

# Corinne Cruaud

## List of Publications by Year in descending order

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Version: 2024-02-01

225  
papers

36,611  
citations

14124

69  
h-index

4131

181  
g-index

246  
all docs

246  
docs citations

246  
times ranked

47578  
citing authors

#	ARTICLE	IF	CITATIONS
1	Providing a phylogenetic framework for trait-based analyses in brown algae: Phylogenomic tree inferred from 32 nuclear protein-coding sequences. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107408.	1.2	2
2	Oxford Nanopore and Bionano Genomics technologies evaluation for plant structural variation detection. <i>BMC Genomics</i> , 2022, 23, 317.	1.2	4
3	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. <i>GigaScience</i> , 2022, 11, .	3.3	26
4	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
5	Genome-wide mapping of individual replication fork velocities using nanopore sequencing. <i>Nature Communications</i> , 2022, 13, .	5.8	15
6	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021, 15, 1767-1781.	4.4	18
7	Large-scale transcriptomics to dissect 2Âyears of the life of a fungal phytopathogen interacting with its host plant. <i>BMC Biology</i> , 2021, 19, 55.	1.7	21
8	Genomic signatures of clonality in the deep water kelp <i>Laminaria rodriguezii</i> . <i>Molecular Ecology</i> , 2021, 30, 1806-1822.	2.0	14
9	Complete Genome Sequences of Two <i>Pseudomonas</i> Species Isolated from Marine Environments of the Pacific Ocean. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
10	Population genomics of apricots unravels domestication history and adaptive events. <i>Nature Communications</i> , 2021, 12, 3956.	5.8	45
11	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
12	Sequencing and Chromosome-Scale Assembly of Plant Genomes, <i>Brassica rapa</i> as a Use Case. <i>Biology</i> , 2021, 10, 732.	1.3	15
13	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	2.0	86
14	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer <i>Adineta vaga</i> . <i>Science Advances</i> , 2021, 7, eabg4216.	4.7	30
15	Serial horizontal transfer of vitamin-biosynthetic genes enables the establishment of new nutritional symbionts in aphidsâ™ di-symbiotic systems. <i>ISME Journal</i> , 2020, 14, 259-273.	4.4	79
16	A framework for in situ molecular characterization of coral holobionts using nanopore sequencing. <i>Scientific Reports</i> , 2020, 10, 15893.	1.6	9
17	The Protector within: Comparative Genomics of APSE Phages across Aphids Reveals Rampant Recombination and Diverse Toxin Arsenals. <i>Genome Biology and Evolution</i> , 2020, 12, 878-889.	1.1	22
18	Biogeography of soil microbial habitats across France. <i>Global Ecology and Biogeography</i> , 2020, 29, 1399-1411.	2.7	22

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19	FORK-seq: replication landscape of the <i>Saccharomyces cerevisiae</i> genome by nanopore sequencing. <i>Genome Biology</i> , 2020, 21, 125.	3.8	39
20	Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, .	3.3	64
21	Two large reciprocal translocations characterized in the disease resistance-rich burmannica genetic group of <i>Musa acuminata</i> . <i>Annals of Botany</i> , 2019, 124, 319-329.	1.4	15
22	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. <i>Scientific Reports</i> , 2019, 9, 14908.	1.6	90
23	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
24	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
25	Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. <i>Nature Microbiology</i> , 2019, 4, 1088-1095.	5.9	57
26	The <i>Wolbachia mobilome</i> in <i>Culex pipiens</i> includes a putative plasmid. <i>Nature Communications</i> , 2019, 10, 1051.	5.8	42
27	Biogeography of Soil Bacterial Networks along a Gradient of Cropping Intensity. <i>Scientific Reports</i> , 2019, 9, 3812.	1.6	53
28	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
29	<i>De novo</i> clustering of long reads by gene from transcriptomics data. <i>Nucleic Acids Research</i> , 2019, 47, e2-e2.	6.5	29
30	Genome evolution across 1,011 <i>Saccharomyces cerevisiae</i> isolates. <i>Nature</i> , 2018, 556, 339-344.	13.7	952
31	Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887.	4.7	316
32	Biogeography of soil bacteria and archaea across France. <i>Science Advances</i> , 2018, 4, eaat1808.	4.7	185
33	The Rise and Fall of African Rice Cultivation Revealed by Analysis of 246 New Genomes. <i>Current Biology</i> , 2018, 28, 2274-2282.e6.	1.8	84
34	A Freeloader? The Highly Eroded Yet Large Genome of the <i>Serratia symbiotica</i> Symbiont of <i>Cinara strobilifera</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2178-2189.	1.1	29
35	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
36	Complete Genome Sequence of the Facultative Methylophile <i>Methylobacterium extorquens</i> TK 0001 Isolated from Soil in Poland. <i>Genome Announcements</i> , 2018, 6, .	0.8	14

