

# Lars Jelsbak

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

9,226  
citations

117625

34  
h-index

138484

58  
g-index

75  
all docs

75  
docs citations

75  
times ranked

12745  
citing authors

#	ARTICLE	IF	CITATIONS
1	Orally active bivalent VHH construct prevents proliferation of F4+ enterotoxigenic Escherichia coli in weaned piglets. IScience, 2022, 25, 104003.	4.1	6
2	A Whole-Cell Biosensor for Detection of 2,4-Diacetylphloroglucinol (DAPG)-Producing Bacteria from Grassland Soil. Applied and Environmental Microbiology, 2021, 87, .	3.1	11
3	The plasmidome of multidrug-resistant emergent Salmonella serovars isolated from poultry. Infection, Genetics and Evolution, 2021, 89, 104716.	2.3	10
4	Identification and Differentiation of Pseudomonas Species in Field Samples Using an <i>rpoD</i> Amplicon Sequencing Methodology. MSystems, 2021, 6, e0070421.	3.8	10
5	Recurrent tuberculosis in patients infected with the predominant Mycobacterium tuberculosis outbreak strain in Denmark. New insights gained through whole genome sequencing. Infection, Genetics and Evolution, 2020, 80, 104169.	2.3	9
6	Complete Genome Sequence of Pseudomonas sp. Strain SK, Isolated from Organic Wheat Rhizosphere. Microbiology Resource Announcements, 2020, 9, .	0.6	2
7	Complete Genome Sequence of a Bioactive Pseudomonas sp. Strain, DTU12.3, Isolated from Soil in Denmark. Microbiology Resource Announcements, 2019, 8, .	0.6	0
8	Within-Host Adaptation Mediated by Intergenic Evolution in Pseudomonas aeruginosa. Genome Biology and Evolution, 2019, 11, 1385-1397.	2.5	53
9	A Rare Thioquinolobactin Siderophore Present in a Bioactive Pseudomonas sp. DTU12.1. Genome Biology and Evolution, 2019, 11, 3529-3533.	2.5	6
10	Application of RNA-seq and Bioimaging Methods to Study Microbe-Microbe Interactions and Their Effects on Biofilm Formation and Gene Expression. Methods in Molecular Biology, 2018, 1734, 131-158.	0.9	5
11	Transcriptomic profiling of interacting nasal staphylococci species reveals global changes in gene and non-coding RNA expression. FEMS Microbiology Letters, 2018, 365, .	1.8	11
12	HldE Is Important for Virulence Phenotypes in Enterotoxigenic Escherichia coli. Frontiers in Cellular and Infection Microbiology, 2018, 8, 253.	3.9	12
13	A Major Mycobacterium tuberculosis outbreak caused by one specific genotype in a low-incidence country: Exploring gene profile virulence explanations. Scientific Reports, 2018, 8, 11869.	3.3	14
14	Intergenic evolution during host adaptation increases expression of the metallophore pseudopaline in Pseudomonas aeruginosa. Microbiology (United Kingdom), 2018, 164, 1038-1047.	1.8	10
15	Reconstruction of the metabolic network of Pseudomonas aeruginosa to interrogate virulence factor synthesis. Nature Communications, 2017, 8, 14631.	12.8	116
16	SERS detection of the biomarker hydrogen cyanide from Pseudomonas aeruginosa cultures isolated from cystic fibrosis patients. Scientific Reports, 2017, 7, 45264.	3.3	26
17	Genomic Epidemiology of a Major Mycobacterium tuberculosis Outbreak: Retrospective Cohort Study in a Low-Incidence Setting Using Sparse Time-Series Sampling. Journal of Infectious Diseases, 2017, 216, 366-374.	4.0	29
18	A Bacteriophage-Acquired O-Antigen Polymerase (Wzyl <sup>2</sup> ) from P. aeruginosa Serotype O16 Performs a Varied Mechanism Compared to Its Cognate Wzyl <sup>±</sup> . Frontiers in Microbiology, 2016, 7, 393.	3.5	7

