

Andrés Moya

List of Publications by Year in descending order

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Version: 2024-02-01

486
papers

29,009
citations

6124

83
h-index

10679

143
g-index

499
all docs

499
docs citations

499
times ranked

29299
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the universal healthy human gut microbiota around the World. Computational and Structural Biotechnology Journal, 2022, 20, 421-433.	1.9	14
2	Kin recognition in <i>Drosophila</i> : rearing environment and relatedness can modulate gut microbiota and cuticular hydrocarbon odour profiles. Oikos, 2022, 2022, .	1.2	3
3	Temporal variations shape the gut microbiome ecology of the moth <i>Brithys crini</i> . Environmental Microbiology, 2022, 24, 3939-3953.	1.8	3
4	Prenatal exposure to antibiotics and risk of childhood overweight or obesity: A systematic review and meta-analysis. Obesity Reviews, 2022, 23, e13382.	3.1	4
5	Microbiota alterations in proline metabolism impact depression. Cell Metabolism, 2022, 34, 681-701.e10.	7.2	77
6	Human Follicular Mites: Ectoparasites Becoming Symbionts. Molecular Biology and Evolution, 2022, 39, .	3.5	6
7	Presence of <i>Blastocystis</i> in gut microbiota is associated with cognitive traits and decreased executive function. ISME Journal, 2022, 16, 2181-2197.	4.4	10
8	A body weight loss- and health-promoting gut microbiota is established after bariatric surgery in individuals with severe obesity. Journal of Pharmaceutical and Biomedical Analysis, 2021, 193, 113747.	1.4	14
9	Insects™ potential: Understanding the functional role of their gut microbiome. Journal of Pharmaceutical and Biomedical Analysis, 2021, 194, 113787.	1.4	32
10	Simulating the impact of non-pharmaceutical interventions limiting transmission in COVID-19 epidemics using a membrane computing model. MicroLife, 2021, 2, uqab011.	1.0	6
11	Metagenomic analysis of formalin-fixed paraffin-embedded tumor and normal mucosa reveals differences in the microbiome of colorectal cancer patients. Scientific Reports, 2021, 11, 391.	1.6	21
12	Fecal microbiota transplantation in HIV: A pilot placebo-controlled study. Nature Communications, 2021, 12, 1139.	5.8	49
13	Human Milk Virome Analysis: Changing Pattern Regarding Mode of Delivery, Birth Weight, and Lactational Stage. Nutrients, 2021, 13, 1779.	1.7	18
14	Interkingdom Gut Microbiome and Resistome of the Cockroach <i>Blattella germanica</i> . MSystems, 2021, 6, .	1.7	13
15	A Dirichlet Autoregressive Model for the Analysis of Microbiota Time-Series Data. Complexity, 2021, 2021, 1-16.	0.9	2
16	Machine learning study of the molecular drivers of natural product prices. Biofuels, Bioproducts and Biorefining, 2021, 15, 1820-1834.	1.9	1
17	Metagenomic Survey of the Highly Polyphagous <i>Anastrepha ludens</i> Developing in Ancestral and Exotic Hosts Reveals the Lack of a Stable Microbiota in Larvae and the Strong Influence of Metamorphosis on Adult Gut Microbiota. Frontiers in Microbiology, 2021, 12, 685937.	1.5	10
18	Analysis of the Microbial Intestinal Tract in Broiler Chickens during the Rearing Period. Biology, 2021, 10, 942.	1.3	10

