

Richard C Cronn

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75
papers

6,505
citations

37
h-index

80
g-index

80
ext. papers

7,863
ext. citations

4.2
avg, IF

5.75
L-index

#	Paper	IF	Citations
75	Range-wide assessment of a SNP panel for individualization and geolocalization of bigleaf maple (<i>Acer macrophyllum</i> Pursh). <i>Forensic Science International Animals and Environments</i> , 2021 , 100033		1
74	Estimating the genetic diversity of Pacific salmon and trout using multigene eDNA metabarcoding. <i>Molecular Ecology</i> , 2021 , 30, 4970-4990	5.7	9
73	Predicting the geographic origin of Spanish Cedar (<i>Cedrela odorata</i> L.) based on DNA variation. <i>Conservation Genetics</i> , 2020 , 21, 625-639	2.6	4
72	An Axiom SNP genotyping array for Douglas-fir. <i>BMC Genomics</i> , 2020 , 21, 9	4.5	14
71	Genomic resources for the Neotropical tree genus <i>Cedrela</i> (Meliaceae) and its relatives. <i>BMC Genomics</i> , 2019 , 20, 58	4.5	5
70	Casting a broader net: Using microfluidic metagenomics to capture aquatic biodiversity data from diverse taxonomic targets. <i>Environmental DNA</i> , 2019 , 1, 251-267	7.6	6
69	A draft genome and transcriptome of common milkweed (<i>Asclepias tuberosa</i>) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. <i>PeerJ</i> , 2019 , 7, e7649	3.1	5
68	eDNA as a tool for identifying freshwater species in sustainable forestry: A critical review and potential future applications. <i>Science of the Total Environment</i> , 2019 , 649, 1157-1170	10.2	35
67	Functional trait divergence and trait plasticity confer polyploid advantage in heterogeneous environments. <i>New Phytologist</i> , 2019 , 221, 2286-2297	9.8	33
66	Comparative Transcriptomics Among Four White Pine Species. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 1461-1474	3.2	20
65	PacBio-Based Mitochondrial Genome Assembly of <i>Leucaena trichandra</i> (Leguminosae) and an Intrageneric Assessment of Mitochondrial RNA Editing. <i>Genome Biology and Evolution</i> , 2018 , 10, 2501-2517	3.9	14
64	Alignment-free genome comparison enables accurate geographic sourcing of white oak DNA. <i>BMC Genomics</i> , 2018 , 19, 896	4.5	2
63	Development of nuclear microsatellite loci for <i>Pinus albicaulis</i> Engelm. (Pinaceae), a conifer of conservation concern. <i>PLoS ONE</i> , 2018 , 13, e0205423	3.7	1
62	Evolution at the tips: <i>Asclepias</i> phylogenomics and new perspectives on leaf surfaces. <i>American Journal of Botany</i> , 2018 , 105, 514-524	2.7	14
61	A time and a place for everything: phylogenetic history and geography as joint predictors of oak plastome phylogeny. <i>Genome</i> , 2017 , 60, 720-732	2.4	42
60	Source identification of western Oregon Douglas-fir wood cores using mass spectrometry and random forest classification. <i>Applications in Plant Sciences</i> , 2017 , 5, 1600158	2.3	22
59	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3157-3167	3.2	55

