

Anthony Levasseur

List of Publications by Citations

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151
papers

7,285
citations

36
h-index

83
g-index

171
ext. papers

9,528
ext. citations

6.9
avg, IF

5.68
L-index

#	Paper	IF	Citations
151	Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. <i>Biotechnology for Biofuels</i> , 2013 , 6, 41	7.8	734
150	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015 , 47, 410-5	36.3	601
149	Culture of previously uncultured members of the human gut microbiota by culturomics. <i>Nature Microbiology</i> , 2016 , 1, 16203	26.6	555
148	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, 9923-8	11.5	461
147	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010 , 28, 957-63	44.5	381
146	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012 , 3, 913	17.4	307
145	Culturing the human microbiota and culturomics. <i>Nature Reviews Microbiology</i> , 2018 , 16, 540-550	22.2	303
144	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	8.4	300
143	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	18.3	261
142	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	6	189
141	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	8.4	162
140	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, 2504-9	11.5	161
139	Tailed giant Tupanvirus possesses the most complete translational apparatus of the known virosphere. <i>Nature Communications</i> , 2018 , 9, 749	17.4	136
138	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, 638-45	3.9	105
137	Insights on the evolution of mycoparasitism from the genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 465-80	3.9	93
136	GPR50 is the mammalian ortholog of Mel1c: evidence of rapid evolution in mammals. <i>BMC Evolutionary Biology</i> , 2008 , 8, 105	3	88
135	RNA-sequencing reveals the complexities of the transcriptional response to lignocellulosic biofuel substrates in. <i>Fungal Biology and Biotechnology</i> , 2014 , 1, 1-14	7.5	83

134	Correction: GPR50 is the mammalian ortholog of Mel1c: Evidence of rapid evolution in mammals. <i>BMC Evolutionary Biology</i> , 2012 , 12, 28	3	78
133	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015 , 8, 107	7.8	74
132	Mimivirus: leading the way in the discovery of giant viruses of amoebae. <i>Nature Reviews Microbiology</i> , 2017 , 15, 243-254	22.2	72
131	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, 433-442	4.7	68
130	Fungal Strategies for Lignin Degradation. <i>Advances in Botanical Research</i> , 2012 , 61, 263-308	2.2	68
129	Characterization of salt-adapted secreted lignocellulolytic enzymes from the mangrove fungus <i>Pestalotiopsis</i> sp. <i>Nature Communications</i> , 2013 , 4, 1810	17.4	64
128	MIMIVIRE is a defence system in mimivirus that confers resistance to viroplasm. <i>Nature</i> , 2016 , 531, 249-520	52.4	63
127	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	4.5	62
126	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	7.2	60
125	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	7.2	58
124	Kaumoebavirus, a New Virus That Clusters with Faustoviruses and Asfarviridae. <i>Viruses</i> , 2016 , 8,	6.2	52
123	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, 8132-40	4.8	50
122	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	4.8	48
121	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, 3451-6	11.5	47
120	Mink, SARS-CoV-2, and the Human-Animal Interface. <i>Frontiers in Microbiology</i> , 2021 , 12, 663815	5.7	47
119	Orpheovirus IHUMI-LCC2: A New Virus among the Giant Viruses. <i>Frontiers in Microbiology</i> , 2017 , 8, 2643	5.7	46
118	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, 872-80	5.7	39
117	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, 126-33	2	38