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19	Obesity status and obesity-associated gut dysbiosis effects on hypothalamic structural covariance. <i>International Journal of Obesity</i> , 2021, , .	1.6	1
20	Obesity-associated deficits in inhibitory control are phenocopied to mice through gut microbiota changes in one-carbon and aromatic amino acids metabolic pathways. <i>Gut</i> , 2021, 70, 2283-2296.	6.1	31
21	The Metabolic Building Blocks of a Minimal Cell. <i>Biology</i> , 2021, 10, 5.	1.3	6
22	A Study of the Coevolution of Digital Organisms with an Evolutionary Cellular Automaton. <i>Biology</i> , 2021, 10, 1147.	1.3	2
23	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	1.7	40
24	Editorial: Searching for the Boundaries of Microbial Speciation in a Rapidly Evolving World. <i>Frontiers in Microbiology</i> , 2021, 12, 808595.	1.5	1
25	Detection of mixed-strain infections by FACS and ultra-low input genome sequencing. <i>Gut Microbes</i> , 2020, 11, 305-309.	4.3	4
26	Functional microbiome deficits associated with ageing: Chronological age threshold. <i>Aging Cell</i> , 2020, 19, e13063.	3.0	49
27	The Gut Microbiota Composition of the Moth <i>Brithys crini</i> Reflects Insect Metamorphosis. <i>Microbial Ecology</i> , 2020, 79, 960-970.	1.4	41
28	Obesity Impairs Short-Term and Working Memory through Gut Microbial Metabolism of Aromatic Amino Acids. <i>Cell Metabolism</i> , 2020, 32, 548-560.e7.	7.2	88
29	Effect of a Nutritional Intervention on the Intestinal Microbiota of Vertically HIV-Infected Children: The PEDIABIO Study. <i>Nutrients</i> , 2020, 12, 2112.	1.7	10
30	Salivary microbiome composition changes after bariatric surgery. <i>Scientific Reports</i> , 2020, 10, 20086.	1.6	13
31	Optimized DNA extraction and purification method for characterization of bacterial and fungal communities in lung tissue samples. <i>Scientific Reports</i> , 2020, 10, 17377.	1.6	15
32	Unveiling the power spectra of γ Scuti stars with TESS. <i>Astronomy and Astrophysics</i> , 2020, 638, A59.	2.1	18
33	Evidence for Succession and Putative Metabolic Roles of Fungi and Bacteria in the Farming Mutualism of the Ambrosia Beetle <i>Xyleborus affinis</i> . <i>MSystems</i> , 2020, 5, .	1.7	23
34	Driven progressive evolution of genome sequence complexity in Cyanobacteria. <i>Scientific Reports</i> , 2020, 10, 19073.	1.6	7
35	The Bacterial Microbiome of Meloidogyne-Based Disease Complex in Coffee and Tomato. <i>Frontiers in Plant Science</i> , 2020, 11, 136.	1.7	34
36	An update on the Symbiotic Genomes Database (SymGenDB): a collection of metadata, genomic, genetic and protein sequences, orthologs and metabolic networks of symbiotic organisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	3

