

Alban Ramette

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

10,224
citations

50276

46
h-index

36028

97
g-index

129
all docs

129
docs citations

129
times ranked

13790
citing authors

#	ARTICLE	IF	CITATIONS
1	Increasing Frequency and Transmission of HIV-1 Non-B Subtypes Among Men Who Have Sex With Men in the Swiss HIV Cohort Study. <i>Journal of Infectious Diseases</i> , 2022, 225, 306-316.	4.0	5
2	External Quality Assessment of SARS-CoV-2 Sequencing: an ESGMD-SSM Pilot Trial across 15 European Laboratories. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0169821.	3.9	13
3	Comparative genomics of 26 complete circular genomes of 18 different serotypes of <i>Actinobacillus pleuropneumoniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	2
4	Similar but different: Integrated phylogenetic analysis of Austrian and Swiss HIV-1 sequences reveal differences in transmission patterns of the local HIV-1 epidemics. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, Publish Ahead of Print, .	2.1	0
5	Investigating the Extent of Primer Dropout in SARS-CoV-2 Genome Sequences During the Early Circulation of Delta Variants. <i>Frontiers in Virology</i> , 2022, 2, .	1.4	14
6	A systematic molecular epidemiology screen reveals numerous HIV-1 superinfections in the Swiss HIV Cohort Study. <i>Journal of Infectious Diseases</i> , 2022, , .	4.0	3
7	Phylogenetic Cluster Analysis Identifies Virological and Behavioral Drivers of Human Immunodeficiency Virus Transmission in Men Who Have Sex With Men. <i>Clinical Infectious Diseases</i> , 2021, 72, 2175-2183.	5.8	10
8	SARS-CoV-2 N501Y Introductions and Transmissions in Switzerland from Beginning of October 2020 to February 2021—Implementation of Swiss-Wide Diagnostic Screening and Whole Genome Sequencing. <i>Microorganisms</i> , 2021, 9, 677.	3.6	32
9	Carbon Source-Dependent Changes of the Structure of <i>Streptococcus pneumoniae</i> Capsular Polysaccharide with Serotype 6F. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4580.	4.1	2
10	Temporal and regional incidence of carbapenemase-producing Enterobacterales, Switzerland, 2013 to 2018. <i>Eurosurveillance</i> , 2021, 26, .	7.0	9
11	Cytokine response in cerebrospinal fluid of meningitis patients and outcome associated with pneumococcal serotype. <i>Scientific Reports</i> , 2021, 11, 19920.	3.3	2
12	Repatriation of a patient with COVID-19 contributed to the importation of an emerging carbapenemase producer. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 27, 267-272.	2.2	8
13	Evaluation of whole-genome sequence data analysis approaches for short- and long-read sequencing of <i>Mycobacterium tuberculosis</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	13
14	Genomic analyses of human adenoviruses unravel novel recombinant genotypes associated with severe infections in pediatric patients. <i>Scientific Reports</i> , 2021, 11, 24038.	3.3	5
15	The Evolving Role of the Clinical Microbiology Laboratory in Identifying Resistance in Gram-Negative Bacteria. <i>Infectious Disease Clinics of North America</i> , 2020, 34, 659-676.	5.1	10
16	Whole-Genome Sequencing of Human Enteroviruses from Clinical Samples by Nanopore Direct RNA Sequencing. <i>Viruses</i> , 2020, 12, 841.	3.3	12
17	The International Virus Bioinformatics Meeting 2020. <i>Viruses</i> , 2020, 12, 1398.	3.3	3
18	Evaluation of primer pairs for microbiome profiling from soils to humans within the One Health framework. <i>Molecular Ecology Resources</i> , 2020, 20, 1558-1571.	4.8	61

