

Laurent Falquet

List of Publications by Year in descending order

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74
papers

7,997
citations

126907

33
h-index

79698

73
g-index

82
all docs

82
docs citations

82
times ranked

10973
citing authors

#	ARTICLE	IF	CITATIONS
1	Dedicated chaperones coordinate co-translational regulation of ribosomal protein production with ribosome assembly to preserve proteostasis. <i>ELife</i> , 2022, 11, .	6.0	11
2	Substrate recognition and cryo-EM structure of the ribosome-bound TAC toxin of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2022, 13, 2641.	12.8	5
3	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.5	51
4	A rationally designed oral vaccine induces immunoglobulin A in the murine gut that directs the evolution of attenuated <i>Salmonella</i> variants. <i>Nature Microbiology</i> , 2021, 6, 830-841.	13.3	21
5	Minimalistic mycoplasmas harbor different functional toxin-antitoxin systems. <i>PLoS Genetics</i> , 2021, 17, e1009365.	3.5	7
6	Signaling via the FLP-14/FRPR-19 neuropeptide pathway sustains nociceptive response to repeated noxious stimuli in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2021, 17, e1009880.	3.5	8
7	Large-Scale Comparison of Toxin and Antitoxins in <i>Listeria monocytogenes</i> . <i>Toxins</i> , 2020, 12, 29.	3.4	4
8	Genome-based characterization of two Colombian clinical <i>Providencia rettgeri</i> isolates co-harboring NDM-1, VIM-2, and other β -lactamases. <i>BMC Microbiology</i> , 2020, 20, 345.	3.3	12
9	Complete Genome Sequence of <i>Mycoplasma feriruminatoris</i> Strain IVB14/OD_0535, Isolated from an Alpine Ibex in a Swiss Zoo. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
10	Study protocol for the ABERRANT study: antibiotic-induced disruption of the maternal and infant microbiome and adverse health outcomes – a prospective cohort study among children born at term. <i>BMJ Open</i> , 2020, 10, e036275.	1.9	4
11	Genome Assembly of the Ragweed Leaf Beetle: A Step Forward to Better Predict Rapid Evolution of a Weed Biocontrol Agent to Environmental Novelty. <i>Genome Biology and Evolution</i> , 2020, 12, 1167-1173.	2.5	10
12	NGS-Based <i>S. aureus</i> Typing and Outbreak Analysis in Clinical Microbiology Laboratories: Lessons Learned From a Swiss-Wide Proficiency Test. <i>Frontiers in Microbiology</i> , 2020, 11, 591093.	3.5	9
13	Removal of a Subset of Non-essential Genes Fully Attenuates a Highly Virulent <i>Mycoplasma</i> Strain. <i>Frontiers in Microbiology</i> , 2019, 10, 664.	3.5	31
14	Large-Scale Analysis of the <i>Mycoplasma bovis</i> Genome Identified Non-essential, Adhesion- and Virulence-Related Genes. <i>Frontiers in Microbiology</i> , 2019, 10, 2085.	3.5	21
15	Injured Axons Instruct Schwann Cells to Build Constricting Actin Spheres to Accelerate Axonal Disintegration. <i>Cell Reports</i> , 2019, 27, 3152-3166.e7.	6.4	43
16	TASmania: A bacterial Toxin-Antitoxin Systems database. <i>PLoS Computational Biology</i> , 2019, 15, e1006946.	3.2	95
17	Reproduction of contagious caprine pleuropneumonia reveals the ability of convalescent sera to reduce hydrogen peroxide production in vitro. <i>Veterinary Research</i> , 2019, 50, 10.	3.0	24
18	Identification of avoidance genes through neural pathway-specific forward optogenetics. <i>PLoS Genetics</i> , 2019, 15, e1008509.	3.5	16