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37	Unraveling Assemblage, Functions and Stability of the Gut Microbiota of <i>Blattella germanica</i> by Antibiotic Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 487.	1.5	15
38	Human milk mycobiota composition: relationship with gestational age, delivery mode, and birth weight. <i>Beneficial Microbes</i> , 2020, 11, 151-162.	1.0	18
39	Inferring Horizontal Gene Transfer with DarkHorse, Phylomizer, and ETE Toolkits. <i>Methods in Molecular Biology</i> , 2020, 2075, 355-369.	0.4	2
40	The Far Ultraviolet Variability of 29 Cygni. <i>Research Notes of the AAS</i> , 2020, 4, 26.	0.3	0
41	AB1035â€¦INTESTINAL MICROBIOTA COMPOSITION OF ADULT PATIENTS WITH FAMILIAL MEDITERRANEAN FEVER AND HEALTHY CONTROLS (THE RHEUMA-BIOTA STUDY). <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1809.2-1809.	0.5	0
42	Bacterial taxa decoupling with ageing. <i>Aging</i> , 2020, 12, 15878-15879.	1.4	0
43	Intestinal microbiota composition of patients with Behçet's disease: differences between eye, mucocutaneous and vascular involvement. The Rheuma-BIOTA study. <i>Clinical and Experimental Rheumatology</i> , 2020, 38 Suppl 127, 60-68.	0.4	4
44	Effects of Immunonutrition in Advanced Human Immunodeficiency Virus Disease: A Randomized Placebo-controlled Clinical Trial (Promaltia Study). <i>Clinical Infectious Diseases</i> , 2019, 68, 120-130.	2.9	31
45	Cross-Regional View of Functional and Taxonomic Microbiota Composition in Obesity and Post-obesity Treatment Shows Country Specific Microbial Contribution. <i>Frontiers in Microbiology</i> , 2019, 10, 2346.	1.5	17
46	Simulating Multilevel Dynamics of Antimicrobial Resistance in a Membrane Computing Model. <i>MBio</i> , 2019, 10, .	1.8	24
47	Modulation of Saliva Microbiota through Prebiotic Intervention in HIV-Infected Individuals. <i>Nutrients</i> , 2019, 11, 1346.	1.7	10
48	The Endobiota Study: Comparison of Vaginal, Cervical and Gut Microbiota Between Women with Stage 3/4 Endometriosis and Healthy Controls. <i>Scientific Reports</i> , 2019, 9, 2204.	1.6	125
49	Profiling of Protein Degradation in Cultures of Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2614.	1.5	74
50	Microbiota of sliced cooked ham packaged in modified atmosphere throughout the shelf life. <i>International Journal of Food Microbiology</i> , 2019, 289, 200-208.	2.1	35
51	Beyond cells â€“ The virome in the human holobiont. <i>Microbial Cell</i> , 2019, 6, 373-396.	1.4	17
52	Effects of HIV, antiretroviral therapy and prebiotics on the active fraction of the gut microbiota. <i>Aids</i> , 2018, 32, 1229-1237.	1.0	25
53	Elevated circulating levels of succinate in human obesity are linked to specific gut microbiota. <i>ISME Journal</i> , 2018, 12, 1642-1657.	4.4	260
54	On the thermodynamic origin of metabolic scaling. <i>Scientific Reports</i> , 2018, 8, 1448.	1.6	35

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55	Rifampicin treatment of <i>Blattella germanica</i> evidences a fecal transmission route of their gut microbiota. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	43
56	Isolation in small populations of Wayampi Amerindians promotes endemicy and homogenisation of their faecal virome, but its distribution is not entirely random. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	0
57	Experimental Epidemiology of Antibiotic Resistance: Looking for an Appropriate Animal Model System. <i>Microbiology Spectrum</i> , 2018, 6, .	1.2	5
58	<i>Tremblaya phenacola</i> PPER: an evolutionary beta-gammaproteobacterium collage. <i>ISME Journal</i> , 2018, 12, 124-135.	4.4	14
59	La ciencia y el arte desde la perspectiva de la transevoluci3n. <i>Arbor</i> , 2018, 194, 477.	0.1	0
60	Evolution of Prokaryote-Animal Endosymbiosis from a Genomics Perspective. <i>Microbiology Monographs</i> , 2018, , 223-255.	0.3	0
61	Impact of Rearing Conditions on the Ambrosia Beetle's Microbiome. <i>Life</i> , 2018, 8, 63.	1.1	18
62	Oxidative stress in the oral cavity is driven by individual-specific bacterial communities. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 29.	2.9	19
63	Impact of gaps in the asteroseismic characterization of pulsating stars. <i>Astronomy and Astrophysics</i> , 2018, 614, A40.	2.1	9
64	To B or Not to B: Comparative Genomics Suggests <i>Arsenophonus</i> as a Source of B Vitamins in Whiteflies. <i>Frontiers in Microbiology</i> , 2018, 9, 2254.	1.5	49
65	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in <i>Pneumocystis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1596-1606.	1.1	9
66	The endobiota study: comparison of vaginal, cervical and intestinal microbiota composition between women with histology proven endometriosis and healthy controls. <i>Fertility and Sterility</i> , 2018, 110, e391.	0.5	1
67	Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , 2018, 12, 1964-1976.	4.4	48
68	Time Series Analysis of the Microbiota of Children Suffering From Acute Infectious Diarrhea and Their Recovery After Treatment. <i>Frontiers in Microbiology</i> , 2018, 9, 1230.	1.5	49
69	Testing the Domino Theory of Gene Loss in <i>Buchnera aphidicola</i> : The Relevance of Epistatic Interactions. <i>Life</i> , 2018, 8, 17.	1.1	2
70	Harassment charges: Injustice done?. <i>Science</i> , 2018, 361, 655-656.	6.0	1
71	The respiratory virome in chronic obstructive pulmonary disease. <i>Future Virology</i> , 2018, 13, 457-466.	0.9	2
72	The analysis of the oral DNA virome reveals which viruses are widespread and rare among healthy young adults in Valencia (Spain). <i>PLoS ONE</i> , 2018, 13, e0191867.	1.1	33

