

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	Gut microbiota are related to Parkinson's disease and clinical phenotype. <i>Movement Disorders</i> , 2015, 30, 350-358.	3.9	1,457
2	Gut microbiota in Parkinson's disease: Temporal stability and relations to disease progression. <i>EBioMedicine</i> , 2019, 44, 691-707.	6.1	236
3	Phylogeny of the Rhizobium-Allorhizobium-Agrobacterium clade supports the delineation of Neorhizobium gen. nov.. <i>Systematic and Applied Microbiology</i> , 2014, 37, 208-215.	2.8	205
4	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
5	Relationships of gut microbiota, short-chain fatty acids, inflammation, and the gut barrier in Parkinson's disease. <i>Molecular Neurodegeneration</i> , 2021, 16, 6.	10.8	197
6	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
7	Cytokinin and Auxin Display Distinct but Interconnected Distribution and Signaling Profiles to Stimulate Cambial Activity. <i>Current Biology</i> , 2016, 26, 1990-1997.	3.9	170
8	Acinetobacter 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
9	Oral and nasal microbiota in Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2017, 38, 61-67.	2.2	159
10	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
11	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
12	Lep-MAP: fast and accurate linkage map construction for large SNP datasets. <i>Bioinformatics</i> , 2013, 29, 3128-3134.	4.1	114
13	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
14	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . <i>Environmental Microbiology Reports</i> , 2016, 8, 1024-1037.	2.4	104
15	The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. <i>Plant Cell</i> , 2018, 30, 2813-2837.	6.6	95
16	Lactobacillus rhamnosus GG Outcompetes Enterococcus faecium via Mucus-Binding Pili: Evidence for a Novel and Heterospecific Probiotic Mechanism. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5756-5762.	3.1	93
17	Bacterial diversity and community structure along different peat soils in boreal forest. <i>Applied Soil Ecology</i> , 2014, 74, 37-45.	4.3	89
18	Mitochondrial Genome of Phlebia radiata 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

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19	Clinically Applicable Multiplex PCR for Four Middle Ear Pathogens. <i>Journal of Clinical Microbiology</i> , 2000, 38, 125-132.	3.9	77
20	Bile microbiota in primary sclerosing cholangitis: Impact on disease progression and development of biliary dysplasia. <i>PLoS ONE</i> , 2017, 12, e0182924.	2.5	71
21	The complexity of titin splicing pattern in human adult skeletal muscles. <i>Skeletal Muscle</i> , 2018, 8, 11.	4.2	65
22	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
23	Genome Sequence of a Food Spoilage Lactic Acid Bacterium, <i>Leuconostoc gasicomitatum</i> LMG 18811, in Association with Specific Spoilage Reactions. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4344-4351.	3.1	56
24	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
25	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
26	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
27	Isotretinoin and lymecycline treatments modify the skin microbiota in acne. <i>Experimental Dermatology</i> , 2018, 27, 30-36.	2.9	48
28	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
29	Genetic Control of Myelin Plasticity after Chronic Psychosocial Stress. <i>ENeuro</i> , 2018, 5, ENEURO.0166-18.2018.	1.9	48
30	Evaluating the mobility potential of antibiotic resistance genes in environmental resistomes without metagenomics. <i>Scientific Reports</i> , 2016, 6, 35790.	3.3	46
31	Bacterial Butyrate in Parkinson's Disease Is Linked to Epigenetic Changes and Depressive Symptoms. <i>Movement Disorders</i> , 2022, 37, 1644-1653.	3.9	44
32	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
33	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
34	Multi-omics analysis identifies mitochondrial pathways associated with anxiety-related behavior. <i>PLoS Genetics</i> , 2019, 15, e1008358.	3.5	43
35	Gut Microbiome Signatures of Risk and Prodromal Markers of Parkinson Disease. <i>Annals of Neurology</i> , 2021, 90, E1-E12.	5.3	41
36	<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

