

# Anthony Levasseur

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/8612414/anthony-levasseur-publications-by-year.pdf>

**Version:** 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Introduction of the SARS-CoV-2 Beta variant from Comoros into the Marseille geographical area.. <i>Travel Medicine and Infectious Disease</i> , <b>2022</b> , 102277	8.4	0
150	Antiviral Activity of Repurposing Ivermectin against a Panel of 30 Clinical SARS-CoV-2 Strains Belonging to 14 Variants.. <i>Pharmaceuticals</i> , <b>2022</b> , 15,	5.2	1
149	Analysis of SARS-CoV-2 Variants From 24,181 Patients Exemplifies the Role of Globalization and Zoonosis in Pandemics.. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 786233	5.7	11
148	Bacterial Infections in Humans and Nonhuman Primates from Africa: Expanding the Knowledge. <i>Yale Journal of Biology and Medicine</i> , <b>2021</b> , 94, 227-248	2.4	
147	Occurrence of a substitution or deletion of SARS-CoV-2 spike amino acid 677 in various lineages in Marseille, France. <i>Virus Genes</i> , <b>2021</b> , 1	2.3	2
146	First evidence of human-to-dog transmission of SARS-CoV-2 B.1.160 variant in France. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> ,	4.2	3
145	Methanobrevibacter smithii Archaemia in Febrile Patients With Bacteremia, Including Those With Endocarditis. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, e2571-e2579	11.6	10
144	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> , <b>2021</b> , 40, 101980	8.4	21
143	Potential zoonotic pathogens hosted by endangered bonobos. <i>Scientific Reports</i> , <b>2021</b> , 11, 6331	4.9	3
142	Occurrence of Ten Protozoan Enteric Pathogens in Three Non-Human Primate Populations. <i>Pathogens</i> , <b>2021</b> , 10,	4.5	3
141	Mink, SARS-CoV-2, and the Human-Animal Interface. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 663815	5.7	47
140	Clinical outcomes in COVID-19 patients infected with different SARS-CoV-2 variants in Marseille, France. <i>Clinical Microbiology and Infection</i> , <b>2021</b> , 27, 1516.e1-1516.e6	9.5	13
139	Emergence and outcomes of the SARS-CoV-2 'Marseille-4' variant. <i>International Journal of Infectious Diseases</i> , <b>2021</b> , 106, 228-236	10.5	23
138	SARS-CoV-2 Infectivity and Severity of COVID-19 According to SARS-CoV-2 Variants: Current Evidence. <i>Journal of Clinical Medicine</i> , <b>2021</b> , 10,	5.1	13
137	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> , <b>2021</b> , 139, 104814	14.5	13
136	Marseilleviruses: An Update in 2021. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 648731	5.7	2
135	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> , <b>2021</b> , 15, e0009555	4.8	0

134	Anaerococcus urinimassiliensis sp. nov., a new bacterium isolated from human urine. <i>Scientific Reports</i> , <b>2021</b> , 11, 2684	4.9	4
133	Running after ghosts: are dead bacteria the dark matter of the human gut microbiota?. <i>Gut Microbes</i> , <b>2021</b> , 13, 1-12	8.8	1
132	Draft Genome Sequence of Comamonas aquatilis Strain LK (= CSUR P6418 = CECT 9772), Isolated from the Planarian Schmidtea mediterranea. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10,	1.3	1
131	Multidrug-Resistant Klebsiella pneumoniae Clones from Wild Chimpanzees and Termites in Senegal. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65, e0255720	5.9	4
130	Clandestinovirus: A Giant Virus With Chromatin Proteins and a Potential to Manipulate the Cell Cycle of Its Host. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 715608	5.7	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> , <b>2021</b> , 8, 737602	4.9	1
128	Spreading of a new SARS-CoV-2 N501Y spike variant in a new lineage. <i>Clinical Microbiology and Infection</i> , <b>2021</b> , 27, 1352.e1-1352.e5	9.5	20
127	Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 719703	5.7	0
126	Spread of Mink SARS-CoV-2 Variants in Humans: A Model of Sarbecovirus Interspecies Evolution. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 675528	5.7	7
125	Incomplete tricarboxylic acid cycle and proton gradient in Pandoravirus massiliensis: is it still a virus?. <i>ISME Journal</i> , <b>2021</b> ,	11.9	4
124	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> , <b>2021</b> , 95, 105092	4.5	7
123	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> , <b>2020</b> , 21,	6.3	7
122	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> , <b>2020</b> , 35, 101738	8.4	300
121	Vermamoeba vermiformis CDC-19 draft genome sequence reveals considerable gene trafficking including with candidate phyla radiation and giant viruses. <i>Scientific Reports</i> , <b>2020</b> , 10, 5928	4.9	7
120	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus Pycnoporus. <i>DNA Research</i> , <b>2020</b> , 27,	4.5	13
119	Yaravirus: A novel 80-nm virus infecting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 16579-16586	11.5	15
118	Adenovirus Infections in African Humans and Wild Non-Human Primates: Great Diversity and Cross-Species Transmission. <i>Viruses</i> , <b>2020</b> , 12,	6.2	8
117	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> , <b>2020</b> , 36, 101791	8.4	162