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37	De novo assembly and annotation of three <i>Leptosphaeria</i> genomes using Oxford Nanopore MinION sequencing. <i>Scientific Data</i> , 2018, 5, 180235.	2.4	53
38	Impact of biotic and abiotic factors on the expression of fungal effector-encoding genes in axenic growth conditions. <i>Fungal Genetics and Biology</i> , 2017, 99, 1-12.	0.9	7
39	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	2.4	147
40	High-Quality <i>de Novo</i> Genome Assembly of the <i>Dekkera bruxellensis</i> Yeast Using Nanopore MinION Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3243-3250.	0.8	44
41	Different waves of effector genes with contrasted genomic location are expressed by <i>Leptosphaeria maculans</i> during cotyledon and stem colonization of oilseed rape. <i>Molecular Plant Pathology</i> , 2017, 18, 1113-1126.	2.0	46
42	Phylogeny and diversification of the cloud forest <i>Morpho sulkowskyi</i> group (Lepidoptera). <i>Trends in Ecology &amp; Evolution</i> , 2017, 32, 1010-1018.	0.7	4
43	de novo assembly and population genomic survey of natural yeast isolates with the Oxford Nanopore MinION sequencer. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	123
44	Mapping and predictive variations of soil bacterial richness across France. <i>PLoS ONE</i> , 2017, 12, e0186766.	1.1	79
45	Geography and life history traits account for the accumulation of cryptic diversity among Indo-West Pacific coral reef fishes. <i>Marine Ecology - Progress Series</i> , 2017, 583, 179-193.	0.9	14
46	Molecular phylogenetics of <i>Sarcoleaceae</i> (Malvales), Madagascar's largest endemic plant family. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 729-743.	0.8	9
47	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629
48	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasite <i>Cytinus hypocistis</i> (Cytinaceae). <i>Annals of Botany</i> , 2016, 118, 885-896.	1.4	55
49	An inter-ocean comparison of coral endemism on seamounts: the case of <i>Chrysogorgia</i> . <i>Journal of Biogeography</i> , 2015, 42, 1907-1918.	1.4	10
50	Full-length <i>de novo</i> assembly of RNA-seq data in pea ( <i>Pisum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. <i>Plant Journal</i> , 2015, 84, 1-19.	2.8	173
51	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
52	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
53	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	1.2	177
54	Improving biodiversity assessment of anuran amphibians using DNA barcoding of tadpoles. Case studies from Southeast Asia. <i>Comptes Rendus - Biologies</i> , 2015, 338, 351-361.	0.1	40

