

# Alice Carolyn McHardy

## List of Publications by Year in descending order

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Version: 2024-02-01

114  
papers

19,241  
citations

36203

51  
h-index

20900

115  
g-index

141  
all docs

141  
docs citations

141  
times ranked

24020  
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
2	Metadata harmonization—Standards are the key for a better usage of omics data for integrative microbiome analysis. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	13
3	Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
4	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	3.2	110
5	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	5.1	20
6	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	5.5	36
7	EpitopeVec: linear epitope prediction using deep protein sequence embeddings. <i>Bioinformatics</i> , 2021, 37, 4517-4525.	1.8	17
8	Haploflow: strain-resolved de novo assembly of viral genomes. <i>Genome Biology</i> , 2021, 22, 212.	3.8	16
9	Hepatitis C reference viruses highlight potent antibody responses and diverse viral functional interactions with neutralising antibodies. <i>Gut</i> , 2021, 70, 1734-1745.	6.1	15
10	Accurate and scalable variant calling from single cell DNA sequencing data with ProSolo. <i>Nature Communications</i> , 2021, 12, 6744.	5.8	8
11	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
12	CAMITAX: Taxon labels for microbial genomes. <i>GigaScience</i> , 2020, 9, .	3.3	6
13	Evolutionary Stabilization of Cooperative Toxin Production through a Bacterium-Plasmid-Phage Interplay. <i>MBio</i> , 2020, 11, .	1.8	7
14	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020, 30, 2909-2922.e6.	2.9	85
15	YBX1 Indirectly Targets Heterochromatin-Repressed Inflammatory Response-Related Apoptosis Genes through Regulating CBX5 mRNA. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4453.	1.8	11
16	Cellular Importin- $\beta$ 3 Expression Dynamics in the Lung Regulate Antiviral Response Pathways against Influenza A Virus Infection. <i>Cell Reports</i> , 2020, 31, 107549.	2.9	11
17	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
18	Phylogeographic reconstruction using air transportation data and its application to the 2009 H1N1 influenza A pandemic. <i>PLoS Computational Biology</i> , 2020, 16, e1007101.	1.5	8

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19	Predicting antimicrobial resistance in <i>Pseudomonas aeruginosa</i> with machine learning-enabled molecular diagnostics. <i>EMBO Molecular Medicine</i> , 2020, 12, e10264.	3.3	111
20	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
21	FRI-133-HCV neutralizing antibody responses in natural infections mapped by metric multi-dimensional scaling reveals new insights into HCV antigenicity and broadly neutralizing antibodies. <i>Journal of Hepatology</i> , 2019, 70, e446.	1.8	0
22	Structures and functions linked to genome-wide adaptation of human influenza A viruses. <i>Scientific Reports</i> , 2019, 9, 6267.	1.6	4
23	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
24	Probabilistic variable-length segmentation of protein sequences for discriminative motif discovery (DiMotif) and sequence embedding (ProtVecX). <i>Scientific Reports</i> , 2019, 9, 3577.	1.6	52
25	Assessing taxonomic metagenome profilers with OPAL. <i>Genome Biology</i> , 2019, 20, 51.	3.8	67
26	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	4.9	117
27	Pediatric ALL relapses after allo-SCT show high individuality, clonal dynamics, selective pressure, and druggable targets. <i>Blood Advances</i> , 2019, 3, 3143-3156.	2.5	4
28	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
29	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. <i>Nature Microbiology</i> , 2019, 4, 470-479.	5.9	164
30	DiTaxa: nucleotide-pair encoding of 16S rRNA for host phenotype and biomarker detection. <i>Bioinformatics</i> , 2019, 35, 2498-2500.	1.8	15
31	Sweep Dynamics (SD) plots: Computational identification of selective sweeps to monitor the adaptation of influenza A viruses. <i>Scientific Reports</i> , 2018, 8, 373.	1.6	16
32	In Silico Vaccine Strain Prediction for Human Influenza Viruses. <i>Trends in Microbiology</i> , 2018, 26, 119-131.	3.5	42
33	A Fr�chet tree distance measure to compare phylogeographic spread paths across trees. <i>Scientific Reports</i> , 2018, 8, 17000.	1.6	2
34	Critical Assessment of Metagenome Interpretation Enters the Second Round. <i>MSystems</i> , 2018, 3, .	1.7	18
35	Software for Characterizing the Antigenic and Genetic Evolution of Human Influenza Viruses. <i>Methods in Molecular Biology</i> , 2018, 1836, 551-565.	0.4	1
36	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. <i>Viruses</i> , 2018, 10, 256.	1.5	6

