

Anders F Andersson

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

15,588
citations

57758

44
h-index

58581

82
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92
all docs

92
docs citations

92
times ranked

20962
citing authors

#	ARTICLE	IF	CITATIONS
1	Salivary Microbiota and Host-Inflammatory Responses in Periodontitis Affected Individuals With and Without Rheumatoid Arthritis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841139.	3.9	11
2	Short- and long-read metabarcoding of the eukaryotic rRNA operon: Evaluation of primers and comparison to shotgun metagenomics sequencing. <i>Molecular Ecology Resources</i> , 2022, 22, 2304-2318.	4.8	16
3	Evaluating metagenomic assembly approaches for biome-specific gene catalogues. <i>Microbiome</i> , 2022, 10, 72.	11.1	18
4	The Fennoscandian Shield deep terrestrial virosphere suggests slow motion "boom and burst" cycles. <i>Communications Biology</i> , 2021, 4, 307.	4.4	19
5	Ecologically coherent population structure of uncultivated bacterioplankton. <i>ISME Journal</i> , 2021, 15, 3034-3049.	9.8	22
6	Machine Learning Predicts the Presence of 2,4,6-Trinitrotoluene in Sediments of a Baltic Sea Munitions Dumpsite Using Microbial Community Compositions. <i>Frontiers in Microbiology</i> , 2021, 12, 626048.	3.5	6
7	The environment drives microbial trait variability in aquatic habitats. <i>Molecular Ecology</i> , 2020, 29, 4605-4617.	3.9	5
8	Deltaproteobacteria and Spirochaetes-Like Bacteria Are Abundant Putative Mercury Methylators in Oxygen-Deficient Water and Marine Particles in the Baltic Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 574080.	3.5	33
9	Gastric Microbiota in a Low "Helicobacter pylori" Prevalence General Population and Their Associations With Gastric Lesions. <i>Clinical and Translational Gastroenterology</i> , 2020, 11, e00191.	2.5	29
10	Genome sequence of segmented filamentous bacteria present in the human intestine. <i>Communications Biology</i> , 2020, 3, 485.	4.4	27
11	Ecosystem-wide metagenomic binning enables prediction of ecological niches from genomes. <i>Communications Biology</i> , 2020, 3, 119.	4.4	64
12	Active sulfur cycling in the terrestrial deep subsurface. <i>ISME Journal</i> , 2020, 14, 1260-1272.	9.8	72
13	DNA metabarcoding reveals microbial community dynamics in a microalgae-based municipal wastewater treatment open photobioreactor. <i>Algal Research</i> , 2020, 51, 102043.	4.6	27
14	Effects of allochthonous dissolved organic matter input on microbial composition and nitrogen-cycling genes at two contrasting estuarine sites. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	3
15	Identification of Salivary Microbiota and Its Association With Host Inflammatory Mediators in Periodontitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 216.	3.9	88
16	Periodontal Health and Oral Microbiota in Patients with Rheumatoid Arthritis. <i>Journal of Clinical Medicine</i> , 2019, 8, 630.	2.4	63
17	Atmospheric Deposition Impact on Bacterial Community Composition in the NW Mediterranean. <i>Frontiers in Microbiology</i> , 2019, 10, 858.	3.5	16
18	New mitochondrial primers for metabarcoding of insects, designed and evaluated using in silico methods. <i>Molecular Ecology Resources</i> , 2019, 19, 90-104.	4.8	69

