AndrÃ©s Moya

List of Publications by Year
in descending order

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486 papers	29,009 citations	5268 83 h-index	9345 143 g-index
499 all docs	499 docs citations	499 times ranked	26609 citing authors

#	Article	IF	Citations
1	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	5.6	913
2	The distribution of fitness effects caused by single-nucleotide substitutions in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8396-8401.	7.1	513
3	Determination of the Core of a Minimal Bacterial Gene Set. Microbiology and Molecular Biology Reviews, 2004, 68, 518-537.	6.6	503
4	Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. Gut, 2013, 62, 1591-1601.	12.1	488
5	Learning how to live together: genomic insights into prokaryoteâ€“animal symbioses. Nature Reviews Genetics, 2008, 9, 218-229.	16.3	465
6	Reductive genome evolution in Buchnera aphidicola. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 581-586.	7.1	461
7	Functional Redundancy-Induced Stability of Gut Microbiota Subjected to Disturbance. Trends in Microbiology, 2016, 24, 402-413.	7.7	451
8	Basic concepts in RNA virus evolution. FASEB Journal, 1996, 10, 859-864.	0.5	416
9	High Diversity of the Viral Community from an Antarctic Lake. Science, 2009, 326, 858-861.	12.6	392
10	Immunity and other defenses in pea aphids, Acyrthosiphon pisum. Genome Biology, 2010, 11, R21.	9.6	389
11	Transmission of Hepatitis C Virus by a Cardiac Surgeon. New England Journal of Medicine, 1996, 334, 555-561.	27.0	360
12	Natural populations of Trypanosoma cruzi, the agent of Chagas disease, have a complex multiclonal structure.. Proceedings of the National Academy of Sciences of the United States of America, 1986, 83, 115-119.	7.1	353
13	Rapid fitness losses in mammalian RNA virus clones due to Muller's ratchet.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 6015-6019.	7.1	353
14	The Gypsy Database (GyDB) of mobile genetic elements: release 2.0. Nucleic Acids Research, 2011, 39, D70-D74.	14.5	344
15	The genome sequence of Blochmannia floridanus: Comparative analysis of reduced genomes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9388-9393.	7.1	338
16	The population genetics and evolutionary epidemiology of RNA viruses. Nature Reviews Microbiology, 2004, 2, 279-288.	28.6	327
17	A Small Microbial Genome: The End of a Long Symbiotic Relationship?. Science, 2006, 314, 312-313.	12.6	309
18	Metatranscriptomic Approach to Analyze the Functional Human Gut Microbiota. PLoS ONE, 2011, 6, e17447.	2.5	302

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19	Meconium microbiota types dominated by lactic acid or enteric bacteria are differentially associated with maternal eczema and respiratory problems in infants. Clinical and Experimental Allergy, 2013, 43, 198-211.	2.9	297
20	Whole Transcriptome Analysis of the Coral Acropora millepora Reveals Complex Responses to CO₂â€driven Acidification during the Initiation of Calcification. Molecular Ecology, 2012, 21, 2440-2454.	3.9	289
21	Side-stepping secondary symbionts: widespread horizontal transfer across and beyond the Aphidoidea. Molecular Ecology, 2003, 12, 1061-1075.	3.9	286
22	Exponential increases of RNA virus fitness during large population transmissions.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5841-5844.	7.1	273
23	TheKeplercharacterization of the variability among A- and F-type stars. Astronomy and Astrophysics, 2011, 534, A125.	5.1	263
24	Elevated circulating levels of succinate in human obesity are linked to specific gut microbiota. ISME Journal, 2018, 12, 1642-1657.	9.8	260
25	Clonal Interference and the Evolution of RNA Viruses. Science, 1999, 285, 1745-1747.	12.6	257
