

Liam D H Elbourne

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7077557/publications.pdf>

Version: 2024-02-01

48
papers

3,657
citations

186265
28
h-index

243625
44
g-index

51
all docs

51
docs citations

51
times ranked

5618
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the transportome of the biosurfactant producing yeast <i>Starmerella bombicola</i> . <i>BMC Genomics</i> , 2022, 23, 22.	2.8	8
2	Physiological Functions of Bacterial Multidrug Efflux Pumps. <i>Chemical Reviews</i> , 2021, 121, 5417-5478.	47.7	78
3	Elucidating Essential Genes in Plant-Associated <i>Pseudomonas protegens</i> Pf-5 Using Transposon Insertion Sequencing. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	11
4	Root Exudates Alter the Expression of Diverse Metabolic, Transport, Regulatory, and Stress Response Genes in Rhizosphere <i>Pseudomonas</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 651282.	3.5	58
5	Increasing the PACE of characterising novel transporters by functional genomics. <i>Current Opinion in Microbiology</i> , 2021, 64, 1-8.	5.1	5
6	Microbial Solute Transporters. , 2019, , 157-157.		0
7	Plastic leachates impair growth and oxygen production in <i>Prochlorococcus</i> , the ocean's most abundant photosynthetic bacteria. <i>Communications Biology</i> , 2019, 2, 184.	4.4	135
8	Interactions of an Emerging Fungal Pathogen <i>Scedosporium aurantiacum</i> with Human Lung Epithelial Cells. <i>Scientific Reports</i> , 2019, 9, 5035.	3.3	11
9	Pacing across the membrane: the novel PACE family of efflux pumps is widespread in Gram-negative pathogens. <i>Research in Microbiology</i> , 2018, 169, 450-454.	2.1	77
10	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018, 20, 2142-2159.	3.8	172
11	Dual Transcriptomics of Host-Pathogen Interaction of Cystic Fibrosis Isolate <i>Pseudomonas aeruginosa</i> PASS1 With Zebrafish. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 406.	3.9	21
12	Long-Term Irrigation Affects the Dynamics and Activity of the Wheat Rhizosphere Microbiome. <i>Frontiers in Plant Science</i> , 2018, 9, 345.	3.6	73
13	Screening of candidate substrates and coupling ions of transporters by thermostability shift assays. <i>ELife</i> , 2018, 7, .	6.0	45
14	MALDI-TOF MS meets WGS in a VRE outbreak investigation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 495-499.	2.9	18
15	Effects of uranium concentration on microbial community structure and functional potential. <i>Environmental Microbiology</i> , 2017, 19, 3323-3341.	3.8	38
16	Zinc stress induces copper depletion in <i>Acinetobacter baumannii</i> . <i>BMC Microbiology</i> , 2017, 17, 59.	3.3	55
17	TransportDB 2.0: a database for exploring membrane transporters in sequenced genomes from all domains of life. <i>Nucleic Acids Research</i> , 2017, 45, D320-D324.	14.5	306
18	The putative drug efflux systems of the <i>Bacillus cereus</i> group. <i>PLoS ONE</i> , 2017, 12, e0176188.	2.5	11