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19	Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain DK1-NH57388A, a Stable Mucoid Cystic Fibrosis Isolate. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
20	Application of Whole-Genome Sequencing Data for O-Specific Antigen Analysis and <i>In Silico</i> Serotyping of <i>Pseudomonas aeruginosa</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1782-1788.	3.9	85
21	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	17.5	2,802
22	The evolution of antimicrobial peptide resistance in <i>Pseudomonas aeruginosa</i> is shaped by strong epistatic interactions. <i>Nature Communications</i> , 2016, 7, 13002.	12.8	106
23	Biofilm as a production platform for heterologous production of rhamnolipids by the non-pathogenic strain <i>Pseudomonas putida</i> KT2440. <i>Microbial Cell Factories</i> , 2016, 15, 181.	4.0	30
24	Substantial molecular evolution and mutation rates in prolonged latent <i>Mycobacterium tuberculosis</i> infection in humans. <i>International Journal of Medical Microbiology</i> , 2016, 306, 580-585.	3.6	38
25	Evolution of metabolic divergence in <i>Pseudomonas aeruginosa</i> during long-term infection facilitates a proto-cooperative interspecies interaction. <i>ISME Journal</i> , 2016, 10, 1323-1336.	9.8	89
26	Antibiotic combination therapy can select for broad-spectrum multidrug resistance in <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2016, 47, 48-55.	2.5	75
27	The phenotypic evolution of <i>Pseudomonas aeruginosa</i> populations changes in the presence of subinhibitory concentrations of ciprofloxacin. <i>Microbiology (United Kingdom)</i> , 2016, 162, 865-875.	1.8	30
28	Utilization and control of ecological interactions in polymicrobial infections and community-based microbial cell factories. <i>F1000Research</i> , 2016, 5, 421.	1.6	2
29	Clinical utilization of genomics data produced by the international <i>Pseudomonas aeruginosa</i> consortium. <i>Frontiers in Microbiology</i> , 2015, 6, 1036.	3.5	144
30	The Widespread Multidrug-Resistant Serotype O12 <i>Pseudomonas aeruginosa</i> Clone Emerged through Concomitant Horizontal Transfer of Serotype Antigen and Antibiotic Resistance Gene Clusters. <i>MBio</i> , 2015, 6, e01396-15.	4.1	47
31	Evolutionary insight from whole-genome sequencing of <i>Pseudomonas aeruginosa</i> from cystic fibrosis patients. <i>Future Microbiology</i> , 2015, 10, 599-611.	2.0	42
32	Bacteriocin-mediated competition in cystic fibrosis lung infections. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150972.	2.6	40
33	Within-Host Evolution of <i>Pseudomonas aeruginosa</i> Reveals Adaptation toward Iron Acquisition from Hemoglobin. <i>MBio</i> , 2014, 5, e00966-14.	4.1	186
34	Environmental Heterogeneity Drives Within-Host Diversification and Evolution of <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2014, 5, e01592-14.	4.1	153
35	<i>Staphylococcus aureus</i> Alters Growth Activity, Autolysis, and Antibiotic Tolerance in a Human Host-Adapted <i>Pseudomonas aeruginosa</i> Lineage. <i>Journal of Bacteriology</i> , 2014, 196, 3903-3911.	2.2	68
36	Typing of <i>Pseudomonas aeruginosa</i> from hemorrhagic pneumonia in mink ( <i>Neovison vison</i> ). <i>Veterinary Microbiology</i> , 2013, 163, 103-109.	1.9	20