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37	BARCOSEL: a tool for selecting an optimal barcode set for high-throughput sequencing. BMC Bioinformatics, 2018, 19, 257.	2.6	35
38	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). Plant Molecular Biology, 1994, 26, 971-978.	3.9	33
39	Genome Sequence and Transcriptome Analysis of Meat-Spoilage-Associated Lactic Acid Bacterium <i>Lactococcus piscium</i> MKFS47. Applied and Environmental Microbiology, 2015, 81, 3800-3811.	3.1	32
40	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. BMC Microbiology, 2012, 12, 121.	3.3	30
41	Comparative genome analysis of 24 bovine-associated <i>Staphylococcus</i> isolates with special focus on the putative virulence genes. PeerJ, 2018, 6, e4560.	2.0	30
42	Pulmonary Infection Caused by an Unusual, Slowly Growing Nontuberculous Mycobacterium. Journal of Clinical Microbiology, 2001, 39, 2668-2671.	3.9	28
43	Flight-induced changes in gene expression in the Glanville fritillary butterfly. Molecular Ecology, 2015, 24, 4886-4900.	3.9	28
44	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
45	Life-history genomic regions explain differences in Atlantic salmon marine diet specialization. Journal of Animal Ecology, 2020, 89, 2677-2691.	2.8	28
46	<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
47	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
48	Skin microbiome in melanomas and melanocytic nevi. European Journal of Dermatology, 2016, 26, 49-55.	0.6	26
49	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. PLoS ONE, 2014, 9, e101467.	2.5	24
50	Isolation and whole genome sequencing of a Ruminococcus-like bacterium, associated with irritable bowel syndrome. Anaerobe, 2016, 39, 60-67.	2.1	24
51	Bracketing phenogenotypic limits of mammalian hybridization. Royal Society Open Science, 2018, 5, 180903.	2.4	24
52	Subgingival microbiota in a population with and without cognitive dysfunction. Journal of Oral Microbiology, 2021, 13, 1854552.	2.7	24
53	Complete genome sequence of <i>Propionibacterium freudenreichii</i> DSM 20271T. Standards in Genomic Sciences, 2015, 10, 83.	1.5	23
54	Characterization of <i>Mycobacterium bohemicum</i> Isolated from Human, Veterinary, and Environmental Sources. Journal of Clinical Microbiology, 2001, 39, 207-211.	3.9	22

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55	Enterococcus rivorum sp. nov., from water of pristine brooks. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2169-2173.	1.7	22
56	Skin Microbiome in Cutaneous T-Cell Lymphoma by 16S and Whole-Genome Shotgun Sequencing. Journal of Investigative Dermatology, 2020, 140, 2304-2308.e7.	0.7	22
57	Loss of cutaneous microbial diversity during first 3 weeks of life in very low birthweight infants. Experimental Dermatology, 2017, 26, 861-867.	2.9	21
58	Genotypic and phenotypic diversity of Lactobacillus rhamnosus clinical isolates, their comparison with strain GG and their recognition by complement system. PLoS ONE, 2017, 12, e0176739.	2.5	21
59	Gut microbiota composition is associated with narcolepsy type 1. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, .	6.0	20
60	Functional genomics provides insights into the role of Propionibacterium freudenreichii ssp. shermanii JS in cheese ripening. International Journal of Food Microbiology, 2017, 241, 39-48.	4.7	19
61	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
62	Cloning of novel bacterial xylanases from lignocellulose-enriched compost metagenomic libraries. AMB Express, 2019, 9, 124.	3.0	18
63	High-pressure processing-induced transcriptome response during recovery of Listeria monocytogenes. BMC Genomics, 2021, 22, 117.	2.8	18
64	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
65	Complete Genome Sequence of Eubacterium hallii Strain L2-7. Genome Announcements, 2017, 5, .	0.8	17
66	Title is missing!. European Journal of Plant Pathology, 2001, 107, 457-465.	1.7	16
67	Complete Genome Sequence of Akkermansia glycaniphila Strain Pyt ^T , a Mucin-Degrading Specialist of the Reticulated Python Gut. Genome Announcements, 2017, 5, .	0.8	16
68	Genome sequence of the model plant pathogen Pectobacterium carotovorum SCC1. Standards in Genomic Sciences, 2017, 12, 87.	1.5	16
69	De novo assembly of genomes from long sequence reads reveals uncharted territories of Propionibacterium freudenreichii. BMC Genomics, 2017, 18, 790.	2.8	16
70	BK polyomavirus microRNA expression and sequence variation in polyomavirus-associated nephropathy. Journal of Clinical Virology, 2018, 102, 70-76.	3.1	16
71	Transcriptomic time-series analysis of cold- and heat-shock response in psychrotrophic lactic acid bacteria. BMC Genomics, 2021, 22, 28.	2.8	16
72	Characterisation of a new isolate of Mycobacterium shimoidei from Finland. Journal of Medical Microbiology, 2000, 49, 937-940.	1.8	16