116	Core gene-based molecular detection and identification of Acanthamoeba species. <i>Scientific Reports</i> , <b>2020</b> , 10, 1583	4.9	6
115	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> , <b>2020</b> , 10, 2548	4.9	1
114	Isolation and genomic characterization of a new mimivirus of lineage B from a Brazilian river. <i>Archives of Virology</i> , <b>2020</b> , 165, 853-863	2.6	1
113	Case Report: Biliary Tract Infections in Two North Africans in France. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2020</b> , 102, 1306-1308	3.2	0
112	Culturing Ancient Bacteria Carrying Resistance Genes from Permafrost and Comparative Genomics with Modern Isolates. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	1
111	Klenkia terrae resistant to DNA extraction in germ-free mice stools illustrates the extraction pitfall faced by metagenomics. <i>Scientific Reports</i> , <b>2020</b> , 10, 10228	4.9	1
110	Rapid Scanning Electron Microscopy Detection and Sequencing of Severe Acute Respiratory Syndrome Coronavirus 2 and Other Respiratory Viruses. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 596180	5.7	4
109	Enteroviruses from Humans and Great Apes in the Republic of Congo: Recombination within Enterovirus C Serotypes. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	3
108	Parasitic Infections in African Humans and Non-Human Primates. <i>Pathogens</i> , <b>2020</b> , 9,	4.5	6
107	How Tupanvirus Degrades the Ribosomal RNA of Its Amoebal Host? The Ribonuclease T2 Track. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1691	5.7	1
106	New Molecular Data on Filaria and its from Red Howler Monkeys () in French Guiana-A Preliminary Study. <i>Pathogens</i> , <b>2020</b> , 9,	4.5	3
105	Host-virus interactions and defense mechanisms for giant viruses. <i>Annals of the New York Academy of Sciences</i> , <b>2020</b> , 1486, 39	6.5	1
104	Phoenicibacter congolensis gen. nov., sp. nov., a new genus isolated from the human gut and its description using a taxonogenomic approach. <i>Antonie Van Leeuwenhoek</i> , <b>2019</b> , 112, 775-784	2.1	2
103	Exhaustive repertoire of human vaginal microbiota. <i>Human Microbiome Journal</i> , <b>2019</b> , 11, 100051	5.6	32
102	Dysgonomonas massiliensis sp. nov., a new species isolated from the human gut and its taxonogenomic description. <i>Antonie Van Leeuwenhoek</i> , <b>2019</b> , 112, 935-945	2.1	4
101	Gut Microbiota Alteration is Characterized by a Proteobacteria and Fusobacteria Bloom in Kwashiorkor and a Bacteroidetes Paucity in Marasmus. <i>Scientific Reports</i> , <b>2019</b> , 9, 9084	4.9	24
100	Guarani Virophage, a New Sputnik-Like Isolate From a Brazilian Lake. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1003	5.7	6
99	Discovery and Further Studies on Giant Viruses at the IHU Mediterranean Infection That Modified the Perception of the Virosphere. <i>Viruses</i> , <b>2019</b> , 11,	6.2	14

