

Corinne Cruaud

List of Publications by Year in descending order

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Version: 2024-02-01

225
papers

36,611
citations

12330

69
h-index

3579

181
g-index

246
all docs

246
docs citations

246
times ranked

43019
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and characterization of a spinal muscular atrophy-determining gene. <i>Cell</i> , 1995, 80, 155-165.	28.9	3,424
2	Mutations in PCSK9 cause autosomal dominant hypercholesterolemia. <i>Nature Genetics</i> , 2003, 34, 154-156.	21.4	2,532
3	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
4	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
5	Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke and dementia. <i>Nature</i> , 1996, 383, 707-710.	27.8	1,893
6	Genome duplication in the teleost fish <i>Tetraodon nigroviridis</i> reveals the early vertebrate proto-karyotype. <i>Nature</i> , 2004, 431, 946-957.	27.8	1,801
7	A candidate gene for familial Mediterranean fever. <i>Nature Genetics</i> , 1997, 17, 25-31.	21.4	1,402
8	Genome evolution across 1,011 <i>Saccharomyces cerevisiae</i> isolates. <i>Nature</i> , 2018, 556, 339-344.	27.8	952
9	Loss-of-function mutations in FGFR1 cause autosomal dominant Kallmann syndrome. <i>Nature Genetics</i> , 2003, 33, 463-465.	21.4	764
10	Strong clustering and stereotyped nature of Notch3 mutations in CADASIL patients. <i>Lancet</i> , The, 1997, 350, 1511-1515.	18.7	651
11	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
12	A human homologue of the <i>Drosophila</i> eyes absent gene underlies Branchio-Oto-Renal (BOR) syndrome and identifies a novel gene family. <i>Nature Genetics</i> , 1997, 15, 157-164.	21.4	628
13	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	12.6	617
14	Mutations in the laminin α 2 chain gene (LAMA2) cause merosin-deficient congenital muscular dystrophy. <i>Nature Genetics</i> , 1995, 11, 216-218.	21.4	603
15	Spastin, a new AAA protein, is altered in the most frequent form of autosomal dominant spastic paraplegia. <i>Nature Genetics</i> , 1999, 23, 296-303.	21.4	575
16	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
17	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.	27.8	505
18	Cardiac myosin binding protein-C gene splice acceptor site mutation is associated with familial hypertrophic cardiomyopathy. <i>Nature Genetics</i> , 1995, 11, 438-440.	21.4	417

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19	New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the <i>trnL</i> approach. <i>Molecular Ecology Resources</i> , 2009, 9, 51-60.	4.8	358
20	A Role for RNAi in the Selective Correction of DNA Methylation Defects. <i>Science</i> , 2009, 323, 1600-1604.	12.6	338
21	Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887.	9.3	316
22	<i>KVLQT1</i> C-Terminal Missense Mutation Causes a Forme Fruste Long-QT Syndrome. <i>Circulation</i> , 1997, 96, 2778-2781.	1.6	311
23	A complete collection of single-gene deletion mutants of <i>Acinetobacter baylyi</i> ADP1. <i>Molecular Systems Biology</i> , 2008, 4, 174.	7.2	289
24	Perlecan, the major proteoglycan of basement membranes, is altered in patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia). <i>Nature Genetics</i> , 2000, 26, 480-483.	21.4	274
25	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
26	DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012, 21, 3647-3655.	3.9	262
27	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.	2.7	261
28	Large-scale species delimitation method for hyperdiverse groups. <i>Molecular Ecology</i> , 2012, 21, 2671-2691.	3.9	259
29	Spectrum of SPC4 mutations in autosomal dominant spastic paraplegia. <i>Human Molecular Genetics</i> , 2000, 9, 637-644.	2.9	255
30	Organization and Sequence of Human Cardiac Myosin Binding Protein C Gene (MYBPC3) and Identification of Mutations Predicted to Produce Truncated Proteins in Familial Hypertrophic Cardiomyopathy. <i>Circulation Research</i> , 1997, 80, 427-434.	4.5	240
31	Structure and Organization of the Human Survival Motor Neurone (SMN) Gene. <i>Genomics</i> , 1996, 32, 479-482.	2.9	234
32	A frameshift deletion in the survival motor neuron gene in Spanish spinal muscular atrophy patients. <i>Nature Genetics</i> , 1995, 11, 335-337.	21.4	220
33	Non-founder mutations in the MEFV gene establish this gene as the cause of familial Mediterranean fever (FMF). <i>Human Molecular Genetics</i> , 1998, 7, 1317-1325.	2.9	214
34	Clustering of mutations responsible for branchio-oto-renal (BOR) syndrome in the eyes absent homologous region (<i>eyaHR</i>) of <i>EYA1</i> . <i>Human Molecular Genetics</i> , 1997, 6, 2247-2255.	2.9	205
35	Phenotypic spectrum of CHARGE syndrome in fetuses with <i>CHD7</i> truncating mutations correlates with expression during human development. <i>Journal of Medical Genetics</i> , 2005, 43, 211-317.	3.2	199
36	Using functional traits and phylogenetic trees to examine the assembly of tropical tree communities. <i>Journal of Ecology</i> , 2012, 100, 690-701.	4.0	191