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73	The respiratory microbiome in bronchial mucosa and secretions from severe IgE-mediated asthma patients. <i>BMC Microbiology</i> , 2017, 17, 20.	1.3	20
74	The Gut Metagenome Changes in Parallel to Waist Circumference, Brain Iron Deposition, and Cognitive Function. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 2962-2973.	1.8	40
75	Bronchial microbiome, PA biofilm-forming capacity and exacerbation in severe COPD patients colonized by <i>P. aeruginosa</i> . <i>Future Microbiology</i> , 2017, 12, 379-392.	1.0	24
76	Health and Disease Imprinted in the Time Variability of the Human Microbiome. <i>MSystems</i> , 2017, 2, .	1.7	43
77	Weighted fitness theory: an approach to symbiotic communities. <i>Environmental Microbiology Reports</i> , 2017, 9, 44-46.	1.0	2
78	The effects of prebiotics on microbial dysbiosis, butyrate production and immunity in HIV-infected subjects. <i>Mucosal Immunology</i> , 2017, 10, 1279-1293.	2.7	103
79	HIV, HPV, and microbiota. <i>Aids</i> , 2017, 31, 591-594.	1.0	29
80	Semi-empirical seismic relations of A-F stars from COROT and Kepler legacy data. <i>Monthly Notices of the Royal Astronomical Society</i> , 2017, 471, 2491-2497.	1.6	34
81	Exploring the human microbiome from multiple perspectives: factors altering its composition and function. <i>FEMS Microbiology Reviews</i> , 2017, 41, 453-478.	3.9	117
82	Antibiotic use and microbiome function. <i>Biochemical Pharmacology</i> , 2017, 134, 114-126.	2.0	240
83	Precise surface gravities of δ Scuti stars from asteroseismology. <i>Monthly Notices of the Royal Astronomical Society: Letters</i> , 2017, 471, L140-L144.	1.2	30
84	Accurate and loggof δ Sct stars using Asteroseismology. <i>EPJ Web of Conferences</i> , 2017, 160, 03003.	0.1	0
85	The genomic sequence of <i>Exiguobacterium chiriqhucha</i> str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. <i>PeerJ</i> , 2017, 5, e3162.	0.9	27
86	Impact of probiotic <i>Saccharomyces boulardii</i> on the gut microbiome composition in HIV-treated patients: A double-blind, randomised, placebo-controlled trial. <i>PLoS ONE</i> , 2017, 12, e0173802.	1.1	46
87	The Monoclonal Antitoxin Antibodies (Actoxumab/Bezlotoxumab) Treatment Facilitates Normalization of the Gut Microbiota of Mice with <i>Clostridium difficile</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 119.	1.8	26
88	Comparative Mitogenomics of Leeches (Annelida: Clitellata): Genome Conservation and Placobdella-Specific trnD Gene Duplication. <i>PLoS ONE</i> , 2016, 11, e0155441.	1.1	18
89	Gut Bacteria Metabolism Impacts Immune Recovery in HIV-infected Individuals. <i>EBioMedicine</i> , 2016, 8, 203-216.	2.7	93
90	Genetic characterization of influenza viruses from influenza-related hospital admissions in the St. Petersburg and Valencia sites of the Global Influenza Hospital Surveillance Network during the 2013/14 influenza season. <i>Journal of Clinical Virology</i> , 2016, 84, 32-38.	1.6	7

