

Anthony Levasseur

List of Publications by Year in descending order

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Version: 2024-02-01

155
papers

10,602
citations

76196

40
h-index

35952

97
g-index

171
all docs

171
docs citations

171
times ranked

13044
citing authors

#	ARTICLE	IF	CITATIONS
1	Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. <i>Biotechnology for Biofuels</i> , 2013, 6, 41.	6.2	994
2	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	9.4	870
3	Culture of previously uncultured members of the human gut microbiota by culturomics. <i>Nature Microbiology</i> , 2016, 1, 16203.	5.9	735
4	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	3.3	595
5	Culturing the human microbiota and culturomics. <i>Nature Reviews Microbiology</i> , 2018, 16, 540-550.	13.6	521
6	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490
7	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012, 3, 913.	5.8	458
8	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
9	Early treatment of COVID-19 patients with hydroxychloroquine and azithromycin: A retrospective analysis of 1061 cases in Marseille, France. <i>Travel Medicine and Infectious Disease</i> , 2020, 35, 101738.	1.5	372
10	Tailed giant Tupanvirus possesses the most complete translational apparatus of the known virosphere. <i>Nature Communications</i> , 2018, 9, 749.	5.8	247
11	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	1.5	226
12	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2504-2509.	3.3	218
13	Outcomes of 3,737 COVID-19 patients treated with hydroxychloroquine/azithromycin and other regimens in Marseille, France: A retrospective analysis. <i>Travel Medicine and Infectious Disease</i> , 2020, 36, 101791.	1.5	209
14	Insights on the Evolution of Mycoparasitism from the Genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 465-480.	1.1	150
15	Mimivirus: leading the way in the discovery of giant viruses of amoebae. <i>Nature Reviews Microbiology</i> , 2017, 15, 243-254.	13.6	132
16	Exploring fungal biodiversity: organic acid production by 66 strains of filamentous fungi. <i>Fungal Biology and Biotechnology</i> , 2014, 1, 1-14.	2.5	119
17	FOLy: An integrated database for the classification and functional annotation of fungal oxidoreductases potentially involved in the degradation of lignin and related aromatic compounds. <i>Fungal Genetics and Biology</i> , 2008, 45, 638-645.	0.9	118
18	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111