26	Altered metabolism of gut microbiota contributes to chronic immune activation in HIV-infected individuals. Mucosal Immunology, 2015, 8, 760-772.	6.0	255
27	GroEL buffers against deleterious mutations. Nature, 2002, 417, 398-398.	27.8	241
28	Antibiotic use and microbiome function. Biochemical Pharmacology, 2017, 134, 114-126.	4.4	240
29	Genetic Lesions Associated with Muller's Ratchet in an RNA Virus. Journal of Molecular Biology, 1996, 264, 255-267.	4.2	224
30	Extreme genome reduction in Buchnera spp.: Toward the minimal genome needed for symbiotic life. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4454-4458.	7.1	221
31	The contribution of epistasis to the architecture of fitness in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15376-15379.	7.1	216
32	Serratia symbiotica from the Aphid Cinara cedri: A Missing Link from Facultative to Obligate Insect Endosymbiont. PLoS Genetics, 2011, 7, e1002357.	3.5	208
33	Genome Degeneration and Adaptation in a Nascent Stage of Symbiosis. Genome Biology and Evolution, 2014, 6, 76-93.	2.5	200
34	Differential Effects of Antibiotic Therapy on the Structure and Function of Human Gut Microbiota. PLoS ONE, 2013, 8, e80201.	2.5	194
35	Evolution of mitochondrial DNA in Drosophila subobscura. Proceedings of the National Academy of Sciences of the United States of America, 1986, 83, 8649-8653.	7.1	191
36	Microbiome Diversity in the Bronchial Tracts of Patients with Chronic Obstructive Pulmonary Disease. Journal of Clinical Microbiology, 2012, 50, 3562-3568.	3.9	181

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37	Severity-Related Changes of Bronchial Microbiome in Chronic Obstructive Pulmonary Disease. Journal of Clinical Microbiology, 2014, 52, 4217-4223.	3.9	181
38	Genetic bottlenecks and population passages cause profound fitness differences in RNA viruses. Journal of Virology, 1993, 67, 222-228.	3.4	181
39	HYBRID Î³ DORADUS-Î´ SCUTI PULSATORS: NEW INSIGHTS INTO THE PHYSICS OF THE OSCILLATIONS FROM KEPLER OBSERVATIONS. Astrophysical Journal Letters, 2010, 713, L192-L197.	8.3	179
40	Environmental distribution of prokaryotic taxa. BMC Microbiology, 2010, 10, 85.	3.3	174
41	Legionella pneumophila pangenome reveals strain-specific virulence factors. BMC Genomics, 2010, 11, 181.	2.8	161
42	The red queen reigns in the kingdom of RNA viruses.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 4821-4824.	7.1	160
43	Selection for Robustness in Mutagenized RNA Viruses. PLoS Genetics, 2007, 3, e93.	3.5	149
44	Size of genetic bottlenecks leading to virus fitness loss is determined by mean initial population fitness. Journal of Virology, 1995, 69, 2869-2872.	3.4	148
45	The evolution of RNA viruses: A population genetics view. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6967-6973.	7.1	146
46	Assessing Gut Microbial Diversity from Feces and Rectal Mucosa. Microbial Ecology, 2011, 61, 123-133.	2.8	143
47	RADIUS DETERMINATION OF SOLAR-TYPE STARS USING ASTEROSEISMOLOGY: WHAT TO EXPECT FROM THE KEPLER MISSION. Astrophysical Journal, 2009, 700, 1589-1602.	4.5	141
48	Effect of Ribavirin on the Mutation Rate and Spectrum of Hepatitis C Virus In Vivo. Journal of Virology, 2009, 83, 5760-5764.	3.4	141
49	Subclonal components of consensus fitness in an RNA virus clone. Journal of Virology, 1994, 68, 4295-4301.	3.4	136
50	Evolutionary Convergence and Nitrogen Metabolism in Blattabacterium strain Bge, Primary Endosymbiont of the Cockroach Blattella germanica. PLoS Genetics, 2009, 5, e1000721.	3.5	134
51	Contribution of Taq polymerase-induced errors to the estimation of RNA virus diversity.. Journal of General Virology, 1998, 79, 2921-2928.	2.9	132
52	A PRECISE ASTEROSEISMIC AGE AND RADIUS FOR THE EVOLVED SUN-LIKE STAR KIC 11026764. Astrophysical Journal, 2010, 723, 1583-1598.	4.5	130
