Amparo Latorre

List of Publications by Year
in descending order

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	Kin recognition in Drosophila: rearing environment and relatedness can modulate gut microbiota and cuticular hydrocarbon odour profiles. Oikos, 2022, 2022, .	1.2	3
2	Of Cockroaches and Symbionts: Recent Advances in the Characterization of the Relationship between Blattella germanica and Its Dual Symbiotic System. Life, 2022, 12, 290.	1.1	4
3	Temporal variations shape the gut microbiome ecology of the moth Brithys crini. Environmental Microbiology, 2022, 24, 3939-3953.	1.8	3
4	Human Follicular Mites: Ectoparasites Becoming Symbionts. Molecular Biology and Evolution, 2022, 39, .	3.5	6
5	Insectsâ€™ potential: Understanding the functional role of their gut microbiome. Journal of Pharmaceutical and Biomedical Analysis, 2021, 194, 113787.	1.4	32
6	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
7	Interkingdom Gut Microbiome and Resistome of the Cockroach Blattella germanica. MSystems, 2021, 6, .	1.7	13
8	Gut Microbiota Cannot Compensate the Impact of (quasi) Aposymbiosis in Blattella germanica. Biology, 2021, 10, 1013.	1.3	6
9	The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC Biology, 2021, 19, 241.	1.7	40
10	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	3.5	29
11	The Gut Microbiota Composition of the Moth Brithys crini Reflects Insect Metamorphosis. Microbial Ecology, 2020, 79, 960-970.	1.4	41
12	gNOMO: a multi-omics pipeline for integrated host and microbiome analysis of non-model organisms. NAR Genomics and Bioinformatics, 2020, 2, lqaa058.	1.5	5
13	Evidence for Succession and Putative Metabolic Roles of Fungi and Bacteria in the Farming Mutualism of the Ambrosia Beetle Xyleborus affinis. MSystems, 2020, 5, .	1.7	23
14	Blattella germanica displays a large arsenal of antimicrobial peptide genes. Scientific Reports, 2020, 10, 21058.	1.6	8
15	The Bacterial Microbiome of Meloidogyne-Based Disease Complex in Coffee and Tomato. Frontiers in Plant Science, 2020, 11, 136.	1.7	34
16	An update on the Symbiotic Genomes Database (SymGenDB): a collection of metadata, genomic, genetic and protein sequences, orthologs and metabolic networks of symbiotic organisms. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	3
17	Unraveling Assemblage, Functions and Stability of the Gut Microbiota of Blattella germanica by Antibiotic Treatment. Frontiers in Microbiology, 2020, 11, 487.	1.5	15
18	Inferring Horizontal Gene Transfer with DarkHorse, Phylomizer, and ETE Toolkits. Methods in Molecular Biology, 2020, 2075, 355-369.	0.4	2

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19	Wolbachia(Alphaproteobacteria: Rickettsiales) Infections in Isolated Aphid Populations from Oceanic Islands of the Azores Archipelago: Revisiting the Supergroups M and N. Environmental Entomology, 2019, 48, 326-334.	0.7	8
20	Unity Makes Strength: A Review on Mutualistic Symbiosis in Representative Insect Clades. Life, 2019, 9, 21.	1.1	25
21	Natural Occurrence of Secondary Bacterial Symbionts in Aphids from Tunisia, with a Focus on Genus Hyalopterus. Environmental Entomology, 2018, 47, 325-333.	0.7	4
22	Rifampicin treatment of Blattella germanica evidences a fecal transmission route of their gut microbiota. FEMS Microbiology Ecology, 2018, 94, .	1.3	43
23	Experimental Epidemiology of Antibiotic Resistance: Looking for an Appropriate Animal Model System. Microbiology Spectrum, 2018, 6, .	1.2	5
24	Tremblaya phenacola PPER: an evolutionary beta-gammaproteobacterium collage. ISME Journal, 2018, 12, 124-135.	4.4	14
25	Evolution of Prokaryote-Animal Endosymbiosis from a Genomics Perspective. Microbiology Monographs, 2018, , 223-255.	0.3	0
26	Oxidative stress in the oral cavity is driven by individual-specific bacterial communities. Npj Biofilms and Microbiomes, 2018, 4, 29.	2.9	19
27	To B or Not to B: Comparative Genomics Suggests Arsenophonus as a Source of B Vitamins in Whiteflies. Frontiers in Microbiology, 2018, 9, 2254.	1.5	49
28	Interplay between gut microbiota metabolism and inflammation in HIV infection. ISME Journal, 2018, 12, 1964-1976.	4.4	48
29	Health and Disease Imprinted in the Time Variability of the Human Microbiome. MSystems, 2017, 2, .	1.7	43
30	Happens in the best of subfamilies: establishment and repeated replacements of coâ€obligate secondary endosymbionts within Lachninae aphids. Environmental Microbiology, 2017, 19, 393-408.	1.8	80
31	The effects of prebiotics on microbial dysbiosis, butyrate production and immunity in HIV-infected subjects. Mucosal Immunology, 2017, 10, 1279-1293.	2.7	103
32	HIV, HPV, and microbiota. Aids, 2017, 31, 591-594.	1.0	29
33	Dissecting genome reduction and trait loss in insect endosymbionts. Annals of the New York Academy of Sciences, 2017, 1389, 52-75.	1.8	87
34	Determinism and Contingency Shape Metabolic Complementation in an Endosymbiotic Consortium. Frontiers in Microbiology, 2017, 8, 2290.	1.5	5
35	The genomic sequence ofExiguobacterium chiriqhuchastr. N139 reveals a species that thrives in cold waters and extreme environmental conditions. PeerJ, 2017, 5, e3162.	0.9	27
36	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