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19	deltaRpkM: an R package for a rapid detection of differential gene presence between related bacterial genomes. BMC Bioinformatics, 2019, 20, 621.	2.6	3
20	Malaria infected red blood cells release small regulatory RNAs through extracellular vesicles. Scientific Reports, 2018, 8, 884.	3.3	60
21	Genetic Separation of <i>Listeria monocytogenes</i> Causing Central Nervous System Infections in Animals. Frontiers in Cellular and Infection Microbiology, 2018, 8, 20.	3.9	22
22	Whole-Genome Sequence of a Colombian <i>Acinetobacter baumannii</i> Strain, a Coproducer of OXA-72 and OXA-255-Like Carbapenemases. Genome Announcements, 2017, 5, .	0.8	5
23	The Discovery of Wild Date Palms in Oman Reveals a Complex Domestication History Involving Centers in the Middle East and Africa. Current Biology, 2017, 27, 2211-2218.e8.	3.9	63
24	<i>Clostridium chauvoei</i> , an Evolutionary Dead-End Pathogen. Frontiers in Microbiology, 2017, 8, 1054.	3.5	33
25	The microbiome of the leaf surface of <i>Arabidopsis</i> protects against a fungal pathogen. New Phytologist, 2016, 210, 1033-1043.	7.3	295
26	The salivary microbiome for differentiating individuals: proof of principle. Microbes and Infection, 2016, 18, 399-405.	1.9	75
27	Cell Cycle Constraints and Environmental Control of Local DNA Hypomethylation in $\hat{\pm}$ -Proteobacteria. PLoS Genetics, 2016, 12, e1006499.	3.5	25
28	The <i>Petunia</i> GRAS Transcription Factor ATA/RAM1 Regulates Symbiotic Gene Expression and Fungal Morphogenesis in Arbuscular Mycorrhiza. Plant Physiology, 2015, 168, 788-797.	4.8	64
29	Field-Applicable Recombinase Polymerase Amplification Assay for Rapid Detection of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> . Journal of Clinical Microbiology, 2015, 53, 2810-2815.	3.9	55
30	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. Frontiers in Microbiology, 2015, 6, 101.	3.5	32
31	SV-AUTOPILOT: optimized, automated construction of structural variation discovery and benchmarking pipelines. BMC Genomics, 2015, 16, 238.	2.8	5
32	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B-13, the first bacterium known to degrade chloroaromatic compounds. Environmental Microbiology, 2015, 17, 91-104.	3.8	52
33	Patho-genetics of <i>Clostridium chauvoei</i> . Research in Microbiology, 2015, 166, 384-392.	2.1	37
34	The Dedicated Chaperone Acl4 Escorts Ribosomal Protein Rpl4 to Its Nuclear Pre-60S Assembly Site. PLoS Genetics, 2015, 11, e1005565.	3.5	59
35	A novel bioinformatics pipeline to discover genes related to arbuscular mycorrhizal symbiosis based on their evolutionary conservation pattern among higher plants. BMC Plant Biology, 2014, 14, 333.	3.6	91
36	Complete Genome Sequences of Virulent <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> Strains F38 and ILRI181. Genome Announcements, 2014, 2, .	0.8	17

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37	Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef (<i>Eragrostis tef</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	2.8	133
38	Análisis genómico del resistoma de la cepa de <i>Acinetobacter baumannii</i> ABIBUN 107m multi-resistente y persistente en hospitales colombianos. Revista Colombiana De Biotecnología, 2014, 16, 104-113.	0.2	2
39	Next Generation Sequencing methods for identification of mutations and large structural variants, 11-12 March 2014. EMBnet Journal, 2014, 20, 752.	0.6	0
40	Report on the ALLBIO minisymposium and workshop: "Next Generation Sequencing (NGS) methods for identification of mutations and large structural variants". EMBnet Journal, 2014, 20, 766.	0.6	0
41	Draft Genome Sequence of the Virulent <i>Clostridium chauvoei</i> Reference Strain JF4335. Genome Announcements, 2013, 1, .	0.8	14
42	Draft Genome Sequences of Multidrug-Resistant <i>Acinetobacter</i> sp. Strains from Colombian Hospitals. Genome Announcements, 2013, 1, .	0.8	3
43	Draft Genome Sequence of the Virulent <i>Avibacterium paragallinarum</i> Serotype A Strain JF4211 and Identification of Two Toxins. Genome Announcements, 2013, 1, .	0.8	4
44	Short Term Evolution of a Highly Transmissible Methicillin-Resistant <i>Staphylococcus aureus</i> Clone (ST228) in a Tertiary Care Hospital. PLoS ONE, 2012, 7, e38969.	2.5	31
45	Genome Sequences of the High-Acetic Acid-Resistant Bacteria <i>Gluconacetobacter europaeus</i> LMG 18890 ^T and <i>G. europaeus</i> LMG 18494 (Reference Strains), <i>G. europaeus</i> 5P3, and <i>Gluconacetobacter oboediens</i> 174Bp2 (Isolated from Vinegar). Journal of Bacteriology, 2011, 193, 2670-2671.	2.2	40
46	The genome of the fire ant <i>Solenopsis invicta</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5679-5684.	7.1	322
47	Visualization and quality assessment of de novo genome assemblies. Bioinformatics, 2011, 27, 3425-3426.	4.1	9
48	Genome-wide comparison of FGFR1 with structurally related surface receptors. Experimental and Therapeutic Medicine, 2010, 1, 161-168.	1.8	8
49	PeroxiBase: a database with new tools for peroxidase family classification. Nucleic Acids Research, 2009, 37, D261-D266.	14.5	141
50	The <i>Mycoplasma conjunctivae</i> genome sequencing, annotation and analysis. BMC Bioinformatics, 2009, 10, S7.	2.6	46
51	Fourmidable: a database for ant genomics. BMC Genomics, 2009, 10, 5.	2.8	38
52	Unexpected vagaries of microsatellite loci in <i>Glomus intraradices</i> : length polymorphisms are rarely caused by variation in repeat number only. New Phytologist, 2008, 180, 568-570.	7.3	3
53	Microsatellites for disentangling underground networks: Strain-specific identification of <i>Glomus intraradices</i> , an arbuscular mycorrhizal fungus. Fungal Genetics and Biology, 2008, 45, 812-817.	2.1	32
54	Experience using web services for biological sequence analysis. Briefings in Bioinformatics, 2008, 9, 493-505.	6.5	24