53	Genome Rearrangement Distances and Gene Order Phylogeny in Î³-Proteobacteria. Molecular Biology and Evolution, 2005, 22, 1456-1467.	8.9	129
54	Network dynamics of eukaryotic LTR retroelements beyond phylogenetic trees. Biology Direct, 2009, 4, 41.	4.6	128

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55	The Endobiota Study: Comparison of Vaginal, Cervical and Gut Microbiota Between Women with Stage 3/4 Endometriosis and Healthy Controls. Scientific Reports, 2019, 9, 2204.	3.3	125
56	Genome size reduction through multiple events of gene disintegration in Buchnera APS. Trends in Genetics, 2001, 17, 615-618.	6.7	124
57	Phylogenomic Evidence for the Presence of a Flagellum and cbb3 Oxidase in the Free-Living Mitochondrial Ancestor. Molecular Biology and Evolution, 2011, 28, 3285-3296.	8.9	124
58	Large-scale gene discovery in the pea aphid Acyrthosiphon pisum (Hemiptera). Genome Biology, 2006, 7, R21.	9.6	123
59	RNA virus quasispecies: significance for viral disease and epidemiology. Infectious Agents and Disease, 1994, 3, 201-14.	1.2	121
60	Genetic diversity of Iberian populations ofBemisia tabaci(Hemiptera: Aleyrodidae) based on random amplified polymorphic DNA-polymerase chain reaction. Molecular Ecology, 2001, 10, 891-897.	3.9	119
61	Coexistence of Wolbachia with Buchnera aphidicola and a Secondary Symbiont in the Aphid Cinara cedri. Journal of Bacteriology, 2004, 186, 6626-6633.	2.2	119
62	Exploring the human microbiome from multiple perspectives: factors altering its composition and function. FEMS Microbiology Reviews, 2017, 41, 453-478.	8.6	117
63	Phylogeny of viroids, viroidlike satellite RNAs, and the viroidlike domain of hepatitis delta virus RNA.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 5631-5634.	7.1	116
64	Identification of the Weevil immune genes and their expression in the bacteriome tissue. BMC Biology, 2008, 6, 43.	3.8	114
65	Is the Quasispecies Concept Relevant to RNA Viruses?. Journal of Virology, 2002, 76, 460-462.	3.4	113
66	Diet shapes the gut microbiota of the omnivorous cockroach Blattella germanica. FEMS Microbiology Ecology, 2015, 91, .	2.7	113
67	Bronchial microbiome of severe COPD patients colonised by Pseudomonas aeruginosa. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 1101-1111.	2.9	112
68	Extreme fitness differences in mammalian and insect hosts after continuous replication of vesicular stomatitis virus in sandfly cells. Journal of Virology, 1995, 69, 6805-6809.	3.4	112
69	Study of the Viral and Microbial Communities Associated With Crohn's Disease: A Metagenomic Approach. Clinical and Translational Gastroenterology, 2013, 4, e36.	2.5	108
70	The frontier between cell and organelle: genome analysis of Candidatus Carsonella ruddii. BMC Evolutionary Biology, 2007, 7, 181.	3.2	106
71	Fitness alteration of foot-and-mouth disease virus mutants: measurement of adaptability of viral quasispecies. Journal of Virology, 1991, 65, 3954-3957.	3.4	106
72	Bacterial endosymbionts of insects: insights from comparative genomics. Environmental Microbiology, 2004, 6, 1109-1122.	3.8	104

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73	The effects of prebiotics on microbial dysbiosis, butyrate production and immunity in HIV-infected subjects. Mucosal Immunology, 2017, 10, 1279-1293.	6.0	103
74	Rapid acclimation of juvenile corals to CO₂â€mediated acidification by upregulation of heat shock protein and Bclâ€2 genes. Molecular Ecology, 2015, 24, 438-452.	3.9	101
75	Evolutionary Trajectories of Beta-Lactamase CTX-M-1 Cluster Enzymes: Predicting Antibiotic Resistance. PLoS Pathogens, 2010, 6, e1000735.	4.7	100