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19	GPR50 is the mammalian ortholog of Mel1c: Evidence of rapid evolution in mammals. <i>BMC Evolutionary Biology</i> , 2008, 8, 105.	3.2	110
20	Mink, SARS-CoV-2, and the Human-Animal Interface. <i>Frontiers in Microbiology</i> , 2021, 12, 663815.	1.5	106
21	MIMIVIRE is a defence system in mimivirus that confers resistance to virophage. <i>Nature</i> , 2016, 531, 249-252.	13.7	98
22	Fungal Strategies for Lignin Degradation. <i>Advances in Botanical Research</i> , 2012, 61, 263-308.	0.5	95
23	Characterization of salt-adapted secreted lignocellulolytic enzymes from the mangrove fungus <i>Pestalotiopsis</i> sp.. <i>Nature Communications</i> , 2013, 4, 1810.	5.8	92
24	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. <i>BMC Genomics</i> , 2014, 15, 486.	1.2	91
25	Description of <i>Mediterraneibacter massiliensis</i> , gen. nov., sp. nov., a new genus isolated from the gut microbiota of an obese patient and reclassification of <i>Ruminococcus faecis</i> , <i>Ruminococcus lactaris</i> , <i>Ruminococcus torques</i> , <i>Ruminococcus gnavus</i> and <i>Clostridium glycyrrhizinilyticum</i> as <i>Mediterraneibacter faecis</i> comb. nov., <i>Mediterraneibacter lactaris</i> comb. nov., <i>Mediterraneibacter torques</i> comb. nov., <i>Mediterraneibacter gnavus</i> comb. nov. and <i>Mediterraneibacter glycyrrhizinilyticus</i> comb. nov.. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2107-2128.	0.7	87
26	The role of duplications in the evolution of genomes highlights the need for evolutionary-based approaches in comparative genomics. <i>Biology Direct</i> , 2011, 6, 11.	1.9	80
27	Multiple markers pyrosequencing reveals highly diverse and host-specific fungal communities on the mangrove trees <i>Avicennia marina</i> and <i>Rhizophora stylosa</i> . <i>FEMS Microbiology Ecology</i> , 2012, 79, 433-444.	1.3	79
28	Kaumoebavirus, a New Virus That Clusters with Faustoviruses and Asfarviridae. <i>Viruses</i> , 2016, 8, 278.	1.5	75
29	Orpheovirus IHUMI-LCC2: A New Virus among the Giant Viruses. <i>Frontiers in Microbiology</i> , 2017, 8, 2643.	1.5	70
30	Probable presence of an ubiquitous cryptic mitochondrial gene on the antisense strand of the cytochrome oxidase I gene. <i>Biology Direct</i> , 2011, 6, 56.	1.9	69
31	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3451-3456.	3.3	63
32	Exhaustive repertoire of human vaginal microbiota. <i>Human Microbiome Journal</i> , 2019, 11, 100051.	3.8	61
33	Exploring laccase-like multicopper oxidase genes from the ascomycete <i>Trichoderma reesei</i> : a functional, phylogenetic and evolutionary study. <i>BMC Biochemistry</i> , 2010, 11, 32.	4.4	60
34	Construction of Engineered Bifunctional Enzymes and Their Overproduction in <i>Aspergillus niger</i> for Improved Enzymatic Tools To Degrade Agricultural By-Products. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8132-8140.	1.4	54
35	Comparison of a Modern and Fossil Pithovirus Reveals Its Genetic Conservation and Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 2333-2339.	1.1	53
36	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015, 5, 11571.	1.6	50

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37	A Large Open Pangenome and a Small Core Genome for Giant Pandoraviruses. <i>Frontiers in Microbiology</i> , 2018, 9, 1486.	1.5	48
38	Analysis of SARS-CoV-2 Variants From 24,181 Patients Exemplifies the Role of Globalization and Zoonosis in Pandemics. <i>Frontiers in Microbiology</i> , 2021, 12, 786233.	1.5	46
39	Tracking the connection between evolutionary and functional shifts using the fungal lipase/feruloyl esterase A family. <i>BMC Evolutionary Biology</i> , 2006, 6, 92.	3.2	45
40	Production of a chimeric enzyme tool associating the <i>Trichoderma reesei</i> swollenin with the <i>Aspergillus niger</i> feruloyl esterase A for release of ferulic acid. <i>Applied Microbiology and Biotechnology</i> , 2006, 73, 872-880.	1.7	44
41	Ancestrality and Mosaicism of Giant Viruses Supporting the Definition of the Fourth TRUC of Microbes. <i>Frontiers in Microbiology</i> , 2018, 9, 2668.	1.5	44
42	Extensive culturomics of 8 healthy samples enhances metagenomics efficiency. <i>PLoS ONE</i> , 2019, 14, e0223543.	1.1	44
43	Emergence and outcomes of the SARS-CoV-2 "Marseille-4" variant. <i>International Journal of Infectious Diseases</i> , 2021, 106, 228-236.	1.5	44
44	Culture of Methanogenic Archaea from Human Colostrum and Milk. <i>Scientific Reports</i> , 2019, 9, 18653.	1.6	43
45	Homologous expression of the feruloyl esterase B gene from <i>Aspergillus niger</i> and characterization of the recombinant enzyme. <i>Protein Expression and Purification</i> , 2004, 37, 126-133.	0.6	41
46	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium <i>Treponema pallidum</i> subsp. <i>pertenue</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	3.0	41
47	Yaravirus: A novel 80-nm virus infecting <i>Acanthamoeba castellanii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16579-16586.	3.3	41
48	Bromodomain testis-specific protein is expressed in mouse oocyte and evolves faster than its ubiquitously expressed paralogs BRD2, -3, and -4. <i>Genomics</i> , 2007, 89, 215-223.	1.3	39
49	Comparative analyses of <i>Podospira anserina</i> secretomes reveal a large array of lignocellulose-active enzymes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7457-7469.	1.7	39
50	A novel glucose dehydrogenase from the white-rot fungus <i>Pycnoporus cinnabarinus</i> : production in <i>Aspergillus niger</i> and physicochemical characterization of the recombinant enzyme. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 10105-10118.	1.7	38
51	Design and Production in <i>Aspergillus niger</i> of a Chimeric Protein Associating a Fungal Feruloyl Esterase and a Clostridial Dockerin Domain. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6984-6991.	1.4	36
52	SARS-CoV-2 Infectivity and Severity of COVID-19 According to SARS-CoV-2 Variants: Current Evidence. <i>Journal of Clinical Medicine</i> , 2021, 10, 2635.	1.0	36
53	Spread of Mink SARS-CoV-2 Variants in Humans: A Model of Sarbecovirus Interspecies Evolution. <i>Frontiers in Microbiology</i> , 2021, 12, 675528.	1.5	35
54	MG-Digger: An Automated Pipeline to Search for Giant Virus-Related Sequences in Metagenomes. <i>Frontiers in Microbiology</i> , 2016, 7, 428.	1.5	34