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37	SEMA3A, a Gene Involved in Axonal Pathfinding, Is Mutated in Patients with Kallmann Syndrome. <i>PLoS Genetics</i> , 2012, 8, e1002896.	3.5	190
38	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.	2.8	189
39	Biogeography of soil bacteria and archaea across France. <i>Science Advances</i> , 2018, 4, eaat1808.	10.3	185
40	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	2.8	177
41	Evolution of the Mitochondrial Genome in Mammals Living at High Altitude: New Insights from a Study of the Tribe Caprini (Bovidae, Antilopinae). <i>Journal of Molecular Evolution</i> , 2009, 68, 293-310.	1.8	174
42	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.	5.7	173
43	The phylogeny and classification of caenophidian snakes inferred from seven nuclear protein-coding genes. <i>Comptes Rendus - Biologies</i> , 2007, 330, 182-187.	0.2	172
44	T-DNA integration into the <i>Arabidopsis</i> genome depends on sequences of pre-insertion sites. <i>EMBO Reports</i> , 2002, 3, 1152-1157.	4.5	162
45	Notch3 Mutations in Cerebral Autosomal Dominant Arteriopathy with Subcortical Infarcts and Leukoencephalopathy (CADASIL), a Mendelian Condition Causing Stroke and Vascular Dementia. <i>Annals of the New York Academy of Sciences</i> , 1997, 826, 213-217.	3.8	157
46	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
47	Origin of tropical American burrowing reptiles by transatlantic rafting. <i>Biology Letters</i> , 2008, 4, 115-118.	2.3	127
48	RNF213, a new nuclear marker for acanthomorph phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 345-363.	2.7	123
49	<i>de novo</i> assembly and population genomic survey of natural yeast isolates with the Oxford Nanopore MinION sequencer. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	123
50	Evolutionary history of the Corallinales (Corallinophycidae, Rhodophyta) inferred from nuclear, plastidial and mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 697-713.	2.7	119
51	A taxonomic and ecological overview of cheese fungi. <i>International Journal of Food Microbiology</i> , 2012, 155, 199-210.	4.7	110
52	Molecular analysis of the CBP gene in 60 patients with Rubinstein-Taybi syndrome. <i>Journal of Medical Genetics</i> , 2002, 39, 415-421.	3.2	109
53	The DNA sequence and analysis of human chromosome 14. <i>Nature</i> , 2003, 421, 601-607.	27.8	108
54	Patterns of genetic structure among Hawaiian corals of the genus <i>Pocillopora</i> yield clusters of individuals that are compatible with morphology. <i>Comptes Rendus - Biologies</i> , 2008, 331, 239-247.	0.2	100