76	Structural alterations of faecal and mucosaâ€associated bacterial communities in irritable bowel syndrome. Environmental Microbiology Reports, 2012, 4, 242-247.	2.4	100
77	Genome reduction and potential metabolic complementation of the dual endosymbionts in the whitefly Bemisia tabaci. BMC Genomics, 2015, 16, 226.	2.8	100
78	Toward minimal bacterial cells: evolution vs. design. FEMS Microbiology Reviews, 2009, 33, 225-235.	8.6	97
79	Instability of the faecal microbiota in diarrhoea-predominant irritable bowel syndrome. FEMS Microbiology Ecology, 2013, 86, 581-589.	2.7	95
80	Gut Bacteria Metabolism Impacts Immune Recovery in HIV-infected Individuals. EBioMedicine, 2016, 8, 203-216.	6.1	93
81	Structural and functional changes in the gut microbiota associated to Clostridium difficile infection. Frontiers in Microbiology, 2014, 5, 335.	3.5	92
82	The cost of replication fidelity in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10233-10237.	7.1	91
83	The Striking Case of Tryptophan Provision in the Cedar Aphid Cinara cedri. Journal of Bacteriology, 2008, 190, 6026-6029.	2.2	91
84	The Active Human Gut Microbiota Differs from the Total Microbiota. PLoS ONE, 2011, 6, e22448.	2.5	90
85	The Evolution of the Heat-Shock Protein GroEL from Buchnera, the Primary Endosymbiont of Aphids, Is Governed by Positive Selection. Molecular Biology and Evolution, 2002, 19, 1162-1170.	8.9	88
86	Obesity Impairs Short-Term and Working Memory through Gut Microbial Metabolism of Aromatic Amino Acids. Cell Metabolism, 2020, 32, 548-560.e7.	16.2	88
87	HD 50844: a new look atÎ´Scuti stars from CoRoT space photometry. Astronomy and Astrophysics, 2009, 506, 85-93.	5.1	88
88	Analysis of and function predictions for previously conserved hypothetical or putative proteins in Blochmannia floridanus. BMC Microbiology, 2006, 6, 1.	3.3	87
89	Mitochondrial DNA evolution in experimental populations of Drosophila subobscura.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 4198-4201.	7.1	86
90	Epistasis and the Adaptability of an RNA Virus. Genetics, 2005, 170, 1001-1008.	2.9	86

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91	Molecular Basis of Adaptive Convergence in Experimental Populations of RNA Viruses. Genetics, 2002, 162, 533-542.	2.9	86
92	Discovery and molecular characterization of a plasmid localized in Buchnera sp. bacterial endosymbiont of the aphid Rhopalosiphum padi. Journal of Molecular Evolution, 1995, 41, 67-73.	1.8	85
93	Mutational and Selective Pressures on Codon and Amino Acid Usage in Buchnera, Endosymbiotic Bacteria of Aphids. Genome Research, 2003, 14, 44-53.	5.5	85
94	Asteroseismic analysis of the CoRoT Î´ Scuti star HD 174936. Astronomy and Astrophysics, 2009, 506, 79-83.	5.1	85
95	Diminishing Returns of Population Size in the Rate of RNA Virus Adaptation. Journal of Virology, 2000, 74, 3566-3571.	3.4	84
96	Gut microbiota disturbance during antibiotic therapy. Gut Microbes, 2014, 5, 64-70.	9.8	83
97	Evolution of small prokaryotic genomes. Frontiers in Microbiology, 2014, 5, 742.	3.5	83
98	Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity. Gut Microbes, 2013, 4, 306-315.	9.8	81
99	Rate of deleterious mutation and the distribution of its effects on fitness in vesicular stomatitis virus. Journal of Evolutionary Biology, 1999, 12, 1078-1088.	1.7	80
100	Why are the genomes of endosymbiotic bacteria so stable?. Trends in Genetics, 2003, 19, 176-180.	6.7	80
101	Complete Genome Sequence of â€œCandidatus Portiera aleyrodidarumâ€•BT-QVLC, an Obligate Symbiont That Supplies Amino Acids and Carotenoids to Bemisia tabaci. Journal of Bacteriology, 2012, 194, 6654-6655.	2.2	80
102	Larval stop, delayed development and survival in overcrowded cultures of Drosophila melanogaster: Effect of urea and uric acid. Journal of Insect Physiology, 1985, 31, 179-185.	2.0	79
