

Amparo Latorre

List of Publications by Year in descending order

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200
papers

13,621
citations

22099

59
h-index

26548

107
g-index

209
all docs

209
docs citations

209
times ranked

13882
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	2.6	913
2	Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. <i>Gut</i> , 2013, 62, 1591-1601.	6.1	488
3	Learning how to live together: genomic insights into prokaryote–animal symbioses. <i>Nature Reviews Genetics</i> , 2008, 9, 218-229.	7.7	465
4	Reductive genome evolution in <i>Buchnera aphidicola</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 581-586.	3.3	461
5	Immunity and other defenses in pea aphids, <i>Acyrtosiphon pisum</i> . <i>Genome Biology</i> , 2010, 11, R21.	13.9	389
6	The Gypsy Database (GyDB) of mobile genetic elements: release 2.0. <i>Nucleic Acids Research</i> , 2011, 39, D70-D74.	6.5	344
7	The genome sequence of <i>Blochmannia floridanus</i> : Comparative analysis of reduced genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9388-9393.	3.3	338
8	A Small Microbial Genome: The End of a Long Symbiotic Relationship?. <i>Science</i> , 2006, 314, 312-313.	6.0	309
9	A classification scheme for mobilization regions of bacterial plasmids. <i>FEMS Microbiology Reviews</i> , 2004, 28, 79-100.	3.9	308
10	Metatranscriptomic Approach to Analyze the Functional Human Gut Microbiota. <i>PLoS ONE</i> , 2011, 6, e17447.	1.1	302
11	Side-stepping secondary symbionts: widespread horizontal transfer across and beyond the Aphidoidea. <i>Molecular Ecology</i> , 2003, 12, 1061-1075.	2.0	286
12	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
13	Extreme genome reduction in <i>Buchnera</i> spp.: Toward the minimal genome needed for symbiotic life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4454-4458.	3.3	221
14	Host–based divergence in populations of the pea aphid: insights from nuclear markers and the prevalence of facultative symbionts. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1703-1712.	1.2	209
15	<i>Serratia symbiotica</i> from the Aphid <i>Cinara cedri</i> : A Missing Link from Facultative to Obligate Insect Endosymbiont. <i>PLoS Genetics</i> , 2011, 7, e1002357.	1.5	208
16	Genome Degeneration and Adaptation in a Nascent Stage of Symbiosis. <i>Genome Biology and Evolution</i> , 2014, 6, 76-93.	1.1	200
17	Differential Effects of Antibiotic Therapy on the Structure and Function of Human Gut Microbiota. <i>PLoS ONE</i> , 2013, 8, e80201.	1.1	194
18	Evolution of mitochondrial DNA in <i>Drosophila subobscura</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 8649-8653.	3.3	191