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55	Heterologous production of cellobiose dehydrogenases from the basidiomycete <i>Coprinopsis cinerea</i> and the ascomycete <i>Podospira anserina</i> and their effect on saccharification of wheat straw. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4873-4885.	1.7	33
56	Differential Gene Expression in <i>Pycnoporus coccineus</i> during Interspecific Mycelial Interactions with Different Competitors. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6626-6636.	1.4	33
57	<i>Fournierella massiliensis</i> gen. nov., sp. nov., a new human-associated member of the family Ruminococcaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1393-1399.	0.8	33
58	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	1.5	32
59	Faustovirus E12 Transcriptome Analysis Reveals Complex Splicing in Capsid Gene. <i>Frontiers in Microbiology</i> , 2018, 9, 2534.	1.5	31
60	Introduction into the Marseille geographical area of a mild SARS-CoV-2 variant originating from sub-Saharan Africa: An investigational study. <i>Travel Medicine and Infectious Disease</i> , 2021, 40, 101980.	1.5	31
61	Paleoproteomics of the Dental Pulp: The plague paradigm. <i>PLoS ONE</i> , 2017, 12, e0180552.	1.1	31
62	Isolation of Yasminevirus, the First Member of Klosneuvirinae Isolated in Coculture with <i>Vermamoeba vermiformis</i> , Demonstrates an Extended Arsenal of Translational Apparatus Components. <i>Journal of Virology</i> , 2019, 94, .	1.5	30
63	Spreading of a new SARS-CoV-2 N501Y spike variant in a new lineage. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1352.e1-1352.e5.	2.8	30
64	Overproduction and characterization of xylanase B from <i>Aspergillus niger</i> . <i>Canadian Journal of Microbiology</i> , 2005, 51, 177-183.	0.8	29
65	Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. <i>Biological Reviews</i> , 2007, 82, 551-572.	4.7	28
66	L-lactic acid production by <i>Aspergillus brasiliensis</i> overexpressing the heterologous <i>ldha</i> gene from <i>Rhizopus oryzae</i> . <i>Microbial Cell Factories</i> , 2015, 14, 66.	1.9	28
67	Virophages of Giant Viruses: An Update at Eleven. <i>Viruses</i> , 2019, 11, 733.	1.5	28
68	A Phylogenomic Study of <i>Acanthamoeba polyphaga</i> Draft Genome Sequences Suggests Genetic Exchanges With Giant Viruses. <i>Frontiers in Microbiology</i> , 2018, 9, 2098.	1.5	27
69	Implementation of an in-house real-time reverse transcription-PCR assay for the rapid detection of the SARS-CoV-2 Marseille-4 variant. <i>Journal of Clinical Virology</i> , 2021, 139, 104814.	1.6	27
70	Integration of Evolutionary Biology Concepts for Functional Annotation and Automation of Complex Research in Evolution: The Multi-Agent Software System DAGOBAN. , 2011, , 71-87.		26
71	Non contiguous-finished genome sequence and description of <i>Microbacterium gorillae</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2016, 11, 32.	1.5	24
72	<i>Staphylococcus aureus</i> Promotes <i>Smed-PGRP-2/Smed-setd8-1</i> Methyltransferase Signalling in Planarian Neoblasts to Sensitize Anti-bacterial Gene Responses During Re-infection. <i>EBioMedicine</i> , 2017, 20, 150-160.	2.7	24