103	Metagenomic Analysis of CrohnÊ¼s Disease Patients Identifies Changes in the Virome and Microbiome Related to Disease Status and Therapy, and Detects Potential Interactions and Biomarkers. Inflammatory Bowel Diseases, 2015, 21, 2515-2532.	1.9	79
104	Evolution of the Secondary Symbiont â€œ Candidatus Serratia symbioticaâ€•in Aphid Species of the Subfamily Lachninae. Applied and Environmental Microbiology, 2008, 74, 4236-4240.	3.1	77
105	Microbiota alterations in proline metabolism impact depression. Cell Metabolism, 2022, 34, 681-701.e10.	16.2	77
106	GroEL and the maintenance of bacterial endosymbiosis. Trends in Genetics, 2004, 20, 413-416.	6.7	76
107	Many-trillionfold amplification of single RNA virus particles fails to overcome the Muller's ratchet effect. Journal of Virology, 1993, 67, 3620-3623.	3.4	75
108	Profiling of Protein Degraders in Cultures of Human Gut Microbiota. Frontiers in Microbiology, 2019, 10, 2614.	3.5	74

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109	Genetic Variability and Antigenic Diversity of Foot-and-Mouth Disease Virus. , 1990, , 233-266.		74
110	Complete Genome Sequence of â€œCandidatus Tremblaya princepsâ€•Strain PCVAL, an Intriguing Translational Machine below the Living-Cell Status. Journal of Bacteriology, 2011, 193, 5587-5588.	2.2	73
111	Comparison of different assembly and annotation tools on analysis of simulated viral metagenomic communities in the gut. BMC Genomics, 2014, 15, 37.	2.8	73
112	Mobile genetic element proliferation and gene inactivation impact over the genome structure and metabolic capabilities of Sodalis glossinidius, the secondary endosymbiont of tsetse flies. BMC Genomics, 2010, 11, 449.	2.8	72
113	Mining metagenomic whole genome sequences revealed subdominant but constant Lactobacillus population in the human gut microbiota. Environmental Microbiology Reports, 2016, 8, 399-406.	2.4	72
114	A Sliding Window-Based Method to Detect Selective Constraints in Protein-Coding Genes and Its Application to RNA Viruses. Journal of Molecular Evolution, 2002, 55, 509-521.	1.8	71
115	Microbial Diversity in the Midguts of Field and Lab-Reared Populations of the European Corn Borer Ostrinia nubilalis. PLoS ONE, 2011, 6, e21751.	2.5	71
116	Solving a Bloody Mess: B-Vitamin Independent Metabolic Convergence among Gammaproteobacterial Obligate Endosymbionts from Blood-Feeding Arthropods and the LeechHaementeria officinalis. Genome Biology and Evolution, 2015, 7, 2871-2884.	2.5	70
117	The Haplotype Distribution of Two Genes of Citrus Tristeza Virus Is Altered after Host Change or Aphid Transmission. Virology, 1999, 255, 32-39.	2.4	69
118	The Genome of Cardinium cBtQ1 Provides Insights into Genome Reduction, Symbiont Motility, and Its Settlement in Bemisia tabaci. Genome Biology and Evolution, 2014, 6, 1013-1030.	2.5	68
119	Ranking the impact of human health disorders on gut metabolism: Systemic lupus erythematosus and obesity as study cases. Scientific Reports, 2015, 5, 8310.	3.3	68
120	Putative evolutionary origin of plasmids carrying the genes involved in leucine biosynthesis in Buchnera aphidicola (endosymbiont of aphids). Journal of Bacteriology, 1997, 179, 4768-4777.	2.2	67
121	A novel intracellular mutualistic bacterium in the invasive ant Cardiocondyla obscurior. ISME Journal, 2016, 10, 376-388.	9.8	67
122	Temperature affects the early life history stages of corals more than near future ocean acidification. Marine Ecology - Progress Series, 2013, 475, 85-92.	1.9	66
123	Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. PLoS ONE, 2011, 6, e19984.	2.5	65
124	High genetic stability in natural populations of the plant RNA virus tobacco mild green mosaic virus. Journal of Molecular Evolution, 1991, 32, 328-332.	1.8	64