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19	Detection and Characterization of Wolbachia Infections in Natural Populations of Aphids: Is the Hidden Diversity Fully Unraveled?. PLoS ONE, 2011, 6, e28695.	1.1	166
20	Legionella pneumophila pangenome reveals strain-specific virulence factors. BMC Genomics, 2010, 11, 181.	1.2	161
21	Assessing Gut Microbial Diversity from Feces and Rectal Mucosa. Microbial Ecology, 2011, 61, 123-133.	1.4	143
22	Evolutionary Convergence and Nitrogen Metabolism in Blattabacterium strain Bge, Primary Endosymbiont of the Cockroach Blattella germanica. PLoS Genetics, 2009, 5, e1000721.	1.5	134
23	Genome size reduction through multiple events of gene disintegration in Buchnera APS. Trends in Genetics, 2001, 17, 615-618.	2.9	124
24	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.	3.5	124
25	Coexistence of Wolbachia with Buchnera aphidicola and a Secondary Symbiont in the Aphid Cinara cedri. Journal of Bacteriology, 2004, 186, 6626-6633.	1.0	119
26	Bacterial antisense RNAs are mainly the product of transcriptional noise. Science Advances, 2016, 2, e1501363.	4.7	118
27	Identification of the Weevil immune genes and their expression in the bacteriome tissue. BMC Biology, 2008, 6, 43.	1.7	114
28	Diet shapes the gut microbiota of the omnivorous cockroach Blattella germanica. FEMS Microbiology Ecology, 2015, 91, .	1.3	113
29	Reconstructing the ancestor of <i>Mycobacterium leprae</i> : The dynamics of gene loss and genome reduction. Genome Research, 2007, 17, 1178-1185.	2.4	110
30	Study of the Viral and Microbial Communities Associated With Crohn's Disease: A Metagenomic Approach. Clinical and Translational Gastroenterology, 2013, 4, e36.	1.3	108
31	The Generalist Inside the Specialist: Gut Bacterial Communities of Two Insect Species Feeding on Toxic Plants Are Dominated by Enterococcus sp.. Frontiers in Microbiology, 2016, 7, 1005.	1.5	108
32	PHYLOGENETIC EVIDENCE FOR HYBRID ORIGINS OF ASEXUAL LINEAGES IN AN APHID SPECIES. Evolution; International Journal of Organic Evolution, 2003, 57, 1291-1303.	1.1	106
33	The frontier between cell and organelle: genome analysis of Candidatus Carsonella ruddii. BMC Evolutionary Biology, 2007, 7, 181.	3.2	106
34	Bacterial endosymbionts of insects: insights from comparative genomics. Environmental Microbiology, 2004, 6, 1109-1122.	1.8	104
35	The effects of prebiotics on microbial dysbiosis, butyrate production and immunity in HIV-infected subjects. Mucosal Immunology, 2017, 10, 1279-1293.	2.7	103
36	Structural alterations of faecal and mucosa-associated bacterial communities in irritable bowel syndrome. Environmental Microbiology Reports, 2012, 4, 242-247.	1.0	100

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37	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
38	Toward minimal bacterial cells: evolution vs. design. <i>FEMS Microbiology Reviews</i> , 2009, 33, 225-235.	3.9	97
39	Instability of the faecal microbiota in diarrhoea-predominant irritable bowel syndrome. <i>FEMS Microbiology Ecology</i> , 2013, 86, 581-589.	1.3	95
40	Gut Bacteria Metabolism Impacts Immune Recovery in HIV-infected Individuals. <i>EBioMedicine</i> , 2016, 8, 203-216.	2.7	93
41	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
42	The Striking Case of Tryptophan Provision in the Cedar Aphid <i>Cinara cedri</i> . <i>Journal of Bacteriology</i> , 2008, 190, 6026-6029.	1.0	91
43	The Active Human Gut Microbiota Differs from the Total Microbiota. <i>PLoS ONE</i> , 2011, 6, e22448.	1.1	90
44	Settling Down: The Genome of <i>Serratia symbiotica</i> from the Aphid <i>Cinara tujafilina</i> Zooms in on the Process of Accommodation to a Cooperative Intracellular Life. <i>Genome Biology and Evolution</i> , 2014, 6, 1683-1698.	1.1	88
45	Dissecting genome reduction and trait loss in insect endosymbionts. <i>Annals of the New York Academy of Sciences</i> , 2017, 1389, 52-75.	1.8	87
46	Mitochondrial DNA evolution in experimental populations of <i>Drosophila subobscura</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 4198-4201.	3.3	86
47	Discovery and molecular characterization of a plasmid localized in <i>Buchnera</i> sp. bacterial endosymbiont of the aphid <i>Rhopalosiphum padi</i> . <i>Journal of Molecular Evolution</i> , 1995, 41, 67-73.	0.8	85
48	Reinventing the Wheel and Making It Round Again: Evolutionary Convergence in <i>Buchnera</i> and <i>Serratia</i> Symbiotic Consortia between the Distantly Related Lachninae Aphids <i>Tuberolachnus salignus</i> and <i>Cinara cedri</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1440-1458.	1.1	85
49	Evolution of small prokaryotic genomes. <i>Frontiers in Microbiology</i> , 2014, 5, 742.	1.5	83
50	Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity. <i>Gut Microbes</i> , 2013, 4, 306-315.	4.3	81
51	Why are the genomes of endosymbiotic bacteria so stable?. <i>Trends in Genetics</i> , 2003, 19, 176-180.	2.9	80
52	Complete Genome Sequence of <i>Candidatus Portiera aleyrodidarum</i> -BT-QVLC, an Obligate Symbiont That Supplies Amino Acids and Carotenoids to <i>Bemisia tabaci</i> . <i>Journal of Bacteriology</i> , 2012, 194, 6654-6655.	1.0	80
53	Happens in the best of subfamilies: establishment and repeated replacements of co-obligate secondary endosymbionts within Lachninae aphids. <i>Environmental Microbiology</i> , 2017, 19, 393-408.	1.8	80
54	Evolution of the Secondary Symbiont <i>Candidatus Serratia symbiotica</i> in Aphid Species of the Subfamily Lachninae. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4236-4240.	1.4	77