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55	MyHits: improvements to an interactive resource for analyzing protein sequences. <i>Nucleic Acids Research</i> , 2007, 35, W433-W437.	14.5	185
56	PeroxiBase: The peroxidase database. <i>Phytochemistry</i> , 2007, 68, 1605-1611.	2.9	187
57	PeroxiBase: A class III plant peroxidase database. <i>Phytochemistry</i> , 2006, 67, 534-539.	2.9	68
58	Hunting for insect-specific protein domains. <i>In Silico Biology</i> , 2006, 6, 35-42.	0.9	1
59	On ubiquitin ligases and cancer. <i>Human Mutation</i> , 2005, 25, 507-512.	2.5	8
60	The <i>Saccharomyces cerevisiae</i> YLL012/YEH1, YLR020/YEH2, and TGL1 Genes Encode a Novel Family of Membrane-Anchored Lipases That Are Required for Steryl Ester Hydrolysis. <i>Molecular and Cellular Biology</i> , 2005, 25, 1655-1668.	2.3	124
61	Transcript Profiling Suggests That Differential Metabolic Adaptation of Mice to a High Fat Diet Is Associated with Changes in Liver to Muscle Lipid Fluxes. <i>Journal of Biological Chemistry</i> , 2004, 279, 50743-50753.	3.4	77
62	MyHits: a new interactive resource for protein annotation and domain identification. <i>Nucleic Acids Research</i> , 2004, 32, W332-W335.	14.5	82
63	Ubiquitin ligases as cancer genes. <i>Nature Reviews Cancer</i> , 2004, 4, 654-654.	28.4	1
64	Swiss EMBnet node web server. <i>Nucleic Acids Research</i> , 2003, 31, 3782-3783.	14.5	11
65	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640
66	PROSITE: A documented database using patterns and profiles as motif descriptors. <i>Briefings in Bioinformatics</i> , 2002, 3, 265-274.	6.5	802
67	The PROSITE database, its status in 2002. <i>Nucleic Acids Research</i> , 2002, 30, 235-238.	14.5	908
68	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	6.5	155
69	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , 2001, 29, 37-40.	14.5	928
70	A ubiquitin-interacting motif conserved in components of the proteasomal and lysosomal protein degradation systems. <i>Trends in Biochemical Sciences</i> , 2001, 26, 347-350.	7.5	414
71	trEST, trGEN and Hits: access to databases of predicted protein sequences. <i>Nucleic Acids Research</i> , 2001, 29, 148-151.	14.5	27
72	The PROSITE database, its status in 1999. <i>Nucleic Acids Research</i> , 1999, 27, 215-219.	14.5	1,089

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73	A human de-ubiquitinating enzyme with both isopeptidase and peptidase activities in vitro. FEBS Letters, 1995, 359, 73-77.	2.8	46
74	cDNA cloning of a human 100 kDa de-ubiquitinating enzyme: the 100 kDa human de-ubiquitinase belongs to the ubiquitin C-terminal hydrolase family 2 (UCH2). FEBS Letters, 1995, 376, 233-237.	2.8	22