

Leighton Pritchard

List of Publications by Year in descending order

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61
papers

8,748
citations

117453

34
h-index

128067

60
g-index

67
all docs

67
docs citations

67
times ranked

10051
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	13.7	1,405
2	Genomics and taxonomy in diagnostics for food security: soft-rotting enterobacterial plant pathogens. <i>Analytical Methods</i> , 2016, 8, 12-24.	1.3	991
3	Using Tablet for visual exploration of second-generation sequencing data. <i>Briefings in Bioinformatics</i> , 2013, 14, 193-202.	3.2	836
4	A translocation signal for delivery of oomycete effector proteins into host plant cells. <i>Nature</i> , 2007, 450, 115-118.	13.7	760
5	An ancestral oomycete locus contains late blight avirulence gene <i>Avr3a</i> , encoding a protein that is recognized in the host cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7766-7771.	3.3	414
6	Resistance gene enrichment sequencing (R-Seq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. <i>Plant Journal</i> , 2013, 76, 530-544.	2.8	367
7	Genome sequence of the enterobacterial phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> and characterization of virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11105-11110.	3.3	366
8	Identification and localisation of the NB-LRR gene family within the potato genome. <i>BMC Genomics</i> , 2012, 13, 75.	1.2	290
9	Trafficking arms: oomycete effectors enter host plant cells. <i>Trends in Microbiology</i> , 2006, 14, 8-11.	3.5	278
10	<i>Dickeya solani</i> sp. nov., a pectinolytic plant-pathogenic bacterium isolated from potato (<i>Solanum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	228
11	Quorum Sensing Coordinates Brute Force and Stealth Modes of Infection in the Plant Pathogen <i>Pectobacterium atrosepticum</i> . <i>PLoS Pathogens</i> , 2008, 4, e1000093.	2.1	216
12	An RxLR Effector from <i>Phytophthora infestans</i> Prevents Re-localisation of Two Plant NAC Transcription Factors from the Endoplasmic Reticulum to the Nucleus. <i>PLoS Pathogens</i> , 2013, 9, e1003670.	2.1	210
13	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. <i>PeerJ</i> , 2013, 1, e167.	0.9	159
14	Oomycete RXLR effectors: delivery, functional redundancy and durable disease resistance. <i>Current Opinion in Plant Biology</i> , 2008, 11, 373-379.	3.5	157
15	Involvement of cathepsin B in the plant disease resistance hypersensitive response. <i>Plant Journal</i> , 2007, 52, 1-13.	2.8	147
16	Colonization outwith the colon: plants as an alternative environmental reservoir for human pathogenic enterobacteria. <i>FEMS Microbiology Reviews</i> , 2009, 33, 689-703.	3.9	147
17	Presence/absence, differential expression and sequence polymorphisms between <i>PiAVR2</i> and <i>PiAVR2</i> -like in <i>Phytophthora infestans</i> determine virulence on <i>R2</i> plants. <i>New Phytologist</i> , 2011, 191, 763-776.	3.5	142
18	Comparative Genomics Reveals What Makes An Enterobacterial Plant Pathogen. <i>Annual Review of Phytopathology</i> , 2006, 44, 305-336.	3.5	138