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55	Complete Genome Sequence of <i>Candidatus Tremblaya princeps</i> Strain PCVAL, an Intriguing Translational Machine below the Living-Cell Status. <i>Journal of Bacteriology</i> , 2011, 193, 5587-5588.	1.0	73
56	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
57	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
58	Snapshots of a shrinking partner: Genome reduction in <i>Serratia symbiotica</i> . <i>Scientific Reports</i> , 2016, 6, 32590.	1.6	68
59	Putative evolutionary origin of plasmids carrying the genes involved in leucine biosynthesis in <i>Buchnera aphidicola</i> (endosymbiont of aphids). <i>Journal of Bacteriology</i> , 1997, 179, 4768-4777.	1.0	67
60	A novel intracellular mutualistic bacterium in the invasive ant <i>Cardiocondyla obscurior</i> . <i>ISME Journal</i> , 2016, 10, 376-388.	4.4	67
61	Comparative Genomics of <i>Blattabacterium cuenoti</i> : The Frozen Legacy of an Ancient Endosymbiont Genome. <i>Genome Biology and Evolution</i> , 2013, 5, 351-361.	1.1	64
62	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
63	Molecular Systematics of Aphids and Their Primary Endosymbionts. <i>Molecular Phylogenetics and Evolution</i> , 2001, 20, 437-449.	1.2	62
64	The effect of superoxide dismutase alleles on aging in <i>Drosophila</i> . <i>Genetica</i> , 1993, 91, 143-149.	0.5	61
65	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
66	Succession of the gut microbiota in the cockroach <i>Blattella germanica</i> . <i>International Microbiology</i> , 2014, 17, 99-109.	1.1	61
67	Colonization Resistance of the Gut Microbiota against <i>Clostridium difficile</i> . <i>Antibiotics</i> , 2015, 4, 337-357.	1.5	60
68	Molecular characterization of cyclic and obligate parthenogens in the aphid <i>Rhopalosiphum padi</i> (L.). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1996, 263, 481-486.	1.2	59
69	New Clues about the Evolutionary History of Metabolic Losses in Bacterial Endosymbionts, Provided by the Genome of <i>Buchnera aphidicola</i> from the Aphid <i>Cinara tujaefilina</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 4446-4454.	1.4	57
70	Metagenomics of human microbiome: beyond 16s rDNA. <i>Clinical Microbiology and Infection</i> , 2012, 18, 47-49.	2.8	57
71	Genomics of intracellular symbionts in insects. <i>International Journal of Medical Microbiology</i> , 2010, 300, 271-278.	1.5	56
72	The Evolutionary Fate of Nonfunctional DNA in the Bacterial Endosymbiont <i>Buchnera aphidicola</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 2172-2181.	3.5	55