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55	Improving soil bacterial taxa-area relationships assessment using DNA meta-barcoding. <i>Heredity</i> , 2015, 114, 468-475.	1.2	23
56	Community assembly on remote islands: a comparison of Hawaiian and Mascarene spiders. <i>Journal of Biogeography</i> , 2015, 42, 39-50.	1.4	16
57	A Phylogenetic Re-Analysis of Groupers with Applications for Ciguatera Fish Poisoning. <i>PLoS ONE</i> , 2014, 9, e98198.	1.1	24
58	Transposable element-assisted evolution and adaptation to host plant within the <i>Leptosphaeria maculans</i> - <i>Leptosphaeria biglobosa</i> species complex of fungal pathogens. <i>BMC Genomics</i> , 2014, 15, 891.	1.2	189
59	Genome sequence of a crustacean iridovirus, IIV31, isolated from the pill bug, <i>Armadillidium vulgare</i> . <i>Journal of General Virology</i> , 2014, 95, 1585-1590.	1.3	24
60	Phylogeny and taxonomy of <i>Syngonanthus</i> and <i>Comanthera</i> (Eriocaulaceae): Evidence from expanded sampling. <i>Taxon</i> , 2014, 63, 47-63.	0.4	26
61	Comparison of library preparation methods reveals their impact on interpretation of metatranscriptomic data. <i>BMC Genomics</i> , 2014, 15, 912.	1.2	56
62	Forest refugia and riverine barriers promote diversification in the <i>W</i> est African pygmy shrew ( <i>C</i> rocicidura obscurior complex,) Tj ETQq0 0 0 rgBT /Overlock 107f 50 457 Td (<sc	1.0	45
63	Evolution within the nuthatches (Sittidae: Aves, Passeriformes): molecular phylogeny, biogeography, and ecological perspectives. <i>Journal of Ornithology</i> , 2014, 155, 755-765.	0.5	31
64	Insights on the Evolution of Plant Succulence from a Remarkable Radiation in Madagascar (Euphorbia). <i>Systematic Biology</i> , 2014, 63, 697-711.	2.7	41
65	Complete genome sequence of invertebrate iridovirus IIV30 isolated from the corn earworm, <i>Helicoverpa zea</i> . <i>Journal of Invertebrate Pathology</i> , 2014, 116, 43-47.	1.5	11
66	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.	13.7	505
67	Characterization of Novel Polycyclic Aromatic Hydrocarbon Dioxygenases from the Bacterial Metagenomic DNA of a Contaminated Soil. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6591-6600.	1.4	60
68	Recognition of a new species of <i>Kallymenia</i> (Gigartinales, Rhodophyta) from Croatia (Mediterranean Sea) based on morphology and DNA barcode. <i>European Journal of Phycology</i> , 2014, 49, 332-344.	0.9	8
69	Complete genome sequence of invertebrate iridovirus IIV-25 isolated from a blackfly larva. <i>Archives of Virology</i> , 2014, 159, 1181-1185.	0.9	12
70	Complete genome sequence of invertebrate iridovirus IIV22A, a variant of IIV22, isolated originally from a blackfly larva. <i>Standards in Genomic Sciences</i> , 2014, 9, 940-947.	1.5	7
71	Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013, 14, 320.	1.2	90
72	Complete genome sequence of invertebrate iridescent virus 22 isolated from a blackfly larva. <i>Journal of General Virology</i> , 2013, 94, 2112-2116.	1.3	22

