

# Lars Paulin

## List of Publications by Year in descending order

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101  
papers

5,964  
citations

117625

34  
h-index

82547

72  
g-index

110  
all docs

110  
docs citations

110  
times ranked

9927  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 variant with mutations in N gene affecting detection by widely used PCR primers. Journal of Medical Virology, 2022, 94, 1227-1231.	5.0	18
2	Improved chromosome-level genome assembly of the Glanville fritillary butterfly ( <i>Melitaea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 11, .	6.4	8
3	Multimomics implicate gut microbiota in altered lipid and energy metabolism in Parkinson's disease. Npj Parkinson's Disease, 2022, 8, 39.	5.3	12
4	Bacterial Butyrate in Parkinson's Disease Is Linked to Epigenetic Changes and Depressive Symptoms. Movement Disorders, 2022, 37, 1644-1653.	3.9	44
5	Transcriptomic time-series analysis of cold- and heat-shock response in psychrotrophic lactic acid bacteria. BMC Genomics, 2021, 22, 28.	2.8	16
6	Subgingival microbiota in a population with and without cognitive dysfunction. Journal of Oral Microbiology, 2021, 13, 1854552.	2.7	24
7	A transcriptomic view to wounding response in young Scots pine stems. Scientific Reports, 2021, 11, 3778.	3.3	9
8	High-pressure processing-induced transcriptome response during recovery of <i>Listeria monocytogenes</i> . BMC Genomics, 2021, 22, 117.	2.8	18
9	Relationships of gut microbiota, short-chain fatty acids, inflammation, and the gut barrier in Parkinson's disease. Molecular Neurodegeneration, 2021, 16, 6.	10.8	197
10	The complete genome sequence of <i>Listeria monocytogenes</i> strain S2542 and expression of selected genes under high-pressure processing. BMC Research Notes, 2021, 14, 137.	1.4	1
11	Comparative Genomics of 42 <i>Arcanobacterium phocae</i> Strains. Antibiotics, 2021, 10, 740.	3.7	1
12	Gut Microbiome Signatures of Risk and Prodromal Markers of Parkinson Disease. Annals of Neurology, 2021, 90, E1-E12.	5.3	41
13	Genomic convergence between <i>Akkermansia muciniphila</i> in different mammalian hosts. BMC Microbiology, 2021, 21, 298.	3.3	10
14	Alu element in the RNA binding motif protein, X-linked 2 (RBMX2) gene found to be linked to bipolar disorder. PLoS ONE, 2021, 16, e0261170.	2.5	2
15	Gut microbiota composition is associated with narcolepsy type 1. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, .	6.0	20
16	Survey of microbes in industrial-scale second-generation bioethanol production for better process knowledge and operation. Applied Microbiology and Biotechnology, 2020, 104, 8049-8064.	3.6	0
17	Immune-microbiota interaction in Finnish and Russian Karelia young people with high and low allergy prevalence. Clinical and Experimental Allergy, 2020, 50, 1148-1158.	2.9	19
18	Complete Genome Sequences and Methylome Analyses of <i>Cutibacterium acnes</i> subsp. <i>acnes</i> Strains DSM 16379 and DSM 1897. Microbiology Resource Announcements, 2020, 9, .	0.6	5