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73	An 18S rDNA-Based Molecular Phylogeny of Aphidiinae (Hymenoptera: Braconidae). <i>Molecular Phylogenetics and Evolution</i> , 2000, 14, 180-194.	1.2	53
74	Plasmids in the aphid endosymbiont <i>Buchnera aphidicola</i> with the smallest genomes. A puzzling evolutionary story. <i>Gene</i> , 2006, 370, 17-25.	1.0	50
75	The cockroach <i>Blattella germanica</i> obtains nitrogen from uric acid through a metabolic pathway shared with its bacterial endosymbiont. <i>Biology Letters</i> , 2014, 10, 20140407.	1.0	50
76	<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
77	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
78	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
79	Genetic differentiation in the striped dolphin <i>Stenella coeruleoalba</i> from European waters according to mitochondrial DNA (mtDNA) restriction analysis. <i>Molecular Ecology</i> , 1999, 8, 1069-1073.	2.0	48
80	Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , 2018, 12, 1964-1976.	4.4	48
81	Characterization of the length polymorphism in the A+T-rich region of the <i>Drosophila obscura</i> group species. <i>Journal of Molecular Evolution</i> , 1993, 36, 214-223.	0.8	47
82	Postsymbiotic plasmid acquisition and evolution of the repA1-replicon in <i>Buchnera aphidicola</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10855-10860.	3.3	45
83	A Genomic Reappraisal of Symbiotic Function in the Aphid/ <i>Buchnera</i> Symbiosis: Reduced Transporter Sets and Variable Membrane Organisations. <i>PLoS ONE</i> , 2011, 6, e29096.	1.1	44
84	Phylogenetic relationships of the endemic Antarctic benthic hydroids (Cnidaria, Hydrozoa): what does the mitochondrial 16S rRNA tell us about it?. <i>Polar Biology</i> , 2010, 33, 41-57.	0.5	43
85	Health and Disease Imprinted in the Time Variability of the Human Microbiome. <i>MSystems</i> , 2017, 2, .	1.7	43
86	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
87	Small but Powerful, the Primary Endosymbiont of Moss Bugs, <i>Candidatus Evansia muelleri</i> , Holds a Reduced Genome with Large Biosynthetic Capabilities. <i>Genome Biology and Evolution</i> , 2014, 6, 1875-1893.	1.1	42
88	Active and secreted IgA-coated bacterial fractions from the human gut reveal an under-represented microbiota core. <i>Scientific Reports</i> , 2013, 3, 3515.	1.6	41
89	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
90	Phylogenetic relationships of the family Campulidae (Trematoda) based on 18S rRNA sequences. <i>Parasitology</i> , 1998, 117, 383-391.	0.7	40