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19	A Sample-to-Report Solution for Taxonomic Identification of Cultured Bacteria in the Clinical Setting Based on Nanopore Sequencing. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	15
20	<p>Epidemiology of Human Adenoviruses: A 20-Year Retrospective Observational Study in Hospitalized Patients in Bern, Switzerland<p>. <i>Clinical Epidemiology</i> , 2020, Volume 12, 353-366.	3.0	32
21	NGS-Based <i>S. aureus</i> Typing and Outbreak Analysis in Clinical Microbiology Laboratories: Lessons Learned From a Swiss-Wide Proficiency Test. <i>Frontiers in Microbiology</i> , 2020, 11, 591093.	3.5	9
22	Recurrent <i>Mycobacterium chelonae</i> Skin Infection Unmasked as Factitious Disorder Using Bacterial Whole Genome Sequence Analysis. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa506.	0.9	2
23	Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. <i>Genes</i> , 2019, 10, 655.	2.4	34
24	Rapid and Cost-Efficient Enterovirus Genotyping from Clinical Samples Using Flongle Flow Cells. <i>Genes</i> , 2019, 10, 659.	2.4	37
25	CO ₂ leakage can cause loss of benthic biodiversity in submarine sands. <i>Marine Environmental Research</i> , 2019, 144, 213-229.	2.5	19
26	Nasal Resistome Development in Infants With Cystic Fibrosis in the First Year of Life. <i>Frontiers in Microbiology</i> , 2019, 10, 212.	3.5	10
27	In situ development of a methanotrophic microbiome in deep-sea sediments. <i>ISME Journal</i> , 2019, 13, 197-213.	9.8	61
28	The Simple 10-Item Predicting Asthma Risk in Children Tool to Predict Childhood Asthma"An External Validation. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2019, 7, 943-953.e4.	3.8	8
29	Draft Genome Sequence of Methicillin-Resistant <i>Staphylococcus aureus</i> Strain AW7, Isolated from a Patient with Bacteremia. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
30	CO ₂ leakage alters biogeochemical and ecological functions of submarine sands. <i>Science Advances</i> , 2018, 4, eaao2040.	10.3	27
31	Influence of Pig Farming on the Human Nasal Microbiota: Key Role of Airborne Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	65
32	Prevalence of carbapenem-resistant <i>Acinetobacter baumannii</i> from 2005 to 2016 in Switzerland. <i>BMC Infectious Diseases</i> , 2018, 18, 159.	2.9	14
33	Longitudinal Associations Between Respiratory Infections and Asthma in Young Children. <i>American Journal of Epidemiology</i> , 2018, 187, 1714-1720.	3.4	9
34	Whole-Genome Sequence of the First Extended-Spectrum β -Lactamase-Producing Strain of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Napoli. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	10
35	Host switching pathogens, infectious outbreaks and zoonosis: A Marie Skłodowska-Curie innovative training network (HONOURS). <i>Virus Research</i> , 2018, 257, 120-124.	2.2	2
36	Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform. <i>Swiss Medical Weekly</i> , 2018, 148, w14693.	1.6	28

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37	The simple 10-item PARC tool predicts childhood asthma in an external validation cohort. , 2018, , .		0
38	Hypoxia causes preservation of labile organic matter and changes seafloor microbial community composition (Black Sea). Science Advances, 2017, 3, e1601897.	10.3	145
39	Heterogeneous Genetic Location of <i>mcr-1</i> in Colistin-Resistant Escherichia coli Isolates from Humans and Retail Chicken Meat in Switzerland: Emergence of <i>mcr-1</i> -Carrying IncK2 Plasmids. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	56
40	Minor impacts of reduced pH on bacterial biofilms on settlement tiles along natural pH gradients at two CO ₂ seeps in Papua New Guinea. ICES Journal of Marine Science, 2017, 74, 978-987.	2.5	11
41	Breastfeeding and respiratory tract infections during the first 2 years of life. ERJ Open Research, 2017, 3, 00143-2016.	2.6	18
42	Prevalence of cough throughout childhood: A cohort study. PLoS ONE, 2017, 12, e0177485.	2.5	25
43	Association between breastfeeding and eczema during childhood and adolescence: A cohort study. PLoS ONE, 2017, 12, e0185066.	2.5	10
44	Early-life respiratory tract infections and the risk of lower lung function and asthma:a meta-analysis of 154,492 children. , 2017, , .		0
45	Methane Seep in Shallow-Water Permeable Sediment Harbors High Diversity of Anaerobic Methanotrophic Communities, Elba, Italy. Frontiers in Microbiology, 2016, 7, 374.	3.5	38
46	Quantification of the effects of ocean acidification on sediment microbial communities in the environment: the importance of ecosystem approaches. FEMS Microbiology Ecology, 2016, 92, fiw027.	2.7	52
47	Diversity and Biogeography of Bathyal and Abyssal Seafloor Bacteria. PLoS ONE, 2016, 11, e0148016.	2.5	132
48	Changes in height and BMI in children and adolescents with primary ciliary dyskinesia (PCD) during the growth period: An iPCD cohort study. , 2016, , .		0
49	Early-life respiratory tract infections and risk of lower lung function and asthma at school-age. The generation R study. , 2016, , .		0
50	Lung growth in children and young adults with primary ciliary dyskinesia (PCD): An iPCD cohort study. , 2016, , .		1
51	Spatial scales of bacterial community diversity at cold seeps (Eastern Mediterranean Sea). ISME Journal, 2015, 9, 1306-1318.	9.8	69
52	Seagrass biofilm communities at a naturally CO_2 -enriched vent. Environmental Microbiology Reports, 2015, 7, 516-525.	2.4	30
53	Global dispersion and local diversification of the methane seep microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4015-4020.	7.1	248
54	Bed-sharing and childhood asthma: from associations to causal modelling. European Respiratory Journal, 2015, 45, 596-600.	6.7	2