98	Virophages of Giant Viruses: An Update at Eleven. <i>Viruses</i> , <b>2019</b> , 11,	6.2	17
97	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> , <b>2019</b> , 57,	9.7	11
96	Molecular Evidence of and in Red Howler Monkey () from French Guiana. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2019</b> , 19, 896-900	2.4	9
95	Extensive culturomics of 8 healthy samples enhances metagenomics efficiency. <i>PLoS ONE</i> , <b>2019</b> , 14, e0233543	3.7	19
94	Multidisciplinary evaluation of Clostridium butyricum clonality isolated from preterm neonates with necrotizing enterocolitis in South France between 2009 and 2017. <i>Scientific Reports</i> , <b>2019</b> , 9, 2077	4.9	5
93	Isolation of Yasminevirus, the First Member of Klosneuvirinae Isolated in Coculture with Vermamoeba vermiformis, Demonstrates an Extended Arsenal of Translational Apparatus Components. <i>Journal of Virology</i> , <b>2019</b> , 94,	6.6	17
92	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> , <b>2019</b> , 85,	4.8	8
91	Culture of Methanogenic Archaea from Human Colostrum and Milk. <i>Scientific Reports</i> , <b>2019</b> , 9, 18653	4.9	26
90	Phylogenomic Analysis of $\beta$ -Lactamase in Archaea and Bacteria Enables the Identification of Putative New Members. <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 1106-1114	3.9	12
89	Tailed giant Tupanvirus possesses the most complete translational apparatus of the known virosphere. <i>Nature Communications</i> , <b>2018</b> , 9, 749	17.4	136
88	Draft Genome Sequence of "Nocardia suismassiliense" Strain S-137 (CSUR P4007). <i>Genome Announcements</i> , <b>2018</b> , 6,		3
87	Microbial Culturomics Broadens Human Vaginal Flora Diversity: Genome Sequence and Description of Prevotella lascolaii sp. nov. Isolated from a Patient with Bacterial Vaginosis. <i>OMICS A Journal of Integrative Biology</i> , <b>2018</b> , 22, 210-222	3.8	8
86	Deciphering viral presences: two novel partial giant viruses detected in marine metagenome and in a mine drainage metagenome. <i>Virology Journal</i> , <b>2018</b> , 15, 66	6.1	15
85	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> , <b>2018</b> , 251, 14-16	6.4	2
84	Morphologic and Genomic Analyses of New Isolates Reveal a Second Lineage of Cedratviruses. <i>Journal of Virology</i> , <b>2018</b> , 92,	6.6	13
83	Mycobacterium ahvazicum sp. nov., the nineteenth species of the Mycobacterium simiae complex. <i>Scientific Reports</i> , <b>2018</b> , 8, 4138	4.9	2
82	Unexpected invasion of miniature inverted-repeat transposable elements in viral genomes. <i>Mobile DNA</i> , <b>2018</b> , 9, 19	4.4	11
81	A Large Open Pangenome and a Small Core Genome for Giant Pandoraviruses. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1486	5.7	23

80	Draft Genome Sequence of Mycobacterium parafortuitum Strain P7335. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	1
79	Pulmonary Isolation of Multidrug resistant "Mycobacterium simulans" and Mycobacterium tuberculosis from a patient in the Horn of Africa. <i>Scientific Reports</i> , <b>2018</b> , 8, 15341	4.9	
78	Faustovirus E12 Transcriptome Analysis Reveals Complex Splicing in Capsid Gene. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2534	5.7	6
77	Ancestrality and Mosaicism of Giant Viruses Supporting the Definition of the Fourth TRUC of Microbes. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2668	5.7	30
76	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> , <b>2018</b> , 7, 157	18.9	30
75	Repertoire of the gut microbiota from stomach to colon using culturomics and next-generation sequencing. <i>BMC Microbiology</i> , <b>2018</b> , 18, 157	4.5	37
74	A Phylogenomic Study of Draft Genome Sequences Suggests Genetic Exchanges With Giant Viruses. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2098	5.7	21
73	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> , <b>2018</b> , 111, 2107-2128	2.1	18
72	Culturing the human microbiota and culturomics. <i>Nature Reviews Microbiology</i> , <b>2018</b> , 16, 540-550	22.2	303
71	<i>Yersinia pestis</i> halotolerance illuminates plague reservoirs. <i>Scientific Reports</i> , <b>2017</b> , 7, 40022	4.9	10
70	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , <b>2017</b> , 18, 28	18.3	261
69	Mimivirus: leading the way in the discovery of giant viruses of amoebae. <i>Nature Reviews Microbiology</i> , <b>2017</b> , 15, 243-254	22.2	72
68	Draft Genome Sequence of CIP 107829. <i>Genome Announcements</i> , <b>2017</b> , 5,		3
67	<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> , <b>2017</b> , 20, 150-160	8.8	19
66	The Rhizome of Lokiarchaeota Illustrates the Mosaicity of Archaeal Genomes. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 2635-2639	3.9	13
65	PCR Detection of Mimivirus. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 1044-1045	10.2	5
64	Genome Sequences of New Faustovirus Strains ST1 and LC9, Isolated from the South of France. <i>Genome Announcements</i> , <b>2017</b> , 5,		8
63	Orpheovirus IHUMI-LCC2: A New Virus among the Giant Viruses. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2643	5.7	46