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91	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	1.7	40
92	The Phylogenetic Analysis of Variable-Length Sequence Data: Elongation Factorâ€™s Introns in European Populations of the Parasitoid Wasp Genus <i>Pauesia</i> (Hymenoptera: Braconidae: Aphidiinae). <i>Molecular Biology and Evolution</i> , 2001, 18, 1117-1131.	3.5	39
93	Chromosomal stasis versus plasmid plasticity in aphid endosymbiont <i>Buchnera aphidicola</i> . <i>Heredity</i> , 2005, 95, 339-347.	1.2	39
94	Structural analyses of a hypothetical minimal metabolism. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1751-1762.	1.8	39
95	Phylogeny of the <i>Drosophila obscura</i> species group deduced from mitochondrial DNA sequences. <i>Journal of Molecular Evolution</i> , 1994, 39, 478-88.	0.8	38
96	Metabolic stasis in an ancient symbiosis: genome-scale metabolic networks from two <i>Blattabacterium cuenoti</i> strains, primary endosymbionts of cockroaches. <i>BMC Microbiology</i> , 2012, 12, S5.	1.3	38
97	Plasmid-Encoded Anthranilate Synthase (TrpEG) in <i>Buchnera aphidicola</i> from Aphids of the Family Pemphigidae. <i>Applied and Environmental Microbiology</i> , 1999, 65, 117-125.	1.4	38
98	Massive presence of insertion sequences in the genome of SOPE, the primary endosymbiont of the rice weevil <i>Sitophilus oryzae</i> . <i>International Microbiology</i> , 2008, 11, 41-8.	1.1	38
99	Mealybugs nested endosymbiosis: going into the â€™matryoshkaâ€™ system in <i>Planococcus citri</i> in depth. <i>BMC Microbiology</i> , 2013, 13, 74.	1.3	37
100	Carriage of Enterobacteria Producing Extended-Spectrum Î²-Lactamases and Composition of the Gut Microbiota in an Amerindian Community. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 507-514.	1.4	37
101	Mitochondrial DNA Haplotype Frequencies in Natural and Experimental Populations of <i>Drosophila subobscura</i> . <i>Genetics</i> , 1998, 149, 1377-1382.	1.2	37
102	Molecular phylogeny of the families Campulidae and Nasitremitidae (Trematoda) based on mtDNA sequence comparisonfn1fn1Note: Nucleotide sequence data reported in this paper are available in the embl, GenBankTM and DDJB data bases under the accession numbers AF034551, AF034552, AF034553, AF034554, AF034555, AF034556 and AF034557.. <i>International Journal for Parasitology</i> , 1998, 28, 767-775.	1.3	36
103	Virulence factor rtx in <i>Legionella pneumophila</i> , evidence suggesting it is a modular multifunctional protein. <i>BMC Genomics</i> , 2008, 9, 14.	1.2	36
104	Mitochondrial Dna Variation in <i>Rhopalosiphum padi</i> (Homoptera: Aphididae) Populations from four Spanish Localities. <i>Annals of the Entomological Society of America</i> , 1992, 85, 241-246.	1.3	35
105	Genome Economization in the Endosymbiont of the Wood Roach <i>Cryptocercus punctulatus</i> Due to Drastic Loss of Amino Acid Synthesis Capabilities. <i>Genome Biology and Evolution</i> , 2011, 3, 1437-1448.	1.1	35
106	The Bacterial Microbiome of Meloidogyne-Based Disease Complex in Coffee and Tomato. <i>Frontiers in Plant Science</i> , 2020, 11, 136.	1.7	34
107	The evolutionary history of <i>Drosophila buzzatii</i> . XXX. Mitochondrial DNA polymorphism in original and colonizing populations. <i>Molecular Biology and Evolution</i> , 1996, 13, 314-323.	3.5	32
108	Insectsâ€™ potential: Understanding the functional role of their gut microbiome. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 194, 113787.	1.4	32