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73	Below-ground fine-scale distribution and soil versus fine root detection of fungal and soil oomycete communities in a French beech forest. <i>Fungal Ecology</i> , 2013, 6, 223-235.	0.7	69
74	Molecular systematics and phylogeography of the tribe Myonycterini (Mammalia, Pteropodidae) inferred from mitochondrial and nuclear markers. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 126-137.	1.2	48
75	DNA barcoding in a biodiversity hot spot: potential value for the identification of <i>M. alagasy</i> Euphorbia L. listed in CITES Appendices I and II. <i>Molecular Ecology Resources</i> , 2013, 13, 57-65.	2.2	32
76	Evolution of Diadromy in Fish: Insights from a Tropical Genus ( <i>Kuhlia</i> Species). <i>American Naturalist</i> , 2013, 181, 52-63.	1.0	22
77	New nuclear markers and exploration of the relationships among Serraniformes (Acanthomorpha). <i>Trends in Ecology and Evolution</i> , 2013, 67, 140-155.	1.2	32
78	Molecular evidence for novel <i>Cantharellus</i> (Cantharellales, Basidiomycota) from tropical African miombo woodland and a key to all tropical African chanterelles. <i>Fungal Diversity</i> , 2013, 58, 281-298.	4.7	35
79	Tracing the history and biogeography of the Australian blindsnake radiation. <i>Journal of Biogeography</i> , 2013, 40, 928-937.	1.4	23
80	Species Diversity, Phylogeny and Large Scale Biogeographic Patterns of the Genus <i>Padina</i> (Phaeophyceae, Dictyotales). <i>Journal of Phycology</i> , 2013, 49, 130-142.	1.0	53
81	Positive selection of protective variants for type 2 diabetes from the Neolithic onward: a case study in Central Asia. <i>European Journal of Human Genetics</i> , 2013, 21, 1146-1151.	1.4	35
82	Purifying selection after episodes of recurrent adaptive diversification in fungal pathogens. <i>Infection, Genetics and Evolution</i> , 2013, 17, 123-131.	1.0	15
83	The contrasted evolutionary fates of deep-sea chemosynthetic mussels ( <i>Bivalvia</i> , <i>Bathymodiolinae</i> ). <i>Ecology and Evolution</i> , 2013, 3, 4748-4766.	0.8	69
84	Status of the Catalan chub <i>Squalius laietanus</i> (Actinopterygii, Cyprinidae) in France: input from morphological and molecular data. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2013, , 04.	0.5	4
85	How Effective Are DNA Barcodes in the Identification of African Rainforest Trees?. <i>PLoS ONE</i> , 2013, 8, e54921.	1.1	81
86	Is the Species Flock Concept Operational? The Antarctic Shelf Case. <i>PLoS ONE</i> , 2013, 8, e68787.	1.1	51
87	The Phylogeny and Biogeographic History of Ashes ( <i>Fraxinus</i> , <i>Oleaceae</i> ) Highlight the Roles of Migration and Vicariance in the Diversification of Temperate Trees. <i>PLoS ONE</i> , 2013, 8, e80431.	1.1	52
88	Non-invasive ancient DNA protocol for fluid-preserved specimens and phylogenetic systematics of the genus <i>Orestias</i> (Teleostei: Cyprinodontidae). <i>Zootaxa</i> , 2013, 3640, 373-94.	0.2	20
89	From endemism to widespread distribution: phylogeography of three amphidromous <i>Sicyopterus</i> species (Teleostei: Gobioidae: Sicydiinae). <i>Marine Ecology - Progress Series</i> , 2012, 455, 269-285.	0.9	45
90	Speciation patterns in gastropods with long-lived larvae from deep-sea seamounts. <i>Molecular Ecology</i> , 2012, 21, 4828-4853.	2.0	36

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91	Phylogenetic footprints of an Antarctic radiation: The Trematominae (Notothenioidei, Teleostei). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 87-101.	1.2	31
92	West-Central African Pleistocene Lowland Forest Evolution Revealed by the Phylogeography of Misonne's Soft-Furred Mouse. <i>African Zoology</i> , 2012, 47, 100-112.	0.2	14
93	Macroevolution of venom apparatus innovations in auger snails (Gastropoda; Conoidea; Terebridae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 64, 21-44.	1.2	36
94	A study of a population of <i>Nyssomyia trapidoi</i> (Diptera: Psychodidae) caught on the Pacific coast of Ecuador. <i>Parasites and Vectors</i> , 2012, 5, 144.	1.0	16
95	Barcoding, molecular taxonomy, and exploration of the diversity of shrews (Soricomorpha: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	1.0	16
96	Are all species of <i>Pseudorhabdosynochus</i> strictly host specific? A molecular study. <i>Parasitology International</i> , 2012, 61, 356-359.	0.6	22
97	SEMA3A, a Gene Involved in Axonal Pathfinding, Is Mutated in Patients with Kallmann Syndrome. <i>PLoS Genetics</i> , 2012, 8, e1002896.	1.5	190
98	Deep-Sea Origin and In-Situ Diversification of Chrysogorgiid Octocorals. <i>PLoS ONE</i> , 2012, 7, e38357.	1.1	50
99	Nucleotide Composition of CO1 Sequences in Chelicerata (Arthropoda): Detecting New Mitogenomic Rearrangements. <i>Journal of Molecular Evolution</i> , 2012, 74, 81-95.	0.8	54
100	A taxonomic and ecological overview of cheese fungi. <i>International Journal of Food Microbiology</i> , 2012, 155, 199-210.	2.1	110
101	Using functional traits and phylogenetic trees to examine the assembly of tropical tree communities. <i>Journal of Ecology</i> , 2012, 100, 690-701.	1.9	191
102	Identification of molecular markers for DNA barcoding in the Aphidiinae (Hym. Braconidae). <i>Molecular Ecology Resources</i> , 2012, 12, 197-208.	2.2	62
103	Morphometric and molecular characterization of the series <i>Guyanensis</i> (Diptera, Psychodidae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 <i>Genetics and Evolution</i> , 2012, 12, 966-977.	1.0	11
104	Testing concordance in species boundaries using acoustic, morphological, and molecular data in the field cricket genus <i>Itaropsis</i> (Orthoptera: Grylloidea, Gryllidae: Gryllinae). <i>Zoological Journal of the Linnean Society</i> , 2012, 164, 285-303.	1.0	11
105	Comprehensive sampling reveals circumpolarity and sympatry in seven mitochondrial lineages of the Southern Ocean crinoid species <i>Promachocrinus kerguelensis</i> (Echinodermata). <i>Molecular Ecology</i> , 2012, 21, 2502-2518.	2.0	73
106	DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012, 21, 3647-3655.	2.0	262
107	Large-scale species delimitation method for hyperdiverse groups. <i>Molecular Ecology</i> , 2012, 21, 2671-2691.	2.0	259
108	The complete phylogeny of <i>Pseudobulweria</i> , the most endangered seabird genus: systematics, species status and conservation implications. <i>Conservation Genetics</i> , 2012, 13, 39-52.	0.8	16