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37	Modular Traits of the Rhizobiales Root Microbiota and Their Evolutionary Relationship with Symbiotic Rhizobia. <i>Cell Host and Microbe</i> , 2018, 24, 155-167.e5.	5.1	244
38	MicroPheno: predicting environments and host phenotypes from 16S rRNA gene sequencing using a k-mer based representation of shallow sub-samples. <i>Bioinformatics</i> , 2018, 34, i32-i42.	1.8	68
39	Transcriptome-wide analysis uncovers the targets of the RNA-binding protein MSI2 and effects of MSI2's RNA-binding activity on IL-6 signaling. <i>Journal of Biological Chemistry</i> , 2018, 293, 15359-15369.	1.6	31
40	AMBER: Assessment of Metagenome BinnERs. <i>GigaScience</i> , 2018, 7, .	3.3	72
41	Reconstructing metabolic pathways of a member of the genus <i>Pelotomaculum</i> suggesting its potential to oxidize benzene to carbon dioxide with direct reduction of sulfate. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw254.	1.3	13
42	Metagenomics and CAZyme Discovery. <i>Methods in Molecular Biology</i> , 2017, 1588, 255-277.	0.4	19
43	Finding Genes in Genome Sequence. <i>Methods in Molecular Biology</i> , 2017, 1525, 271-291.	0.4	4
44	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
45	Characterisation of a stable laboratory co-culture of acidophilic nanoorganisms. <i>Scientific Reports</i> , 2017, 7, 3289.	1.6	57
46	EDEN: evolutionary dynamics within environments. <i>Bioinformatics</i> , 2017, 33, 3292-3295.	1.8	2
47	T-cell acute lymphoblastic leukemia in infants has distinct genetic and epigenetic features compared to childhood cases. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 159-167.	1.5	15
48	Genome-guided design of a defined mouse microbiota that confers colonization resistance against <i>Salmonella enterica</i> serovar Typhimurium. <i>Nature Microbiology</i> , 2017, 2, 16215.	5.9	313
49	Investigation of different nitrogen reduction routes and their key microbial players in wood chip-driven denitrification beds. <i>Scientific Reports</i> , 2017, 7, 17028.	1.6	33
50	Comparative whole-genome analysis reveals artificial selection effects on <i>Ustilago esculenta</i> genome. <i>DNA Research</i> , 2017, 24, 635-648.	1.5	58
51	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 264.	6.2	50
52	<i>Candidatus</i> <i>Adiutrix intracellularis</i> ™, an endosymbiont of termite gut flagellates, is the first representative of a deep branching clade of <i>Deltaproteobacteria</i> and a putative homoacetogen. <i>Environmental Microbiology</i> , 2016, 18, 2548-2564.	1.8	50
53	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , 2016, 101, 1380-1389.	1.7	43
54	From Genomes to Phenotypes: TraitAr, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	1.7	102

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55	Determination of antigenicity-altering patches on the major surface protein of human influenza A/H3N2 viruses. <i>Virus Evolution</i> , 2016, 2, vev025.	2.2	21
56	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. <i>Nature Communications</i> , 2016, 7, 11362.	5.8	214
57	Evolution of 2009 H1N1 influenza viruses during the pandemic correlates with increased viral pathogenicity and transmissibility in the ferret model. <i>Scientific Reports</i> , 2016, 6, 28583.	1.6	24
58	Denoising DNA deep sequencing data—high-throughput sequencing errors and their correction. <i>Briefings in Bioinformatics</i> , 2016, 17, 154-179.	3.2	254
59	<i>PhyloPythiaS+</i> : a self-training method for the rapid reconstruction of low-ranking taxonomic bins from metagenomes. <i>PeerJ</i> , 2016, 4, e1603.	0.9	87
60	The PARA-suite: PAR-CLIP specific sequence read simulation and processing. <i>PeerJ</i> , 2016, 4, e2619.	0.9	8
61	Bioboxes: standardised containers for interchangeable bioinformatics software. <i>GigaScience</i> , 2015, 4, 47.	3.3	84
62	Biochemical and bioinformatic methods for elucidating the role of RNA-protein interactions in posttranscriptional regulation. <i>Briefings in Functional Genomics</i> , 2015, 14, 102-114.	1.3	10
63	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015, 17, 603-616.	5.1	628
64	Structure and Function of the Bacterial Root Microbiota in Wild and Domesticated Barley. <i>Cell Host and Microbe</i> , 2015, 17, 392-403.	5.1	1,102
65	Genomics and drug profiling of fatal TCF3-HLF <sup>+</sup> positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. <i>Nature Genetics</i> , 2015, 47, 1020-1029.	9.4	190
66	Coupling of diversification and pH adaptation during the evolution of terrestrial Thaumarchaeota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9370-9375.	3.3	98
67	Functional overlap of the Arabidopsis leaf and root microbiota. <i>Nature</i> , 2015, 528, 364-369.	13.7	1,062
68	How to Grow a Computational Biology Lab. <i>PLoS Computational Biology</i> , 2015, 11, e1004397.	1.5	1
69	Inference of phenotype-defining functional modules of protein families for microbial plant biomass degraders. <i>Biotechnology for Biofuels</i> , 2014, 7, 124.	6.2	19
70	RidgeRace: ridge regression for continuous ancestral character estimation on phylogenetic trees. <i>Bioinformatics</i> , 2014, 30, i527-i533.	1.8	28
71	Microbial genome-enabled insights into plant-microorganism interactions. <i>Nature Reviews Genetics</i> , 2014, 15, 797-813.	7.7	187
72	De novo prediction of the genomic components and capabilities for microbial plant biomass degradation from (meta-)genomes. <i>Biotechnology for Biofuels</i> , 2013, 6, 24.	6.2	18