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19	Towards understanding the virulence functions of RXLR effectors of the oomycete plant pathogen <i>Phytophthora infestans</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 1133-1140.	2.4	92
20	Schemes of flux control in a model of <i>Saccharomyces cerevisiae</i> glycolysis. <i>FEBS Journal</i> , 2002, 269, 3894-3904.	0.2	91
21	Detection of phytopathogens of the genus <i>Dickeya</i> using a PCR primer prediction pipeline for draft bacterial genome sequences. <i>Plant Pathology</i> , 2013, 62, 587-596.	1.2	87
22	GenomeDiagram: a python package for the visualization of large-scale genomic data. <i>Bioinformatics</i> , 2006, 22, 616-617.	1.8	83
23	Expressed sequence tag (EST) analysis of the pine wood nematode <i>Bursaphelenchus xylophilus</i> and <i>B. mucronatus</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 155, 9-17.	0.5	83
24	Easy phylotyping of <i>Escherichia coli</i> via the EzClermont web app and command-line tool. <i>Access Microbiology</i> , 2020, 2, acmi000143.	0.2	68
25	A systems biology perspective on plant-microbe interactions: Biochemical and structural targets of pathogen effectors. <i>Plant Science</i> , 2011, 180, 584-603.	1.7	65
26	The zigzag model of plant-microbe interactions: is it time to move on?. <i>Molecular Plant Pathology</i> , 2014, 15, 865-870.	2.0	64
27	Toward collaborative open data science in metabolomics using Jupyter Notebooks and cloud computing. <i>Metabolomics</i> , 2019, 15, 125.	1.4	59
28	Evolutionary trace analysis of the Kunitz/BPTI family of proteins: functional divergence may have been based on conformational adjustment 1 Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 1999, 285, 1589-1607.	2.0	56
29	Genetic characterization of the HrpL regulon of the fire blight pathogen <i>Erwinia amylovora</i> reveals novel virulence factors. <i>Molecular Plant Pathology</i> , 2012, 13, 160-173.	2.0	54
30	A general model of error-prone PCR. <i>Journal of Theoretical Biology</i> , 2005, 234, 497-509.	0.8	53
31	<i>Pectobacterium parvum</i> sp. nov., having a <i>Salmonella</i> SPI-1-like Type III secretion system and low virulence. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2440-2448.	0.8	51
32	Bacterial chemoattraction towards jasmonate plays a role in the entry of <i>Dickeya dadantii</i> through wounded tissues. <i>Molecular Microbiology</i> , 2009, 74, 662-671.	1.2	50
33	Efflux Pump Gene Expression in <i>Erwinia chrysanthemi</i> Is Induced by Exposure to Phenolic Acids. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 313-320.	1.4	43
34	Draft Genome Sequences of Four <i>Dickeya dianthicola</i> and Four <i>Dickeya solani</i> Strains. <i>Genome Announcements</i> , 2013, 1, .	0.8	43
35	Metabarcoding reveals a high diversity of woody host-associated <i>Phytophthora</i> spp. in soils at public gardens and amenity woodlands in Britain. <i>PeerJ</i> , 2019, 7, e6931.	0.9	40
36	Alignment-Free Design of Highly Discriminatory Diagnostic Primer Sets for <i>Escherichia coli</i> O104:H4 Outbreak Strains. <i>PLoS ONE</i> , 2012, 7, e34498.	1.1	35