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55	Blindsnake evolutionary tree reveals long history on Gondwana. <i>Biology Letters</i> , 2010, 6, 558-561.	2.3	98
56	Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013, 14, 320.	2.8	90
57	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. <i>Scientific Reports</i> , 2019, 9, 14908.	3.3	90
58	Molecular Phylogenetics of Thecata (Hydrozoa, Cnidaria) Reveals Long-Term Maintenance of Life History Traits despite High Frequency of Recent Character Changes. <i>Systematic Biology</i> , 2009, 58, 509-526.	5.6	88
59	Laying the foundations for a new classification of Agaonidae (Hymenoptera: Chalcidoidea), a multilocus phylogenetic approach. <i>Cladistics</i> , 2010, 26, 359-387.	3.3	86
60	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	4.4	86
61	The Rise and Fall of African Rice Cultivation Revealed by Analysis of 246 New Genomes. <i>Current Biology</i> , 2018, 28, 2274-2282.e6.	3.9	84
62	Assessment of Three Mitochondrial Genes (16S, Cytb, CO1) for Identifying Species in the Praomyini Tribe (Rodentia: Muridae). <i>PLoS ONE</i> , 2012, 7, e36586.	2.5	84
63	A mutation in HERG Associated with Notched T waves in Long QT Syndrome. <i>Journal of Molecular and Cellular Cardiology</i> , 1996, 28, 1609-1615.	1.9	83
64	Several deep-sea mussels and their associated symbionts are able to live both on wood and on whale falls. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 177-185.	2.6	81
65	How Effective Are DNA Barcodes in the Identification of African Rainforest Trees?. <i>PLoS ONE</i> , 2013, 8, e54921.	2.5	81
66	Evolutionary history of the <i>Paradoxurus</i> palm civets – a new model for Asian biogeography. <i>Journal of Biogeography</i> , 2010, 37, 2077-2097.	3.0	79
67	Incongruence between morphotypes and genetically delimited species in the coral genus <i>Stylophora</i> : phenotypic plasticity, morphological convergence, morphological stasis or interspecific hybridization?. <i>BMC Ecology</i> , 2011, 11, 22.	3.0	79
68	Serial horizontal transfer of vitamin-biosynthetic genes enables the establishment of new nutritional symbionts in aphids' di-symbiotic systems. <i>ISME Journal</i> , 2020, 14, 259-273.	9.8	79
69	Mapping and predictive variations of soil bacterial richness across France. <i>PLoS ONE</i> , 2017, 12, e0186766.	2.5	79
70	Improved PCR-Walking for Large-Scale Isolation of Plant T-DNA Borders. <i>BioTechniques</i> , 2001, 30, 496-504.	1.8	78
71	DNA markers to disentangle complexes of cryptic taxa in mealybugs (Hemiptera: Pseudococcidae). <i>Journal of Applied Entomology</i> , 2011, 135, 142-155.	1.8	77
72	High quality draft sequences for prokaryotic genomes using a mix of new sequencing technologies. <i>BMC Genomics</i> , 2008, 9, 603.	2.8	76

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73	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.	3.9	73
74	Whole Genome Sequence Comparisons and "Full-Length" cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation. <i>Genome Research</i> , 2004, 14, 406-413.	5.5	72
75	New insights into diversity and evolution of deep-sea Mytilidae (Mollusca: Bivalvia). <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 71-83.	2.7	72
76	A molecular phylogenetic framework for the Muricidae, a diverse family of carnivorous gastropods. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 1025-1039.	2.7	71
77	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	6.5	70
78	Starting to unravel the toxoglossan knot: Molecular phylogeny of the <i>œturrids</i> (Neogastropoda). <i>Tj ETQq0 0 0,rgBT /Overlock 10 T</i>	2.7	69
79	Molecular phylogeny of the Dictyotales and their position within the Phaeophyceae, based on nuclear, plastid and mitochondrial DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 211-226.	2.7	69
80	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.	1.6	69
81	The contrasted evolutionary fates of deep-sea chemosynthetic mussels (Bivalvia, Bathymodiolinae). <i>Ecology and Evolution</i> , 2013, 3, 4748-4766.	1.9	69
82	Large-scale characterization of Tos17 insertion sites in a rice T-DNA mutant library. <i>Plant Molecular Biology</i> , 2007, 65, 587-601.	3.9	66
83	A physical map of the heterozygous grapevine 'Cabernet Sauvignon' allows mapping candidate genes for disease resistance. <i>BMC Plant Biology</i> , 2008, 8, 66.	3.6	66
84	cDNA Isolation, Expression, and Chromosomal Localization of the Mouse Survival Motor Neuron Gene (<i>Smn</i>). <i>Genomics</i> , 1997, 40, 185-188.	2.9	64
85	Molecular phylogeny in mytilids supports the wooden steps to deep-sea vents hypothesis. <i>Comptes Rendus - Biologies</i> , 2007, 330, 446-456.	0.2	64
86	Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, .	6.4	64
87	A 94 kb genomic sequence 3' to the murine Xist gene reveals an AT rich region containing a new testis specific gene <i>Tsx</i> . <i>Human Molecular Genetics</i> , 1996, 5, 1713-1726.	2.9	63
88	Detection and analysis of alternative splicing in <i>Yarrowia lipolytica</i> reveal structural constraints facilitating nonsense-mediated decay of intron-retaining transcripts. <i>Genome Biology</i> , 2010, 11, R65.	9.6	63
89	The actinopterygian diversity of the CEAMARC cruises: Barcoding and molecular taxonomy as a multi-level tool for new findings. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2011, 58, 250-263.	1.4	63
90	Did glacial advances during the Pleistocene influence differently the demographic histories of benthic and pelagic Antarctic shelf fishes? Inferences from intraspecific mitochondrial and nuclear DNA sequence diversity. <i>BMC Evolutionary Biology</i> , 2007, 7, 220.	3.2	62