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109	Deciduous Trees and the Application of Universal DNA Barcodes: A Case Study on the Circumpolar <i>Fraxinus</i> . PLoS ONE, 2012, 7, e34089.	1.1	40
110	Assessment of Three Mitochondrial Genes (16S, Cytb, CO1) for Identifying Species in the Praomyini Tribe (Rodentia: Muridae). PLoS ONE, 2012, 7, e36586.	1.1	84
111	In and out of Madagascar: Dispersal to Peripheral Islands, Insular Speciation and Diversification of Indian Ocean Daisy Trees ( <i>Psiadia</i> , Asteraceae). PLoS ONE, 2012, 7, e42932.	1.1	58
112	Barcoding type specimens helps to identify synonyms and an unnamed new species in Eumunida Smith, 1883 (Decapoda : Eumunididae). Invertebrate Systematics, 2011, 25, 322.	0.5	48
113	<i>Cantharellus texensis</i> sp. nov. from Texas, a southern lookalike of <i>C. cinnabarinus</i> revealed by <i>tef-1</i> sequence data. Mycologia, 2011, 103, 1037-1046.	0.8	38
114	DNA barcoding and molecular systematics of the benthic and demersal organisms of the CEAMARC survey. Polar Science, 2011, 5, 298-312.	0.5	25
115	DNA barcoding of African fruit bats (Mammalia, Pteropodidae). The mitochondrial genome does not provide a reliable discrimination between <i>Epomophorus gambianus</i> and <i>Micropteropus pusillus</i> . Comptes Rendus - Biologies, 2011, 334, 544-554.	0.1	55
116	The actinopterygian diversity of the CEAMARC cruises: Barcoding and molecular taxonomy as a multi-level tool for new findings. Deep-Sea Research Part II: Topical Studies in Oceanography, 2011, 58, 250-263.	0.6	63
117	Evolutionary history of the Corallinales (Corallinophycidae, Rhodophyta) inferred from nuclear, plastidial and mitochondrial genomes. Molecular Phylogenetics and Evolution, 2011, 61, 697-713.	1.2	119
118	Antarctic Ascidians (Tunicata) of the French-Australian survey CEAMARC in Terre Adélie. Zootaxa, 2011, 2817, 1.	0.2	19
119	Contribution of DNA-typing to bushmeat surveys: assessment of a roadside market in south-western Nigeria. Wildlife Research, 2011, 38, 696.	0.7	21
120	Evolution of acoustic communication in the Gomphocerinae (Orthoptera: Caelifera: Acrididae). Zoologica Scripta, 2011, 40, 479-497.	0.7	22
121	DNA markers to disentangle complexes of cryptic taxa in mealybugs (Hemiptera: Pseudococcidae). Journal of Applied Entomology, 2011, 135, 142-155.	0.8	77
122	Phylogeography of the Eurasian green woodpecker ( <i>Picus viridis</i> ). Journal of Biogeography, 2011, 38, 311-325.	1.4	46
123	Comparative phylogeography of two African carnivorans presumably introduced into Europe: disentangling natural versus human-mediated dispersal across the Strait of Gibraltar. Journal of Biogeography, 2011, 38, 341-358.	1.4	58
124	Geographical origin and endemism of Corsican Kuhl's pipistrelles assessed from mitochondrial DNA. Journal of Zoology, 2011, 284, 31-39.	0.8	11
125	Incongruence between morphotypes and genetically delimited species in the coral genus <i>Stylophora</i> : phenotypic plasticity, morphological convergence, morphological stasis or interspecific hybridization?. BMC Ecology, 2011, 11, 22.	3.0	79
126	Multilocus analyses of an Antarctic fish species flock (Teleostei, Notothenioidei, Trematominae): Phylogenetic approach and test of the early-radiation event. Molecular Phylogenetics and Evolution, 2011, 60, 305-316.	1.2	34



