

# Richard C Cronn

## List of Publications by Year in descending order

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74  
papers

8,673  
citations

76326

40  
h-index

82547

72  
g-index

80  
all docs

80  
docs citations

80  
times ranked

7571  
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimating the genetic diversity of Pacific salmon and trout using multigene eDNA metabarcoding. <i>Molecular Ecology</i> , 2021, 30, 4970-4990.	3.9	33
2	Range-wide assessment of a SNP panel for individualization and geolocalization of bigleaf maple ( <i>Acer</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	1
3	An Axiom SNP genotyping array for Douglas-fir. <i>BMC Genomics</i> , 2020, 21, 9.	2.8	25
4	Predicting the geographic origin of Spanish Cedar ( <i>Cedrela odorata</i> L.) based on DNA variation. <i>Conservation Genetics</i> , 2020, 21, 625-639.	1.5	11
5	Casting a broader net: Using microfluidic metagenomics to capture aquatic biodiversity data from diverse taxonomic targets. <i>Environmental DNA</i> , 2019, 1, 251-267.	5.8	12
6	Genomic resources for the Neotropical tree genus <i>Cedrela</i> (Meliaceae) and its relatives. <i>BMC Genomics</i> , 2019, 20, 58.	2.8	15
7	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.	8.0	60
8	Functional trait divergence and trait plasticity confer polyploid advantage in heterogeneous environments. <i>New Phytologist</i> , 2019, 221, 2286-2297.	7.3	84
9	A draft genome and transcriptome of common milkweed ( <i>Asclepias syriaca</i> ) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. <i>PeerJ</i> , 2019, 7, e7649.	2.0	19
10	Comparative Transcriptomics Among Four White Pine Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1461-1474.	1.8	35
11	Alignment-free genome comparison enables accurate geographic sourcing of white oak DNA. <i>BMC Genomics</i> , 2018, 19, 896.	2.8	6
12	Development of nuclear microsatellite loci for <i>Pinus albicaulis</i> Engelm. (Pinaceae), a conifer of conservation concern. <i>PLoS ONE</i> , 2018, 13, e0205423.	2.5	2
13	Evolution at the tips: <i>Asclepias</i> phylogenomics and new perspectives on leaf surfaces. <i>American Journal of Botany</i> , 2018, 105, 514-524.	1.7	19
14	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.	2.5	49
15	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.	2.0	64
16	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.	2.1	32
17	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3157-3167.	1.8	103
18	A New Species and Introgression in Eastern Asian Hemlocks (Pinaceae: <i>Tsuga</i> ). <i>Systematic Botany</i> , 2017, 42, 733-746.	0.5	15

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19	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.	2.8	35
20	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks ( <i>Quercus L. sect. Quercus</i> ). <i>PLoS ONE</i> , 2016, 11, e0158221.	2.5	34
21	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.	3.6	38
22	Phylogenetic marker development for target enrichment from transcriptome and genome skim data: the pipeline and its application in southern African <i>Oxalis</i> ( <i>Oxalidaceae</i> ). <i>Molecular Ecology Resources</i> , 2016, 16, 1124-1135.	4.8	101
23	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0145031.	2.5	28
24	<i>Fragaria</i> : A genus with deep historical roots and ripe for evolutionary and ecological insights. <i>American Journal of Botany</i> , 2014, 101, 1686-1699.	1.7	149
25	Hyb-Seq: Combining target enrichment and genome skimming for plant phylogenomics. <i>Applications in Plant Sciences</i> , 2014, 2, 1400042.	2.1	405
26	Dual RNA-seq of the plant pathogen <i>Phytophthora ramorum</i> and its tanoak host. <i>Tree Genetics and Genomes</i> , 2014, 10, 489-502.	1.6	45
27	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.	3.2	21
28	Insights into phylogeny, sex function and age of <i>Fragaria</i> based on whole chloroplast genome sequencing. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 17-29.	2.7	144
29	Microsatellite Primers for the Pacific Northwest Conifer <i>Callitropsis nootkatensis</i> ( <i>Cupressaceae</i> ). <i>Applications in Plant Sciences</i> , 2013, 1, 1300025.	2.1	0
30	A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation. <i>BMC Genomics</i> , 2013, 14, 137.	2.8	55
31	Transcriptome characterization and detection of gene expression differences in aspen ( <i>Populus</i> ) Tj ETQq1 1 0.784314 rgBT /Qverlock 1.6 8		
32	Horizontal Transfer of DNA from the Mitochondrial to the Plastid Genome and Its Subsequent Evolution in Milkweeds ( <i>Apocynaceae</i> ). <i>Genome Biology and Evolution</i> , 2013, 5, 1872-1885.	2.5	129
33	Low Diversity in the Mitogenome of Sperm Whales Revealed by Next-Generation Sequencing. <i>Genome Biology and Evolution</i> , 2013, 5, 113-129.	2.5	37
34	Navigating the tip of the genomic iceberg: Next-generation sequencing for plant systematics. <i>American Journal of Botany</i> , 2012, 99, 349-364.	1.7	558
35	Separating the wheat from the chaff: mitigating the effects of noise in a plastome phylogenomic data set from <i>Pinus L.</i> ( <i>Pinaceae</i> ). <i>BMC Evolutionary Biology</i> , 2012, 12, 100.	3.2	96
36	Targeted enrichment strategies for next-generation plant biology. <i>American Journal of Botany</i> , 2012, 99, 291-311.	1.7	212

