Leighton Pritchard

List of Publications by Year
in descending order

61 papers	**8,748** citations	117625 **34** h-index	128289 **60** g-index
67 all docs	**67** docs citations	**67** times ranked	**10051** citing authors

#	Article	IF	Citations
1	ActinoBase: tools and protocols for researchers working on Streptomyces and other filamentous actinobacteria. Microbial Genomics, 2022, 8, .	2.0	2
2	Isolation, Detection and Characterization of Pectobacterium and Dickeya Species. , 2021, , 149-173.		5
3	Proposal for the creation of a new genus Musicola gen. nov., reclassification of Dickeya paradisiaca (Samson et al. 2005) as Musicola paradisiaca comb. nov. and description of a new species Musicola keenii sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	22
4	PHYTO-THREATS: Addressing Threats to UK Forests and Woodlands from Phytophthora; Identifying Risks of Spread in Trade and Methods for Mitigation. Forests, 2021, 12, 1617.	2.1	18
5	A high-throughput genomic screen identifies a role for the plasmid-borne type II secretion system of Escherichia coli O157:H7 (Sakai) in plant-microbe interactions. Genomics, 2020, 112, 4242-4253.	2.9	2
6	Dataset of Escherichia coli O157: H7 genes enriched in adherence to spinach root tissue. Data in Brief, 2020, 31, 105769.	1.0	0
7	Easy phylotyping of Escherichia coli via the EzClermont web app and command-line tool. Access Microbiology, 2020, 2, acmi000143.	0.5	68
8	Pectobacterium parvum sp. nov., having a Salmonella SPI-1-like Type III secretion system and low virulence. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2440-2448.	1.7	51
9	Toward collaborative open data science in metabolomics using Jupyter Notebooks and cloud computing. Metabolomics, 2019, 15, 125.	3.0	59
10	Metabarcoding reveals a high diversity of woody host-associated *Phytophthora* spp. in soils at public gardens and amenity woodlands in Britain. PeerJ, 2019, 7, e6931.	2.0	40
11	riboSeed: leveraging prokaryotic genomic architecture to assemble across ribosomal regions. Nucleic Acids Research, 2018, 46, e68-e68.	14.5	10
12	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. Frontiers in Sustainable Food Systems, 2018, 2, .	3.9	14
13	Absence of Curli in Soil-Persistent Escherichia coli Is Mediated by a C-di-GMP Signaling Defect and Suggests Evidence of Biofilm-Independent Niche Specialization. Frontiers in Microbiology, 2018, 9, 1340.	3.5	4
14	Metagenomic Analysis of the Gut Microbiome of the Common Black Slug Arion ater in Search of Novel Lignocellulose Degrading Enzymes. Frontiers in Microbiology, 2017, 8, 2181.	3.5	33
15	Genomics and taxonomy in diagnostics for food security: soft-rotting enterobacterial plant pathogens. Analytical Methods, 2016, 8, 12-24.	2.7	991
16	Why Genomics Research on Pectobacterium and Dickeya Makes a Difference. American Journal of Potato Research, 2015, 92, 218-222.	0.9	8
17	Detection of the Bacterial Potato Pathogens Pectobacterium and Dickeya spp. Using Conventional and Real-Time PCR. Methods in Molecular Biology, 2015, 1302, 1-16.	0.9	30
18	Epidemiology of Dickeya dianthicola and Dickeya solani in ornamental hosts and potato studied using variable number tandem repeat analysis. European Journal of Plant Pathology, 2015, 141, 63-70.	1.7	26

#	Article	IF	Citations
19	Dickeya solani sp. nov., a pectinolytic plant-pathogenic bacterium isolated from potato (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlock	1.7	228
20	The zigzag model of plant–microbe interactions: is it time to move on?. Molecular Plant Pathology, 2014, 15, 865-870.	4.2	64
21	Galaxy as a Platform for Identifying Candidate Pathogen Effectors. Methods in Molecular Biology, 2014, 1127, 3-15.	0.9	5
22	On the Statistics of Identifying Candidate Pathogen Effectors. Methods in Molecular Biology, 2014, 1127, 53-64.	0.9	6
23	Resistance gene enrichment sequencing (<scp>R</scp>en<scp>S</scp>eq) enables reannotation of the <scp>NB</scp>–<scp>LRR</scp> gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. Plant Journal, 2013, 76, 530-544.	5.7	367
24	Using Tablet for visual exploration of second-generation sequencing data. Briefings in Bioinformatics, 2013, 14, 193-202.	6.5	836
25	Detection of phytopathogens of the genus <i>Dickeya</i> using a PCR primer prediction pipeline for draft bacterial genome sequences. Plant Pathology, 2013, 62, 587-596.	2.4	87
26	Draft Genome Sequences of Four Dickeya dianthicola and Four Dickeya solani Strains. Genome Announcements, 2013, 1, .	0.8	43
27	Draft Genome Sequences of 17 Isolates of the Plant Pathogenic Bacterium <i>Dickeya</i>. Genome Announcements, 2013, 1, .	0.8	32
28	An RxLR Effector from Phytophthora infestans Prevents Re-localisation of Two Plant NAC Transcription Factors from the Endoplasmic Reticulum to the Nucleus. PLoS Pathogens, 2013, 9, e1003670.	4.7	210
29	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. PeerJ, 2013, 1, e167.	2.0	159
30	Genome-Wide Analysis of the Response of <i>Dickeya dadantii</i> 3937 to Plant Antimicrobial Peptides. Molecular Plant-Microbe Interactions, 2012, 25, 523-533.	2.6	18
31	Identification and localisation of the NB-LRR gene family within the potato genome. BMC Genomics, 2012, 13, 75.	2.8	290
32	Genetic characterization of the HrpL regulon of the fire blight pathogen<i>Erwinia amylovora</i>reveals novel virulence factors. Molecular Plant Pathology, 2012, 13, 160-173.	4.2	54
33	Alignment-Free Design of Highly Discriminatory Diagnostic Primer Sets for Escherichia coli O104:H4 Outbreak Strains. PLoS ONE, 2012, 7, e34498.	2.5	35
34	A systems biology perspective on plant–microbe interactions: Biochemical and structural targets of pathogen effectors. Plant Science, 2011, 180, 584-603.	3.6	65
35	Presence/absence, differential expression and sequence polymorphisms between <i>PiAVR2</i> and <i>PiAVR2–like</i> in <i>Phytophthora infestans</i> determine virulence on <i>R2</i> plants. New Phytologist, 2011, 191, 763-776.	7.3	142
36	Genome-Wide Identification of HrpL-Regulated Genes in the Necrotrophic Phytopathogen Dickeya dadantii 3937. PLoS ONE, 2010, 5, e13472.	2.5	25