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73	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
74	Polyadenylation and degradation of structurally abnormal mitochondrial tRNAs in human cells. <i>Nucleic Acids Research</i> , 2018, 46, 5209-5226.	14.5	14
75	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffold output. <i>PLoS ONE</i> , 2019, 14, e0216885.	2.5	14
76	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
77	Single-Molecule Sequencing Revealing the Presence of Distinct JC Polyomavirus Populations in Patients With Progressive Multifocal Leukoencephalopathy. <i>Journal of Infectious Diseases</i> , 2016, 215, jiw399.	4.0	13
78	Genomic features separating ten strains of <i>Neorhizobium galegae</i> with different symbiotic phenotypes. <i>BMC Genomics</i> , 2015, 16, 348.	2.8	12
79	Multimiomics implicate gut microbiota in altered lipid and energy metabolism in Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2022, 8, 39.	5.3	12
80	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
81	Genomic convergence between <i>Akkermansia muciniphila</i> in different mammalian hosts. <i>BMC Microbiology</i> , 2021, 21, 298.	3.3	10
82	Skin Microbiome in Small- and Large-plaque Parapsoriasis. <i>Acta Dermato-Venereologica</i> , 2017, 97, 685-691.	1.3	9
83	A transcriptomic view to wounding response in young Scots pine stems. <i>Scientific Reports</i> , 2021, 11, 3778.	3.3	9
84	<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
85	Breakpoint mapping and haplotype analysis of translocation t(1;12)(q43;q21.1) in two apparently independent families with vascular phenotypes. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 56-68.	1.2	8
86	Phenotypic effects of dietary stress in combination with a respiratory chain bypass in mice. <i>Physiological Reports</i> , 2019, 7, e14159.	1.7	8
87	Improved chromosome-level genome assembly of the Glanville fritillary butterfly (<i>Melitaea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 11, .	6.4	8
88	<i>Streptococcus halichoeri</i> : Comparative Genomics of an Emerging Pathogen. <i>International Journal of Genomics</i> , 2020, 2020, 1-9.	1.6	7
89	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
90	The Sequence of a 36 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

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91	Complete Genome Sequences and Methylome Analyses of <i>Cutibacterium acnes</i> subsp. <i>acnes</i> Strains DSM 16379 and DSM 1897 ^T . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
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	Genome Sequences of Four <i>Staphylococcus aureus</i> Strains Isolated from Bovine Mastitis. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
94	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
95	Increased transcriptome sequencing efficiency with modified Mint-2 digestion and ligation protocol. <i>Analytical Biochemistry</i> , 2015, 477, 38-40.	2.4	2
96	Complete Genome Sequence of <i>Enterococcus faecium</i> Commensal Isolate E1002. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
97	Alu element in the RNA binding motif protein, X-linked 2 (RBMX2) gene found to be linked to bipolar disorder. <i>PLoS ONE</i> , 2021, 16, e0261170.	2.5	2
98	The complete genome sequence of <i>Listeria monocytogenes</i> strain S2542 and expression of selected genes under high-pressure processing. <i>BMC Research Notes</i> , 2021, 14, 137.	1.4	1
99	Comparative Genomics of 42 <i>Arcanobacterium phocae</i> Strains. <i>Antibiotics</i> , 2021, 10, 740.	3.7	1
100	Identification of nodulation promoter (nod-box) regions of <i>Rhizobium galegae</i> . <i>FEMS Microbiology Letters</i> , 1999, 177, 217-223.	1.8	1
101	Survey of microbes in industrial-scale second-generation bioethanol production for better process knowledge and operation. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 8049-8064.	3.6	0