62	Paleoproteomics of the Dental Pulp: The plague paradigm. <i>PLoS ONE</i> , <b>2017</b> , 12, e0180552	3.7	21
61	<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> , <b>2017</b> , 67, 1393-1399 <sup>2,2</sup>		19
60	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> , <b>2017</b> , 66, 1523-1530	3.2	3
59	Comparison of a Modern and Fossil Pithovirus Reveals Its Genetic Conservation and Evolution. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 2333-9	3.9	24
58	Culture of previously uncultured members of the human gut microbiota by culturomics. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16203	26.6	555
57	Draft Genome Sequence of <i>Mycobacterium houstonense</i> Strain ATCC 49403T. <i>Genome Announcements</i> , <b>2016</b> , 4,		3
56	Characterization of extracellular amylase produced by haloalkalophilic strain <i>Kocuria</i> sp. HJ014. <i>International Journal of Environmental Health Research</i> , <b>2016</b> , 26, 396-404	3.6	4
55	MIMIVIRE is a defence system in mimivirus that confers resistance to virophage. <i>Nature</i> , <b>2016</b> , 531, 249-52.4	52.4	63
54	Kaumobavirus, a New Virus That Clusters with Faustoviruses and Asfarviridae. <i>Viruses</i> , <b>2016</b> , 8,	6.2	52
53	MG-Digger: An Automated Pipeline to Search for Giant Virus-Related Sequences in Metagenomes. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 428	5.7	24
52	Non contiguous-finished genome sequence and description of <i>Microbacterium gorillae</i> sp. nov. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 32		12
51	<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> , <b>2016</b> , 73, 255-64	2.4	5
50	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> , <b>2015</b> , 112, 3451-6	11.5	47
49	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , <b>2015</b> , 47, 410-5	36.3	601
48	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , <b>2015</b> , 5, 11571	4.9	36
47	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , <b>2015</b> , 8, 107	7.8	74
46	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> , <b>2015</b> , 14, 66	6.4	26
45	Insights on the evolution of mycoparasitism from the genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 465-80	3.9	93

44	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> , <b>2014</b> , 111, 9923-8	11.5	461
43	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> , <b>2014</b> , 15, 486	4.5	62
42	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> , <b>2014</b> , 98, 10105-18	5.7	29
41	RNA-sequencing reveals the complexities of the transcriptional response to lignocellulosic biofuel substrates in. <i>Fungal Biology and Biotechnology</i> , <b>2014</b> , 1, 1-14	7.5	83
40	Comparative analyses of <i>Podospora anserina</i> secretomes reveal a large array of lignocellulose-active enzymes. <i>Applied Microbiology and Biotechnology</i> , <b>2014</b> , 98, 7457-69	5.7	33
39	Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. <i>Biotechnology for Biofuels</i> , <b>2013</b> , 6, 41	7.8	734
38	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> , <b>2013</b> , 97, 4873-85	5.7	30
37	Characterization of salt-adapted secreted lignocellulolytic enzymes from the mangrove fungus <i>Pestalotiopsis</i> sp. <i>Nature Communications</i> , <b>2013</b> , 4, 1810	17.4	64
36	Differential gene expression in <i>Pycnoporus coccineus</i> during interspecific mycelial interactions with different competitors. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 6626-36	4.8	27
35	Correction: GPR50 is the mammalian ortholog of Mel1c: Evidence of rapid evolution in mammals. <i>BMC Evolutionary Biology</i> , <b>2012</b> , 12, 28	3	78
34	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , <b>2012</b> , 3, 913	17.4	307
33	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> , <b>2012</b> , 79, 433-44	4.2	68
32	The chordate proteome history database. <i>Evolutionary Bioinformatics</i> , <b>2012</b> , 8, 437-47	1.9	5
31	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> , <b>2012</b> , 8, e1003088	6	189
30	Fungal Strategies for Lignin Degradation. <i>Advances in Botanical Research</i> , <b>2012</b> , 61, 263-308	2.2	68
29	Integration of Evolutionary Biology Concepts for Functional Annotation and Automation of Complex Research in Evolution: The Multi-Agent Software System DAGOBAN <b>2011</b> , 71-87		24
28	Fungal protein production: design and production of chimeric proteins. <i>Annual Review of Microbiology</i> , <b>2011</b> , 65, 57-69	17.5	15
27	Phylogeographic relationships in the polypore fungus <i>Pycnoporus</i> inferred from molecular data. <i>FEMS Microbiology Letters</i> , <b>2011</b> , 325, 37-48	2.9	13