116	Repertoire of the gut microbiota from stomach to colon using culturomics and next-generation sequencing. <i>BMC Microbiology</i> , 2018 , 18, 157	4.5	37
115	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015 , 5, 11571	4.9	36
114	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	36
113	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, 6984-91	4.8	34
112	Comparative analyses of <i>Podospora anserina</i> secretomes reveal a large array of lignocellulose-active enzymes. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 7457-69	5.7	33
111	Exhaustive repertoire of human vaginal microbiota. <i>Human Microbiome Journal</i> , 2019 , 11, 100051	5.6	32
110	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, 215-23	4.3	32
109	Heterologous production of cellobiose dehydrogenases from the basidiomycete <i>Coprinopsis cinerea</i> and the ascomycete <i>Podospora anserina</i> and their effect on saccharification of wheat straw. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 4873-85	5.7	30
108	Ancestrality and Mosaicism of Giant Viruses Supporting the Definition of the Fourth TRUC of Microbes. <i>Frontiers in Microbiology</i> , 2018 , 9, 2668	5.7	30
107	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, 157	18.9	30
106	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, 10105-18	5.7	29
105	Differential gene expression in <i>Pycnoporus coccineus</i> during interspecific mycelial interactions with different competitors. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6626-36	4.8	27
104	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	6.4	26
103	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, 551-72	13.5	26
102	Culture of Methanogenic Archaea from Human Colostrum and Milk. <i>Scientific Reports</i> , 2019 , 9, 18653	4.9	26
101	Gut Microbiota Alteration is Characterized by a Proteobacteria and Fusobacteria Bloom in Kwashiorkor and a Bacteroidetes Paucity in Marasmus. <i>Scientific Reports</i> , 2019 , 9, 9084	4.9	24
100	Comparison of a Modern and Fossil Pithovirus Reveals Its Genetic Conservation and Evolution. <i>Genome Biology and Evolution</i> , 2016 , 8, 2333-9	3.9	24
99	Integration of Evolutionary Biology Concepts for Functional Annotation and Automation of Complex Research in Evolution: The Multi-Agent Software System DAGOBAN 2011 , 71-87		24

98	MG-Digger: An Automated Pipeline to Search for Giant Virus-Related Sequences in Metagenomes. <i>Frontiers in Microbiology</i> , 2016 , 7, 428	5.7	24
97	A Large Open Pangenome and a Small Core Genome for Giant Pandoraviruses. <i>Frontiers in Microbiology</i> , 2018 , 9, 1486	5.7	23
96	Emergence and outcomes of the SARS-CoV-2 'Marseille-4' variant. <i>International Journal of Infectious Diseases</i> , 2021 , 106, 228-236	10.5	23
95	Overproduction and characterization of xylanase B from <i>Aspergillus niger</i> . <i>Canadian Journal of Microbiology</i> , 2005 , 51, 177-83	3.2	21
94	Paleoproteomics of the Dental Pulp: The plague paradigm. <i>PLoS ONE</i> , 2017 , 12, e0180552	3.7	21
93	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	8.4	21
92	A Phylogenomic Study of Draft Genome Sequences Suggests Genetic Exchanges With Giant Viruses. <i>Frontiers in Microbiology</i> , 2018 , 9, 2098	5.7	21
91	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	9.5	20
90	<i>Staphylococcus aureus</i> Promotes Smed-PGRP-2/Smed-setd8-1 Methyltransferase Signalling in Planarian Neoblasts to Sensitize Anti-bacterial Gene Responses During Re-infection. <i>EBioMedicine</i> , 2017 , 20, 150-160	8.8	19
89	Extensive culturomics of 8 healthy samples enhances metagenomics efficiency. <i>PLoS ONE</i> , 2019 , 14, e0233543	3.7	19
88	<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	3.2	19
87	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, 135-43	2.8	18
86	Ancestral animal genomes reconstruction. <i>Current Opinion in Immunology</i> , 2007 , 19, 542-6	7.8	18
85	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. Antonie van Leeuwenhoek, 2019 , 111, 2107-2128	2.1	18
84	Virophages of Giant Viruses: An Update at Eleven. <i>Viruses</i> , 2019 , 11,	6.2	17
83	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,	6.6	17
82	Yaravirus: A novel 80-nm virus infecting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16579-16586	11.5	15
81	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	6.1	15