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91	HIV infection results in metabolic alterations in the gut microbiota different from those induced by other diseases. <i>Scientific Reports</i> , 2016, 6, 26192.	1.6	50
92	Active and Secretory IgA-Coated Bacterial Fractions Elucidate Dysbiosis in <i>Clostridium difficile</i> Infection. <i>MSphere</i> , 2016, 1, .	1.3	20
93	Mining metagenomic whole genome sequences revealed subdominant but constant <i>Lactobacillus</i> population in the human gut microbiota. <i>Environmental Microbiology Reports</i> , 2016, 8, 399-406.	1.0	72
94	Functional Redundancy-Induced Stability of Gut Microbiota Subjected to Disturbance. <i>Trends in Microbiology</i> , 2016, 24, 402-413.	3.5	451
95	Carriage of Enterobacteria Producing Extended-Spectrum β -Lactamases and Composition of the Gut Microbiota in an Amerindian Community. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 507-514.	1.4	37
96	A novel intracellular mutualistic bacterium in the invasive ant <i>Cardiocondyla obscurior</i> . <i>ISME Journal</i> , 2016, 10, 376-388.	4.4	67
97	Filosofía, ciencia y biología sintética. <i>Isegoria</i> , 2016, , 659.	0.1	1
98	Solving a Bloody Mess: B-Vitamin Independent Metabolic Convergence among Gammaproteobacterial Obligate Endosymbionts from Blood-Feeding Arthropods and the Leech <i>Haementeria officinalis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 2871-2884.	1.1	70
99	A membrane computing simulator of trans-hierarchical antibiotic resistance evolution dynamics in nested ecological compartments (ARES). <i>Biology Direct</i> , 2015, 10, 41.	1.9	21
100	Effect of daily intake of pomegranate juice on fecal microbiota and feces metabolites from healthy volunteers. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1942-1953.	1.5	64
101	SymbioGenomesDB: a database for the integration and access to knowledge on host-symbiont relationships. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav109.	1.4	7
102	Metagenomic Analysis of Crohn's Disease Patients Identifies Changes in the Virome and Microbiome Related to Disease Status and Therapy, and Detects Potential Interactions and Biomarkers. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 2515-2532.	0.9	79
103	Fragmentation and Coverage Variation in Viral Metagenome Assemblies, and Their Effect in Diversity Calculations. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 141.	2.0	33
104	Colonization Resistance of the Gut Microbiota against <i>Clostridium difficile</i> . <i>Antibiotics</i> , 2015, 4, 337-357.	1.5	60
105	The link between independent acquisition of intracellular gamma-endosymbionts and concerted evolution in <i>Tremblaya princeps</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 642.	1.5	18
106	Direct sequencing of human gut virome fractions obtained by flow cytometry. <i>Frontiers in Microbiology</i> , 2015, 6, 955.	1.5	18
107	<i>Clostridium difficile</i> heterogeneously impacts intestinal community architecture but drives stable metabolome responses. <i>ISME Journal</i> , 2015, 9, 2206-2220.	4.4	50
108	Identification of Xenologs and Their Characteristic Low Expression Levels in the Cyanobacterium <i>Synechococcus elongatus</i> . <i>Journal of Molecular Evolution</i> , 2015, 80, 292-304.	0.8	2