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91	Identification of molecular markers for DNA barcoding in the Aphidiinae (Hym. Braconidae). <i>Molecular Ecology Resources</i> , 2012, 12, 197-208.	4.8	62
92	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.	3.1	60
93	Comparative phylogeography of two African carnivorans presumably introduced into Europe: disentangling natural versus human-mediated dispersal across the Strait of Gibraltar. <i>Journal of Biogeography</i> , 2011, 38, 341-358.	3.0	58
94	In and out of Madagascar: Dispersal to Peripheral Islands, Insular Speciation and Diversification of Indian Ocean Daisy Trees (<i>Psiadia</i> , Asteraceae). <i>PLoS ONE</i> , 2012, 7, e42932.	2.5	58
95	Substitution of a conserved cysteine-996 in a cysteine-rich motif of the laminin alpha2-chain in congenital muscular dystrophy with partial deficiency of the protein. <i>American Journal of Human Genetics</i> , 1996, 58, 1177-84.	6.2	58
96	Genetics of laminin $\alpha 2$ chain (or merosin) deficient congenital muscular dystrophy: from identification of mutations to prenatal diagnosis. <i>Neuromuscular Disorders</i> , 1997, 7, 180-186.	0.6	57
97	PCR based mutation screening of the laminin alpha2 chain gene (LAMA2): application to prenatal diagnosis and search for founder effects in congenital muscular dystrophy.. <i>Journal of Medical Genetics</i> , 1998, 35, 211-217.	3.2	57
98	Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. <i>Nature Microbiology</i> , 2019, 4, 1088-1095.	13.3	57
99	Comparisons between mitochondrial genomes of domestic goat (<i>Capra hircus</i>) reveal the presence of numts and multiple sequencing errors. <i>Mitochondrial DNA</i> , 2010, 21, 68-76.	0.6	56
100	Comparison of library preparation methods reveals their impact on interpretation of metatranscriptomic data. <i>BMC Genomics</i> , 2014, 15, 912.	2.8	56
101	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> . <i>Comptes Rendus - Biologies</i> , 2011, 334, 544-554.	0.2	55
102	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.	2.9	55
103	Dissecting the major African snake radiation: a molecular phylogeny of the Lamprophiidae Fitzinger (Serpentes, Caenophidia). <i>Zootaxa</i> , 2008, 1945, 51-66.	0.5	55
104	Nucleotide Composition of CO1 Sequences in Chelicerata (Arthropoda): Detecting New Mitogenomic Rearrangements. <i>Journal of Molecular Evolution</i> , 2012, 74, 81-95.	1.8	54
105	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.	2.3	53
106	Biogeography of Soil Bacterial Networks along a Gradient of Cropping Intensity. <i>Scientific Reports</i> , 2019, 9, 3812.	3.3	53
107	De novo assembly and annotation of three <i>Leptosphaeria</i> genomes using Oxford Nanopore MinION sequencing. <i>Scientific Data</i> , 2018, 5, 180235.	5.3	53
108	The Phylogeny and Biogeographic History of Ashes (<i>Fraxinus</i> , Oleaceae) Highlight the Roles of Migration and Vicariance in the Diversification of Temperate Trees. <i>PLoS ONE</i> , 2013, 8, e80431.	2.5	52

