

Andreas SjÅrdin

List of Publications by Year in descending order

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66
papers

4,766
citations

159585

30
h-index

106344

65
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docs citations

68
times ranked

7673
citing authors

#	ARTICLE	IF	CITATIONS
1	Alphacoronavirus in a Daubenton's Myotis Bat (<i>Myotis daubentonii</i>) in Sweden. <i>Viruses</i> , 2022, 14, 556.	3.3	5
2	Co-Occurrence of Francisella, Spotted Fever Group Rickettsia, and Midichloria in Avian-Associated <i>Hyalomma rufipes</i> . <i>Microorganisms</i> , 2022, 10, 1393.	3.6	5
3	Community-led, integrated, reproducible multi-omics with anvio. <i>Nature Microbiology</i> , 2021, 6, 3-6.	13.3	370
4	Complete Genome Sequence of <i>Francisella</i> sp. Strain LA11-2445 (FDC406), a Novel <i>Francisella</i> Species Isolated from a Human Skin Lesion. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
5	Reorganized Genomic Taxonomy of Francisellaceae Enables Design of Robust Environmental PCR Assays for Detection of <i>Francisella tularensis</i> . <i>Microorganisms</i> , 2021, 9, 146.	3.6	19
6	Biological amplification of low frequency mutations unravels laboratory culture history of the bio-threat agent <i>Francisella tularensis</i> . <i>Forensic Science International: Genetics</i> , 2020, 45, 102230.	3.1	6
7	Complete Genome Sequence of <i>Francisella halioticida</i> Type Strain DSM 23729 (FSC1005). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
8	A whole-genome sequenced control population in northern Sweden reveals subregional genetic differences. <i>PLoS ONE</i> , 2020, 15, e0237721.	2.5	1
9	Complete Genome Sequence of <i>Francisella tularensis</i> subsp. <i>holarctica</i> Strain A271_1 (FDC408), Isolated from a Eurasian Beaver (<i>Castor fiber</i>). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
10	Reclassification of <i>Francisella noatunensis</i> subsp. <i>orientalis</i> Ottem et al. 2009 as <i>Francisella orientalis</i> sp. nov., <i>Francisella noatunensis</i> subsp. <i>chilensis</i> subsp. nov. and emended description of <i>Francisella noatunensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2034-2048.	1.7	38
11	Complete Genome Sequences of <i>Allofrancisella inopinata</i> SYSU YG23 and <i>Allofrancisella frigidaquae</i> SYSU 10HL1970, Isolated from Water from Cooling Systems in China. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
12	doepipeline: a systematic approach to optimizing multi-level and multi-step data processing workflows. <i>BMC Bioinformatics</i> , 2019, 20, 498.	2.6	2
13	A geographically matched control population efficiently limits the number of candidate disease-causing variants in an unbiased whole-genome analysis. <i>PLoS ONE</i> , 2019, 14, e0213350.	2.5	8
14	A New Species of the $\hat{3}$ -Proteobacterium <i>Francisella</i> , <i>F. adeliensis</i> Sp. Nov., Endocytobiont in an Antarctic Marine Ciliate and Potential Evolutionary Forerunner of Pathogenic Species. <i>Microbial Ecology</i> , 2019, 77, 587-596.	2.8	22
15	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. <i>Frontiers in Microbiology</i> , 2018, 9, 2364.	3.5	16
16	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	19.0	714
17	Predators and nutrient availability favor protozoa-resisting bacteria in aquatic systems. <i>Scientific Reports</i> , 2018, 8, 8415.	3.3	20
18	<i>Galleria mellonella</i> Reveals Niche Differences Between Highly Pathogenic and Closely Related Strains of <i>Francisella</i> spp.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 188.	3.9	14