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37	Comparative Mitogenomics of Leeches (Annelida: Clitellata): Genome Conservation and Placobdella-Specific trnD Gene Duplication. PLoS ONE, 2016, 11, e0155441.	1.1	18
38	Gut Bacteria Metabolism Impacts Immune Recovery in HIV-infected Individuals. EBioMedicine, 2016, 8, 203-216.	2.7	93
39	Seasonal Changes in the Endosymbiotic Consortia of Aphids from the Genus <i>Cinara</i>. Microbes and Environments, 2016, 31, 137-144.	0.7	5
40	HIV infection results in metabolic alterations in the gut microbiota different from those induced by other diseases. Scientific Reports, 2016, 6, 26192.	1.6	50
41	Bacterial antisense RNAs are mainly the product of transcriptional noise. Science Advances, 2016, 2, e1501363.	4.7	118
42	Snapshots of a shrinking partner: Genome reduction in Serratia symbiotica. Scientific Reports, 2016, 6, 32590.	1.6	68
43	Reinventing the Wheel and Making It Round Again: Evolutionary Convergence inBuchneraâ€“SerratiaSymbiotic Consortia between the Distantly Related Lachninae AphidsTuberolachnus salignusandCinara cedri. Genome Biology and Evolution, 2016, 8, 1440-1458.	1.1	85
44	Carriage of Enterobacteria Producing Extended-Spectrum Î²-Lactamases and Composition of the Gut Microbiota in an Amerindian Community. Antimicrobial Agents and Chemotherapy, 2016, 60, 507-514.	1.4	37
45	A novel intracellular mutualistic bacterium in the invasive ant Cardiocondyla obscurior. ISME Journal, 2016, 10, 376-388.	4.4	67
46	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.	1.1	70
47	A membrane computing simulator of trans-hierarchical antibiotic resistance evolution dynamics in nested ecological compartments (ARES). Biology Direct, 2015, 10, 41.	1.9	21
48	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.	1.5	64
49	SymbioGenomesDB: a database for the integration and access to knowledge on hostâ€“symbiont relationships. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav109.	1.4	7
50	Colonization Resistance of the Gut Microbiota against Clostridium difficile. Antibiotics, 2015, 4, 337-357.	1.5	60
51	The link between independent acquisition of intracellular gamma-endosymbionts and concerted evolution in Tremblaya princeps. Frontiers in Microbiology, 2015, 6, 642.	1.5	18
52	Clostridium difficile heterogeneously impacts intestinal community architecture but drives stable metabolome responses. ISME Journal, 2015, 9, 2206-2220.	4.4	50
53	Two Host Clades, Two Bacterial Arsenals: Evolution through Gene Losses in Facultative Endosymbionts. Genome Biology and Evolution, 2015, 7, 839-855.	1.1	26
54	Genome Evolution in the Primary Endosymbiont of Whiteflies Sheds Light on Their Divergence. Genome Biology and Evolution, 2015, 7, 873-888.	1.1	61