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37	Archetypal analysis of diverse <i>Pseudomonas aeruginosa</i> transcriptomes reveals adaptation in cystic fibrosis airways. <i>BMC Bioinformatics</i> , 2013, 14, 279.	2.6	42
38	Draft Genome Sequences of <i>Pseudomonas aeruginosa</i> B3 Strains Isolated from a Cystic Fibrosis Patient Undergoing Antibiotic Chemotherapy. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
39	Evolutionary remodeling of global regulatory networks during long-term bacterial adaptation to human hosts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7766-7771.	7.1	77
40	Genome Analysis of a Transmissible Lineage of <i>Pseudomonas aeruginosa</i> Reveals Pathoadaptive Mutations and Distinct Evolutionary Paths of Hypermutators. <i>PLoS Genetics</i> , 2013, 9, e1003741.	3.5	191
41	Evolution and diversification of <i>Pseudomonas aeruginosa</i> in the paranasal sinuses of cystic fibrosis children have implications for chronic lung infection. <i>ISME Journal</i> , 2012, 6, 31-45.	9.8	184
42	Mutations in 23S rRNA Confer Resistance against Azithromycin in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4519-4521.	3.2	26
43	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1355-1361.	3.9	1,925
44	Adaptation of <i>Pseudomonas aeruginosa</i> to the cystic fibrosis airway: an evolutionary perspective. <i>Nature Reviews Microbiology</i> , 2012, 10, 841-851.	28.6	635
45	Deletion and acquisition of genomic content during early stage adaptation of <i>Pseudomonas aeruginosa</i> to a human host environment. <i>Environmental Microbiology</i> , 2012, 14, 2200-2211.	3.8	88
46	Microbial ecology and adaptation in cystic fibrosis airways. <i>Environmental Microbiology</i> , 2011, 13, 1682-1689.	3.8	64
47	Bacterial adaptation during chronic infection revealed by independent component analysis of transcriptomic data. <i>BMC Microbiology</i> , 2011, 11, 184.	3.3	20
48	Evolutionary dynamics of bacteria in a human host environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7481-7486.	7.1	327
49	Early adaptive developments of <i>Pseudomonas aeruginosa</i> after the transition from life in the environment to persistent colonization in the airways of human cystic fibrosis hosts. <i>Environmental Microbiology</i> , 2010, 12, 1643-1658.	3.8	124
50	In Situ Growth Rates and Biofilm Development of <i>Pseudomonas aeruginosa</i> Populations in Chronic Lung Infections. <i>Journal of Bacteriology</i> , 2008, 190, 2767-2776.	2.2	201
51	Molecular Epidemiology and Dynamics of <i>Pseudomonas aeruginosa</i> Populations in Lungs of Cystic Fibrosis Patients. <i>Infection and Immunity</i> , 2007, 75, 2214-2224.	2.2	220
52	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	17.5	354
53	Enhancer-binding proteins with a forkhead-associated domain and the $\Delta 54$ regulon in <i>Myxococcus xanthus</i> fruiting body development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3010-3015.	7.1	46
54	$\Delta 54$ Enhancer Binding Proteins and <i>Myxococcus xanthus</i> Fruiting Body Development. <i>Journal of Bacteriology</i> , 2004, 186, 4361-4368.	2.2	61

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55	Coupling gene expression and multicellular morphogenesis during fruiting body formation in <i>Myxococcus xanthus</i> . <i>Molecular Microbiology</i> , 2003, 48, 1-8.	2.5	66
56	Cell behavior and cell-cell communication during fruiting body morphogenesis in <i>Myxococcus xanthus</i> . <i>Journal of Microbiological Methods</i> , 2003, 55, 829-839.	1.6	41
57	Pattern formation by a cell surface-associated morphogen in <i>Myxococcus xanthus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2032-2037.	7.1	90
58	Pattern formation: fruiting body morphogenesis in <i>Myxococcus xanthus</i> . <i>Current Opinion in Microbiology</i> , 2000, 3, 637-642.	5.1	59
59	The cell surface-associated intercellular C-signal induces behavioral changes in individual <i>Myxococcus xanthus</i> cells during fruiting body morphogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 5031-5036.	7.1	66