#	ARTICLE	IF	CITATIONS
19	Revealing colonisation and biofilm formation of an adherent coal seam associated microbial community on a coal surface. <i>International Journal of Coal Geology</i> , 2016, 160-161, 42-50.	5.0	27
20	Fluorescence-Based Flow Sorting in Parallel with Transposon Insertion Site Sequencing Identifies Multidrug Efflux Systems in <i>Acinetobacter baumannii</i> . <i>MBio</i> , 2016, 7, .	4.1	27
21	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	21
22	Insights on virulence from the complete genome of <i>Staphylococcus capitis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 980.	3.5	56
23	6. Microbial Slime Curtain Communities of the Nullarbor Caves. , 2015, , 125-136.		0
24	An ace up their sleeve: a transcriptomic approach exposes the <i>AceI</i> efflux protein of <i>Acinetobacter baumannii</i> and reveals the drug efflux potential hidden in many microbial pathogens. <i>Frontiers in Microbiology</i> , 2015, 6, 333.	3.5	35
25	A novel family of integrases associated with prophages and genomic islands integrated within the <i>tRNA-dihydrouridine synthase A (dusA)</i> gene. <i>Nucleic Acids Research</i> , 2015, 43, 4547-4557.	14.5	34
26	The <i>Rsm</i> regulon of plant growth-promoting <i>Pseudomonas fluorescens</i> SS101: role of small RNAs in regulation of lipopeptide biosynthesis. <i>Microbial Biotechnology</i> , 2015, 8, 296-310.	4.2	31
27	Genomic analyses of <i>Clostridium perfringens</i> isolates from five toxinotypes. <i>Research in Microbiology</i> , 2015, 166, 255-263.	2.1	71
28	Genome Sequence of the Neurotoxicogenic <i>Clostridium butyricum</i> Strain 5521. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
29	Next Generation Barcode Tagged Sequencing for Monitoring Microbial Community Dynamics. <i>Methods in Molecular Biology</i> , 2014, 1096, 101-110.	0.9	2
30	Microbial Solute Transporters. , 2014, , .		0
31	Life in the dark: metagenomic evidence that a microbial slime community is driven by inorganic nitrogen metabolism. <i>ISME Journal</i> , 2013, 7, 1227-1236.	9.8	63
32	Genome Sequence of the Group III <i>Clostridium botulinum</i> Strain Eklund-C. <i>Genome Announcements</i> , 2013, 1, e0004413.	0.8	5
33	Maintenance of essential amino acid synthesis pathways in the <i>Blattabacterium cuenoti</i> symbiont of a wood-feeding cockroach. <i>Biology Letters</i> , 2013, 9, 20121153.	2.3	45
34	H-NS Plays a Role in Expression of <i>Acinetobacter baumannii</i> Virulence Features. <i>Infection and Immunity</i> , 2013, 81, 2574-2583.	2.2	100
35	The Complete Genome and Phenome of a Community-Acquired <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2013, 8, e58628.	2.5	93
36	Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. <i>ISME Journal</i> , 2012, 6, 1403-1414.	9.8	120

#	ARTICLE	IF	CITATIONS
37	Comparative Genomics of Plant-Associated <i>Pseudomonas</i> spp.: Insights into Diversity and Inheritance of Traits Involved in Multitrophic Interactions. <i>PLoS Genetics</i> , 2012, 8, e1002784.	3.5	578
38	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	17.5	428
39	Genome of alkaliphilic <i>Bacillus pseudofirmus</i> OF4 reveals adaptations that support the ability to grow in an external pH range from 7.5 to 11.4. <i>Environmental Microbiology</i> , 2011, 13, 3289-3309.	3.8	73
40	Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213.	2.2	155
41	Inactivation of the GacA response regulator in <i>Pseudomonas fluorescens</i> Pf-5 has far-reaching transcriptomic consequences. <i>Environmental Microbiology</i> , 2010, 12, 899-915.	3.8	137
42	Complete Genome Sequence of the Multiresistant Taxonomic Outlier <i>Pseudomonas aeruginosa</i> PA7. <i>PLoS ONE</i> , 2010, 5, e8842.	2.5	236
43	Statistical Analysis of Microarray Data with Replicated Spots: A Case Study with <i>Synechococcus</i> WH8102. <i>Comparative and Functional Genomics</i> , 2009, 2009, 1-11.	2.0	5
44	Tn 1403 , a Multiple-Antibiotic Resistance Transposon Made Up of Three Distinct Transposons. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 1827-1829.	3.2	56
45	Gene Cassette Encoding a 3- N -Aminoglycoside Acetyltransferase in a Chromosomal Integron. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 2270-2271.	3.2	9
46	New Integron-Associated Gene Cassette Encoding a Trimethoprim-Resistant DfrB-Type Dihydrofolate Reductase. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 2863-2865.	3.2	19
47	Evolutionary Relationships of Pathogenic Clones of <i>Vibrio cholerae</i> by Sequence Analysis of Four Housekeeping Genes. <i>Infection and Immunity</i> , 1999, 67, 1116-1124.	2.2	87
48	Unravelling Stratified Microbial Assemblages in Australia's Only Deep Anchialine System, The Bundera Sinkhole. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	10