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55	Diversity of Iron Oxidizing and Reducing Bacteria in Flow Reactors in the Åspåq Hard Rock Laboratory. <i>Geomicrobiology Journal</i> , 2015, 32, 207-220.	2.0	26
56	Changes in microbial communities in coastal sediments along natural CO_2 gradients at a volcanic vent in <i>Papua New Guinea</i> . <i>Environmental Microbiology</i> , 2015, 17, 3678-3691.	3.8	64
57	Causal relationships between infections and asthma throughout childhood: A path analysis approach. , 2015, , .		0
58	Risk factors for chronic non-specific cough in 0-2 year olds: A cohort study. , 2015, , .		1
59	Does breastfeeding protect against childhood eczema?. , 2015, , .		0
60	Dual symbiosis with co-occurring sulfur-oxidizing symbionts in vestimentiferan tubeworms from a <i>Mediterranean</i> hydrothermal vent. <i>Environmental Microbiology</i> , 2014, 16, 3638-3656.	3.8	38
61	The R package <i>otu2ot</i> for implementing the entropy decomposition of nucleotide variation in sequence data. <i>Frontiers in Microbiology</i> , 2014, 5, 601.	3.5	19
62	Spatial patterns and links between microbial community composition and function in cyanobacterial mats. <i>Frontiers in Microbiology</i> , 2014, 5, 406.	3.5	22
63	Bacterial taxa "area and distance" decay relationships in marine environments. <i>Molecular Ecology</i> , 2014, 23, 954-964.	3.9	147
64	Ecological coherence of diversity patterns derived from classical fingerprinting and <i>Next-Generation Sequencing</i> techniques. <i>Environmental Microbiology</i> , 2014, 16, 2672-2681.	3.8	73
65	A guide to statistical analysis in microbial ecology: a community-focused, living review of multivariate data analyses. <i>FEMS Microbiology Ecology</i> , 2014, 90, 543-550.	2.7	314
66	Biogeographic patterns of bacterial microdiversity in Arctic deep-sea sediments (HAUSGARTEN, Fram) <i>Journal of Biogeography</i> , 2013, 40, 800-811.	3.5	17
67	Macroecological patterns of marine bacteria on a global scale. <i>Journal of Biogeography</i> , 2013, 40, 800-811.	3.0	53
68	Microbial Communities of Deep-Sea Methane Seeps at Hikurangi Continental Margin (New Zealand). <i>PLoS ONE</i> , 2013, 8, e72627.	2.5	78
69	Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. <i>Frontiers in Microbiology</i> , 2013, 4, 207.	3.5	28
70	Relationships between Host Phylogeny, Host Type and Bacterial Community Diversity in Cold-Water Coral Reef Sponges. <i>PLoS ONE</i> , 2013, 8, e55505.	2.5	64
71	Biogeography of Deep-Sea Benthic Bacteria at Regional Scale (LTER HAUSGARTEN, Fram Strait, Arctic). <i>PLoS ONE</i> , 2013, 8, e72779.	2.5	65
72	The energy "diversity" relationship of complex bacterial communities in Arctic deep-sea sediments. <i>ISME Journal</i> , 2012, 6, 724-732.	9.8	131