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109	Ranking the impact of human health disorders on gut metabolism: Systemic lupus erythematosus and obesity as study cases. <i>Scientific Reports</i> , 2015, 5, 8310.	1.6	68
110	Two Host Clades, Two Bacterial Arsenals: Evolution through Gene Losses in Facultative Endosymbionts. <i>Genome Biology and Evolution</i> , 2015, 7, 839-855.	1.1	26
111	Genome Evolution in the Primary Endosymbiont of Whiteflies Sheds Light on Their Divergence. <i>Genome Biology and Evolution</i> , 2015, 7, 873-888.	1.1	61
112	Diet shapes the gut microbiota of the omnivorous cockroach <i>Blattella germanica</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	113
113	The Calculus of Life. <i>SpringerBriefs in Biology</i> , 2015, , .	0.5	3
114	Reply to "Chronic Obstructive Pulmonary Disease Lung Microbiota Diversity May Be Mediated by Age or Inhaled Corticosteroid Use". <i>Journal of Clinical Microbiology</i> , 2015, 53, 1051-1051.	1.8	0
115	Gödel and the Blind Watchmaker. <i>SpringerBriefs in Biology</i> , 2015, , 73-81.	0.5	0
116	Genome reduction and potential metabolic complementation of the dual endosymbionts in the whitefly <i>Bemisia tabaci</i> . <i>BMC Genomics</i> , 2015, 16, 226.	1.2	100
117	Rapid acclimation of juvenile corals to CO ₂ -mediated acidification by upregulation of heat shock protein and Bcl-2 genes. <i>Molecular Ecology</i> , 2015, 24, 438-452.	2.0	101
118	Altered metabolism of gut microbiota contributes to chronic immune activation in HIV-infected individuals. <i>Mucosal Immunology</i> , 2015, 8, 760-772.	2.7	255
119	Functional Metagenomics of the Bronchial Microbiome in COPD. <i>PLoS ONE</i> , 2015, 10, e0144448.	1.1	40
120	Direct Sequencing from the Minimal Number of DNA Molecules Needed to Fill a 454 Picotiterplate. <i>PLoS ONE</i> , 2014, 9, e97379.	1.1	12
121	Obsolescence and Intervention: On Synthetic-Biological Entities. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 59.	2.0	2
122	Structural and functional changes in the gut microbiota associated to <i>Clostridium difficile</i> infection. <i>Frontiers in Microbiology</i> , 2014, 5, 335.	1.5	92
123	Gut microbiota disturbance during antibiotic therapy. <i>Gut Microbes</i> , 2014, 5, 64-70.	4.3	83
124	Genome Degeneration and Adaptation in a Nascent Stage of Symbiosis. <i>Genome Biology and Evolution</i> , 2014, 6, 76-93.	1.1	200
125	The Genome of <i>Cardinium</i> cBtQ1 Provides Insights into Genome Reduction, Symbiont Motility, and Its Settlement in <i>Bemisia tabaci</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 1013-1030.	1.1	68
126	Molecular evidence for ongoing complementarity and horizontal gene transfer in endosymbiotic systems of mealybugs. <i>Frontiers in Microbiology</i> , 2014, 5, 449.	1.5	12

