

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	The PROSITE database, its status in 1999. <i>Nucleic Acids Research</i> , 1999, 27, 215-219.	14.5	1,089
2	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
3	The PROSITE database, its status in 2002. <i>Nucleic Acids Research</i> , 2002, 30, 235-238.	14.5	908
4	PROSITE: A documented database using patterns and profiles as motif descriptors. <i>Briefings in Bioinformatics</i> , 2002, 3, 265-274.	6.5	802
5	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640
6	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
7	The genome of the fire ant <i>Solenopsis invicta</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5679-5684.	7.1	322
8	The microbiome of the leaf surface of <i>Arabidopsis</i> protects against a fungal pathogen. <i>New Phytologist</i> , 2016, 210, 1033-1043.	7.3	295
9	PeroxiBase: The peroxidase database. <i>Phytochemistry</i> , 2007, 68, 1605-1611.	2.9	187
10	MyHits: improvements to an interactive resource for analyzing protein sequences. <i>Nucleic Acids Research</i> , 2007, 35, W433-W437.	14.5	185
11	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	6.5	155
12	PeroxiBase: a database with new tools for peroxidase family classification. <i>Nucleic Acids Research</i> , 2009, 37, D261-D266.	14.5	141
13	Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef (<i>Eragrostis tef</i>) Tj ETQq1 1 0.784314 rrgBT /Ove 2.8 133		
14	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
15	TASmania: A bacterial Toxin-Antitoxin Systems database. <i>PLoS Computational Biology</i> , 2019, 15, e1006946.	3.2	95
16	A novel bioinformatics pipeline to discover genes related to arbuscular mycorrhizal symbiosis based on their evolutionary conservation pattern among higher plants. <i>BMC Plant Biology</i> , 2014, 14, 333.	3.6	91
17	MyHits: a new interactive resource for protein annotation and domain identification. <i>Nucleic Acids Research</i> , 2004, 32, W332-W335.	14.5	82
18	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

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19	The salivary microbiome for differentiating individuals: proof of principle. <i>Microbes and Infection</i> , 2016, 18, 399-405.	1.9	75
20	PeroxiBase: A class III plant peroxidase database. <i>Phytochemistry</i> , 2006, 67, 534-539.	2.9	68
21	The <i>Petunia</i> GRAS Transcription Factor ATA/RAM1 Regulates Symbiotic Gene Expression and Fungal Morphogenesis in Arbuscular Mycorrhiza. <i>Plant Physiology</i> , 2015, 168, 788-797.	4.8	64
22	The Discovery of Wild Date Palms in Oman Reveals a Complex Domestication History Involving Centers in the Middle East and Africa. <i>Current Biology</i> , 2017, 27, 2211-2218.e8.	3.9	63
23	Malaria infected red blood cells release small regulatory RNAs through extracellular vesicles. <i>Scientific Reports</i> , 2018, 8, 884.	3.3	60
24	The Dedicated Chaperone Acl4 Escorts Ribosomal Protein Rpl4 to Its Nuclear Pre-60S Assembly Site. <i>PLoS Genetics</i> , 2015, 11, e1005565.	3.5	59
25	Field-Applicable Recombinase Polymerase Amplification Assay for Rapid Detection of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 2810-2815.	3.9	55
26	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015, 17, 91-104.	3.8	52
27	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.5	51
28	A human de-ubiquitinating enzyme with both isopeptidase and peptidase activities in vitro. <i>FEBS Letters</i> , 1995, 359, 73-77.	2.8	46
29	The <i>Mycoplasma conjunctivae</i> genome sequencing, annotation and analysis. <i>BMC Bioinformatics</i> , 2009, 10, S7.	2.6	46
30	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
31	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). <i>Journal of Bacteriology</i> , 2011, 193, 2670-2671.	2.2	40
32	Fourmidable: a database for ant genomics. <i>BMC Genomics</i> , 2009, 10, 5.	2.8	38
33	Patho-genetics of <i>Clostridium chauvoei</i> . <i>Research in Microbiology</i> , 2015, 166, 384-392.	2.1	37
34	<i>Clostridium chauvoei</i> , an Evolutionary Dead-End Pathogen. <i>Frontiers in Microbiology</i> , 2017, 8, 1054.	3.5	33
35	Microsatellites for disentangling underground networks: Strain-specific identification of <i>Glomus intraradices</i> , an arbuscular mycorrhizal fungus. <i>Fungal Genetics and Biology</i> , 2008, 45, 812-817.	2.1	32
36	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015, 6, 101.	3.5	32