125	Comparative Genomics of Blattabacterium cuenoti: The Frozen Legacy of an Ancient Endosymbiont Genome. Genome Biology and Evolution, 2013, 5, 351-361.	2.5	64
126	Effect of daily intake of pomegranate juice on fecal microbiota and feces metabolites from healthy volunteers. Molecular Nutrition and Food Research, 2015, 59, 1942-1953.	3.3	64

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127	Mapping Natural Polymorphisms of Hepatitis C virus NS3/4A Protease and Antiviral Resistance to Inhibitors in Worldwide Isolates. Antiviral Therapy, 2008, 13, 481-494.	1.0	63
128	Molecular Systematics of Aphids and Their Primary Endosymbionts. Molecular Phylogenetics and Evolution, 2001, 20, 437-449.	2.7	62
129	Age determination of the HR8799 planetary system using asteroseismology. Monthly Notices of the Royal Astronomical Society: Letters, 2010, 405, L81-L85.	3.3	61
130	Molecular evolution in court: analysis of a large hepatitis C virus outbreak from an evolving source. BMC Biology, 2013, 11, 76.	3.8	61
131	Genome Evolution in the Primary Endosymbiont of Whiteflies Sheds Light on Their Divergence. Genome Biology and Evolution, 2015, 7, 873-888.	2.5	61
132	Succession of the gut microbiota in the cockroach Blattella germanica. International Microbiology, 2014, 17, 99-109.	2.4	61
133	Molecular systematics of aphids (Homoptera: Aphididae): new insights from the long-wavelength opsin gene. Molecular Phylogenetics and Evolution, 2004, 30, 24-37.	2.7	60
134	Colonization Resistance of the Gut Microbiota against Clostridium difficile. Antibiotics, 2015, 4, 337-357.	3.7	60
135	Gene encoding capsid protein VP1 of foot-and-mouth disease virus: a quasispecies model of molecular evolution.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 6811-6815.	7.1	59
136	Molecular characterization of cyclic and obligate parthenogens in the aphid Rhopalosiphum padi (L.). Proceedings of the Royal Society B: Biological Sciences, 1996, 263, 481-486.	2.6	59
137	Genomic Determinants of Protein Folding Thermodynamics in Prokaryotic Organisms. Journal of Molecular Biology, 2004, 343, 1451-1466.	4.2	59
138	Estimating the extent of horizontal gene transfer in metagenomic sequences. BMC Genomics, 2008, 9, 136.	2.8	59
139	Sequences of isopenicillin N synthetase genes suggest horizontal gene transfer from prokaryotes to eukaryotes. Proceedings of the Royal Society B: Biological Sciences, 1990, 241, 164-169.	2.6	58
140	Evidence for Positive Selection in the Capsid Protein-Coding Region of the Foot-and-Mouth Disease Virus (FMDV) Subjected to Experimental Passage Regimens. Molecular Biology and Evolution, 2001, 18, 10-21.	8.9	58
141	New Clues about the Evolutionary History of Metabolic Losses in Bacterial Endosymbionts, Provided by the Genome of Buchnera aphidicola from the Aphid Cinara tujafilina. Applied and Environmental Microbiology, 2011, 77, 4446-4454.	3.1	57
142	Metagenomics of human microbiome: beyond 16s rDNA. Clinical Microbiology and Infection, 2012, 18, 47-49.	6.0	57
143	Genomics of intracellular symbionts in insects. International Journal of Medical Microbiology, 2010, 300, 271-278.	3.6	56
144	The ten grand challenges of synthetic life. Systems and Synthetic Biology, 2011, 5, 1-9.	1.0	54

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145	Variability and evolution of the plant RNA virus pepper mild mottle virus. Journal of Virology, 1989, 63, 2198-2203.	3.4	54
146	Evidence of Recombination in Intrapatient Populations of Hepatitis C Virus. PLoS ONE, 2008, 3, e3239.	2.5	54
147	Long-term outcome of â€˜long-term liver transplant survivorsâ€™. Transplant International, 2013, 26, 740-750.	1.6	53