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127	The theoretical instability strip of M dwarf stars. Monthly Notices of the Royal Astronomical Society, 2014, 438, 2371-2379.	1.6	15
128	No exception to the rule: <i>Candidatus</i> Portiera aleyrodidarum cell wall revisited. FEMS Microbiology Letters, 2014, 360, 132-136.	0.7	7
129	Severity-Related Changes of Bronchial Microbiome in Chronic Obstructive Pulmonary Disease. Journal of Clinical Microbiology, 2014, 52, 4217-4223.	1.8	181
130	Genome Sequence of Lactobacillus plantarum 19L3, a Strain Proposed as a Starter Culture for Slovensk Bryndza Ovine Cheese. Genome Announcements, 2014, 2, .	0.8	1
131	Small but Powerful, the Primary Endosymbiont of Moss Bugs, <i>Candidatus</i> Evansia muelleri, Holds a Reduced Genome with Large Biosynthetic Capabilities. Genome Biology and Evolution, 2014, 6, 1875-1893.	1.1	42
132	DNA barcodes reveal the presence of the introduced freshwater leech <i>Helobdella europaea</i> in Spain. Mitochondrial DNA, 2014, 25, 387-393.	0.6	12
133	Scanty microbes, the "symbionelle"™ concept. Environmental Microbiology, 2014, 16, 335-338.	1.8	18
134	Bronchial microbiome of severe COPD patients colonised by Pseudomonas aeruginosa. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 1101-1111.	1.3	112
135	Live Genomics for Pathogen Monitoring in Public Health. Pathogens, 2014, 3, 93-108.	1.2	4
136	Comparison of different assembly and annotation tools on analysis of simulated viral metagenomic communities in the gut. BMC Genomics, 2014, 15, 37.	1.2	73
137	Protective effect of <i>Bifidobacterium pseudocatenulatum</i> CECT7765 against induced bacterial antigen translocation in experimental cirrhosis. Liver International, 2014, 34, 850-858.	1.9	41
138	The cockroach <i>Blattella germanica</i> obtains nitrogen from uric acid through a metabolic pathway shared with its bacterial endosymbiont. Biology Letters, 2014, 10, 20140407.	1.0	50
139	Selective growth-inhibitory effect of 8-hydroxyquinoline towards Clostridium difficile and Bifidobacterium longum subsp. longum in co-culture analysed by flow cytometry. Journal of Medical Microbiology, 2014, 63, 1663-1669.	0.7	11
140	Retrospective case-control study of viral pathogen screening in proliferative verrucous leukoplakia lesions. Clinical Otolaryngology, 2014, 39, 272-280.	0.6	15
141	Plasmid Conjugation from Proteobacteria as Evidence for the Origin of Xenologous Genes in Cyanobacteria. Journal of Bacteriology, 2014, 196, 1551-1559.	1.0	15
142	Evolution of small prokaryotic genomes. Frontiers in Microbiology, 2014, 5, 742.	1.5	83
143	Measuring mean densities of <i>γ</i> Scuti stars with asteroseismology. Astronomy and Astrophysics, 2014, 563, A7.	2.1	48
144	Relating the outcome of HCV infection and different host SNP polymorphisms in a Majorcan population coinfecting with HCV-HIV and treated with pegIFN-RBV. International Microbiology, 2014, 17, 11-20.	1.1	4

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145	Succession of the gut microbiota in the cockroach <i>Blattella germanica</i> . <i>International Microbiology</i> , 2014, 17, 99-109.	1.1	61
146	Near-future reductions in pH will have no consistent ecological effects on the early life-history stages of reef corals. <i>Marine Ecology - Progress Series</i> , 2013, 486, 143-151.	0.9	26
147	Mealybugs nested endosymbiosis: going into the "matryoshka" system in <i>Planococcus citri</i> in depth. <i>BMC Microbiology</i> , 2013, 13, 74.	1.3	37
148	Molecular evolution in court: analysis of a large hepatitis C virus outbreak from an evolving source. <i>BMC Biology</i> , 2013, 11, 76.	1.7	61
149	Generalized Linear Model (GLM) framework for the association of host variables and viral strains with liver fibrosis in HCV/HIV coinfecting patients. <i>Infection, Genetics and Evolution</i> , 2013, 13, 284-291.	1.0	7
150	Instability of the faecal microbiota in diarrhoea-predominant irritable bowel syndrome. <i>FEMS Microbiology Ecology</i> , 2013, 86, 581-589.	1.3	95
151	Long-term outcome of "long-term liver transplant survivors". <i>Transplant International</i> , 2013, 26, 740-750.	0.8	53
152	Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. <i>Gut</i> , 2013, 62, 1591-1601.	6.1	488
153	Meconium microbiota types dominated by lactic acid or enteric bacteria are differentially associated with maternal eczema and respiratory problems in infants. <i>Clinical and Experimental Allergy</i> , 2013, 43, 198-211.	1.4	297
154	Study of the Viral and Microbial Communities Associated With Crohn's Disease: A Metagenomic Approach. <i>Clinical and Translational Gastroenterology</i> , 2013, 4, e36.	1.3	108
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