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55	Diet shapes the gut microbiota of the omnivorous cockroach Blattella germanica. FEMS Microbiology Ecology, 2015, 91, .	1.3	113
56	Genome reduction and potential metabolic complementation of the dual endosymbionts in the whitefly Bemisia tabaci. BMC Genomics, 2015, 16, 226.	1.2	100
57	Altered metabolism of gut microbiota contributes to chronic immune activation in HIV-infected individuals. Mucosal Immunology, 2015, 8, 760-772.	2.7	255
58	Endosymbiosis. , 2015, , 733-734.		0
59	Selecting Microbial Strains from Pine Tree Resin: Biotechnological Applications from a Terpene World. PLoS ONE, 2014, 9, e100740.	1.1	21
60	Structural and functional changes in the gut microbiota associated to Clostridium difficile infection. Frontiers in Microbiology, 2014, 5, 335.	1.5	92
61	Genome Degeneration and Adaptation in a Nascent Stage of Symbiosis. Genome Biology and Evolution, 2014, 6, 76-93.	1.1	200
62	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.	1.1	68
63	Molecular evidence for ongoing complementarity and horizontal gene transfer in endosymbiotic systems of mealybugs. Frontiers in Microbiology, 2014, 5, 449.	1.5	12
64	No exception to the rule:CandidatusPortiera aleyrodidarum cell wall revisited. FEMS Microbiology Letters, 2014, 360, 132-136.	0.7	7
65	Settling Down: The Genome of Serratia symbiotica from the Aphid Cinara tujafilina Zooms in on the Process of Accommodation to a Cooperative Intracellular Life. Genome Biology and Evolution, 2014, 6, 1683-1698.	1.1	88
66	Small but Powerful, the Primary Endosymbiont of Moss Bugs, Candidatus Evansia muelleri, Holds a Reduced Genome with Large Biosynthetic Capabilities. Genome Biology and Evolution, 2014, 6, 1875-1893.	1.1	42
67	DNA barcodes reveal the presence of the introduced freshwater leechHelobdella europaeain Spain. Mitochondrial DNA, 2014, 25, 387-393.	0.6	12
68	Scanty microbes, the â€˜symbionelleâ€™ concept. Environmental Microbiology, 2014, 16, 335-338.	1.8	18
69	The cockroachBlattella germanicaobtains nitrogen from uric acid through a metabolic pathway shared with its bacterial endosymbiont. Biology Letters, 2014, 10, 20140407.	1.0	50
70	Evolution of small prokaryotic genomes. Frontiers in Microbiology, 2014, 5, 742.	1.5	83
71	Succession of the gut microbiota in the cockroach Blattella germanica. International Microbiology, 2014, 17, 99-109.	1.1	61
72	Mealybugs nested endosymbiosis: going into the â€˜matryoshkaâ€™ system in Planococcus citri in depth. BMC Microbiology, 2013, 13, 74.	1.3	37

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73	Instability of the faecal microbiota in diarrhoea-predominant irritable bowel syndrome. FEMS Microbiology Ecology, 2013, 86, 581-589.	1.3	95
74	Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. Gut, 2013, 62, 1591-1601.	6.1	488
75	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
76	Comparative Genomics of Blattabacterium cuenoti: The Frozen Legacy of an Ancient Endosymbiont Genome. Genome Biology and Evolution, 2013, 5, 351-361.	1.1	64
77	Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity. Gut Microbes, 2013, 4, 306-315.	4.3	81
78	Active and secreted IgA-coated bacterial fractions from the human gut reveal an under-represented microbiota core. Scientific Reports, 2013, 3, 3515.	1.6	41
79	What Symbionts Teach us about Modularity. Frontiers in Bioengineering and Biotechnology, 2013, 1, 14.	2.0	11
80	Differential Effects of Antibiotic Therapy on the Structure and Function of Human Gut Microbiota. PLoS ONE, 2013, 8, e80201.	1.1	194
81	A New Method for Extracting Skin Microbes Allows Metagenomic Analysis of Whole-Deep Skin. PLoS ONE, 2013, 8, e74914.	1.1	19
82	How Does Tremblaya princeps Get Essential Proteins from Its Nested Partner Moranella endobia in the Mealybug Planoccocus citri?. PLoS ONE, 2013, 8, e77307.	1.1	16
83	Effect of Dietary Carbohydrate Restriction on an Obesity-Related Prevotella-Dominated Human Fecal Microbiota. Metagenomics (Cairo, Egypt), 2013, 2, 1-4.	1.2	19
84	Role of Symbiosis in Evolution. Social and Ecological Interactions in the Galapagos Islands, 2013, , 63-70.	0.4	0
85	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.	1.0	80
86	Metagenomics of human microbiome: beyond 16s rDNA. Clinical Microbiology and Infection, 2012, 18, 47-49.	2.8	57
87	Comparative Genomics of Serratia spp.: Two Paths towards Endosymbiotic Life. PLoS ONE, 2012, 7, e47274.	1.1	29
88	Factors Behind Junk DNA in Bacteria. Genes, 2012, 3, 634-650.	1.0	26
89	Metabolic stasis in an ancient symbiosis: genome-scale metabolic networks from two Blattabacterium cuenoti strains, primary endosymbionts of cockroaches. BMC Microbiology, 2012, 12, S5.	1.3	38
90	Structural alterations of faecal and mucosaâ€associated bacterial communities in irritable bowel syndrome. Environmental Microbiology Reports, 2012, 4, 242-247.	1.0	100