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73	Discovery and Further Studies on Giant Viruses at the IHU Mediterranean Infection That Modified the Perception of the Virophere. <i>Viruses</i> , 2019, 11, 312.	1.5	23
74	An Earliest Endosymbiont, <i>Wolbachia massiliensis</i> sp. nov., Strain PL13 from the Bed Bug (<i>Cimex</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 8064.	1.8	23
75	Clinical outcomes in patients infected with different SARS-CoV-2 variants at one hospital during three phases of the COVID-19 epidemic in Marseille, France. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105092.	1.0	22
76	First evidence of human-to-dog transmission of SARS-CoV-2 B.1.160 variant in France. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	22
77	The Rhizome of Lokiarchaeota Illustrates the Mosaicity of Archaeal Genomes. <i>Genome Biology and Evolution</i> , 2017, 9, 2635-2639.	1.1	21
78	Morphologic and Genomic Analyses of New Isolates Reveal a Second Lineage of Cedratviruses. <i>Journal of Virology</i> , 2018, 92, .	1.5	21
79	Ancestral animal genomes reconstruction. <i>Current Opinion in Immunology</i> , 2007, 19, 542-546.	2.4	20
80	Unexpected invasion of miniature inverted-repeat transposable elements in viral genomes. <i>Mobile DNA</i> , 2018, 9, 19.	1.3	20
81	<i>Vermamoeba vermiformis</i> CDC-19 draft genome sequence reveals considerable gene trafficking including with candidate phyla radiation and giant viruses. <i>Scientific Reports</i> , 2020, 10, 5928.	1.6	20
82	Adenovirus Infections in African Humans and Wild Non-Human Primates: Great Diversity and Cross-Species Transmission. <i>Viruses</i> , 2020, 12, 657.	1.5	20
83	Running after ghosts: are dead bacteria the dark matter of the human gut microbiota?. <i>Gut Microbes</i> , 2021, 13, 1-12.	4.3	20
84	Phylogeny of fungal hemoglobins and expression analysis of the <i>Aspergillus oryzae</i> flavohemoglobin gene <i>fhbA</i> during hyphal growth. <i>Fungal Biology</i> , 2010, 114, 135-143.	1.1	19
85	Phylogenomic Analysis of β -Lactamase in Archaea and Bacteria Enables the Identification of Putative New Members. <i>Genome Biology and Evolution</i> , 2018, 10, 1106-1114.	1.1	19
86	Deciphering viral presences: two novel partial giant viruses detected in marine metagenome and in a mine drainage metagenome. <i>Virology Journal</i> , 2018, 15, 66.	1.4	19
87	Guarani Virophage, a New Sputnik-Like Isolate From a Brazilian Lake. <i>Frontiers in Microbiology</i> , 2019, 10, 1003.	1.5	19
88	<i>Methanobrevibacter smithii</i> Archaemia in Febrile Patients With Bacteremia, Including Those With Endocarditis. <i>Clinical Infectious Diseases</i> , 2021, 73, e2571-e2579.	2.9	19
89	Fungal Protein Production: Design and Production of Chimeric Proteins. <i>Annual Review of Microbiology</i> , 2011, 65, 57-69.	2.9	18
90	<i>Yersinia pestis</i> halotolerance illuminates plague reservoirs. <i>Scientific Reports</i> , 2017, 7, 40022.	1.6	18