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19	AFISsys - An autonomous instrument for the preservation of brackish water samples for microbial metatranscriptome analysis. <i>Water Research</i> , 2019, 149, 351-361.	11.3	4
20	Multiscale patterns and drivers of arbuscular mycorrhizal fungal communities in the roots and root-associated soil of a wild perennial herb. <i>New Phytologist</i> , 2018, 220, 1248-1261.	7.3	48
21	BARM and BalticMicrobeDB, a reference metagenome and interface to meta-omic data for the Baltic Sea. <i>Scientific Data</i> , 2018, 5, 180146.	5.3	54
22	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. <i>Nature Communications</i> , 2018, 9, 5091.	12.8	190
23	Biogeochemical Cycling by a Low-Diversity Microbial Community in Deep Groundwater. <i>Frontiers in Microbiology</i> , 2018, 9, 2129.	3.5	35
24	Genomes from uncultivated prokaryotes: a comparison of metagenome-assembled and single-amplified genomes. <i>Microbiome</i> , 2018, 6, 173.	11.1	86
25	Prevalent reliance of bacterioplankton on exogenous vitamin B1 and precursor availability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10447-E10456.	7.1	64
26	Coupling biogeochemical process rates and metagenomic blueprints of coastal bacterial assemblages in the context of environmental change. <i>Environmental Microbiology</i> , 2018, 20, 3083-3099.	3.8	11
27	Stationary and portable sequencing-based approaches for tracing wastewater contamination in urban stormwater systems. <i>Scientific Reports</i> , 2018, 8, 11907.	3.3	24
28	Metapopulation theory identifies biogeographical patterns among core and satellite marine bacteria scaling from tens to thousands of kilometers. <i>Environmental Microbiology</i> , 2017, 19, 1222-1236.	3.8	38
29	Lake bacterioplankton dynamics over diurnal timescales. <i>Freshwater Biology</i> , 2017, 62, 191-204.	2.4	11
30	Ninety-nine <i>de novo</i> assembled genomes from the moose (<i>Alces alces</i>) rumen microbiome provide new insights into microbial plant biomass degradation. <i>ISME Journal</i> , 2017, 11, 2538-2551.	9.8	120
31	Potential for hydrogen-oxidizing chemolithoautotrophic and diazotrophic populations to initiate biofilm formation in oligotrophic, deep terrestrial subsurface waters. <i>Microbiome</i> , 2017, 5, 37.	11.1	39
32	Mineral Type Structures Soil Microbial Communities. <i>Geomicrobiology Journal</i> , 2017, 34, 538-545.	2.0	16
33	Colonization and Succession within the Human Gut Microbiome by Archaea, Bacteria, and Microeukaryotes during the First Year of Life. <i>Frontiers in Microbiology</i> , 2017, 8, 738.	3.5	207
34	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 1561.	3.5	265
35	Improvement of identification methods for honeybee specific Lactic Acid Bacteria; future approaches. <i>PLoS ONE</i> , 2017, 12, e0174614.	2.5	16
36	Diversity of Pico- to Mesoplankton along the 2000 km Salinity Gradient of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 679.	3.5	96

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37	Phylogenetic Signals of Salinity and Season in Bacterial Community Composition Across the Salinity Gradient of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 1883.	3.5	81
38	Reconstructing a hydrogen-driven microbial metabolic network in Opalinus Clay rock. <i>Nature Communications</i> , 2016, 7, 12770.	12.8	120
39	Whole genome sequencing identifies a novel species of the genus <i>Capnocytophaga</i> isolated from dog and cat bite wounds in humans. <i>Scientific Reports</i> , 2016, 6, 22919.	3.3	28
40	A minimalistic microbial food web in an excavated deep subsurface clay rock. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv138.	2.7	29
41	Experimental insights into the importance of aquatic bacterial community composition to the degradation of dissolved organic matter. <i>ISME Journal</i> , 2016, 10, 533-545.	9.8	418
42	Metagenome-assembled genomes uncover a global brackish microbiome. <i>Genome Biology</i> , 2015, 16, 279.	8.8	186
43	Disentangling seasonal bacterioplankton population dynamics by high-frequency sampling. <i>Environmental Microbiology</i> , 2015, 17, 2459-2476.	3.8	142
44	Phasing of single DNA molecules by massively parallel barcoding. <i>Nature Communications</i> , 2015, 6, 7173.	12.8	31
45	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. <i>PLoS ONE</i> , 2014, 9, e89549.	2.5	184
46	Olsson, B. (1956–2014): pioneer of the archaeal cell cycle. <i>Molecular Microbiology</i> , 2014, 92, 903-909.	2.5	1
47	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. <i>PLoS ONE</i> , 2014, 9, e95567.	2.5	218
48	Decreased gut microbiota diversity, delayed <i>Bacteroidetes</i> colonisation and reduced Th1 responses in infants delivered by Caesarean section. <i>Gut</i> , 2014, 63, 559-566.	12.1	823
49	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014, 11, 1144-1146.	19.0	1,709
50	DegePrime, a Program for Degenerate Primer Design for Broad-Taxonomic-Range PCR in Microbial Ecology Studies. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5116-5123.	3.1	355
51	Low gut microbiota diversity in early infancy precedes asthma at school age. <i>Clinical and Experimental Allergy</i> , 2014, 44, 842-850.	2.9	577
52	The impact of Crohn's disease genes on healthy human gut microbiota: a pilot study. <i>Gut</i> , 2013, 62, 952.1-954.	12.1	32
53	Active nitrogen-fixing heterotrophic bacteria at and below the chemocline of the central Baltic Sea. <i>ISME Journal</i> , 2013, 7, 1413-1423.	9.8	146
54	Reply. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 248-249.	2.9	6