80	Fungal protein production: design and production of chimeric proteins. <i>Annual Review of Microbiology</i> , 2011 , 65, 57-69	17.5	15
79	Discovery and Further Studies on Giant Viruses at the IHU Mediterranee Infection That Modified the Perception of the Virosphere. <i>Viruses</i> , 2019 , 11,	6.2	14
78	The Rhizome of Lokiarchaeota Illustrates the Mosaicity of Archaeal Genomes. <i>Genome Biology and Evolution</i> , 2017 , 9, 2635-2639	3.9	13
77	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020 , 27,	4.5	13
76	Morphologic and Genomic Analyses of New Isolates Reveal a Second Lineage of Cedratviruses. <i>Journal of Virology</i> , 2018 , 92,	6.6	13
75	Phylogeographic relationships in the polypore fungus <i>Pycnoporus</i> inferred from molecular data. <i>FEMS Microbiology Letters</i> , 2011 , 325, 37-48	2.9	13
74	Strategies for reliable exploitation of evolutionary concepts in high throughput biology. <i>Evolutionary Bioinformatics</i> , 2008 , 4, 121-37	1.9	13
73	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	9.5	13
72	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,	5.1	13
71	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	14.5	13
70	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	3.9	12
69	Non contiguous-finished genome sequence and description of <i>Microbacterium gorillae</i> sp. nov. <i>Standards in Genomic Sciences</i> , 2016 , 11, 32		12
68	Unexpected invasion of miniature inverted-repeat transposable elements in viral genomes. <i>Mobile DNA</i> , 2018 , 9, 19	4.4	11
67	Passive Filtration, Rapid Scanning Electron Microscopy, and Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry for Culture and Identification from the Oral Cavity. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	11
66	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	5.7	11
65	<i>Yersinia pestis</i> halotolerance illuminates plague reservoirs. <i>Scientific Reports</i> , 2017 , 7, 40022	4.9	10
64	<i>Methanobrevibacter smithii</i> Archaemia in Febrile Patients With Bacteremia, Including Those With Endocarditis. <i>Clinical Infectious Diseases</i> , 2021 , 73, e2571-e2579	11.6	10
63	Molecular Evidence of and in Red Howler Monkey () from French Guiana. <i>Vector-Borne and Zoonotic Diseases</i> , 2019 , 19, 896-900	2.4	9

62	Adenovirus Infections in African Humans and Wild Non-Human Primates: Great Diversity and Cross-Species Transmission. <i>Viruses</i> , 2020 , 12,	6.2	8
61	Genome Sequences of New Faustovirus Strains ST1 and LC9, Isolated from the South of France. <i>Genome Announcements</i> , 2017 , 5,		8
60	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	3.8	8
59	CASSIOPE: an expert system for conserved regions searches. <i>BMC Bioinformatics</i> , 2009 , 10, 284	3.6	8
58	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,	4.8	8
57	An Earliest Endosymbiont, sp. nov., Strain PL13 from the Bed Bug (), Type Strain of a New Supergroup T. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	7
56	Vermamoeba vermiformis CDC-19 draft genome sequence reveals considerable gene trafficking including with candidate phyla radiation and giant viruses. <i>Scientific Reports</i> , 2020 , 10, 5928	4.9	7
55	Spread of Mink SARS-CoV-2 Variants in Humans: A Model of Sarbecovirus Interspecies Evolution. <i>Frontiers in Microbiology</i> , 2021 , 12, 675528	5.7	7
54	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	4.5	7
53	Guarani Virophage, a New Sputnik-Like Isolate From a Brazilian Lake. <i>Frontiers in Microbiology</i> , 2019 , 10, 1003	5.7	6
52	Core gene-based molecular detection and identification of Acanthamoeba species. <i>Scientific Reports</i> , 2020 , 10, 1583	4.9	6
51	Was the ancestral MHC involved in innate immunity?. <i>European Journal of Immunology</i> , 2010 , 40, 2682-5	6.1	6
50	Genomic diversity and evolution of coronavirus (SARS-CoV-2) in France from 309 COVID-19-infected patients		6
49	Tricarboxylic acid cycle and proton gradient in Pandoravirus massiliensis: Is it still a virus?		6
48	Parasitic Infections in African Humans and Non-Human Primates. <i>Pathogens</i> , 2020 , 9,	4.5	6
47	Faustovirus E12 Transcriptome Analysis Reveals Complex Splicing in Capsid Gene. <i>Frontiers in Microbiology</i> , 2018 , 9, 2534	5.7	6
46	PCR Detection of Mimivirus. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1044-1045	10.2	5
45	The chordate proteome history database. <i>Evolutionary Bioinformatics</i> , 2012 , 8, 437-47	1.9	5