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37	Mitochondrial genome sequences illuminate maternal lineages of conservation concern in a rare carnivore. <i>BMC Ecology</i> , 2011, 11, 10.	3.0	66
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.	2.8	104
39	Transcriptome characterization and polymorphism detection between subspecies of big sagebrush ( <i>Artemisia tridentata</i> ). <i>BMC Genomics</i> , 2011, 12, 370.	2.8	46
40	Microsatellite primers for the Pacific Northwest endemic conifer <i>Chamaecyparis lawsoniana</i> (Cupressaceae). <i>American Journal of Botany</i> , 2011, 98, e323-5.	1.7	3
41	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.	2.5	41
42	What are the best seed sources for ecosystem restoration on BLM and USFS lands?. <i>Native Plants Journal</i> , 2010, 11, 117-131.	0.2	114
43	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, 738-740.	4.8	11
44	Tangled trios?: Characterizing a hybrid zone in <i>Castilleja</i> (Orobanchaceae). <i>American Journal of Botany</i> , 2009, 96, 1519-1531.	1.7	21
45	Evolution and Natural History of the Cotton Genus. , 2009, , 3-22.		169
46	Increasing phylogenetic resolution at low taxonomic levels using massively parallel sequencing of chloroplast genomes. <i>BMC Biology</i> , 2009, 7, 84.	3.8	504
47	Reticulate evolution and incomplete lineage sorting among the ponderosa pines. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 498-511.	2.7	127
48	Multiplex sequencing of plant chloroplast genomes using Solexa sequencing-by-synthesis technology. <i>Nucleic Acids Research</i> , 2008, 36, e122-e122.	14.5	356
49	Multiple Nuclear Loci Reveal the Distinctiveness of the Threatened, Neotropical <i>Pinus chiapensis</i> . <i>Systematic Botany</i> , 2007, 32, 703-717.	0.5	16
50	Widespread Genealogical Nonmonophyly in Species of <i>Pinus</i> Subgenus <i>Strobus</i> . <i>Systematic Biology</i> , 2007, 56, 163-181.	5.6	158
51	Fossil Calibration of Molecular Divergence Infers a Moderate Mutation Rate and Recent Radiations for <i>Pinus</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 90-101.	8.9	197
52	Interspecific phylogenetic analysis enhances intraspecific phylogeographical inference: a case study in <i>Pinus lambertiana</i> . <i>Molecular Ecology</i> , 2007, 16, 3926-3937.	3.9	66
53	Length polymorphism scanning is an efficient approach for revealing chloroplast DNA variation. <i>Genome</i> , 2006, 49, 134-142.	2.0	8
54	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.	0.9	52

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55	Evolutionary relationships among <i>Pinus</i> (Pinaceae) subsections inferred from multiple low-copy nuclear loci. <i>American Journal of Botany</i> , 2005, 92, 2086-2100.	1.7	83
56	Use of nuclear genes for phylogeny reconstruction in plants. <i>Australian Systematic Botany</i> , 2004, 17, 145.	0.9	367
57	Cryptic trysts, genomic mergers, and plant speciation. <i>New Phytologist</i> , 2004, 161, 133-142.	7.3	124
58	Pacific Northwest Forest Tree Seed Zones: A Template for Native Plants?. <i>Native Plants Journal</i> , 2004, 5, 131-140.	0.2	104
59	CRYPTIC REPEATED GENOMIC RECOMBINATION DURING SPECIATION IN GOSSYPIUM GOSSYPIOIDES. Evolution; <i>International Journal of Organic Evolution</i> , 2003, 57, 2475-2489.	2.3	77
60	Polyploidy and the evolutionary history of cotton. <i>Advances in Agronomy</i> , 2003, 78, 139-186.	5.2	694
61	Rate Variation Among Nuclear Genes and the Age of Polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 633-643.	8.9	325
62	CRYPTIC REPEATED GENOMIC RECOMBINATION DURING SPECIATION IN GOSSYPIUM GOSSYPIOIDES. Evolution; <i>International Journal of Organic Evolution</i> , 2003, 57, 2475.	2.3	6
63	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, 4649-4654.	7.1	793
64	Quantitative Analysis of Transcript Accumulation from Genes Duplicated by Polyploidy Using cDNASSCP. <i>BioTechniques</i> , 2003, 34, 726-734.	1.8	23
65	Intron Size and Genome Size in Plants. <i>Molecular Biology and Evolution</i> , 2002, 19, 2346-2352.	8.9	67
66	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, 707-725.	1.7	249
67	Length and sequence heterogeneity in 5S rDNA of <i>Populus deltoides</i> . <i>Genome</i> , 2002, 45, 1181-1188.	2.0	38
68	Feast and famine in plant genomes. <i>Genetica</i> , 2002, 115, 37-47.	1.1	135
69	Comparative development of fiber in wild and cultivated cotton. <i>Evolution &amp; Development</i> , 2001, 3, 3-17.	2.0	145
70	Simple methods for isolating homoeologous loci from allopolyploid genomes. <i>Genome</i> , 1998, 41, 756-762.	2.0	22
71	The tortoise and the hare: choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group. <i>American Journal of Botany</i> , 1998, 85, 1301-1315.	1.7	423
72	Monitoring Fluoride with Honey Bees in the Upper Snake River Plain of Idaho. <i>Journal of Environmental Quality</i> , 1996, 25, 868-877.	2.0	6

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73	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.	1.8	217
74	Inhibition of reverse transcriptase from feline immunodeficiency virus by analogs of 2'-deoxyadenosine-5'-triphosphate. <i>Biochemical Pharmacology</i> , 1992, 44, 1375-1381.	4.4	31