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37	Evaluation of a novel method for the identification of coevolving protein residues. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 549-555.	1.0	33
38	Metagenomic Analysis of the Gut Microbiome of the Common Black Slug <i>Arion ater</i> in Search of Novel Lignocellulose Degrading Enzymes. <i>Frontiers in Microbiology</i> , 2017, 8, 2181.	1.5	33
39	Draft Genome Sequences of 17 Isolates of the Plant Pathogenic Bacterium <i>Dickeya</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	32
40	Detection of the Bacterial Potato Pathogens <i>Pectobacterium</i> and <i>Dickeya</i> spp. Using Conventional and Real-Time PCR. <i>Methods in Molecular Biology</i> , 2015, 1302, 1-16.	0.4	30
41	A novel non-protein-coding infection-specific gene family is clustered throughout the genome of <i>Phytophthora infestans</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 747-759.	0.7	27
42	Epidemiology of <i>Dickeya dianthicola</i> and <i>Dickeya solani</i> in ornamental hosts and potato studied using variable number tandem repeat analysis. <i>European Journal of Plant Pathology</i> , 2015, 141, 63-70.	0.8	26
43	Genome-Wide Identification of HrpL-Regulated Genes in the Necrotrophic Phytopathogen <i>Dickeya dadantii</i> 3937. <i>PLoS ONE</i> , 2010, 5, e13472.	1.1	25
44	Proposal for the creation of a new genus <i>Musicola</i> gen. nov., reclassification of <i>Dickeya paradisiaca</i> (Samson et al. 2005) as <i>Musicola paradisiaca</i> comb. nov. and description of a new species <i>Musicola keenii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	22
45	Do Proteins Learn to Evolve? The Hopfield Network as a Basis for the Understanding of Protein Evolution. <i>Journal of Theoretical Biology</i> , 2000, 202, 77-86.	0.8	19
46	Families of short interspersed elements in the genome of the oomycete plant pathogen, <i>Phytophthora infestans</i> . <i>Fungal Genetics and Biology</i> , 2005, 42, 351-365.	0.9	19
47	Genome-Wide Analysis of the Response of <i>Dickeya dadantii</i> 3937 to Plant Antimicrobial Peptides. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 523-533.	1.4	18
48	PHYTO-THREATS: Addressing Threats to UK Forests and Woodlands from <i>Phytophthora</i> ; Identifying Risks of Spread in Trade and Methods for Mitigation. <i>Forests</i> , 2021, 12, 1617.	0.9	18
49	Toward Assessing Farm-Based Anaerobic Digestate Public Health Risks: Comparative Investigation With Slurry, Effect of Pasteurization Treatments, and Use of Miniature Bioreactors as Proxies for Pathogen Spiking Trials. <i>Frontiers in Sustainable Food Systems</i> , 2018, 2, .	1.8	14
50	riboSeed: leveraging prokaryotic genomic architecture to assemble across ribosomal regions. <i>Nucleic Acids Research</i> , 2018, 46, e68-e68.	6.5	10
51	Microarray Comparative Genomic Hybridisation Analysis Incorporating Genomic Organisation, and Application to Enterobacterial Plant Pathogens. <i>PLoS Computational Biology</i> , 2009, 5, e1000473.	1.5	9
52	Why Genomics Research on <i>Pectobacterium</i> and <i>Dickeya</i> Makes a Difference. <i>American Journal of Potato Research</i> , 2015, 92, 218-222.	0.5	8
53	On the Statistics of Identifying Candidate Pathogen Effectors. <i>Methods in Molecular Biology</i> , 2014, 1127, 53-64.	0.4	6
54	Isolation, Detection and Characterization of <i>Pectobacterium</i> and <i>Dickeya</i> Species. , 2021, , 149-173.		5

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55	Galaxy as a Platform for Identifying Candidate Pathogen Effectors. <i>Methods in Molecular Biology</i> , 2014, 1127, 3-15.	0.4	5
56	Absence of Curli in Soil-Persistent <i>Escherichia coli</i> Is Mediated by a C-di-GMP Signaling Defect and Suggests Evidence of Biofilm-Independent Niche Specialization. <i>Frontiers in Microbiology</i> , 2018, 9, 1340.	1.5	4
57	Simple intrasequence difference (SID) analysis: an original method to highlight and rank sub-structural interfaces in protein folds. Application to the folds of bovine pancreatic trypsin inhibitor, phospholipase A2, chymotrypsin and carboxypeptidase A. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 87-101.	1.0	3
58	A high-throughput genomic screen identifies a role for the plasmid-borne type II secretion system of <i>Escherichia coli</i> O157:H7 (Sakai) in plant-microbe interactions. <i>Genomics</i> , 2020, 112, 4242-4253.	1.3	2
59	ActinoBase: tools and protocols for researchers working on <i>Streptomyces</i> and other filamentous actinobacteria. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
60	Bacterial chemoattraction towards jasmonate plays a role in the entry of <i>Dickeya dadantii</i> through wounded tissues. <i>Molecular Microbiology</i> , 2009, 74, 1543-1543.	1.2	1
61	Dataset of <i>Escherichia coli</i> O157: H7 genes enriched in adherence to spinach root tissue. <i>Data in Brief</i> , 2020, 31, 105769.	0.5	0