44	Mycobacterium icosiumassiliensis sp. nov., a New Member in the Mycobacterium terrae Complex Isolated from Surface Water in Algeria. <i>Current Microbiology</i> , 2016 , 73, 255-64	2.4	5
43	Multidisciplinary evaluation of Clostridium butyricum clonality isolated from preterm neonates with necrotizing enterocolitis in South France between 2009 and 2017. <i>Scientific Reports</i> , 2019 , 9, 2077	4.9	5
42	Dysgonomonas massiliensis sp. nov., a new species isolated from the human gut and its taxonogenomic description. <i>Antonie Van Leeuwenhoek</i> , 2019 , 112, 935-945	2.1	4
41	Characterization of extracellular amylase produced by haloalkalophilic strain Kocuria sp. HJ014. <i>International Journal of Environmental Health Research</i> , 2016 , 26, 396-404	3.6	4
40	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	5.7	4
39	Anaerococcus urinimassiliensis sp. nov., a new bacterium isolated from human urine. <i>Scientific Reports</i> , 2021 , 11, 2684	4.9	4
38	Multidrug-Resistant Klebsiella pneumoniae Clones from Wild Chimpanzees and Termites in Senegal. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0255720	5.9	4
37	Clandestinovirus: A Giant Virus With Chromatin Proteins and a Potential to Manipulate the Cell Cycle of Its Host. <i>Frontiers in Microbiology</i> , 2021 , 12, 715608	5.7	4
36	Analysis of SARS-CoV-2 variants from 24,181 patients exemplifies the role of globalisation and zoonosis in pandemics		4
35	Incomplete tricarboxylic acid cycle and proton gradient in Pandoravirus massiliensis: is it still a virus?. <i>ISME Journal</i> , 2021 ,	11.9	4
34	Draft Genome Sequence of CIP 107829. <i>Genome Announcements</i> , 2017 , 5,		3
33	Draft Genome Sequence of "Nocardia suismassiliense" Strain S-137 (CSUR P4007). <i>Genome Announcements</i> , 2018 , 6,		3
32	Draft Genome Sequence of Mycobacterium houstonense Strain ATCC 49403T. <i>Genome Announcements</i> , 2016 , 4,		3
31	First evidence of human-to-dog transmission of SARS-CoV-2 B.1.160 variant in France. <i>Transboundary and Emerging Diseases</i> , 2021 ,	4.2	3
30	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	3.2	3
29	A mysterious 80 nm amoeba virus with a near-complete Φ RFan genome challenges the classification of DNA viruses		3
28	Enteroviruses from Humans and Great Apes in the Republic of Congo: Recombination within Enterovirus C Serotypes. <i>Microorganisms</i> , 2020 , 8,	4.9	3
27	New Molecular Data on Filaria and its from Red Howler Monkeys () in French Guiana-A Preliminary Study. <i>Pathogens</i> , 2020 , 9,	4.5	3