148	Evolution of Fitness in Experimental Populations of Vesicular Stomatitis Virus. Genetics, 1996, 142, 673-679.	2.9	53
149	The strands of both polarities of a small circular RNA from carnation self-cleavein vitrothrough alternative double- and single-hammerhead structures. Nucleic Acids Research, 1992, 20, 6323-6329.	14.5	52
150	From Phylogenetics to Phylogenomics: The Evolutionary Relationships of Insect Endosymbiotic Î³-Proteobacteria as a Test Case. Systematic Biology, 2007, 56, 1-16.	5.6	52
151	Relationships of Gag-pol Diversity between Ty3/Gypsy and Retroviridae LTR retroelements and the three kings hypothesis. BMC Evolutionary Biology, 2008, 8, 276.	3.2	50
152	Early Progress in Aphid Genomics and Consequences for Plantâ€“Aphid Interactions Studies. Molecular Plant-Microbe Interactions, 2008, 21, 701-708.	2.6	50
153	The cockroachBlattella germanicaobtains nitrogen from uric acid through a metabolic pathway shared with its bacterial endosymbiont. Biology Letters, 2014, 10, 20140407.	2.3	50
154	Clostridium difficile heterogeneously impacts intestinal community architecture but drives stable metabolome responses. ISME Journal, 2015, 9, 2206-2220.	9.8	50
155	HIV infection results in metabolic alterations in the gut microbiota different from those induced by other diseases. Scientific Reports, 2016, 6, 26192.	3.3	50
156	EFFECT OF DELETERIOUS MUTATION-ACCUMULATION ON THE FITNESS OF RNA BACTERIOPHAGE MS2. Evolution; International Journal of Organic Evolution, 2000, 54, 686.	2.3	49
157	To B or Not to B: Comparative Genomics Suggests Arsenophonus as a Source of B Vitamins in Whiteflies. Frontiers in Microbiology, 2018, 9, 2254.	3.5	49
158	Time Series Analysis of the Microbiota of Children Suffering From Acute Infectious Diarrhea and Their Recovery After Treatment. Frontiers in Microbiology, 2018, 9, 1230.	3.5	49
159	Functional microbiome deficits associated with ageing: Chronological age threshold. Aging Cell, 2020, 19, e13063.	6.7	49
160	Fecal microbiota transplantation in HIV: A pilot placebo-controlled study. Nature Communications, 2021, 12, 1139.	12.8	49
161	Population structure and mitochondrial DNA gene flow in Old World populations of Drosophila subobscura. Heredity, 1992, 68, 15-24.	2.6	48
162	Genetic differentiation in the striped dolphin Stenella coeruleoalba from European waters according to mitochondrial DNA (mtDNA) restriction analysis. Molecular Ecology, 1999, 8, 1069-1073.	3.9	48

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163	An in-depth study of HDâ€‰174966 with CoRoT photometry and HARPS spectroscopy. Astronomy and Astrophysics, 2013, 559, A63.	5.1	48
164	Interplay between gut microbiota metabolism and inflammation in HIV infection. ISME Journal, 2018, 12, 1964-1976.	9.8	48
165	Measuring mean densities ofÎ´Scuti stars with asteroseismology. Astronomy and Astrophysics, 2014, 563, A7.	5.1	48
166	EFFECT OF DELETERIOUS MUTATION-ACCUMULATION ON THE FITNESS OF RNA BACTERIOPHAGE MS2. Evolution; International Journal of Organic Evolution, 2000, 54, 686-691.	2.3	47
167	Evolution of RNA virus in spatially structured heterogeneous environments. Journal of Evolutionary Biology, 2003, 16, 456-466.	1.7	47
168	Impact of probiotic Saccharomyces boulardii on the gut microbiome composition in HIV-treated patients: A double-blind, randomised, placebo-controlled trial. PLoS ONE, 2017, 12, e0173802.	2.5	46
169	Postsymbiotic plasmid acquisition and evolution of the repA1-replicon in Buchnera aphidicola. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10855-10860.	7.1	45
170	Phylogenetic Analysis of Viroid and Viroid-Like Satellite RNAs from Plants: A Reassessment. Journal of Molecular Evolution, 2001, 53, 155-159.	1.8	45
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