#	ARTICLE	IF	CITATIONS
37	Towards understanding the virulence functions of RXLR effectors of the oomycete plant pathogen Phytophthora infestans. Journal of Experimental Botany, 2009, 60, 1133-1140.	4.8	92
38	Microarray Comparative Genomic Hybridisation Analysis Incorporating Genomic Organisation, and Application to Enterobacterial Plant Pathogens. PLoS Computational Biology, 2009, 5, e1000473.	3.2	9
39	Bacterial chemoattraction towards jasmonate plays a role in the entry of *Dickeya dadantii* through wounded tissues. Molecular Microbiology, 2009, 74, 662-671.	2.5	50
40	Bacterial chemoattraction towards jasmonate plays a role in the entry of *Dickeya dadantii* through wounded tissues. Molecular Microbiology, 2009, 74, 1543-1543.	2.5	1
41	Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. Nature, 2009, 461, 393-398.	27.8	1,405
42	Colonization outwith the colon: plants as an alternative environmental reservoir for human pathogenic enterobacteria. FEMS Microbiology Reviews, 2009, 33, 689-703.	8.6	147
43	Quorum Sensing Coordinates Brute Force and Stealth Modes of Infection in the Plant Pathogen Pectobacterium atrosepticum. PLoS Pathogens, 2008, 4, e1000093.	4.7	216
44	Oomycete RXLR effectors: delivery, functional redundancy and durable disease resistance. Current Opinion in Plant Biology, 2008, 11, 373-379.	7.1	157
45	A novel non-protein-coding infection-specific gene family is clustered throughout the genome of Phytophthora infestans. Microbiology (United Kingdom), 2007, 153, 747-759.	1.8	27
46	Efflux Pump Gene Expression in Erwinia chrysanthemi Is Induced by Exposure to Phenolic Acids. Molecular Plant-Microbe Interactions, 2007, 20, 313-320.	2.6	43
47	A translocation signal for delivery of oomycete effector proteins into host plant cells. Nature, 2007, 450, 115-118.	27.8	760
48	Involvement of cathepsin B in the plant disease resistance hypersensitive response. Plant Journal, 2007, 52, 1-13.	5.7	147
49	Expressed sequence tag (EST) analysis of the pine wood nematode Bursaphelenchus xylophilus and B. mucronatus. Molecular and Biochemical Parasitology, 2007, 155, 9-17.	1.1	83
50	Comparative Genomics Reveals What Makes An Enterobacterial Plant Pathogen. Annual Review of Phytopathology, 2006, 44, 305-336.	7.8	138
51	GenomeDiagram: a python package for the visualization of large-scale genomic data. Bioinformatics, 2006, 22, 616-617.	4.1	83
52	Trafficking arms: oomycete effectors enter host plant cells. Trends in Microbiology, 2006, 14, 8-11.	7.7	278
53	A general model of error-prone PCR. Journal of Theoretical Biology, 2005, 234, 497-509.	1.7	53
54	An ancestral oomycete locus contains late blight avirulence gene Avr3a, encoding a protein that is recognized in the host cytoplasm. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7766-7771.	7.1	414

#	Article	IF	Citations
55	Families of short interspersed elements in the genome of the oomycete plant pathogen, Phytophthora infestans. Fungal Genetics and Biology, 2005, 42, 351-365.	2.1	19
56	Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11105-11110.	7.1	366
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. Protein Engineering, Design and Selection, 2003, 16, 87-101.	2.1	3
58	Schemes of flux control in a model ofSaccharomyces cerevisiaeglycolysis. FEBS Journal, 2002, 269, 3894-3904.	0.2	91
59	Evaluation of a novel method for the identification of coevolving protein residues. Protein Engineering, Design and Selection, 2001, 14, 549-555.	2.1	33
60	Do Proteins Learn to Evolve? The Hopfield Network as a Basis for the Understanding of Protein Evolution. Journal of Theoretical Biology, 2000, 202, 77-86.	1.7	19
61	Evolutionary trace analysis of the Kunitz/BPTI family of proteins: functional divergence may have been based on conformational adjustment 1 1Edited by F. Cohen. Journal of Molecular Biology, 1999, 285, 1589-1607.	4.2	56