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73	Diversity and dynamics of rare and of resident bacterial populations in coastal sands. ISME Journal, 2012, 6, 542-553.	9.8	224
74	Distribution and <i>in situ</i> abundance of sulfate-reducing bacteria in diverse marine hydrocarbon seep sediments. Environmental Microbiology, 2012, 14, 2689-2710.	3.8	128
75	Repeatedly Evolved Host-Specific Ectosymbioses between Sulfur-Oxidizing Bacteria and Amphipods Living in a Cave Ecosystem. PLoS ONE, 2012, 7, e50254.	2.5	40
76	Mats of psychrophilic thiotrophic bacteria associated with cold seeps of the Barents Sea. Biogeosciences, 2012, 9, 2947-2960.	3.3	47
77	Bacterial diversity and biogeochemistry of different chemosynthetic habitats of the REGAB cold seep (West African margin, 3160 m water depth). Biogeosciences, 2012, 9, 5031-5048.	3.3	43
78	Microbial diversity of eolian dust sources from saline lake sediments and biological soil crusts in arid Southern Australia. FEMS Microbiology Ecology, 2012, 80, 294-304.	2.7	43
79	Spatial Scales of Bacterial Diversity in Cold-Water Coral Reef Ecosystems. PLoS ONE, 2012, 7, e32093.	2.5	44
80	Microbial and Chemical Characterization of Underwater Fresh Water Springs in the Dead Sea. PLoS ONE, 2012, 7, e38319.	2.5	161
81	Effects of Eutrophication, Seasonality and Macrofouling on the Diversity of Bacterial Biofilms in Equatorial Coral Reefs. PLoS ONE, 2012, 7, e39951.	2.5	44
82	Factors controlling the distribution of anaerobic methanotrophic communities in marine environments: Evidence from intact polar membrane lipids. Geochimica Et Cosmochimica Acta, 2011, 75, 164-184.	3.9	111
83	<i>Pseudomonas protegens</i> sp. nov., widespread plant-protecting bacteria producing the biocontrol compounds 2,4-diacetylphloroglucinol and pyoluteorin. Systematic and Applied Microbiology, 2011, 34, 180-188.	2.8	304
84	Global Patterns of Bacterial Beta-Diversity in Seafloor and Seawater Ecosystems. PLoS ONE, 2011, 6, e24570.	2.5	525
85	Drivers of bacterial diversity dynamics in permeable carbonate and silicate coral reef sands from the Red Sea. Environmental Microbiology, 2011, 13, 1815-1826.	3.8	45
86	Determinants of the distribution of nitrogen-cycling microbial communities at the landscape scale. ISME Journal, 2011, 5, 532-542.	9.8	336
87	Quantifying the effect of environment stability on the transcription factor repertoire of marine microbes. Microbial Informatics and Experimentation, 2011, 1, 9.	7.6	5
88	Temporal shifts of the Norway lobster (<i>Nephrops norvegicus</i>) gut bacterial communities. FEMS Microbiology Ecology, 2010, 74, 472-484.	2.7	60
89	Bacterial diversity and biogeography in deep-sea surface sediments of the South Atlantic Ocean. ISME Journal, 2010, 4, 159-170.	9.8	227
90	Novel observations of <i>Thiobacterium</i> , a sulfur-storing Gammaproteobacterium producing gelatinous mats. ISME Journal, 2010, 4, 1031-1043.	9.8	12