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91	Clinical outcomes in COVID-19 patients infected with different SARS-CoV-2 variants in Marseille, France. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1516.e1-1516.e6.	2.8	18
92	Parasitic Infections in African Humans and Non-Human Primates. <i>Pathogens</i> , 2020, 9, 561.	1.2	17
93	Clandestinovirus: A Giant Virus With Chromatin Proteins and a Potential to Manipulate the Cell Cycle of Its Host <i>Vermamoeba vermiformis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 715608.	1.5	17
94	Phylogeographic relationships in the polypore fungus <i>Pycnoporus</i> inferred from molecular data. <i>FEMS Microbiology Letters</i> , 2011, 325, 37-48.	0.7	16
95	<i>Mycobacterium icosiumassiliensis</i> sp. nov., a New Member in the <i>Mycobacterium terrae</i> Complex Isolated from Surface Water in Algeria. <i>Current Microbiology</i> , 2016, 73, 255-264.	1.0	16
96	Microbial Culturomics Broadens Human Vaginal Flora Diversity: Genome Sequence and Description of <i>Prevotella lascolaii</i> sp. nov. Isolated from a Patient with Bacterial Vaginosis. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 210-222.	1.0	16
97	Incomplete tricarboxylic acid cycle and proton gradient in <i>Pandoravirus massiliensis</i> : is it still a virus?. <i>ISME Journal</i> , 2022, 16, 695-704.	4.4	16
98	Strategies for Reliable Exploitation of Evolutionary Concepts in High Throughput Biology. <i>Evolutionary Bioinformatics</i> , 2008, 4, EBO.S597.	0.6	15
99	Passive Filtration, Rapid Scanning Electron Microscopy, and Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry for <i>Treponema</i> Culture and Identification from the Oral Cavity. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	14
100	Molecular Evidence of <i>Leishmania infantum</i> and <i>Leishmania guyanensis</i> in Red Howler Monkey (<i>Alouatta seniculus</i>) from French Guiana. <i>Vector-Borne and Zoonotic Diseases</i> , 2019, 19, 896-900.	0.6	14
101	Marseilleviruses: An Update in 2021. <i>Frontiers in Microbiology</i> , 2021, 12, 648731.	1.5	14
102	Genome Sequences of New Faustovirus Strains ST1 and LC9, Isolated from the South of France. <i>Genome Announcements</i> , 2017, 5, .	0.8	13
103	<i>Trichoderma reesei</i> Dehydrogenase, a Pyrroloquinoline Quinone-Dependent Member of Auxiliary Activity Family 12 of the Carbohydrate-Active Enzymes Database: Functional and Structural Characterization. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
104	Enteroviruses from Humans and Great Apes in the Republic of Congo: Recombination within Enterovirus C Serotypes. <i>Microorganisms</i> , 2020, 8, 1779.	1.6	13
105	Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clones from Wild Chimpanzees and Termites in Senegal. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0255720.	1.4	13
106	Sequential Appearance and Isolation of a SARS-CoV-2 Recombinant between Two Major SARS-CoV-2 Variants in a Chronically Infected Immunocompromised Patient. <i>Viruses</i> , 2022, 14, 1266.	1.5	13
107	Core gene-based molecular detection and identification of <i>Acanthamoeba</i> species. <i>Scientific Reports</i> , 2020, 10, 1583.	1.6	12
108	New Molecular Data on <i>Filaria</i> and its <i>Wolbachia</i> from Red Howler Monkeys (<i>Alouatta macconnelli</i>) in French Guiana—A Preliminary Study. <i>Pathogens</i> , 2020, 9, 626.	1.2	11

