

# Alban Ramette

## List of Publications by Year in descending order

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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	Multivariate analyses in microbial ecology. <i>FEMS Microbiology Ecology</i> , 2007, 62, 142-160.	2.7	1,477
2	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
3	Global Patterns of Bacterial Beta-Diversity in Seafloor and Seawater Ecosystems. <i>PLoS ONE</i> , 2011, 6, e24570.	2.5	525
4	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
5	<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
6	Determinants of the distribution of nitrogen-cycling microbial communities at the landscape scale. <i>ISME Journal</i> , 2011, 5, 532-542.	9.8	336
7	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
8	<i>Pseudomonas protegens</i> sp. nov., widespread plant-protecting bacteria producing the biocontrol compounds 2,4-diacetylphloroglucinol and pyoluteorin. <i>Systematic and Applied Microbiology</i> , 2011, 34, 180-188.	2.8	304
9	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
10	Global dispersion and local diversification of the methane seep microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4015-4020.	7.1	248
11	Biogeography: An Emerging Cornerstone for Understanding Prokaryotic Diversity, Ecology, and Evolution. <i>Microbial Ecology</i> , 2007, 53, 197-207.	2.8	228
12	Bacterial diversity and biogeography in deep-sea surface sediments of the South Atlantic Ocean. <i>ISME Journal</i> , 2010, 4, 159-170.	9.8	227
13	Diversity and dynamics of rare and of resident bacterial populations in coastal sands. <i>ISME Journal</i> , 2012, 6, 542-553.	9.8	224
14	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
15	Toward a More Robust Assessment of Intraspecies Diversity, Using Fewer Genetic Markers— <i>¿</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 7286-7293.	3.1	196
16	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
17	Phylogeny of HCN Synthase-Encoding hcnBC Genes in Biocontrol Fluorescent <i>Pseudomonads</i> and Its Relationship with Host Plant Species and HCN Synthesis Ability. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 525-535.	2.6	163
18	Microbial and Chemical Characterization of Underwater Fresh Water Springs in the Dead Sea. <i>PLoS ONE</i> , 2012, 7, e38319.	2.5	161

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19	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
20	Bacterial taxaâ€‘area and distanceâ€‘decay relationships in marine environments. <i>Molecular Ecology</i> , 2014, 23, 954-964.	3.9	147
21	Hypoxia causes preservation of labile organic matter and changes seafloor microbial community composition (Black Sea). <i>Science Advances</i> , 2017, 3, e1601897.	10.3	145
22	Diversity and Biogeography of Bathyal and Abyssal Seafloor Bacteria. <i>PLoS ONE</i> , 2016, 11, e0148016.	2.5	132
23	The energyâ€‘diversity relationship of complex bacterial communities in Arctic deep-sea sediments. <i>ISME Journal</i> , 2012, 6, 724-732.	9.8	131
24	Distribution and <i>in situ</i> abundance of sulfateâ€‘reducing bacteria in diverse marine hydrocarbon seep sediments. <i>Environmental Microbiology</i> , 2012, 14, 2689-2710.	3.8	128
25	Factors controlling the distribution of anaerobic methanotrophic communities in marine environments: Evidence from intact polar membrane lipids. <i>Geochimica Et Cosmochimica Acta</i> , 2011, 75, 164-184.	3.9	111
26	Multivariate Cutoff Level Analysis (MultiCoLA) of large community data sets. <i>Nucleic Acids Research</i> , 2010, 38, e155-e155.	14.5	108
27	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
28	Species Abundance and Diversity of Burkholderia cepacia Complex in the Environment. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1193-1201.	3.1	104
29	Cosmopolitan distribution of phlD-containing dicotyledonous crop-associated biocontrol pseudomonads of worldwide origin. <i>FEMS Microbiology Ecology</i> , 2001, 37, 105-116.	2.7	102
30	Dual symbiosis of the vent shrimp <i>Rimicaris exoculata</i> with filamentous gammaâ€‘and epsilonproteobacteria at four Midâ€‘Atlantic Ridge hydrothermal vent fields. <i>Environmental Microbiology</i> , 2010, 12, 2204-2218.	3.8	102
31	Genetic diversity and biocontrol potential of fluorescent pseudomonads producing phloroglucinols and hydrogen cyanide from Swiss soils naturally suppressive or conducive to Thielaviopsis basicola-mediated black root rot of tobacco. <i>FEMS Microbiology Ecology</i> , 2006, 55, 369-381.	2.7	91
32	Microbial Communities of Deep-Sea Methane Seeps at Hikurangi Continental Margin (New Zealand). <i>PLoS ONE</i> , 2013, 8, e72627.	2.5	78
33	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
34	Spatial scales of bacterial community diversity at cold seeps (Eastern Mediterranean Sea). <i>ISME Journal</i> , 2015, 9, 1306-1318.	9.8	69
35	Polymorphism of the Polyketide Synthase Gene phlD in Biocontrol Fluorescent Pseudomonads Producing 2,4-Diacetylphloroglucinol and Comparison of PhlD with Plant Polyketide Synthases. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 639-652.	2.6	68
36	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