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55	Metagenomic <i>De Novo</i> Assembly of an Aquatic Representative of the Verrucomicrobial Class <i>Spartobacteria</i> . <i>MBio</i> , 2013, 4, e00569-12.	4.1	107
56	Low diversity of the gut microbiota in infants with atopic eczema. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 434-440.e2.	2.9	659
57	Bacterial Community Composition in the Water Column of a Lake Formed by a Former Uranium Open Pit Mine. <i>Microbial Ecology</i> , 2012, 64, 870-880.	2.8	9
58	Freshwater bacterioplankton richness in oligotrophic lakes depends on nutrient availability rather than on species-area relationships. <i>ISME Journal</i> , 2012, 6, 1127-1136.	9.8	105
59	Which sequencing depth is sufficient to describe patterns in bacterial α - and β -diversity?. <i>Environmental Microbiology Reports</i> , 2012, 4, 367-372.	2.4	117
60	Genome Sequencing Reveals a Phage in <i>Helicobacter pylori</i> . <i>MBio</i> , 2011, 2, .	4.1	60
61	Titration-free 454 sequencing using Y adapters. <i>Nature Protocols</i> , 2011, 6, 1367-1376.	12.0	24
62	Novel primers for 16S rRNA-based archaeal community analyses in environmental samples. <i>Journal of Microbiological Methods</i> , 2011, 84, 12-18.	1.6	218
63	High archaeal diversity in Antarctic circumpolar deep waters. <i>Environmental Microbiology Reports</i> , 2011, 3, 689-697.	2.4	31
64	Transitions in bacterial communities along the 2000‰ salinity gradient of the Baltic Sea. <i>ISME Journal</i> , 2011, 5, 1571-1579.	9.8	2,219
65	Rapid Screening of Complex DNA Samples by Single-Molecule Amplification and Sequencing. <i>PLoS ONE</i> , 2011, 6, e19723.	2.5	2
66	A Method for Metagenomics of <i>Helicobacter pylori</i> from Archived Formalin-Fixed Gastric Biopsies Permitting Longitudinal Studies of Carcinogenic Risk. <i>PLoS ONE</i> , 2011, 6, e26442.	2.5	14
67	Nitrogenase Gene Amplicons from Global Marine Surface Waters Are Dominated by Genes of Non-Cyanobacteria. <i>PLoS ONE</i> , 2011, 6, e19223.	2.5	176
68	Replication-biased genome organisation in the crenarchaeon <i>Sulfolobus</i> . <i>BMC Genomics</i> , 2010, 11, 454.	2.8	22
69	Pyrosequencing reveals contrasting seasonal dynamics of taxa within Baltic Sea bacterioplankton communities. <i>ISME Journal</i> , 2010, 4, 171-181.	9.8	263
70	Short-Term Antibiotic Treatment Has Differing Long-Term Impacts on the Human Throat and Gut Microbiome. <i>PLoS ONE</i> , 2010, 5, e9836.	2.5	936
71	A Pyrosequencing Study in Twins Shows That Gastrointestinal Microbial Profiles Vary With Inflammatory Bowel Disease Phenotypes. <i>Gastroenterology</i> , 2010, 139, 1844-1854.e1.	1.3	916
72	Titration-free massively parallel pyrosequencing using trace amounts of starting material. <i>Nucleic Acids Research</i> , 2010, 38, e137-e137.	14.5	28

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73	Community-wide analysis of microbial genome sequence signatures. <i>Genome Biology</i> , 2009, 10, R85.	9.6	479
74	Virus Population Dynamics and Acquired Virus Resistance in Natural Microbial Communities. <i>Science</i> , 2008, 320, 1047-1050.	12.6	469
75	Community proteogenomics highlights microbial strain-variant protein expression within activated sludge performing enhanced biological phosphorus removal. <i>ISME Journal</i> , 2008, 2, 853-864.	9.8	156
76	Comparative Analysis of Human Gut Microbiota by Barcoded Pyrosequencing. <i>PLoS ONE</i> , 2008, 3, e2836.	2.5	901
77	Functional Analysis of the M.HpyAIV DNA Methyltransferase of <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 2007, 189, 8914-8921.	2.2	29
78	Global analysis of mRNA stability in the archaeon <i>Sulfolobus</i> . <i>Genome Biology</i> , 2006, 7, R99.	9.6	74
79	Identification of the Missing Links in Prokaryotic Pentose Oxidation Pathways. <i>Journal of Biological Chemistry</i> , 2006, 281, 27378-27388.	3.4	102
80	9 Functional Genomics of the Thermo-Acidophilic Archaeon <i>Sulfolobus solfataricus</i> . <i>Methods in Microbiology</i> , 2006, 35, 201-231.	0.8	0
81	Dual-genome primer design for construction of DNA microarrays. <i>Bioinformatics</i> , 2005, 21, 325-332.	4.1	18
82	Three replication origins in <i>Sulfolobus</i> species: Synchronous initiation of chromosome replication and asynchronous termination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7046-7051.	7.1	205
83	A transcriptional timetable of autumn senescence. <i>Genome Biology</i> , 2004, 5, R24.	9.6	226