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37	Removal of a Subset of Non-essential Genes Fully Attenuates a Highly Virulent Mycoplasma Strain. <i>Frontiers in Microbiology</i> , 2019, 10, 664.	3.5	31
38	Short Term Evolution of a Highly Transmissible Methicillin-Resistant <i>Staphylococcus aureus</i> Clone (ST228) in a Tertiary Care Hospital. <i>PLoS ONE</i> , 2012, 7, e38969.	2.5	31
39	trEST, trGEN and Hits: access to databases of predicted protein sequences. <i>Nucleic Acids Research</i> , 2001, 29, 148-151.	14.5	27
40	Cell Cycle Constraints and Environmental Control of Local DNA Hypomethylation in $\hat{\pm}$ -Proteobacteria. <i>PLoS Genetics</i> , 2016, 12, e1006499.	3.5	25
41	Experience using web services for biological sequence analysis. <i>Briefings in Bioinformatics</i> , 2008, 9, 493-505.	6.5	24
42	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
43	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). <i>FEBS Letters</i> , 1995, 376, 233-237.	2.8	22
44	Genetic Separation of <i>Listeria monocytogenes</i> Causing Central Nervous System Infections in Animals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 20.	3.9	22
45	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
46	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
47	Complete Genome Sequences of Virulent <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> Strains F38 and ILRI181. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
48	Identification of avoidance genes through neural pathway-specific forward optogenetics. <i>PLoS Genetics</i> , 2019, 15, e1008509.	3.5	16
49	Draft Genome Sequence of the Virulent <i>Clostridium chauvoei</i> Reference Strain JF4335. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
50	Genome-based characterization of two Colombian clinical <i>Providencia rettgeri</i> isolates co-harboring NDM-1, VIM-2, and other $\hat{\pm}$ -lactamases. <i>BMC Microbiology</i> , 2020, 20, 345.	3.3	12
51	Swiss EMBnet node web server. <i>Nucleic Acids Research</i> , 2003, 31, 3782-3783.	14.5	11
52	Dedicated chaperones coordinate co-translational regulation of ribosomal protein production with ribosome assembly to preserve proteostasis. <i>ELife</i> , 2022, 11, .	6.0	11
53	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
54	Visualization and quality assessment of de novo genome assemblies. <i>Bioinformatics</i> , 2011, 27, 3425-3426.	4.1	9

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55	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
56	On ubiquitin ligases and cancer. <i>Human Mutation</i> , 2005, 25, 507-512.	2.5	8
57	Genome-wide comparison of FGFRL1 with structurally related surface receptors. <i>Experimental and Therapeutic Medicine</i> , 2010, 1, 161-168.	1.8	8
58	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
59	Minimalistic mycoplasmas harbor different functional toxin-antitoxin systems. <i>PLoS Genetics</i> , 2021, 17, e1009365.	3.5	7
60	SV-AUTOPILOT: optimized, automated construction of structural variation discovery and benchmarking pipelines. <i>BMC Genomics</i> , 2015, 16, 238.	2.8	5
61	Whole-Genome Sequence of a Colombian <i>Acinetobacter baumannii</i> Strain, a Coproducer of OXA-72 and OXA-255-Like Carbapenemases. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
62	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
63	Draft Genome Sequence of the Virulent <i>Avibacterium paragallinarum</i> Serotype A Strain JF4211 and Identification of Two Toxins. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
64	Large-Scale Comparison of Toxin and Antitoxins in <i>Listeria monocytogenes</i> . <i>Toxins</i> , 2020, 12, 29.	3.4	4
65	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
66	Unexpected vagaries of microsatellite loci in <i>Glomus intraradices</i> : length polymorphisms are rarely caused by variation in repeat number only. <i>New Phytologist</i> , 2008, 180, 568-570.	7.3	3
67	Draft Genome Sequences of Multidrug-Resistant <i>Acinetobacter</i> sp. Strains from Colombian Hospitals. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
68	deltaRpkM: an R package for a rapid detection of differential gene presence between related bacterial genomes. <i>BMC Bioinformatics</i> , 2019, 20, 621.	2.6	3
69	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
70	Análisis genómico del resistoma de la cepa de <i>Acinetobacter baumannii</i> ABIBUN 107m multi-resistente y persistente en hospitales colombianos. <i>Revista Colombiana De Biotecnología</i> , 2014, 16, 104-113.	0.2	2
71	Ubiquitin ligases as cancer genes. <i>Nature Reviews Cancer</i> , 2004, 4, 654-654.	28.4	1
72	Hunting for insect-specific protein domains. <i>In Silico Biology</i> , 2006, 6, 35-42.	0.9	1

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73	Next Generation Sequencing methods for identification of mutations and large structural variants, 11-12 March 2014. EMBnet Journal, 2014, 20, 752.	0.6	0
74	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