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37	Biogeography of Deep-Sea Benthic Bacteria at Regional Scale (LTER HAUSGARTEN, Fram Strait, Arctic). PLoS ONE, 2013, 8, e72779.	2.5	65
38	Identification and Onion Pathogenicity of <i>Burkholderia cepacia</i> Complex Isolates from the Onion Rhizosphere and Onion Field Soil. Applied and Environmental Microbiology, 2008, 74, 3121-3129.	3.1	64
39	Changes in microbial communities in coastal sediments along natural $\text{CO}_2$ gradients at a volcanic vent in Papua New Guinea. Environmental Microbiology, 2015, 17, 3678-3691.	3.8	64
40	Relationships between Host Phylogeny, Host Type and Bacterial Community Diversity in Cold-Water Coral Reef Sponges. PLoS ONE, 2013, 8, e55505.	2.5	64
41	In situ development of a methanotrophic microbiome in deep-sea sediments. ISME Journal, 2019, 13, 197-213.	9.8	61
42	Evaluation of primer pairs for microbiome profiling from soils to humans within the One Health framework. Molecular Ecology Resources, 2020, 20, 1558-1571.	4.8	61
43	Temporal shifts of the Norway lobster ( <i>Nephrops norvegicus</i> ) gut bacterial communities. FEMS Microbiology Ecology, 2010, 74, 472-484.	2.7	60
44	Inter- and intra-habitat bacterial diversity associated with cold-water corals. ISME Journal, 2009, 3, 756-759.	9.8	57
45	Heterogeneous Genetic Location of <i>mcr-1</i> in Colistin-Resistant <i>Escherichia coli</i> 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
46	Macroecological patterns of marine bacteria on a global scale. Journal of Biogeography, 2013, 40, 800-811.	3.0	53
47	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
48	High symbiont diversity in the bone-eating worm <i>Osedax mucofloris</i> from shallow whale-falls in the North Atlantic. Environmental Microbiology, 2010, 12, 2355-2370.	3.8	47
49	Mats of psychrophilic thiotrophic bacteria associated with cold seeps of the Barents Sea. Biogeosciences, 2012, 9, 2947-2960.	3.3	47
50	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
51	Spatial Scales of Bacterial Diversity in Cold-Water Coral Reef Ecosystems. PLoS ONE, 2012, 7, e32093.	2.5	44
52	Effects of Eutrophication, Seasonality and Macrofouling on the Diversity of Bacterial Biofilms in Equatorial Coral Reefs. PLoS ONE, 2012, 7, e39951.	2.5	44
53	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
54	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