58	A New Species and Introgression in Eastern Asian Hemlocks (Pinaceae: Tsuga). <i>Systematic Botany</i> , 2017 , 42, 733-746	0.7	10
57	Transcription through the eye of a needle: daily and annual cyclic gene expression variation in Douglas-fir needles. <i>BMC Genomics</i> , 2017 , 18, 558	4.5	18
56	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks (Quercus L. sect. Quercus). <i>PLoS ONE</i> , 2016 , 11, e0158221	3.7	24
55	Targeted Capture Sequencing in Whitebark Pine Reveals Range-Wide Demographic and Adaptive Patterns Despite Challenges of a Large, Repetitive Genome. <i>Frontiers in Plant Science</i> , 2016 , 7, 484	6.2	25
54	Phylogenetic marker development for target enrichment from transcriptome and genome skim data: the pipeline and its application in southern African Oxalis (Oxalidaceae). <i>Molecular Ecology Resources</i> , 2016 , 16, 1124-35	8.4	53
53	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. <i>PLoS ONE</i> , 2015 , 10, e0145031	3.7	17
52	Dual RNA-seq of the plant pathogen Phytophthora ramorum and its tanoak host. <i>Tree Genetics and Genomes</i> , 2014 , 10, 489-502	2.1	37
51	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , 2014 , 14, 67	3	18
50	Fragaria: a genus with deep historical roots and ripe for evolutionary and ecological insights. <i>American Journal of Botany</i> , 2014 , 101, 1686-99	2.7	88
49	Hyb-Seq: Combining target enrichment and genome skimming for plant phylogenomics. <i>Applications in Plant Sciences</i> , 2014 , 2, 1400042	2.3	227
48	Insights into phylogeny, sex function and age of Fragaria based on whole chloroplast genome sequencing. <i>Molecular Phylogenetics and Evolution</i> , 2013 , 66, 17-29	4.1	111
47	Microsatellite primers for the Pacific Northwest conifer Callitropsis nootkatensis (Cupressaceae). <i>Applications in Plant Sciences</i> , 2013 , 1, 1300025	2.3	
46	A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation. <i>BMC Genomics</i> , 2013 , 14, 137	4.5	50
45	Transcriptome characterization and detection of gene expression differences in aspen (Populus tremuloides). <i>Tree Genetics and Genomes</i> , 2013 , 9, 1031-1041	2.1	8
44	Horizontal transfer of DNA from the mitochondrial to the plastid genome and its subsequent evolution in milkweeds (apocynaceae). <i>Genome Biology and Evolution</i> , 2013 , 5, 1872-85	3.9	79
43	Low diversity in the mitogenome of sperm whales revealed by next-generation sequencing. <i>Genome Biology and Evolution</i> , 2013 , 5, 113-29	3.9	25
42	Separating the wheat from the chaff: mitigating the effects of noise in a plastome phylogenomic data set from Pinus L. (Pinaceae). <i>BMC Evolutionary Biology</i> , 2012 , 12, 100	3	82
41	Targeted enrichment strategies for next-generation plant biology. <i>American Journal of Botany</i> , 2012 , 99, 291-311	2.7	149

40	Navigating the tip of the genomic iceberg: Next-generation sequencing for plant systematics. <i>American Journal of Botany</i> , 2012 , 99, 349-64	2.7	386
39	Mitochondrial genome sequences illuminate maternal lineages of conservation concern in a rare carnivore. <i>BMC Ecology</i> , 2011 , 11, 10	2.7	56
38	Building a model: developing genomic resources for common milkweed (<i>Asclepias syriaca</i>) with low coverage genome sequencing. <i>BMC Genomics</i> , 2011 , 12, 211	4.5	89
37	Transcriptome characterization and polymorphism detection between subspecies of big sagebrush (<i>Artemisia tridentata</i>). <i>BMC Genomics</i> , 2011 , 12, 370	4.5	42
36	Microsatellite primers for the Pacific Northwest endemic conifer <i>Chamaecyparis lawsoniana</i> (Cupressaceae). <i>American Journal of Botany</i> , 2011 , 98, e323-5	2.7	3
35	Adventures in the enormous: a 1.8 million clone BAC library for the 21.7 Gb genome of loblolly pine. <i>PLoS ONE</i> , 2011 , 6, e16214	3.7	38
34	Development of novel chloroplast microsatellite markers to identify species in the <i>Agrostis</i> complex (Poaceae) and related genera. <i>Molecular Ecology Resources</i> , 2010 , 10, 738-40	8.4	9
33	What are the best seed sources for ecosystem restoration on BLM and USFS lands?. <i>Native Plants Journal</i> , 2010 , 11, 117-131	0.6	92
32	Tangled trios?: Characterizing a hybrid zone in <i>Castilleja</i> (Orobanchaceae). <i>American Journal of Botany</i> , 2009 , 96, 1519-31	2.7	14
31	Evolution and Natural History of the Cotton Genus 2009 , 3-22		89
30	Increasing phylogenetic resolution at low taxonomic levels using massively parallel sequencing of chloroplast genomes. <i>BMC Biology</i> , 2009 , 7, 84	7.3	372
29	Reticulate evolution and incomplete lineage sorting among the ponderosa pines. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 52, 498-511	4.1	101
28	Multiplex sequencing of plant chloroplast genomes using Solexa sequencing-by-synthesis technology. <i>Nucleic Acids Research</i> , 2008 , 36, e122	20.1	291
27	Fossil calibration of molecular divergence infers a moderate mutation rate and recent radiations for pinus. <i>Molecular Biology and Evolution</i> , 2007 , 24, 90-101	8.3	166
26	Interspecific phylogenetic analysis enhances intraspecific phylogeographical inference: a case study in <i>Pinus lambertiana</i> . <i>Molecular Ecology</i> , 2007 , 16, 3926-37	5.7	62
25	Multiple Nuclear Loci Reveal the Distinctiveness of the Threatened, Neotropical <i>Pinus chiapensis</i> . <i>Systematic Botany</i> , 2007 , 32, 703-717	0.7	12
24	Widespread genealogical nonmonophyly in species of <i>Pinus</i> subgenus <i>Strobus</i> . <i>Systematic Biology</i> , 2007 , 56, 163-81	8.4	131
23	Length polymorphism scanning is an efficient approach for revealing chloroplast DNA variation. <i>Genome</i> , 2006 , 49, 134-42	2.4	7