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19	Life's history genomic regions explain differences in Atlantic salmon marine diet specialization. <i>Journal of Animal Ecology</i> , 2020, 89, 2677-2691.	2.8	28
20	Skin Microbiome in Cutaneous T-Cell Lymphoma by 16S and Whole-Genome Shotgun Sequencing. <i>Journal of Investigative Dermatology</i> , 2020, 140, 2304-2308.e7.	0.7	22
21	<i>Streptococcus halichoeri</i> : Comparative Genomics of an Emerging Pathogen. <i>International Journal of Genomics</i> , 2020, 2020, 1-9.	1.6	7
22	Identification and Characterization of Splicing Defects by Single-Molecule Real-Time Sequencing Technology (PacBio). <i>Journal of Neuromuscular Diseases</i> , 2020, 7, 477-481.	2.6	7
23	Cloning of novel bacterial xylanases from lignocellulose-enriched compost metagenomic libraries. <i>AMB Express</i> , 2019, 9, 124.	3.0	18
24	Red-Brown Pigmentation of <i>Acidipropionibacterium jensenii</i> Is Tied to Haemolytic Activity and <i>cyl</i> -Like Gene Cluster. <i>Microorganisms</i> , 2019, 7, 512.	3.6	10
25	Phenotypic effects of dietary stress in combination with a respiratory chain bypass in mice. <i>Physiological Reports</i> , 2019, 7, e14159.	1.7	8
26	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffold output. <i>PLoS ONE</i> , 2019, 14, e0216885.	2.5	14
27	Multi-omics analysis identifies mitochondrial pathways associated with anxiety-related behavior. <i>PLoS Genetics</i> , 2019, 15, e1008358.	3.5	43
28	Gut microbiota in Parkinson's disease: Temporal stability and relations to disease progression. <i>EBioMedicine</i> , 2019, 44, 691-707.	6.1	236
29	BK polyomavirus microRNA expression and sequence variation in polyomavirus-associated nephropathy. <i>Journal of Clinical Virology</i> , 2018, 102, 70-76.	3.1	16
30	Polyadenylation and degradation of structurally abnormal mitochondrial tRNAs in human cells. <i>Nucleic Acids Research</i> , 2018, 46, 5209-5226.	14.5	14
31	Secretome profiling of <i>Propionibacterium freudenreichii</i> reveals highly variable responses even among the closely related strains. <i>Microbial Biotechnology</i> , 2018, 11, 510-526.	4.2	15
32	Food Spoilage-Associated <i>Leuconostoc</i> , <i>Lactococcus</i> , and <i>Lactobacillus</i> Species Display Different Survival Strategies in Response to Competition. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	50
33	Breakpoint mapping and haplotype analysis of translocation t(1;12)(q43;q21.1) in two apparently independent families with vascular phenotypes. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2018, 6, 56-68.	1.2	8
34	Mu transpososome activity-profiling yields hyperactive MuA variants for highly efficient genetic and genome engineering. <i>Nucleic Acids Research</i> , 2018, 46, 4649-4661.	14.5	4
35	The complexity of titin splicing pattern in human adult skeletal muscles. <i>Skeletal Muscle</i> , 2018, 8, 11.	4.2	65
36	Isotretinoin and lymecycline treatments modify the skin microbiota in acne. <i>Experimental Dermatology</i> , 2018, 27, 30-36.	2.9	48

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37	Gut microbiome in gestational diabetes: a cross-sectional study of mothers and offspring 5 years postpartum. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2018, 97, 38-46.	2.8	51
38	Bracketing phenogenotypic limits of mammalian hybridization. <i>Royal Society Open Science</i> , 2018, 5, 180903.	2.4	24
39	Cloning of the wheat Yr15 resistance gene sheds light on the plant tandem kinase-pseudokinase family. <i>Nature Communications</i> , 2018, 9, 3735.	12.8	204
40	The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. <i>Plant Cell</i> , 2018, 30, 2813-2837.	6.6	95
41	Metagenomic and metatranscriptomic analysis of the microbial community in Swiss-type Maasdam cheese during ripening. <i>International Journal of Food Microbiology</i> , 2018, 281, 10-22.	4.7	63
42	Dietary supplementation with yeast hydrolysate in pregnancy influences colostrum yield and gut microbiota of sows and piglets after birth. <i>PLoS ONE</i> , 2018, 13, e0197586.	2.5	48
43	BARCOSEL: a tool for selecting an optimal barcode set for high-throughput sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 257.	2.6	35
44	<i>Acidipropionibacterium virtanenii</i> sp. nov., isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3175-3183.	1.7	9
45	<i>Romboutsia hominis</i> sp. nov., the first human gut-derived representative of the genus <i>Romboutsia</i> , isolated from ileostoma effluent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3479-3486.	1.7	37
46	Genetic Control of Myelin Plasticity after Chronic Psychosocial Stress. <i>ENeuro</i> , 2018, 5, ENEURO.0166-18.2018.	1.9	48
47	Comparative genome analysis of 24 bovine-associated <i>Staphylococcus</i> isolates with special focus on the putative virulence genes. <i>PeerJ</i> , 2018, 6, e4560.	2.0	30
48	Complete Genome Sequence of <i>Akkermansia glycaniphila</i> Strain Pyt <sup>T</sup> , a Mucin-Degrading Specialist of the Reticulated Python Gut. <i>Genome Announcements</i> , 2017, 5, .	0.8	16
49	Oral and nasal microbiota in Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2017, 38, 61-67.	2.2	159
50	Loss of cutaneous microbial diversity during first 3 weeks of life in very low birthweight infants. <i>Experimental Dermatology</i> , 2017, 26, 861-867.	2.9	21
51	Complete Genome Sequence of <i>Eubacterium hallii</i> Strain L2-7. <i>Genome Announcements</i> , 2017, 5, .	0.8	17
52	An Inducible Operon Is Involved in Inulin Utilization in <i>Lactobacillus plantarum</i> Strains, as Revealed by Comparative Proteogenomics and Metabolic Profiling. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	43
53	Functional genomics provides insights into the role of <i>Propionibacterium freudenreichii</i> ssp. <i>shermanii</i> JS in cheese ripening. <i>International Journal of Food Microbiology</i> , 2017, 241, 39-48.	4.7	19
54	Skin Microbiome in Small- and Large-plaque Parapsoriasis. <i>Acta Dermato-Venereologica</i> , 2017, 97, 685-691.	1.3	9