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55	Repeatedly Evolved Host-Specific Ectosymbioses between Sulfur-Oxidizing Bacteria and Amphipods Living in a Cave Ecosystem. PLoS ONE, 2012, 7, e50254.	2.5	40
56	Dual symbiosis with co-occurring sulfur-oxidizing symbionts in vestimentiferan tubeworms from a Mediterranean hydrothermal vent. Environmental Microbiology, 2014, 16, 3638-3656.	3.8	38
57	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
58	Rapid and Cost-Efficient Enterovirus Genotyping from Clinical Samples Using Flow Cytometry. Genes, 2019, 10, 659.	2.4	37
59	Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. Genes, 2019, 10, 655.	2.4	34
60	Epidemiology of Human Adenoviruses: A 20-Year Retrospective Observational Study in Hospitalized Patients in Bern, Switzerland. Clinical Epidemiology, 2020, Volume 12, 353-366.	3.0	32
61	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. Microorganisms, 2021, 9, 677.	3.6	32
62	Seagrass biofilm communities at a naturally CO <sub>2</sub> -rich vent. Environmental Microbiology Reports, 2015, 7, 516-525.	2.4	30
63	Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. Frontiers in Microbiology, 2013, 4, 207.	3.5	28
64	Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform. Swiss Medical Weekly, 2018, 148, w14693.	1.6	28
65	CO <sub>2</sub> leakage alters biogeochemical and ecological functions of submarine sands. Science Advances, 2018, 4, eaao2040.	10.3	27
66	Effects of nitrobenzene contamination and of bioaugmentation on nitrification and ammonia-oxidizing bacteria in soil. FEMS Microbiology Ecology, 2009, 70, 315-323.	2.7	26
67	Diversity of Iron Oxidizing and Reducing Bacteria in Flow Reactors in the Åspå Hard Rock Laboratory. Geomicrobiology Journal, 2015, 32, 207-220.	2.0	26
68	Prevalence of cough throughout childhood: A cohort study. PLoS ONE, 2017, 12, e0177485.	2.5	25
69	Application of a gene-based identification approach to the maize rhizosphere reveals novel diversity in Burkholderia species. FEMS Microbiology Letters, 2006, 259, 126-132.	1.8	23
70	Multilevel analysis of the bacterial diversity along the environmental gradient Río de la Plata—South Atlantic Ocean. Aquatic Microbial Ecology, 2010, 61, 57-72.	1.8	22
71	Spatial patterns and links between microbial community composition and function in cyanobacterial mats. Frontiers in Microbiology, 2014, 5, 406.	3.5	22
72	Response of benthic microbial communities to chitin enrichment: an in situ study in the deep Arctic Ocean. Polar Biology, 2009, 32, 105-112.	1.2	20

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73	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
74	CO2 leakage can cause loss of benthic biodiversity in submarine sands. <i>Marine Environmental Research</i> , 2019, 144, 213-229.	2.5	19
75	Breastfeeding and respiratory tract infections during the first 2 years of life. <i>ERJ Open Research</i> , 2017, 3, 00143-2016.	2.6	18
76	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
77	Biogeographic patterns of bacterial microdiversity in Arctic deep-sea sediments (HAUSGARTEN, Fram) Tj ETQq1 1 0,784314 rgBT /Ovelde	3.5	17
78	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
79	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
80	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
81	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
82	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
83	Novel observations of <i>Thiobacterium</i> , a sulfur-storing Gammaproteobacterium producing gelatinous mats. <i>ISME Journal</i> , 2010, 4, 1031-1043.	9.8	12
84	Whole-Genome Sequencing of Human Enteroviruses from Clinical Samples by Nanopore Direct RNA Sequencing. <i>Viruses</i> , 2020, 12, 841.	3.3	12
85	Minor impacts of reduced pH on bacterial biofilms on settlement tiles along natural pH gradients at two CO2 seeps in Papua New Guinea. <i>ICES Journal of Marine Science</i> , 2017, 74, 978-987.	2.5	11
86	Microbial colonisation of artificial and deep-sea sediments in the Arctic Ocean. <i>Marine Ecology</i> , 2009, 30, 391-404.	1.1	10
87	Whole-Genome Sequence of the First Extended-Spectrum $\beta$ -Lactamase-Producing Strain of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Napoli. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	10
88	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
89	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
90	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