26	Potential zoonotic pathogens hosted by endangered bonobos. <i>Scientific Reports</i> , 2021 , 11, 6331	4.9	3
25	Occurrence of Ten Protozoan Enteric Pathogens in Three Non-Human Primate Populations. <i>Pathogens</i> , 2021 , 10,	4.5	3
24	Phoenicibacter congonensis 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	2.1	2
23	Deciphering the genomes of 16 Acanthamoeba species does not provide evidence of integration of known giant virus-associated mobile genetic elements. <i>Virus Research</i> , 2018 , 251, 14-16	6.4	2
22	Mycobacterium ahvazicum sp. nov., the nineteenth species of the Mycobacterium simiae complex. <i>Scientific Reports</i> , 2018 , 8, 4138	4.9	2
21	Occurrence of a substitution or deletion of SARS-CoV-2 spike amino acid 677 in various lineages in Marseille, France. <i>Virus Genes</i> , 2021 , 1	2.3	2
20	Marseilleviruses: An Update in 2021. <i>Frontiers in Microbiology</i> , 2021 , 12, 648731	5.7	2
19	Full-length title: 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	4.9	1
18	Isolation and genomic characterization of a new mimivirus of lineage B from a Brazilian river. <i>Archives of Virology</i> , 2020 , 165, 853-863	2.6	1
17	The emergence, spread and vanishing of a French SARS-CoV-2 variant exemplifies the fate of RNA virus epidemics and obeys the Black Queen rule		1
16	An Overview of Evolutionary Biology Concepts for Functional Annotation: Advances and Challenges 2008 , 209-215		1
15	Culturing Ancient Bacteria Carrying Resistance Genes from Permafrost and Comparative Genomics with Modern Isolates. <i>Microorganisms</i> , 2020 , 8,	4.9	1
14	Klenkia terrae resistant to DNA extraction in germ-free mice stools illustrates the extraction pitfall faced by metagenomics. <i>Scientific Reports</i> , 2020 , 10, 10228	4.9	1
13	How Tupanvirus Degrades the Ribosomal RNA of Its Amoebal Host? The Ribonuclease T2 Track. <i>Frontiers in Microbiology</i> , 2020 , 11, 1691	5.7	1
12	Host-virus interactions and defense mechanisms for giant viruses. <i>Annals of the New York Academy of Sciences</i> , 2020 , 1486, 39	6.5	1
11	Running after ghosts: are dead bacteria the dark matter of the human gut microbiota?. <i>Gut Microbes</i> , 2021 , 13, 1-12	8.8	1
10	Draft Genome Sequence of Comamonas aquatilis Strain LK (= CSUR P6418 = CECT 9772), Isolated from the Planarian Schmidtea mediterranea. <i>Microbiology Resource Announcements</i> , 2021 , 10,	1.3	1
9	Draft Genome Sequence of Mycobacterium parafortuitum Strain P7335. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1

8	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	4.9	1
7	Antiviral Activity of Repurposing Ivermectin against a Panel of 30 Clinical SARS-CoV-2 Strains Belonging to 14 Variants.. <i>Pharmaceuticals</i> , 2022 , 15,	5.2	1
6	Introduction of the SARS-CoV-2 Beta variant from Comoros into the Marseille geographical area.. <i>Travel Medicine and Infectious Disease</i> , 2022 , 102277	8.4	0
5	Case Report: Biliary Tract Infections in Two North Africans in France. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020 , 102, 1306-1308	3.2	0
4	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	4.8	0
3	Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. <i>Frontiers in Microbiology</i> , 2021 , 12, 719703	5.7	0
2	Bacterial Infections in Humans and Nonhuman Primates from Africa: Expanding the Knowledge. <i>Yale Journal of Biology and Medicine</i> , 2021 , 94, 227-248	2.4	
1	Pulmonary Isolation of Multidrug resistant " <i>Mycobacterium simulans</i> " and <i>Mycobacterium tuberculosis</i> from a patient in the Horn of Africa. <i>Scientific Reports</i> , 2018 , 8, 15341	4.9	