

Anna Edlund

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

5,422
citations

201674

27
h-index

233421

45
g-index

55
all docs

55
docs citations

55
times ranked

9196
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>mucG</i> , <i>mucH</i> , and <i>mucK</i> Modulate Production of Mutanocyclin and Reutericyclins in <i>Streptococcus mutans</i> B04Sm5. <i>Journal of Bacteriology</i> , 2022, 204, e0004222.	2.2	4
2	Oral Microbial Species and Virulence Factors Associated with Oral Squamous Cell Carcinoma. <i>Microbial Ecology</i> , 2021, 82, 1030-1046.	2.8	29
3	Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. <i>Genome Research</i> , 2021, 31, 64-74.	5.5	59
4	The Oral Host-Microbial Interactome: An Ecological Chronometer of Health?. <i>Trends in Microbiology</i> , 2021, 29, 551-561.	7.7	41
5	Identification of Bacterial Biosynthetic Gene Associated with Caries. <i>Methods in Molecular Biology</i> , 2021, 2327, 161-189.	0.9	2
6	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.	8.0	81
7	E-073...Clot bank collaborative registry protocol: Novel method for evaluating ischemic thrombus. , 2021, , .		0
8	Multi-Omics Study of Keystone Species in a Cystic Fibrosis Microbiome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12050.	4.1	14
9	Tetramic Acids Mutanocyclin and Reutericyclin A, Produced by <i>Streptococcus mutans</i> Strain B04Sm5 Modulate the Ecology of an in vitro Oral Biofilm. <i>Frontiers in Oral Health</i> , 2021, 2, 796140.	3.0	5
10	Cariogenic <i>Streptococcus mutans</i> Produces Tetramic Acid Strain-Specific Antibiotics That Impair Commensal Colonization. <i>ACS Infectious Diseases</i> , 2020, 6, 563-571.	3.8	40
11	Composite Long- and Short-Read Sequencing Delivers a Complete Genome Sequence of B04Sm5, a Reutericyclin- and Mutanocyclin-Producing Strain of <i>Streptococcus mutans</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	9
12	Commensal Oral <i>Rothia mucilaginosa</i> Produces Enterobactin, a Metal-Chelating Siderophore. <i>MSystems</i> , 2020, 5, .	3.8	30
13	Caries-Associated Biosynthetic Gene Clusters in <i>Streptococcus mutans</i> . <i>Journal of Dental Research</i> , 2020, 99, 969-976.	5.2	13
14	Salivary Bioscience and Periodontal Medicine. , 2020, , 419-447.		1
15	Discovery of a Novel Periodontal Disease-Associated Bacterium. <i>Microbial Ecology</i> , 2019, 77, 267-276.	2.8	26
16	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	12.8	428
17	Identification of the Bacterial Biosynthetic Gene Clusters of the Oral Microbiome Illuminates the Unexplored Social Language of Bacteria during Health and Disease. <i>MBio</i> , 2019, 10, .	4.1	73
18	<i>Klebsiella</i> and <i>Providencia</i> emerge as lone survivors following long-term starvation of oral microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8499-8504.	7.1	30