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55	Bile microbiota in primary sclerosing cholangitis: Impact on disease progression and development of biliary dysplasia. PLoS ONE, 2017, 12, e0182924.	2.5	71
56	Genome sequence of the model plant pathogen <i>Pectobacterium carotovorum</i> SCC1. Standards in Genomic Sciences, 2017, 12, 87.	1.5	16
57	De novo assembly of genomes from long sequence reads reveals uncharted territories of <i>Propionibacterium freudenreichii</i> . BMC Genomics, 2017, 18, 790.	2.8	16
58	Genotypic and phenotypic diversity of <i>Lactobacillus rhamnosus</i> clinical isolates, their comparison with strain GG and their recognition by complement system. PLoS ONE, 2017, 12, e0176739.	2.5	21
59	<i>Lactobacillus oligofermentans</i> glucose, ribose and xylose transcriptomes show higher similarity between glucose and xylose catabolism-induced responses in the early exponential growth phase. BMC Genomics, 2016, 17, 539.	2.8	27
60	Complete Genome Sequence of <i>Enterococcus faecium</i> Commensal Isolate E1002. Genome Announcements, 2016, 4, .	0.8	2
61	Skin microbiome in melanomas and melanocytic nevi. European Journal of Dermatology, 2016, 26, 49-55.	0.6	26
62	Polymorphisms, Chromosomal Rearrangements, and Mutator Phenotype Development during Experimental Evolution of <i>Lactobacillus rhamnosus</i> GG. Applied and Environmental Microbiology, 2016, 82, 3783-3792.	3.1	27
63	<i>Lactobacillus rhamnosus</i> GG Outcompetes <i>Enterococcus faecium</i> via Mucus-Binding Pili: Evidence for a Novel and Heterospecific Probiotic Mechanism. Applied and Environmental Microbiology, 2016, 82, 5756-5762.	3.1	93
64	Single-Molecule Sequencing Revealing the Presence of Distinct JC Polyomavirus Populations in Patients With Progressive Multifocal Leukoencephalopathy. Journal of Infectious Diseases, 2016, 215, jiw399.	4.0	13
65	Cytokinin and Auxin Display Distinct but Interconnected Distribution and Signaling Profiles to Stimulate Cambial Activity. Current Biology, 2016, 26, 1990-1997.	3.9	170
66	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . Environmental Microbiology Reports, 2016, 8, 1024-1037.	2.4	104
67	Evaluating the mobility potential of antibiotic resistance genes in environmental resistomes without metagenomics. Scientific Reports, 2016, 6, 35790.	3.3	46
68	Complete genome sequence of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1, isolated from vacuum-packaged vegetable sausages. Standards in Genomic Sciences, 2016, 11, 40.	1.5	28
69	Isolation and whole genome sequencing of a <i>Ruminococcus</i> -like bacterium, associated with irritable bowel syndrome. Anaerobe, 2016, 39, 60-67.	2.1	24
70	Genomic features separating ten strains of <i>Neorhizobium galegae</i> with different symbiotic phenotypes. BMC Genomics, 2015, 16, 348.	2.8	12
71	Genome Sequences of Four <i>Staphylococcus aureus</i> Strains Isolated from Bovine Mastitis. Genome Announcements, 2015, 3, .	0.8	4
72	Increased transcriptome sequencing efficiency with modified Mint-2 digestion-ligation protocol. Analytical Biochemistry, 2015, 477, 38-40.	2.4	2