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73	Alignment-Free Genome Tree Inference by Learning Group-Specific Distance Metrics. <i>Genome Biology and Evolution</i> , 2013, 5, 1470-1484.	1.1	16
74	High-Throughput miRNA and mRNA Sequencing of Paired Colorectal Normal, Tumor and Metastasis Tissues and Bioinformatic Modeling of miRNA-1 Therapeutic Applications. <i>PLoS ONE</i> , 2013, 8, e67461.	1.1	53
75	PTree: pattern-based, stochastic search for maximum parsimony phylogenies. <i>PeerJ</i> , 2013, 1, e89.	0.9	3
76	Inference of Genotype-Phenotype Relationships in the Antigenic Evolution of Human Influenza A (H3N2) Viruses. <i>PLoS Computational Biology</i> , 2012, 8, e1002492.	1.5	26
77	Detecting Patches of Protein Sites of Influenza A Viruses under Positive Selection. <i>Molecular Biology and Evolution</i> , 2012, 29, 2063-2071.	3.5	27
78	Taxonomic binning of metagenome samples generated by next-generation sequencing technologies. <i>Briefings in Bioinformatics</i> , 2012, 13, 646-655.	3.2	98
79	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	4.4	928
80	The PhyloPythiaS Web Server for Taxonomic Assignment of Metagenome Sequences. <i>PLoS ONE</i> , 2012, 7, e38581.	1.1	108
81	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. <i>PLoS ONE</i> , 2012, 7, e38571.	1.1	190
82	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011, 8, 191-192.	9.0	198
83	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011, 5, 122-130.	4.4	114
84	Inferring functional modules of protein families with probabilistic topic models. <i>BMC Bioinformatics</i> , 2011, 12, 141.	1.2	11
85	The impact of seasonal and year-round transmission regimes on the evolution of influenza A virus. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2249-2256.	1.2	12
86	Allele dynamics plots for the study of evolutionary dynamics in viral populations. <i>Nucleic Acids Research</i> , 2011, 39, e4-e4.	6.5	32
87	Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7503-7508.	3.3	414
88	The Role of Genomics in Tracking the Evolution of Influenza A Virus. <i>PLoS Pathogens</i> , 2009, 5, e1000566.	2.1	81
89	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	9.4	254
90	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	2.4	456

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91	The Genome Sequence of the Tomato-Pathogenic Actinomycete <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB382 Reveals a Large Island Involved in Pathogenicity. <i>Journal of Bacteriology</i> , 2008, 190, 2138-2149.	1.0	153
92	Finding Genes in Genome Sequence. <i>Methods in Molecular Biology</i> , 2008, 452, 163-177.	0.4	4
93	What's in the mix: phylogenetic classification of metagenome sequence samples. <i>Current Opinion in Microbiology</i> , 2007, 10, 499-503.	2.3	100
94	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	9.4	354
95	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	9.0	322
96	Accurate phylogenetic classification of variable-length DNA fragments. <i>Nature Methods</i> , 2007, 4, 63-72.	9.0	524
97	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	13.7	1,181
98	REGANOR. <i>Applied Bioinformatics</i> , 2006, 5, 193-198.	1.7	44
99	GISMO—gene identification using a support vector machine for ORF classification. <i>Nucleic Acids Research</i> , 2006, 35, 540-549.	6.5	47
100	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium <i>Alcanivorax borkumensis</i> . <i>Nature Biotechnology</i> , 2006, 24, 997-1004.	9.4	417
101	Complete genome of the mutualistic, N <sub>2</sub> -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. <i>Nature Biotechnology</i> , 2006, 24, 1384-1390.	9.4	237
102	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	9.4	634
103	Short blocks from the noncoding parts of the human genome have instances within nearly all known genes and relate to biological processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6605-6610.	3.3	111
104	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5691-5702.	6.5	1,806
105	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	1.0	321
106	Comparing expression level-dependent features in codon usage with protein abundance: An analysis of "predictive proteomics". <i>Proteomics</i> , 2004, 4, 46-58.	1.3	16
107	Development of joint application strategies for two microbial gene finders. <i>Bioinformatics</i> , 2004, 20, 1622-1631.	1.8	72
108	The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of l-aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , 2003, 104, 5-25.	1.9	844

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109	Genome-based analysis of biosynthetic aminotransferase genes of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2003, 104, 229-240.	1.9	33
110	GenDB—an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , 2003, 31, 2187-2195.	6.5	644
111	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , 2003, 106, 157-167.	1.9	22
112	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003, 106, 147-156.	1.9	31
113	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80.	0.8	8
114	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80.	0.8	0