

# Lars Jelsbak

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

9,226  
citations

117453

34  
h-index

138251

58  
g-index

75  
all docs

75  
docs citations

75  
times ranked

12745  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	9.4	2,802
2	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1355-1361.	1.8	1,925
3	Adaptation of <i>Pseudomonas aeruginosa</i> to the cystic fibrosis airway: an evolutionary perspective. <i>Nature Reviews Microbiology</i> , 2012, 10, 841-851.	13.6	635
4	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	9.4	354
5	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.	3.3	327
6	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.	1.0	220
7	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.	1.0	201
8	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.	1.5	191
9	Within-Host Evolution of <i>Pseudomonas aeruginosa</i> Reveals Adaptation toward Iron Acquisition from Hemoglobin. <i>MBio</i> , 2014, 5, e00966-14.	1.8	186
10	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.	4.4	184
11	Environmental Heterogeneity Drives Within-Host Diversification and Evolution of <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2014, 5, e01592-14.	1.8	153
12	Clinical utilization of genomics data produced by the international <i>Pseudomonas aeruginosa</i> consortium. <i>Frontiers in Microbiology</i> , 2015, 6, 1036.	1.5	144
13	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.	1.8	124
14	Reconstruction of the metabolic network of <i>Pseudomonas aeruginosa</i> to interrogate virulence factor synthesis. <i>Nature Communications</i> , 2017, 8, 14631.	5.8	116
15	The evolution of antimicrobial peptide resistance in <i>Pseudomonas aeruginosa</i> is shaped by strong epistatic interactions. <i>Nature Communications</i> , 2016, 7, 13002.	5.8	106
16	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.	3.3	90
17	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.	4.4	89
18	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.	1.8	88

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19	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.	1.8	85
20	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.	3.3	77
21	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.	1.1	75
22	<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.	1.0	68
23	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.	3.3	66
24	Coupling gene expression and multicellular morphogenesis during fruiting body formation in <i>Myxococcus xanthus</i> . <i>Molecular Microbiology</i> , 2003, 48, 1-8.	1.2	66
25	Microbial ecology and adaptation in cystic fibrosis airways. <i>Environmental Microbiology</i> , 2011, 13, 1682-1689.	1.8	64
26	Ïf54 Enhancer Binding Proteins and <i>Myxococcus xanthus</i> Fruiting Body Development. <i>Journal of Bacteriology</i> , 2004, 186, 4361-4368.	1.0	61
27	Pattern formation: fruiting body morphogenesis in <i>Myxococcus xanthus</i> . <i>Current Opinion in Microbiology</i> , 2000, 3, 637-642.	2.3	59
28	Within-Host Adaptation Mediated by Intergenic Evolution in <i>Pseudomonas aeruginosa</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1385-1397.	1.1	53
29	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.	1.8	47
30	Enhancer-binding proteins with a forkhead-associated domain and the Æ54 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.	3.3	46
31	Archetypal analysis of diverse <i>Pseudomonas aeruginosa</i> transcriptomes reveals adaptation in cystic fibrosis airways. <i>BMC Bioinformatics</i> , 2013, 14, 279.	1.2	42
32	Evolutionary insight from whole-genome sequencing of <i>Pseudomonas aeruginosa</i> from cystic fibrosis patients. <i>Future Microbiology</i> , 2015, 10, 599-611.	1.0	42
33	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.	0.7	41
34	Bacteriocin-mediated competition in cystic fibrosis lung infections. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150972.	1.2	40
35	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.	1.5	38
36	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.	1.9	30

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37	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.	0.7	30
38	Genomic Epidemiology of a Major <i>Mycobacterium tuberculosis</i> Outbreak: Retrospective Cohort Study in a Low-Incidence Setting Using Sparse Time-Series Sampling. <i>Journal of Infectious Diseases</i> , 2017, 216, 366-374.	1.9	29
39	Mutations in 23S rRNA Confer Resistance against Azithromycin in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4519-4521.	1.4	26
40	SERS detection of the biomarker hydrogen cyanide from <i>Pseudomonas aeruginosa</i> cultures isolated from cystic fibrosis patients. <i>Scientific Reports</i> , 2017, 7, 45264.	1.6	26
41	Bacterial adaptation during chronic infection revealed by independent component analysis of transcriptomic data. <i>BMC Microbiology</i> , 2011, 11, 184.	1.3	20
42	Typing of <i>Pseudomonas aeruginosa</i> from hemorrhagic pneumonia in mink ( <i>Neovison vison</i> ). <i>Veterinary Microbiology</i> , 2013, 163, 103-109.	0.8	20
43	A Major <i>Mycobacterium tuberculosis</i> outbreak caused by one specific genotype in a low-incidence country: Exploring gene profile virulence explanations. <i>Scientific Reports</i> , 2018, 8, 11869.	1.6	14
44	HldE Is Important for Virulence Phenotypes in Enterotoxigenic <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 253.	1.8	12
45	Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain DK1-NH57388A, a Stable Mucoïd Cystic Fibrosis Isolate. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
46	Transcriptomic profiling of interacting nasal staphylococci species reveals global changes in gene and non-coding RNA expression. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	11
47	A Whole-Cell Biosensor for Detection of 2,4-Diacetylphloroglucinol (DAPG)-Producing Bacteria from Grassland Soil. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	11
48	The plasmidome of multidrug-resistant emergent <i>Salmonella</i> serovars isolated from poultry. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104716.	1.0	10
49	Identification and Differentiation of <i>Pseudomonas</i> Species in Field Samples Using an <i>rpoD</i> Amplicon Sequencing Methodology. <i>MSystems</i> , 2021, 6, e0070421.	1.7	10
50	Intergenic evolution during host adaptation increases expression of the metallophore pseudopaline in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 1038-1047.	0.7	10
51	Recurrent tuberculosis in patients infected with the predominant <i>Mycobacterium tuberculosis</i> outbreak strain in Denmark. New insights gained through whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104169.	1.0	9
52	A Bacteriophage-Acquired O-Antigen Polymerase (Wzy <sup>12</sup> ) from <i>P. aeruginosa</i> Serotype O16 Performs a Varied Mechanism Compared to Its Cognate Wzy <sup>1±</sup> . <i>Frontiers in Microbiology</i> , 2016, 7, 393.	1.5	7
53	A Rare Thioquinolobactin Siderophore Present in a Bioactive <i>Pseudomonas</i> sp. DTU12.1. <i>Genome Biology and Evolution</i> , 2019, 11, 3529-3533.	1.1	6
54	Orally active bivalent VHH construct prevents proliferation of F4+ enterotoxigenic <i>Escherichia coli</i> in weaned piglets. <i>IScience</i> , 2022, 25, 104003.	1.9	6

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55	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
56	Application of RNA-seq and Bioimaging Methods to Study Microbe–Microbe Interactions and Their Effects on Biofilm Formation and Gene Expression. <i>Methods in Molecular Biology</i> , 2018, 1734, 131-158.	0.4	5
57	Complete Genome Sequence of <i>Pseudomonas</i> sp. Strain SK, Isolated from Organic Wheat Rhizosphere. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
58	Utilization and control of ecological interactions in polymicrobial infections and community-based microbial cell factories. <i>F1000Research</i> , 2016, 5, 421.	0.8	2
59	Complete Genome Sequence of a Bioactive <i>Pseudomonas</i> sp. Strain, DTU12.3, Isolated from Soil in Denmark. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0