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91	Daily follow-up of bacterial communities in the human gut reveals stable composition and host-specific patterns of interaction. FEMS Microbiology Ecology, 2012, 81, 427-437.	1.3	24
92	A Bacillus thuringiensis strain producing epizootics on Plodia interpunctella: A case study. Journal of Stored Products Research, 2012, 48, 52-60.	1.2	12
93	Staphylococcus prevails in the skin microbiota of longâ€term immunodeficient mice. Environmental Microbiology, 2012, 14, 2087-2098.	1.8	13
94	The role of symbiosis in eukaryotic evolution. , 2011, , 326-344.		3
95	Symbionts and Pathogens: What is the Difference?. Current Topics in Microbiology and Immunology, 2011, 358, 215-243.	0.7	27
96	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
97	The Gypsy Database (GyDB) of mobile genetic elements: release 2.0. Nucleic Acids Research, 2011, 39, D70-D74.	6.5	344
98	A Genomic Reappraisal of Symbiotic Function in the Aphid/Buchnera Symbiosis: Reduced Transporter Sets and Variable Membrane Organisations. PLoS ONE, 2011, 6, e29096.	1.1	44
99	Molecular evidence to suggest the origin of a colonization: Drosophila subobscura in America. Genetica, 2011, 139, 1477-1486.	0.5	4
100	Assessing Gut Microbial Diversity from Feces and Rectal Mucosa. Microbial Ecology, 2011, 61, 123-133.	1.4	143
101	Genome Economization in the Endosymbiont of the Wood Roach Cryptocercus punctulatus Due to Drastic Loss of Amino Acid Synthesis Capabilities. Genome Biology and Evolution, 2011, 3, 1437-1448.	1.1	35
102	Complete Genome Sequence of Acidaminococcus intestini RYC-MR95, a Gram-Negative Bacterium from the Phylum Firmicutes. Journal of Bacteriology, 2011, 193, 7008-7009.	1.0	22
103	New Insights on the Evolutionary History of Aphids and Their Primary Endosymbiont Buchnera aphidicola. International Journal of Evolutionary Biology, 2011, 2011, 1-9.	1.0	10
104	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
105	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.	1.4	57
106	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.	1.0	73
107	Serratia symbiotica from the Aphid Cinara cedri: A Missing Link from Facultative to Obligate Insect Endosymbiont. PLoS Genetics, 2011, 7, e1002357.	1.5	208
108	Metatranscriptomic Approach to Analyze the Functional Human Gut Microbiota. PLoS ONE, 2011, 6, e17447.	1.1	302