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109	Analysis of major repetitive DNA sequences in the dog (<i>Canis familiaris</i>) genome. <i>Mammalian Genome</i> , 1999, 10, 699-705.	2.2	51
110	Is the Species Flock Concept Operational? The Antarctic Shelf Case. <i>PLoS ONE</i> , 2013, 8, e68787.	2.5	51
111	Some considerations for analyzing biodiversity using integrative metagenomics and gene networks. <i>Biology Direct</i> , 2010, 5, 47.	4.6	50
112	Deep-Sea Origin and In-Situ Diversification of Chrysogorgiid Octocorals. <i>PLoS ONE</i> , 2012, 7, e38357.	2.5	50
113	An integrative approach to species delimitation in <i>Benthomangelia</i> (Mollusca: Conoidea). <i>Biological Journal of the Linnean Society</i> , 2009, 96, 696-708.	1.6	49
114	Barcoding type specimens helps to identify synonyms and an unnamed new species in <i>Eumunida</i> Smith, 1883 (Decapoda : Eumunidae). <i>Invertebrate Systematics</i> , 2011, 25, 322.	1.3	48
115	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.	2.7	48
116	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.	2.9	47
117	Tracing the colonization history of the Indian Ocean scops-owls (Strigiformes: Otus) with further insight into the spatio-temporal origin of the Malagasy avifauna. <i>BMC Evolutionary Biology</i> , 2008, 8, 197.	3.2	46
118	Phylogeography of the Eurasian green woodpecker (<i>Picus viridis</i>). <i>Journal of Biogeography</i> , 2011, 38, 311-325.	3.0	46
119	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.	4.2	46
120	Early onset autosomal dominant spastic paraplegia caused by novel mutations in SPG3A. <i>Neurogenetics</i> , 2004, 5, 239-243.	1.4	45
121	Invasion of the French Paleolithic painted cave of Lascaux by members of the <i>Fusarium solani</i> species complex. <i>Mycologia</i> , 2007, 99, 526-533.	1.9	45
122	From endemism to widespread distribution: phylogeography of three amphidromous <i>Sicyopterus</i> species (Teleostei: Gobioidi: Sicydiinae). <i>Marine Ecology - Progress Series</i> , 2012, 455, 269-285.	1.9	45
123	Population genomics of apricots unravels domestication history and adaptive events. <i>Nature Communications</i> , 2021, 12, 3956.	12.8	45
124	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.	3.9	44
125	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.	1.8	44
126	Studying sources of incongruence in arthropod molecular phylogenies: Sea spiders (Pycnogonida) as a case study. <i>Comptes Rendus - Biologies</i> , 2010, 333, 438-453.	0.2	43

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127	The Wolbachia mobilome in <i>Culex pipiens</i> includes a putative plasmid. <i>Nature Communications</i> , 2019, 10, 1051.	12.8	42
128	Genotype-phenotype analysis in four families with mutations in β -myosin heavy chain gene responsible for familial hypertrophic cardiomyopathy. <i>Human Mutation</i> , 1998, 12, 385-392.	2.5	41
129	Insights on the Evolution of Plant Succulence from a Remarkable Radiation in Madagascar (Euphorbia). <i>Systematic Biology</i> , 2014, 63, 697-711.	5.6	41
130	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.	0.2	40
131	Deciduous Trees and the Application of Universal DNA Barcodes: A Case Study on the Circumpolar <i>Fraxinus</i> . <i>PLoS ONE</i> , 2012, 7, e34089.	2.5	40
132	Phylogeography of spiny mice (genus <i>Acomys</i> , Rodentia: Muridae) from the south-western margin of the Sahara with taxonomic implications. <i>Biological Journal of the Linnean Society</i> , 0, 98, 29-46.	1.6	39
133	FORK-seq: replication landscape of the <i>Saccharomyces cerevisiae</i> genome by nanopore sequencing. <i>Genome Biology</i> , 2020, 21, 125.	8.8	39
134	CpDNA-based species identification and phylogeography: application to African tropical tree species. <i>Molecular Ecology</i> , 2010, 19, 5469-5483.	3.9	38
135	<i>Cantharellus texensis</i> sp. nov. from Texas, a southern lookalike of <i>C. cinnabarinus</i> revealed by <i>tef-1</i> sequence data. <i>Mycologia</i> , 2011, 103, 1037-1046.	1.9	38
136	Evolutionary history and biogeography of the drongos (Dicruridae), a tropical Old World clade of corvid passerines. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 158-167.	2.7	37
137	Hidden diversity and endemism on seamounts: focus on poorly dispersive neogastropods. <i>Biological Journal of the Linnean Society</i> , 0, 100, 420-438.	1.6	37
138	Mitochondrial sequences of <i>Seriatopora</i> corals show little agreement with morphology and reveal the duplication of a tRNA gene near the control region. <i>Coral Reefs</i> , 2008, 27, 789-794.	2.2	36
139	Speciation patterns in gastropods with long-lived larvae from deep-sea seamounts. <i>Molecular Ecology</i> , 2012, 21, 4828-4853.	3.9	36
140	Macroevolution of venom apparatus innovations in auger snails (Gastropoda; Conoidea; Terebridae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 64, 21-44.	2.7	36
141	Molecular taxonomy and identification within the Antarctic genus <i>Trematomus</i> (Notothenioidei.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 1</i>	1.2	35
142	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.	12.3	35
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157	De novo clustering of long reads by gene from transcriptomics data. <i>Nucleic Acids Research</i> , 2019, 47, e2-e2.	14.5	29
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