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19	Microbial community response to growing season and plant nutrient optimisation in a boreal Norway spruce forest. <i>Soil Biology and Biochemistry</i> , 2018, 125, 197-209.	8.8	64
20	Reassessing the Role of Type II Toxin-Antitoxin Systems in Formation of <i>Escherichia coli</i> Type II Persister Cells. <i>MBio</i> , 2018, 9, .	4.1	174
21	Hematopoietic Age at Onset of Triple-Negative Breast Cancer Dictates Disease Aggressiveness and Progression. <i>Cancer Research</i> , 2016, 76, 2932-2943.	0.9	17
22	Scaffolding of a bacterial genome using MinION nanopore sequencing. <i>Scientific Reports</i> , 2015, 5, 11996.	3.3	70
23	Complete Genome Sequence of <i>Francisella guangzhouensis</i> Strain 08HL01032 , Isolated from Air-Conditioning Systems in China. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
24	The Plant Genome Integrative Explorer Resource: PlantGen.org. <i>New Phytologist</i> , 2015, 208, 1149-1156.	7.3	282
25	Phylogeographical pattern of <i>Francisella tularensis</i> in a nationwide outbreak of tularaemia in Norway, 2011. <i>Eurosurveillance</i> , 2015, 20, .	7.0	22
26	Genomic analyses of <i>Francisella tularensis</i> strains confirm disease transmission from drinking water sources, Turkey, 2008, 2009 and 2012. <i>Eurosurveillance</i> , 2015, 20, .	7.0	26
27	Eight New Genomes and Synthetic Controls Increase the Accessibility of Rapid Melt-MAMA SNP Typing of <i>Coxiella burnetii</i> . <i>PLoS ONE</i> , 2014, 9, e85417.	2.5	17
28	Complete Genome Sequence of <i>Francisella endociliophora</i> Strain FSC1006, Isolated from a Laboratory Culture of the Marine Ciliate <i>Euplotes raikovi</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	23
29	<i>Francisella tularensis</i> subsp. <i>tularensis</i> Group A.I, United States. <i>Emerging Infectious Diseases</i> , 2014, 20, 861-5.	4.3	18
30	CanSNPer: a hierarchical genotype classifier of clonal pathogens. <i>Bioinformatics</i> , 2014, 30, 1762-1764.	4.1	63
31	Genome sequence of <i>Coxiella burnetii</i> strain Namibia. <i>Standards in Genomic Sciences</i> , 2014, 9, 22.	1.5	12
32	An improved multiple-locus variable-number of tandem repeat analysis (MLVA) for the fish pathogen <i>Francisella noatunensis</i> using capillary electrophoresis. <i>BMC Veterinary Research</i> , 2013, 9, 252.	1.9	5
33	The phylogeographic pattern of <i>Francisella tularensis</i> in Sweden indicates a Scandinavian origin of Eurasian tularaemia. <i>Environmental Microbiology</i> , 2013, 15, 634-645.	3.8	68
34	The Need for High-Quality Whole-Genome Sequence Databases in Microbial Forensics. <i>Biosecurity and Bioterrorism</i> , 2013, 11, S78-S86.	1.2	17
35	<i>Trans</i> -Golgi Network Localized ECHIDNA/Ypt Interacting Protein Complex Is Required for the Secretion of Cell Wall Polysaccharides in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 2633-2646.	6.6	111
36	Indigenous Infection with <i>Francisella tularensis</i> holarctica in The Netherlands. <i>Case Reports in Infectious Diseases</i> , 2013, 2013, 1-3.	0.5	12