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109	The Active Human Gut Microbiota Differs from the Total Microbiota. PLoS ONE, 2011, 6, e22448.	1.1	90
110	Bacteria Associated with Copestylum (Diptera, Syrphidae) Larvae and Their Cactus Host Isolatocereus dumortieri. PLoS ONE, 2011, 6, e27443.	1.1	8
111	Phylogenetic relationships of the endemic Antarctic benthic hydroids (Cnidaria, Hydrozoa): what does the mitochondrial 16S rRNA tell us about it?. Polar Biology, 2010, 33, 41-57.	0.5	43
112	Legionella pneumophila pangenome reveals strain-specific virulence factors. BMC Genomics, 2010, 11, 181.	1.2	161
113	Effects ofBacillus thuringiensisCry1Ab and Cry3Aa endotoxins on predatory Coleoptera tested through artificial diet-incorporation bioassays. Bulletin of Entomological Research, 2010, 100, 297-302.	0.5	26
114	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	2.6	913
115	Genomics of intracellular symbionts in insects. International Journal of Medical Microbiology, 2010, 300, 271-278.	1.5	56
116	Immunity and other defenses in pea aphids, Acyrthosiphon pisum. Genome Biology, 2010, 11, R21.	13.9	389
117	Evolution of Prokaryote-Animal Symbiosis from a Genomics Perspective. Microbiology Monographs, 2010, , 207-233.	0.3	11
118	Life With a Few Genes: A Survey on Naturally Evolved Reduced Genomes~!2009-11-30~!2010-01-24~!2010-05-07~!. The Open Evolution Journal, 2010, 4, 12-22.	0.2	11
119	Unravelling the bacterial diversity found in the semi-arid Tablas de Daimiel National Park wetland (central Spain). Aquatic Microbial Ecology, 2010, 59, 33-44.	0.9	6
120	Goethe's dream. EMBO Reports, 2009, 10, S28-32.	2.0	15
121	Toward minimal bacterial cells: evolution vs. design. FEMS Microbiology Reviews, 2009, 33, 225-235.	3.9	97
122	The evolutionary history of symbiotic associations among bacteria and their animal hosts: a model. Clinical Microbiology and Infection, 2009, 15, 11-13.	2.8	15
123	Evolutionary Convergence and Nitrogen Metabolism in Blattabacterium strain Bge, Primary Endosymbiont of the Cockroach Blattella germanica. PLoS Genetics, 2009, 5, e1000721.	1.5	134
124	Identification of the Weevil immune genes and their expression in the bacteriome tissue. BMC Biology, 2008, 6, 43.	1.7	114
125	Learning how to live together: genomic insights into prokaryoteâ€“animal symbioses. Nature Reviews Genetics, 2008, 9, 218-229.	7.7	465
126	Blattabacteria, the endosymbionts of cockroaches, have small genome sizes and high genome copy numbers. Environmental Microbiology, 2008, 10, 3417-3422.	1.8	31

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127	Patterns and rates of nucleotide substitution, insertion and deletion in the endosymbiont of ants Blochmannia floridanus. Molecular Ecology, 2008, 17, 4382-4392.	2.0	13
128	Molecular variation in the Odh gene in Chilean natural populations of Drosophila subobscura. Hereditas, 2008, 145, 154-162.	0.5	7
129	Virulence factor rtx in Legionella pneumophila, evidence suggesting it is a modular multifunctional protein. BMC Genomics, 2008, 9, 14.	1.2	36
130	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.	1.4	77
131	The Striking Case of Tryptophan Provision in the Cedar Aphid Cinara cedri. Journal of Bacteriology, 2008, 190, 6026-6029.	1.0	91
132	Massive presence of insertion sequences in the genome of SOPE, the primary endosymbiont of the rice weevil Sitophilus oryzae. International Microbiology, 2008, 11, 41-8.	1.1	38
133	Reconstructing the ancestor of Mycobacterium leprae: The dynamics of gene loss and genome reduction. Genome Research, 2007, 17, 1178-1185.	2.4	110
134	Structural analyses of a hypothetical minimal metabolism. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1751-1762.	1.8	39
135	Genome reduction of the aphid endosymbiont Buchnera aphidicola in a recent evolutionary time scale. Gene, 2007, 389, 87-95.	1.0	29
136	Genomic Changes in Bacteria: From Free-Living to Endosymbiotic Life. Biological and Medical Physics Series, 2007, , 149-165.	0.3	4
137	A simple DNA extraction method suitable for PCR detection of genetically modified maize. Journal of the Science of Food and Agriculture, 2007, 87, 2728-2731.	1.7	8
138	The frontier between cell and organelle: genome analysis of Candidatus Carsonella ruddii. BMC Evolutionary Biology, 2007, 7, 181.	3.2	106
139	A Small Microbial Genome: The End of a Long Symbiotic Relationship?. Science, 2006, 314, 312-313.	6.0	309
140	Plasmids in the aphid endosymbiont Buchnera aphidicola with the smallest genomes. A puzzling evolutionary story. Gene, 2006, 370, 17-25.	1.0	50
141	Chromosomal stasis versus plasmid plasticity in aphid endosymbiont Buchnera aphidicola. Heredity, 2005, 95, 339-347.	1.2	39
142	Comparative analysis of two genomic regions among four strains of Buchnera aphidicola, primary endosymbiont of aphids. Gene, 2005, 345, 73-80.	1.0	9
143	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
144	Evolution of the Leucine Gene Cluster in Buchnera aphidicola : Insights from Chromosomal Versions of the Cluster. Journal of Bacteriology, 2004, 186, 2646-2654.	1.0	18