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109	Blattabacteria, the endosymbionts of cockroaches, have small genome sizes and high genome copy numbers. <i>Environmental Microbiology</i> , 2008, 10, 3417-3422.	1.8	31
110	Structure and evolution of the leucine plasmids carried by the endosymbiont (<i>Buchnera aphidicola</i>) from aphids of the family Aphididae. <i>FEMS Microbiology Letters</i> , 1998, 168, 43-49.	0.7	30
111	Genome reduction of the aphid endosymbiont <i>Buchnera aphidicola</i> in a recent evolutionary time scale. <i>Gene</i> , 2007, 389, 87-95.	1.0	29
112	Comparative Genomics of <i>Serratia</i> spp.: Two Paths towards Endosymbiotic Life. <i>PLoS ONE</i> , 2012, 7, e47274.	1.1	29
113	HIV, HPV, and microbiota. <i>Aids</i> , 2017, 31, 591-594.	1.0	29
114	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. <i>Molecular Biology and Evolution</i> , 2020, 37, 730-756.	3.5	29
115	Symbionts and Pathogens: What is the Difference?. <i>Current Topics in Microbiology and Immunology</i> , 2011, 358, 215-243.	0.7	27
116	The genomic sequence of <i>Exiguobacterium chiriquhucha</i> str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. <i>PeerJ</i> , 2017, 5, e3162.	0.9	27
117	Effects of <i>Bacillus thuringiensis</i> Cry1Ab and Cry3Aa endotoxins on predatory Coleoptera tested through artificial diet-incorporation bioassays. <i>Bulletin of Entomological Research</i> , 2010, 100, 297-302.	0.5	26
118	Factors Behind Junk DNA in Bacteria. <i>Genes</i> , 2012, 3, 634-650.	1.0	26
119	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
120	Comparative Molecular Evolution of Primary (<i>Buchnera</i>) and Secondary Symbionts of Aphids Based on Two Protein-Coding Genes. <i>Journal of Molecular Evolution</i> , 2002, 55, 127-137.	0.8	25
121	Unity Makes Strength: A Review on Mutualistic Symbiosis in Representative Insect Clades. <i>Life</i> , 2019, 9, 21.	1.1	25
122	Genetic differentiation between natural populations of <i>Drosophila subobscura</i> in the Western Mediterranean Area with respect to chromosomal variation. <i>Genetics Selection Evolution</i> , 1984, 16, 143.	1.2	24
123	Daily follow-up of bacterial communities in the human gut reveals stable composition and host-specific patterns of interaction. <i>FEMS Microbiology Ecology</i> , 2012, 81, 427-437.	1.3	24
124	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
125	Conservation genetics of insular <i>Podarcis</i> lizards using partial cytochrome b sequences. <i>Molecular Ecology</i> , 1998, 7, 1407-1411.	2.0	22
126	Mitochondrial DNA Divergence Suggests That <i>Podarcis hispanica atrata</i> (Squamata: Lacertidae) from the Columbretes Islands Merits Specific Distinction. <i>Copeia</i> , 1998, 1998, 1037.	1.4	22

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127	Complete Genome Sequence of <i>Acidaminococcus intestini</i> RYC-MR95, a Gram-Negative Bacterium from the Phylum Firmicutes. <i>Journal of Bacteriology</i> , 2011, 193, 7008-7009.	1.0	22
128	Selecting Microbial Strains from Pine Tree Resin: Biotechnological Applications from a Terpene World. <i>PLoS ONE</i> , 2014, 9, e100740.	1.1	21
129	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
130	Metagenomic analysis of formalin-fixed paraffin-embedded tumor and normal mucosa reveals differences in the microbiome of colorectal cancer patients. <i>Scientific Reports</i> , 2021, 11, 391.	1.6	21
131	Assessing the nucleotide diversity of three aphid species by RAPD. <i>Journal of Evolutionary Biology</i> , 1997, 10, 459.	0.8	21
132	Mitochondrial DNA variability in three Mediterranean populations of <i>Aphanius iberus</i> . <i>Biological Conservation</i> , 1995, 72, 251-256.	1.9	20
133	Molecular characterization and cytonuclear disequilibria of two <i>Drosophila subobscura</i> mitochondrial haplotypes. <i>Genome</i> , 1993, 36, 890-898.	0.9	19
134	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
135	A New Method for Extracting Skin Microbes Allows Metagenomic Analysis of Whole-Deep Skin. <i>PLoS ONE</i> , 2013, 8, e74914.	1.1	19
136	Effect of Dietary Carbohydrate Restriction on an Obesity-Related <i>Prevotella</i> -Dominated Human Fecal Microbiota. <i>Metagenomics (Cairo, Egypt)</i> , 2013, 2, 1-4.	1.2	19
137	Evolution of the Leucine Gene Cluster in <i>Buchnera aphidicola</i> : Insights from Chromosomal Versions of the Cluster. <i>Journal of Bacteriology</i> , 2004, 186, 2646-2654.	1.0	18
138	Scanty microbes, the "symbionelle"™ concept. <i>Environmental Microbiology</i> , 2014, 16, 335-338.	1.8	18
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