22	Phylogeny of the New World diploid cottons (<i>Gossypium</i> L., Malvaceae) based on sequences of three low-copy nuclear genes. <i>Plant Systematics and Evolution</i> , 2005 , 252, 199-214	1.3	37
21	Evolutionary relationships among <i>Pinus</i> (Pinaceae) subsections inferred from multiple low-copy nuclear loci. <i>American Journal of Botany</i> , 2005 , 92, 2086-100	2.7	75
20	Use of nuclear genes for phylogeny reconstruction in plants. <i>Australian Systematic Botany</i> , 2004 , 17, 145-1		325
19	Cryptic trysts, genomic mergers, and plant speciation. <i>New Phytologist</i> , 2004 , 161, 133-142	9.8	96
18	Pacific Northwest Forest Tree Seed Zones: A Template for Native Plants?. <i>Native Plants Journal</i> , 2004 , 5, 131-140	0.6	82
17	Genes duplicated by polyploidy show unequal contributions to the transcriptome and organ-specific reciprocal silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4649-54	11.5	652
16	Quantitative analysis of transcript accumulation from genes duplicated by polyploidy using cDNA-SSCP. <i>BioTechniques</i> , 2003 , 34, 726-30, 732, 734	2.5	22
15	Cryptic repeated genomic recombination during speciation in <i>Gossypium gossypoides</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 2475-89	3.8	63
14	Polyploidy and the evolutionary history of cotton. <i>Advances in Agronomy</i> , 2003 , 78, 139-186	7.7	494
13	Rate variation among nuclear genes and the age of polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003 , 20, 633-43	8.3	246
12	CRYPTIC REPEATED GENOMIC RECOMBINATION DURING SPECIATION IN GOSSYPIMUM GOSSYPIOIDES. <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 2475	3.8	5
11	Feast and famine in plant genomes. <i>Genetica</i> , 2002 , 115, 37-47	1.5	113
10	Intron size and genome size in plants. <i>Molecular Biology and Evolution</i> , 2002 , 19, 2346-52	8.3	62
9	Rapid diversification of the cotton genus (<i>Gossypium</i> : Malvaceae) revealed by analysis of sixteen nuclear and chloroplast genes. <i>American Journal of Botany</i> , 2002 , 89, 707-25	2.7	193
8	Length and sequence heterogeneity in 5S rDNA of <i>Populus deltoides</i> . <i>Genome</i> , 2002 , 45, 1181-8	2.4	34
7	Comparative development of fiber in wild and cultivated cotton. <i>Evolution & Development</i> , 2001 , 3, 3-17	2.6	119
6	Simple methods for isolating homoeologous loci from allopolyploid genomes. <i>Genome</i> , 1998 , 41, 756-762	2.4	20
5	The tortoise and the hare: choosing between noncoding plastome and nuclear <i>Adh</i> sequences for phylogeny reconstruction in a recently diverged plant group. <i>American Journal of Botany</i> , 1998 , 85, 1301-1315	2.7	380

4	Monitoring Fluoride with Honey Bees in the Upper Snake River Plain of Idaho. <i>Journal of Environmental Quality</i> , 1996 , 25, 868-877	3-4	6
3	Polymorphism and concerted evolution in a tandemly repeated gene family: 5S ribosomal DNA in diploid and allopolyploid cottons. <i>Journal of Molecular Evolution</i> , 1996 , 42, 685-705	3-1	193
2	Inhibition of reverse transcriptase from feline immunodeficiency virus by analogs of 2-Deoxyadenosine-5-Phosphate. <i>Biochemical Pharmacology</i> , 1992 , 44, 1375-81	6	22
1	Transcription through the eye of a needle: daily and annual cycles of gene expression variation in Douglas-fir needles		2