26	The role of duplications in the evolution of genomes highlights the need for evolutionary-based approaches in comparative genomics. <i>Biology Direct</i> , <b>2011</b> , 6, 11	7.2	58
25	Probable presence of an ubiquitous cryptic mitochondrial gene on the antisense strand of the cytochrome oxidase I gene. <i>Biology Direct</i> , <b>2011</b> , 6, 56	7.2	60
24	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> , <b>2011</b> , 108, 2504-9	11.5	161
23	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , <b>2010</b> , 28, 957-63	44.5	381
22	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> , <b>2010</b> , 114, 135-43	2.8	18
21	Was the ancestral MHC involved in innate immunity?. <i>European Journal of Immunology</i> , <b>2010</b> , 40, 2682-5	6.1	6
20	Exploring laccase-like multicopper oxidase genes from the ascomycete <i>Trichoderma reesei</i> : a functional, phylogenetic and evolutionary study. <i>BMC Biochemistry</i> , <b>2010</b> , 11, 32	4.8	48
19	CASSIOPE: an expert system for conserved regions searches. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 284	3.6	8
18	GPR50 is the mammalian ortholog of <i>Mel1c</i> : evidence of rapid evolution in mammals. <i>BMC Evolutionary Biology</i> , <b>2008</b> , 8, 105	3	88
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> , <b>2008</b> , 45, 638-45	3.9	105
16	Strategies for reliable exploitation of evolutionary concepts in high throughput biology. <i>Evolutionary Bioinformatics</i> , <b>2008</b> , 4, 121-37	1.9	13
15	An Overview of Evolutionary Biology Concepts for Functional Annotation: Advances and Challenges <b>2008</b> , 209-215		1
14	Ancestral animal genomes reconstruction. <i>Current Opinion in Immunology</i> , <b>2007</b> , 19, 542-6	7.8	18
13	Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. <i>Biological Reviews</i> , <b>2007</b> , 82, 551-72	13.5	26
12	Bromodomain testis-specific protein is expressed in mouse oocyte and evolves faster than its ubiquitously expressed paralogs BRD2, -3, and -4. <i>Genomics</i> , <b>2007</b> , 89, 215-23	4.3	32
11	Tracking the connection between evolutionary and functional shifts using the fungal lipase/feruloyl esterase A family. <i>BMC Evolutionary Biology</i> , <b>2006</b> , 6, 92	3	36
10	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> , <b>2006</b> , 73, 872-80	5.7	39
9	Overproduction and characterization of xylanase B from <i>Aspergillus niger</i> . <i>Canadian Journal of Microbiology</i> , <b>2005</b> , 51, 177-83	3.2	21

8	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> , <b>2005</b> , 71, 8132-40	4.8	50
7	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> , <b>2004</b> , 70, 6984-91	4.8	34
6	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> , <b>2004</b> , 37, 126-33	2	38
5	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
4	A mysterious 80 nm amoeba virus with a near-complete ORFan genome challenges the classification of DNA viruses		3
3	Genomic diversity and evolution of coronavirus (SARS-CoV-2) in France from 309 COVID-19-infected patients		6
2	Tricarboxylic acid cycle and proton gradient in <i>Pandoravirus massiliensis</i> : Is it still a virus?		6
1	Analysis of SARS-CoV-2 variants from 24,181 patients exemplifies the role of globalisation and zoonosis in pandemics		4