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91	Site and plant species are important determinants of the <i>Methylobacterium</i> community composition in the plant phyllosphere. <i>ISME Journal</i> , 2010, 4, 719-728.	9.8	297
92	Dual symbiosis of the vent shrimp <i>Rimicaris exoculata</i> with filamentous gamma- and epsilon-proteobacteria at four Mid-Atlantic Ridge hydrothermal vent fields. <i>Environmental Microbiology</i> , 2010, 12, 2204-2218.	3.8	102
93	High symbiont diversity in the bone-eating worm <i>Osedax mucofloris</i> from shallow whale-falls in the North Atlantic. <i>Environmental Microbiology</i> , 2010, 12, 2355-2370.	3.8	47
94	Improved <i>dsrA</i> -Based Terminal Restriction Fragment Length Polymorphism Analysis of Sulfate-Reducing Bacteria. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5308-5311.	3.1	17
95	Multilevel analysis of the bacterial diversity along the environmental gradient Río de la Plata "South Atlantic Ocean. <i>Aquatic Microbial Ecology</i> , 2010, 61, 57-72.	1.8	22
96	Impact of natural oil and higher hydrocarbons on microbial diversity, distribution, and activity in Gulf of Mexico cold-seep sediments. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2010, 57, 2008-2021.	1.4	171
97	Multivariate Cutoff Level Analysis (MultiCoLA) of large community data sets. <i>Nucleic Acids Research</i> , 2010, 38, e155-e155.	14.5	108
98	Quantitative Community Fingerprinting Methods for Estimating the Abundance of Operational Taxonomic Units in Natural Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2495-2505.	3.1	205
99	Response of benthic microbial communities to chitin enrichment: an in situ study in the deep Arctic Ocean. <i>Polar Biology</i> , 2009, 32, 105-112.	1.2	20
100	Inter- and intra-habitat bacterial diversity associated with cold-water corals. <i>ISME Journal</i> , 2009, 3, 756-759.	9.8	57
101	Time- and sediment depth-related variations in bacterial diversity and community structure in subtidal sands. <i>ISME Journal</i> , 2009, 3, 780-791.	9.8	159
102	Effects of nitrobenzene contamination and of bioaugmentation on nitrification and ammonia-oxidizing bacteria in soil. <i>FEMS Microbiology Ecology</i> , 2009, 70, 315-323.	2.7	26
103	Microbial colonisation of artificial and deep-sea sediments in the Arctic Ocean. <i>Marine Ecology</i> , 2009, 30, 391-404.	1.1	10
104	Impact of space, time and complex environments on microbial communities. <i>Clinical Microbiology and Infection</i> , 2009, 15, 60-62.	6.0	4
105	Crystal ball " 2009. <i>Environmental Microbiology Reports</i> , 2009, 1, 3-26.	2.4	5
106	Identification and Onion Pathogenicity of <i>Burkholderia cepacia</i> Complex Isolates from the Onion Rhizosphere and Onion Field Soil. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3121-3129.	3.1	64
107	Multiscale responses of microbial life to spatial distance and environmental heterogeneity in a patchy ecosystem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2761-2766.	7.1	376
108	Multivariate analyses in microbial ecology. <i>FEMS Microbiology Ecology</i> , 2007, 62, 142-160.	2.7	1,477

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109	Biogeography: An Emerging Cornerstone for Understanding Prokaryotic Diversity, Ecology, and Evolution. <i>Microbial Ecology</i> , 2007, 53, 197-207.	2.8	228
110	The bacterial species definition in the genomic era. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1929-1940.	4.0	550
111	Application of <i>arcA</i> gene-based identification approach to the maize rhizosphere reveals novel diversity in <i>Burkholderia</i> species. <i>FEMS Microbiology Letters</i> , 2006, 259, 126-132.	1.8	23
112	Genetic diversity and biocontrol potential of fluorescent pseudomonads producing phloroglucinols and hydrogen cyanide from Swiss soils naturally suppressive or conducive to <i>Thielaviopsis basicola</i> -mediated black root rot of tobacco. <i>FEMS Microbiology Ecology</i> , 2006, 55, 369-381.	2.7	91
113	Toward a More Robust Assessment of Intraspecies Diversity, Using Fewer Genetic Markers— <i>z</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 7286-7293.	3.1	196
114	<i>Burkholderia xenovorans</i> LB400 harbors a multi-replicon, 9.73-Mbp genome shaped for versatility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15280-15287.	7.1	339
115	Species Abundance and Diversity of <i>Burkholderia cepacia</i> Complex in the Environment. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1193-1201.	3.1	104
116	Prevalence of fluorescent pseudomonads producing antifungal phloroglucinols and/or hydrogen cyanide in soils naturally suppressive or conducive to tobacco black root rot. <i>FEMS Microbiology Ecology</i> , 2003, 44, 35-43.	2.7	105
117	Phylogeny of HCN Synthase-Encoding <i>hcnBC</i> Genes in Biocontrol Fluorescent Pseudomonads and Its Relationship with Host Plant Species and HCN Synthesis Ability. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 525-535.	2.6	163
118	Prevalence of fluorescent pseudomonads producing antifungal phloroglucinols and/or hydrogen cyanide in soils naturally suppressive or conducive to tobacco black root rot. <i>FEMS Microbiology Ecology</i> , 2003, 44, 35-43.	2.7	3
119	Polymorphism of the Polyketide Synthase Gene <i>phlD</i> in Biocontrol Fluorescent Pseudomonads Producing 2,4-Diacetylphloroglucinol and Comparison of <i>PhlD</i> with Plant Polyketide Synthases. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 639-652.	2.6	68
120	Cosmopolitan distribution of <i>phlD</i> -containing dicotyledonous crop-associated biocontrol pseudomonads of worldwide origin. <i>FEMS Microbiology Ecology</i> , 2001, 37, 105-116.	2.7	102