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37	Draft genome sequence of <i>Francisella tularensis</i> subsp. <i>holarctica</i> BD11-00177. <i>Standards in Genomic Sciences</i> , 2013, 8, 539-547.	1.5	5
38	The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. <i>Nucleic Acids Research</i> , 2012, 40, D1313-D1317.	14.5	35
39	Genome Sequence of <i>Francisella tularensis</i> subspecies <i>holarctica</i> Strain FSC200, Isolated from a Child with Tularemia. <i>Journal of Bacteriology</i> , 2012, 194, 6965-6966.	2.2	34
40	Real-time PCR assays targeting unique DNA sequences of fish-pathogenic <i>Francisella noatunensis</i> subspecies <i>noatunensis</i> and <i>orientalis</i> . <i>Diseases of Aquatic Organisms</i> , 2012, 101, 225-234.	1.0	20
41	Genome characterisation of the genus <i>Francisella</i> reveals insight into similar evolutionary paths in pathogens of mammals and fish. <i>BMC Genomics</i> , 2012, 13, 268.	2.8	121
42	Increased knowledge of <i>Francisella</i> genus diversity highlights the benefits of optimised DNA-based assays. <i>BMC Microbiology</i> , 2012, 12, 220.	3.3	16
43	The Distribution of <i>Francisella</i> -like Bacteria Associated with Coastal Waters in Norway. <i>Microbial Ecology</i> , 2012, 64, 370-377.	2.8	26
44	Analysis of global changes in gene expression during activity-dormancy cycle in hybrid aspen apex. <i>Plant Biotechnology</i> , 2010, 27, 1-16.	1.0	79
45	Whole-Genome Sequencing Reveals Distinct Mutational Patterns in Closely Related Laboratory and Naturally Propagated <i>Francisella tularensis</i> Strains. <i>PLoS ONE</i> , 2010, 5, e11556.	2.5	24
46	Components Acting Downstream of Short Day Perception Regulate Differential Cessation of Cambial Activity and Associated Responses in Early and Late Clones of Hybrid Poplar. <i>Plant Physiology</i> , 2010, 154, 1294-1303.	4.8	31
47	The Control of Autumn Senescence in European Aspen. <i>Plant Physiology</i> , 2009, 149, 1982-1991.	4.8	239
48	Local and systemic transcriptome responses to herbivory and jasmonic acid in <i>Populus</i> . <i>Tree Genetics and Genomes</i> , 2009, 5, 459-474.	1.6	30
49	A unique program for cell death in xylem fibers of <i>Populus</i> stem. <i>Plant Journal</i> , 2009, 58, 260-274.	5.7	147
50	The <i>Populus</i> Genome Integrative Explorer (PopGenIE): a new resource for exploring the <i>Populus</i> genome. <i>New Phytologist</i> , 2009, 182, 1013-1025.	7.3	208
51	A cross-species transcriptomics approach to identify genes involved in leaf development. <i>BMC Genomics</i> , 2008, 9, 589.	2.8	37
52	Global expression profiling in leaves of free-growing aspen. <i>BMC Plant Biology</i> , 2008, 8, 61.	3.6	29
53	Environmental and hormonal regulation of the activity-dormancy cycle in the cambial meristem involves stage-specific modulation of transcriptional and metabolic networks. <i>Plant Journal</i> , 2007, 50, 557-573.	5.7	161
54	Growth-phase-dependent gene expression profiling of poplar (<i>Populus alba</i> L.— <i>Populus tremula</i> var.) Tj ETQq0 0 0 rgBT/Overlock 10 Tf	9.2	15

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55	Orthogonal projections to latent structures as a strategy for microarray data normalization. BMC Bioinformatics, 2007, 8, 207.	2.6	67
56	The genetics and genomics of the drought response in Populus. Plant Journal, 2006, 48, 321-341.	5.7	216
57	UPSC-BASE -Populustranscriptomics online. Plant Journal, 2006, 48, 806-817.	5.7	53
58	Protease gene families in Populus and Arabidopsis. BMC Plant Biology, 2006, 6, 30.	3.6	129
59	MASQOT-GUI: spot quality assessment for the two-channel microarray platform. Bioinformatics, 2006, 22, 2554-2555.	4.1	8
60	Abundantly and Rarely Expressed Lhc Protein Genes Exhibit Distinct Regulation Patterns in Plants. Plant Physiology, 2006, 140, 793-804.	4.8	146
61	Molecular targets of elevated [CO ₂] in leaves and stems of Populus deltoides: implications for future tree growth and carbon sequestration. Functional Plant Biology, 2006, 33, 121.	2.1	41
62	The transcriptome of Populus in elevated CO ₂ . New Phytologist, 2005, 167, 143-154.	7.3	88
63	MASQOT: a method for cDNA microarray spot quality control. BMC Bioinformatics, 2005, 6, 250.	2.6	16
64	A transcriptional timetable of autumn senescence. Genome Biology, 2004, 5, R24.	9.6	226
65	Cadherins regulate aggregation of pancreatic Î ² -cells in vivo. Development (Cambridge), 1996, 122, 2895-2902.	2.5	210
66	Mouse R-Cadherin: Expression during the Organogenesis of Pancreas and Gastrointestinal Tract. Experimental Cell Research, 1995, 221, 413-425.	2.6	37