evolution of the <i>Bartonella</i> Gene Transfer Agent. <i>Molecular Biology and Evolution</i> , 2018, 35, 451-464.	8.9	24

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19	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.. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 444-451.	1.7	22
20	Molecular Characterization of Multidrug-Resistant <i>Yersinia enterocolitica</i> From Foodborne Outbreaks in Sweden. Frontiers in Microbiology, 2021, 12, 664665.	3.5	22
21	Experimental Determination and Prediction of the Fitness Effects of Random Point Mutations in the Biosynthetic Enzyme HisA. Molecular Biology and Evolution, 2018, 35, 704-718.	8.9	21
22	M-protein and other intrinsic virulence factors of <i>Streptococcus pyogenes</i> are encoded on an ancient pathogenicity island. BMC Genomics, 2009, 10, 198.	2.8	19
23	~Geoarchaeote NAG1~™ is a deeply rooting lineage of the archaeal order Thermoproteales rather than a new phylum. ISME Journal, 2014, 8, 1353-1357.	9.8	19
24	Resurrecting ancestral genes in bacteria to interpret ancient biosignatures. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2017, 375, 20160352.	3.4	19
25	Describing ancient horizontal gene transfers at the nucleotide and gene levels by comparative pathogenicity island genomics. Bioinformatics, 2006, 22, 1072-1079.	4.1	18
26	A genome-wide study of recombination rate variation in <i>Bartonella henselae</i> . BMC Evolutionary Biology, 2012, 12, 65.	3.2	18
27	phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics. Bioinformatics, 2017, 33, 1230-1232.	4.1	18
28	The all-intracellular order Legionellales is unexpectedly diverse, globally distributed and lowly abundant. FEMS Microbiology Ecology, 2018, 94, .	2.7	18
29	<i>Legionella pneumophila</i> recurrently isolated in a Spanish hospital: Two years of antimicrobial resistance surveillance. Environmental Research, 2018, 166, 638-646.	7.5	16
30	Adaptive Mutations and Replacements of Virulence Traits in the <i>Escherichia coli</i> O104:H4 Outbreak Population. PLoS ONE, 2013, 8, e63027.	2.5	15
31	Host Adaptation in <i>Legionellales</i> Is 1.9 Ga, Coincident with Eukaryogenesis. Molecular Biology and Evolution, 2022, 39, .	8.9	15
32	Genomics as an essential tool for the assembly of whole genome sequences: the example of the chromosome of <i>Bifidobacterium longum</i> NCC2705. BMC Microbiology, 2005, 5, 60.	3.3	12
33	Identification and characterization of pathogenicity and other genomic islands using base composition analyses. Future Microbiology, 2006, 1, 309-316.	2.0	11
34	Heimdallarchaea encodes profilin with eukaryotic-like actin regulation and polyproline binding. Communications Biology, 2021, 4, 1024.	4.4	11
35	<i>Coetzyea brasiliensis</i> gen. nov., sp. nov. isolated from larvae of <i>Anopheles darlingi</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5211-5217.	1.7	10
36	<i>Chlamydia psittaci</i> in fulmars on the Faroe Islands: a causative link to South American psittacines eight decades after a severe epidemic. Microbes and Infection, 2020, 22, 356-359.	1.9	9

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37	Genomic diversity of the 2011 European outbreaks of <i>Escherichia coli</i> O104:H4. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3627-8.	7.1	8
38	Paralogization and New Protein Architectures in Planctomycetes Bacteria with Complex Cell Structures. Molecular Biology and Evolution, 2020, 37, 1020-1040.	8.9	6
39	Withdrawn as Duplicate: The all-intracellular order Legionellales is unexpectedly diverse, globally distributed and lowly abundant. FEMS Microbiology Ecology, 2018, , .	2.7	5
40	Expression of the <i>qepA1</i> gene is induced under antibiotic exposure. Journal of Antimicrobial Chemotherapy, 2021, 76, 1433-1440.	3.0	5
41	Solving ambiguities in contig assembly of <i>Idiomarina loihiensis</i> L2TR chromosome by in silico analyses. FEMS Microbiology Letters, 2007, 271, 187-192.	1.8	3
42	Chromosomal Location Determines the Rate of Intrachromosomal Homologous Recombination in <i>Salmonella</i> . MBio, 2021, 12, e0115121.	4.1	2