

# Andreas Wilm

## List of Publications by Year in descending order

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28  
papers

18,033  
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293460

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563245

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g-index

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all docs

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docs citations

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times ranked

39608  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	0.8	188
2	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	0.8	642
3	Reproducible, scalable, and shareable analysis pipelines with bioinformatics workflow managers. Nature Methods, 2021, 18, 1161-1168.	9.0	83
4	The nf-core framework for community-curated bioinformatics pipelines. Nature Biotechnology, 2020, 38, 276-278.	9.4	963
5	Structure mapping of dengue and Zika viruses reveals functional long-range interactions. Nature Communications, 2019, 10, 1408.	5.8	104
6	Human pharyngeal microbiota in age-related macular degeneration. PLoS ONE, 2018, 13, e0201768.	1.1	23
7	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202.	2.7	94
8	In Vivo Mapping of Eukaryotic RNA Interactomes Reveals Principles of Higher-Order Organization and Regulation. Molecular Cell, 2016, 62, 603-617.	4.5	290
9	Whole metagenome profiling reveals skin microbiome-dependent susceptibility to atopic dermatitis flare. Nature Microbiology, 2016, 1, 16106.	5.9	298
10	INC-Seq: accurate single molecule reads using nanopore sequencing. GigaScience, 2016, 5, 34.	3.3	133
11	Analysis of Dengue Virus Genetic Diversity during Human and Mosquito Infection Reveals Genetic Constraints. PLoS Neglected Tropical Diseases, 2015, 9, e0004044.	1.3	47
12	Tracking Dengue Virus Intra-host Genetic Diversity during Human-to-Mosquito Transmission. PLoS Neglected Tropical Diseases, 2015, 9, e0004052.	1.3	70
13	Draft Genome Sequence of Polychlorinated Biphenyl-Dechlorinating Dehalococcoides mccartyi Strain SG1, Which Carries a Circular Putative Plasmid. Genome Announcements, 2014, 2, .	0.8	6
14	Genomic characterization of three unique <i>Dehalococcoides</i> that respire on persistent polychlorinated biphenyls. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12103-12108.	3.3	168
15	Next-Generation Whole Genome Sequencing of Dengue Virus. Methods in Molecular Biology, 2014, 1138, 175-195.	0.4	14
16	Making automated multiple alignments of very large numbers of protein sequences. Bioinformatics, 2013, 29, 989-995.	1.8	49
17	Species Identification and Profiling of Complex Microbial Communities Using Shotgun Illumina Sequencing of 16S rRNA Amplicon Sequences. PLoS ONE, 2013, 8, e60811.	1.1	93
18	A Randomized, Double-Blind Placebo Controlled Trial of Balapiravir, a Polymerase Inhibitor, in Adult Dengue Patients. Journal of Infectious Diseases, 2013, 207, 1442-1450.	1.9	201

#	ARTICLE	IF	CITATIONS
19	LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. <i>Nucleic Acids Research</i> , 2012, 40, 11189-11201.	6.5	1,074
20	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011, 7, 539.	3.2	12,778
21	Sequence embedding for fast construction of guide trees for multiple sequence alignment. <i>Algorithms for Molecular Biology</i> , 2010, 5, 21.	0.3	94
22	Fast embedding methods for clustering tens of thousands of sequences. <i>Computational Biology and Chemistry</i> , 2008, 32, 282-286.	1.1	4
23	ConStruct: Improved construction of RNA consensus structures. <i>BMC Bioinformatics</i> , 2008, 9, 219.	1.2	37
24	R-Coffee: a method for multiple alignment of non-coding RNA. <i>Nucleic Acids Research</i> , 2008, 36, e52-e52.	6.5	116
25	R-Coffee: a web server for accurately aligning noncoding RNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, W10-W13.	6.5	53
26	An enhanced RNA alignment benchmark for sequence alignment programs. <i>Algorithms for Molecular Biology</i> , 2006, 1, 19.	0.3	103
27	STRAL: progressive alignment of non-coding RNA using base pairing probability vectors in quadratic time. <i>Bioinformatics</i> , 2006, 22, 1593-1599.	1.8	65
28	A benchmark of multiple sequence alignment programs upon structural RNAs. <i>Nucleic Acids Research</i> , 2005, 33, 2433-2439.	6.5	242