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109	Multidisciplinary evaluation of <i>Clostridium butyricum</i> clonality isolated from preterm neonates with necrotizing enterocolitis in South France between 2009 and 2017. <i>Scientific Reports</i> , 2019, 9, 20777.	1.6	10
110	Potential zoonotic pathogens hosted by endangered bonobos. <i>Scientific Reports</i> , 2021, 11, 6331.	1.6	10
111	CASSIOPE: An expert system for conserved regions searches. <i>BMC Bioinformatics</i> , 2009, 10, 284.	1.2	9
112	Rapid Scanning Electron Microscopy Detection and Sequencing of Severe Acute Respiratory Syndrome Coronavirus 2 and Other Respiratory Viruses. <i>Frontiers in Microbiology</i> , 2020, 11, 596180.	1.5	9
113	Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. <i>Frontiers in Microbiology</i> , 2021, 12, 719703.	1.5	9
114	Occurrence of Ten Protozoan Enteric Pathogens in Three Non-Human Primate Populations. <i>Pathogens</i> , 2021, 10, 280.	1.2	8
115	Occurrence of a substitution or deletion of SARS-CoV-2 spike amino acid 677 in various lineages in Marseille, France. <i>Virus Genes</i> , 2022, 58, 53-58.	0.7	8
116	<i>Anaerococcus urinimassiliensis</i> sp. nov., a new bacterium isolated from human urine. <i>Scientific Reports</i> , 2021, 11, 2684.	1.6	7
117	A <i>Listeria monocytogenes</i> clone in human breast milk associated with severe acute malnutrition in West Africa: A multicentric case-controlled study. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009555.	1.3	7
118	Antiviral Activity of Repurposing Ivermectin against a Panel of 30 Clinical SARS-CoV-2 Strains Belonging to 14 Variants. <i>Pharmaceuticals</i> , 2022, 15, 445.	1.7	7
119	Screening and Whole Genome Sequencing of SARS-CoV-2 Circulating During the First Three Waves of the COVID-19 Pandemic in Libreville and the Haut-Ogooué Province in Gabon. <i>Frontiers in Medicine</i> , 2022, 9, .	1.2	7
120	Was the ancestral MHC involved in innate immunity?. <i>European Journal of Immunology</i> , 2010, 40, 2682-2685.	1.6	6
121	Characterization of extracellular amylase produced by haloalkalophilic strain <i>Kocuria</i> sp. HJ014. <i>International Journal of Environmental Health Research</i> , 2016, 26, 396-404.	1.3	6
122	PCR Detection of Mimivirus. <i>Emerging Infectious Diseases</i> , 2017, 23, 1044-1045.	2.0	6
123	<i>Dysgonomonas massiliensis</i> sp. nov., a new species isolated from the human gut and its taxonogenomic description. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 935-945.	0.7	6
124	Culturing Ancient Bacteria Carrying Resistance Genes from Permafrost and Comparative Genomics with Modern Isolates. <i>Microorganisms</i> , 2020, 8, 1522.	1.6	6
125	How Tupanvirus Degrades the Ribosomal RNA of Its Amoebal Host? The Ribonuclease T2 Track. <i>Frontiers in Microbiology</i> , 2020, 11, 1691.	1.5	6
126	The Chordate Proteome History Database. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9186.	0.6	5