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19	Uncovering complex microbiome activities via metatranscriptomics during 24h hours of oral biofilm assembly and maturation. <i>Microbiome</i> , 2018, 6, 217.	11.1	34
20	Quorum Sensing Modulates the Epibiotic-Parasitic Relationship Between <i>Actinomyces odontolyticus</i> and Its <i>Saccharibacteria</i> epibiont, a <i>Nanosynbacter lyticus</i> Strain, TM7x. <i>Frontiers in Microbiology</i> , 2018, 9, 2049.	3.5	32
21	Exploiting the Oral Microbiome to Prevent Tooth Decay: Has Evolution Already Provided the Best Tools?. <i>Frontiers in Microbiology</i> , 2018, 9, 3323.	3.5	70
22	Uncovering the Horseshoe Effect in Microbial Analyses. <i>MSystems</i> , 2017, 2, .	3.8	67
23	Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules. <i>MSystems</i> , 2017, 2, .	3.8	30
24	Targeted Antimicrobial Peptides: A Novel Technology to Eradicate Harmful. <i>Journal of the California Dental Association</i> , 2017, 45, 557-564.	0.1	10
25	Metagenome and Metatranscriptome Analyses Using Protein Family Profiles. <i>PLoS Computational Biology</i> , 2016, 12, e1004991.	3.2	21
26	Spatial Molecular Architecture of the Microbial Community of a <i>Peltigera</i> Lichen. <i>MSystems</i> , 2016, 1, .	3.8	36
27	The Denture-Associated Oral Microbiome in Health and Stomatitis. <i>MSphere</i> , 2016, 1, .	2.9	44
28	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
29	High-Quality Draft Genome Sequence of Low-pH-Active <i>Veillonella parvula</i> Strain SHI-1, Isolated from Human Saliva within an In Vitro Oral Biofilm Model. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
30	Draft Genome Sequence of <i>Candidatus Bacteroides pericalifornicus</i> , a New Member of the <i>Bacteroidetes</i> Phylum Found within the Oral Microbiome of Periodontitis Patients. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
31	Bacteriophage and their potential roles in the human oral cavity. <i>Journal of Oral Microbiology</i> , 2015, 7, 27423.	2.7	109
32	Meta-omics uncover temporal regulation of pathways across oral microbiome genera during <i>in vitro</i> sugar metabolism. <i>ISME Journal</i> , 2015, 9, 2605-2619.	9.8	63
33	Cultivation of a human-associated TM7 phylotype reveals a reduced genome and epibiotic parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 244-249.	7.1	405
34	Bacteria-Mediated Effects of Antibiotics on <i>Daphnia</i> Nutrition. <i>Environmental Science & Technology</i> , 2015, 49, 5779-5787.	10.0	79
35	An <i>in vitro</i> biofilm model system maintaining a highly reproducible species and metabolic diversity approaching that of the human oral microbiome. <i>Microbiome</i> , 2013, 1, 25.	11.1	106
36	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2390-9.	7.1	192

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37	Genome of the pathogen <i>Porphyromonas gingivalis</i> recovered from a biofilm in a hospital sink using a high-throughput single-cell genomics platform. <i>Genome Research</i> , 2013, 23, 867-877.	5.5	58
38	Observing the invisible through imaging mass spectrometry, a window into the metabolic exchange patterns of microbes. <i>Journal of Proteomics</i> , 2012, 75, 5069-5076.	2.4	39
39	Antibiotic-Induced Change of Bacterial Communities Associated with the Copepod <i>Nitocra spinipes</i> . <i>PLoS ONE</i> , 2012, 7, e33107.	2.5	29
40	Microdiversity and evidence for high dispersal rates in the marine actinomycete <i>Salinispora pacifica</i> . <i>Environmental Microbiology</i> , 2012, 14, 480-493.	3.8	40
41	Geographic Distribution of Secondary Metabolite Genes in the Marine Actinomycete <i>Salinispora arenicola</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 5916-5925.	3.1	30
42	Use of bromodeoxyuridine immunocapture to identify psychrotolerant phenanthrene-degrading bacteria in phenanthrene-enriched polluted Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , 2008, 65, 513-525.	2.7	35
43	Active bacterial community structure along vertical redox gradients in Baltic Sea sediment. <i>Environmental Microbiology</i> , 2008, 10, 2051-2063.	3.8	74
44	Nucleic acid levels in copepods: dynamic response to phytoplankton blooms in the northern Baltic proper. <i>Marine Ecology - Progress Series</i> , 2007, 349, 213-225.	1.9	9
45	Microbial community structure in polluted Baltic Sea sediments. <i>Environmental Microbiology</i> , 2006, 8, 223-232.	3.8	48
46	Changes in Active Bacterial Communities before and after Dredging of Highly Polluted Baltic Sea Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6800-6807.	3.1	46
47	Thrombus-associated microbiota in acute ischemic stroke patients. , 0, 13, 247.		1