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91	Association between breastfeeding and eczema during childhood and adolescence: A cohort study. PLoS ONE, 2017, 12, e0185066.	2.5	10
92	Longitudinal Associations Between Respiratory Infections and Asthma in Young Children. American Journal of Epidemiology, 2018, 187, 1714-1720.	3.4	9
93	Temporal and regional incidence of carbapenemase-producing Enterobacterales, Switzerland, 2013 to 2018. Eurosurveillance, 2021, 26, .	7.0	9
94	NGS-Based S. aureus Typing and Outbreak Analysis in Clinical Microbiology Laboratories: Lessons Learned From a Swiss-Wide Proficiency Test. Frontiers in Microbiology, 2020, 11, 591093.	3.5	9
95	The Simple 10-Item Predicting Asthma Risk in Children Tool to Predict Childhood Asthma—An External Validation. Journal of Allergy and Clinical Immunology: in Practice, 2019, 7, 943-953.e4.	3.8	8
96	Repatriation of a patient with COVID-19 contributed to the importation of an emerging carbapenemase producer. Journal of Global Antimicrobial Resistance, 2021, 27, 267-272.	2.2	8
97	Draft Genome Sequence of Methicillin-Resistant Staphylococcus aureus Strain AW7, Isolated from a Patient with Bacteremia. Microbiology Resource Announcements, 2019, 8, .	0.6	7
98	Crystal ball “ 2009. Environmental Microbiology Reports, 2009, 1, 3-26.	2.4	5
99	Quantifying the effect of environment stability on the transcription factor repertoire of marine microbes. Microbial Informatics and Experimentation, 2011, 1, 9.	7.6	5
100	Increasing Frequency and Transmission of HIV-1 Non-B Subtypes Among Men Who Have Sex With Men in the Swiss HIV Cohort Study. Journal of Infectious Diseases, 2022, 225, 306-316.	4.0	5
101	Genomic analyses of human adenoviruses unravel novel recombinant genotypes associated with severe infections in pediatric patients. Scientific Reports, 2021, 11, 24038.	3.3	5
102	Impact of space, time and complex environments on microbial communities. Clinical Microbiology and Infection, 2009, 15, 60-62.	6.0	4
103	The International Virus Bioinformatics Meeting 2020. Viruses, 2020, 12, 1398.	3.3	3
104	Prevalence of fluorescent pseudomonads producing antifungal phloroglucinols and/or hydrogen cyanide in soils naturally suppressive or conducive to tobacco black root rot. FEMS Microbiology Ecology, 2003, 44, 35-43.	2.7	3
105	A systematic molecular epidemiology screen reveals numerous HIV-1 superinfections in the Swiss HIV Cohort Study. Journal of Infectious Diseases, 2022, , .	4.0	3
106	Bed-sharing and childhood asthma: from associations to causal modelling. European Respiratory Journal, 2015, 45, 596-600.	6.7	2
107	Host switching pathogens, infectious outbreaks and zoonosis: A Marie Skłodowska-Curie innovative training network (HONOURS). Virus Research, 2018, 257, 120-124.	2.2	2
108	Carbon Source-Dependent Changes of the Structure of Streptococcus pneumoniae Capsular Polysaccharide with Serotype 6F. International Journal of Molecular Sciences, 2021, 22, 4580.	4.1	2

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109	Cytokine response in cerebrospinal fluid of meningitis patients and outcome associated with pneumococcal serotype. <i>Scientific Reports</i> , 2021, 11, 19920.	3.3	2
110	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
111	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
112	Risk factors for chronic non-specific cough in 0-2 year olds: A cohort study. , 2015, , .		1
113	Lung growth in children and young adults with primary ciliary dyskinesia (PCD): An iPCD cohort study. , 2016, , .		1
114	Causal relationships between infections and asthma throughout childhood: A path analysis approach. , 2015, , .		0
115	Does breastfeeding protect against childhood eczema?. , 2015, , .		0
116	Changes in height and BMI in children and adolescents with primary ciliary dyskinesia (PCD) during the growth period: An iPCD cohort study. , 2016, , .		0
117	Early-life respiratory tract infections and risk of lower lung function and asthma at school-age. The generation R study. , 2016, , .		0
118	Early-life respiratory tract infections and the risk of lower lung function and asthma:a meta-analysis of 154,492 children. , 2017, , .		0
119	The simple 10-item PARC tool predicts childhood asthma in an external validation cohort. , 2018, , .		0
120	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</i> (1999), 2022, Publish Ahead of Print, .	2.1	0