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127	Phylogenetics, species boundaries and timing of resource tracking in a highly specialized group of seed beetles (Coleoptera: Chrysomelidae: Bruchinae). <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 746-760.	1.2	29
128	Molecular phylogeny of the nutmeg shells (Neogastropoda, Cancellariidae). <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 685-697.	1.2	15
129	Diversity gradients and phylogeographic patterns in <i>Santiria trimera</i> (Burseraceae), a widespread African tree typical of mature rainforests. <i>American Journal of Botany</i> , 2011, 98, 254-264.	0.8	25
130	Evolution of oil-producing trichomes in <i>Sisyrinchium</i> (Iridaceae): insights from the first comprehensive phylogenetic analysis of the genus. <i>Annals of Botany</i> , 2011, 107, 1287-1312.	1.4	47
131	Complete Genome Sequence of the Commensal <i>Streptococcus salivarius</i> Strain JIM8777. <i>Journal of Bacteriology</i> , 2011, 193, 5024-5025.	1.0	19
132	Complete Genome Sequence of the Clinical <i>Streptococcus salivarius</i> Strain CCHSS3. <i>Journal of Bacteriology</i> , 2011, 193, 5041-5042.	1.0	9
133	Laying the foundations for a new classification of Agaonidae (Hymenoptera: Chalcidoidea), a multilocus phylogenetic approach. <i>Cladistics</i> , 2010, 26, 359-387.	1.5	86
134	Some considerations for analyzing biodiversity using integrative metagenomics and gene networks. <i>Biology Direct</i> , 2010, 5, 47.	1.9	50
135	A molecular phylogenetic framework for the Muricidae, a diverse family of carnivorous gastropods. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 1025-1039.	1.2	71
136	Finding candidate genes under positive selection in Non-model species: examples of genes involved in host specialization in pathogens. <i>Molecular Ecology</i> , 2010, 19, 292-306.	2.0	44
137	CpDNA-based species identification and phylogeography: application to African tropical tree species. <i>Molecular Ecology</i> , 2010, 19, 5469-5483.	2.0	38
138	Evolutionary history of the <i>Paradoxurus</i> palm civets – a new model for Asian biogeography. <i>Journal of Biogeography</i> , 2010, 37, 2077-2097.	1.4	79
139	A multi-locus time-calibrated phylogeny of the brown algae (Heterokonta, Ochrophyta, Phaeophyceae): Investigating the evolutionary nature of the “brown algal crown radiation” <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 659-674.	1.2	261
140	New insights into diversity and evolution of deep-sea Mytilidae (Mollusca: Bivalvia). <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 71-83.	1.2	72
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