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127	Draft Genome Sequence of <i>Mycobacterium houstonense</i> Strain ATCC 49403 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
128	Deciphering the genomes of 16 <i>Acanthamoeba</i> species does not provide evidence of integration of known giant virus-associated mobile genetic elements. <i>Virus Research</i> , 2018, 251, 14-16.	1.1	4
129	Whole Genome Sequencing of SARS-CoV-2 Strains in COVID-19 Patients From Djibouti Shows Novel Mutations and Clades Replacing Over Time. <i>Frontiers in Medicine</i> , 2021, 8, 737602.	1.2	4
130	Investigation of a COVID-19 outbreak on the Charles de Gaulle aircraft carrier, March to April 2020: a retrospective cohort study. <i>Eurosurveillance</i> , 2022, 27, .	3.9	4
131	Draft Genome Sequence of <i>Mycobacterium boenickei</i> CIP 107829. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
132	Draft Genome Sequence of <i>Nocardia suis</i> strain S-137 (CSUR P4007). <i>Genome Announcements</i> , 2018, 6, .	0.8	3
133	<i>Mycobacterium ahvazicum</i> sp. nov., the nineteenth species of the <i>Mycobacterium simiae</i> complex. <i>Scientific Reports</i> , 2018, 8, 4138.	1.6	3
134	Dramatic HIV DNA degradation associated with spontaneous HIV suppression and disease-free outcome in a young seropositive woman following her infection. <i>Scientific Reports</i> , 2020, 10, 2548.	1.6	3
135	Isolation and genomic characterization of a new mimivirus of lineage B from a Brazilian river. <i>Archives of Virology</i> , 2020, 165, 853-863.	0.9	3
136	Host-virus interactions and defense mechanisms for giant viruses. <i>Annals of the New York Academy of Sciences</i> , 2021, 1486, 39-57.	1.8	3
137	In vitro detection of bacterial contamination in platelet concentrates by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry: a preliminary study. <i>Journal of Medical Microbiology</i> , 2017, 66, 1523-1530.	0.7	3
138	Case Report: <i>Vibrio cholerae</i> Biliary Tract Infections in Two North Africans in France. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 1306-1308.	0.6	3
139	Introduction of the SARS-CoV-2 Beta variant from Comoros into the Marseille geographical area. <i>Travel Medicine and Infectious Disease</i> , 2022, 46, 102277.	1.5	3
140	<i>Phoenicibacter congongensis</i> gen. nov., sp. nov., a new genus isolated from the human gut and its description using a taxonogenomic approach. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 775-784.	0.7	2
141	Draft Genome Sequence of <i>Mycobacterium parafortuitum</i> Strain P7335. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
142	Draft Genome Sequence of <i>Mycobacterium setense</i> CSUR47. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
143	<i>Klenkia terrae</i> resistant to DNA extraction in germ-free mice stools illustrates the extraction pitfall faced by metagenomics. <i>Scientific Reports</i> , 2020, 10, 10228.	1.6	1
144	Draft Genome Sequence of <i>Comamonas aquatilis</i> Strain LK (=CSUR P6418=CECT 9772), Isolated from the Planarian <i>Schmidtea mediterranea</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1

#	ARTICLE	IF	CITATIONS
145	An Overview of Evolutionary Biology Concepts for Functional Annotation: Advances and Challenges. , 2008, , 209-215.		1
146	Bacterial Infections in Humans and Nonhuman Primates from Africa: Expanding the Knowledge. Yale Journal of Biology and Medicine, 2021, 94, 227-248.	0.2	1
147	Draft Genome Sequence of Mycobacterium interjectum Strain ATCC 51457 T. Genome Announcements, 2016, 4, .	0.8	0
148	Draft Genome Sequence of Mycobacterium colombiense. Genome Announcements, 2017, 5, .	0.8	0
149	Complete Genome Sequence of Mycobacterium sp. Strain 3519A. Genome Announcements, 2018, 6, .	0.8	0
150	Complete Genome Sequence of <i>Mycobacterium</i> sp. Strain 4858. Genome Announcements, 2018, 6, .	0.8	0
151	Draft Genome Sequence of Mycobacterium shimoidei Strain P7336. Microbiology Resource Announcements, 2018, 7, .	0.3	0
152	Pulmonary Isolation of Multidrug resistant <i>Mycobacterium simulans</i> and <i>Mycobacterium tuberculosis</i> from a patient in the Horn of Africa. Scientific Reports, 2018, 8, 15341.	1.6	0
153	Draft Genome Sequence of Streptomyces mexicanus Strain Q0842, Isolated from Human Skin. Microbiology Resource Announcements, 2020, 9, .	0.3	0
154	Draft Genome Sequence of Comamonas jiangduensis Strain YW1 ^T . Microbiology Resource Announcements, 2021, 10, .	0.3	0
155	Draft Genome Sequence of Vogesella oryzae L3B39 ^T , Isolated from the Rhizosphere of Saline-Tolerant Pokkali Rice. Microbiology Resource Announcements, 2021, 10, .	0.3	0