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73	Multilocus Sequence Typing of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> , a Psychrotrophic Lactic Acid Bacterium Causing Spoilage of Packaged Perishable Foods. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2474-2480.	3.1	13
74	Genome Sequence and Transcriptome Analysis of Meat-Spoilage-Associated Lactic Acid Bacterium <i>Lactococcus piscium</i> MKFS47. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3800-3811.	3.1	32
75	Flight-induced changes in gene expression in the Glanville fritillary butterfly. <i>Molecular Ecology</i> , 2015, 24, 4886-4900.	3.9	28
76	Complete genome sequence of <i>Propionibacterium freudenreichii</i> DSM 20271T. <i>Standards in Genomic Sciences</i> , 2015, 10, 83.	1.5	23
77	Gut microbiota are related to Parkinson's disease and clinical phenotype. <i>Movement Disorders</i> , 2015, 30, 350-358.	3.9	1,457
78	Comparative Genomics and Characterization of Hybrid Shigatoxigenic and Enterotoxigenic <i>Escherichia coli</i> (STEC/ETEC) Strains. <i>PLoS ONE</i> , 2015, 10, e0135936.	2.5	50
79	A Comparative Pan-Genome Perspective of Niche-Adaptable Cell-Surface Protein Phenotypes in <i>Lactobacillus rhamnosus</i> . <i>PLoS ONE</i> , 2014, 9, e102762.	2.5	43
80	Mitochondrial Genome of <i>Phlebia radiata</i> Is the Second Largest (156 kbp) among Fungi and Features Signs of Genome Flexibility and Recent Recombination Events. <i>PLoS ONE</i> , 2014, 9, e97141.	2.5	80
81	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. <i>PLoS ONE</i> , 2014, 9, e101467.	2.5	24
82	Taxonomically and functionally diverse microbial communities in deep crystalline rocks of the Fennoscandian shield. <i>ISME Journal</i> , 2014, 8, 126-138.	9.8	107
83	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , 2014, 5, 4737.	12.8	196
84	<i>Acinetobacter</i> species in the skin microbiota protect against allergic sensitization and inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 1301-1309.e11.	2.9	163
85	Bacterial diversity and community structure along different peat soils in boreal forest. <i>Applied Soil Ecology</i> , 2014, 74, 37-45.	4.3	89
86	Phylogeny of the <i>Rhizobium</i> "Allorhizobium" <i>Agrobacterium</i> clade supports the delineation of <i>Neorhizobium</i> gen. nov.. <i>Systematic and Applied Microbiology</i> , 2014, 37, 208-215.	2.8	205
87	Faecal Microbiota Composition in Adults Is Associated with the FUT2 Gene Determining the Secretor Status. <i>PLoS ONE</i> , 2014, 9, e94863.	2.5	129
88	Lep-MAP: fast and accurate linkage map construction for large SNP datasets. <i>Bioinformatics</i> , 2013, 29, 3128-3134.	4.1	114
89	<i>Enterococcus rivorum</i> sp. nov., from water of pristine brooks. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2169-2173.	1.7	22
90	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. <i>BMC Microbiology</i> , 2012, 12, 121.	3.3	30

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91	Genome Sequence of a Food Spoilage Lactic Acid Bacterium, <i>Leuconostoc gasicomitatum</i> LMG 18811 <sup>T</sup> , in Association with Specific Spoilage Reactions. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4344-4351.	3.1	56
92	<i>Suillus bovinus</i> glutamine synthetase gene organization, transcription and enzyme activities in the Scots pine mycorrhizosphere developed on forest humus. <i>New Phytologist</i> , 2004, 164, 389-399.	7.3	4
93	Title is missing!. <i>European Journal of Plant Pathology</i> , 2001, 107, 457-465.	1.7	16
94	Identification of a nonsense mutation in the PAX9 gene in molar oligodontia. <i>European Journal of Human Genetics</i> , 2001, 9, 743-746.	2.8	147
95	Pulmonary Infection Caused by an Unusual, Slowly Growing Nontuberculous Mycobacterium. <i>Journal of Clinical Microbiology</i> , 2001, 39, 2668-2671.	3.9	28
96	Characterization of <i>Mycobacterium bohemicum</i> Isolated from Human, Veterinary, and Environmental Sources. <i>Journal of Clinical Microbiology</i> , 2001, 39, 207-211.	3.9	22
97	Characterisation of a new isolate of <i>Mycobacterium shimoidei</i> from Finland. <i>Journal of Medical Microbiology</i> , 2000, 49, 937-940.	1.8	16
98	Clinically Applicable Multiplex PCR for Four Middle Ear Pathogens. <i>Journal of Clinical Microbiology</i> , 2000, 38, 125-132.	3.9	77
99	Identification of nodulation promoter (nod-box) regions of <i>Rhizobium galegae</i> . <i>FEMS Microbiology Letters</i> , 1999, 177, 217-223.	1.8	1
100	The Sequence of a 36Â·7â€%kb Segment on the Left Arm of Chromosome IV from <i>Saccharomyces cerevisiae</i> Reveals 20 Non-overlapping Open Reading Frames (ORFs) Including SIT4, FAD1, NAM1, RNA11, SIR2, NAT1, PRP9, ACT2 and MPS1 and 11 New ORFs. , 1997, 13, 65-71.		6
101	A corolla-and carpel-abundant, non-specific lipid transfer protein gene is expressed in the epidermis and parenchyma of <i>Gerbera hybrida</i> var. <i>Regina</i> (Compositae). <i>Plant Molecular Biology</i> , 1994, 26, 971-978.	3.9	33