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145	The Evolutionary Fate of Nonfunctional DNA in the Bacterial Endosymbiont Buchnera aphidicola. Molecular Biology and Evolution, 2004, 21, 2172-2181.	3.5	55
146	Bacterial endosymbionts of insects: insights from comparative genomics. Environmental Microbiology, 2004, 6, 1109-1122.	1.8	104
147	A classification scheme for mobilization regions of bacterial plasmids. FEMS Microbiology Reviews, 2004, 28, 79-100.	3.9	308
148	Colonization of America by Drosophila subobscura: Association between Odh gene haplotypes, lethal genes and chromosomal arrangements. Genes and Genetic Systems, 2004, 79, 233-244.	0.2	10
149	The effect of superoxide dismutase alleles on aging in Drosophila. , 2004, , 198-204.		0
150	Why are the genomes of endosymbiotic bacteria so stable?. Trends in Genetics, 2003, 19, 176-180.	2.9	80
151	Side-stepping secondary symbionts: widespread horizontal transfer across and beyond the Aphidoidea. Molecular Ecology, 2003, 12, 1061-1075.	2.0	286
152	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
153	PHYLOGENETIC EVIDENCE FOR HYBRID ORIGINS OF ASEXUAL LINEAGES IN AN APHID SPECIES. Evolution; International Journal of Organic Evolution, 2003, 57, 1291.	1.1	7
154	Hostâ€“based divergence in populations of the pea aphid: insights from nuclear markers and the prevalence of facultative symbionts. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 1703-1712.	1.2	209
155	Reductive genome evolution in Buchnera aphidicola. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 581-586.	3.3	461
156	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.	3.3	338
157	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.	3.3	221
158	Molecular Characterization of the Leucine Cluster in Buchnera sp. Strain PSY, a Primary Endosymbiont of the Aphid Pemphigus spyrothecae. Applied and Environmental Microbiology, 2002, 68, 2572-2575.	1.4	8
159	Comparative Molecular Evolution of Primary (Buchnera) and Secondary Symbionts of Aphids Based on Two Protein-Coding Genes. Journal of Molecular Evolution, 2002, 55, 127-137.	0.8	25
160	Linkage disequilibria between mtDNA haplotypes and chromosomal arrangements in a natural population of Drosophila subobscura. Heredity, 2002, 89, 133-138.	1.2	13
161	The Phylogenetic Analysis of Variable-Length Sequence Data: Elongation Factorâ€“1Î± Introns in European Populations of the Parasitoid Wasp Genus Pauesia (Hymenoptera: Braconidae: Aphidiinae). Molecular Biology and Evolution, 2001, 18, 1117-1131.	3.5	39
162	Molecular Systematics of Aphids and Their Primary Endosymbionts. Molecular Phylogenetics and Evolution, 2001, 20, 437-449.	1.2	62

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163	Genome size reduction through multiple events of gene disintegration in Buchnera APS. Trends in Genetics, 2001, 17, 615-618.	2.9	124
164	An 18S rDNA-Based Molecular Phylogeny of Aphidiinae (Hymenoptera: Braconidae). Molecular Phylogenetics and Evolution, 2000, 14, 180-194.	1.2	53
165	Molecular Characterization of the Leucine Plasmid from Buchnera aphidicola , Primary Endosymbiont of the Aphid Acyrthosiphon pisum. Current Microbiology, 2000, 40, 264-268.	1.0	6
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