

# Christopher A Saski

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

4,683  
citations

186265

28  
h-index

106344

65  
g-index

77  
all docs

77  
docs citations

77  
times ranked

5267  
citing authors

#	ARTICLE	IF	CITATIONS
1	An InÂVtro Co-Culture System for Rapid Differential Response to <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> Race 4 in Three Cotton Cultivars. <i>Plant Disease</i> , 2022, 106, 990-995.	1.4	5
2	Ppe.XapF: High throughput KASP assays to identify fruit response to <i>Xanthomonas arboricola</i> pv. <i>pruni</i> (Xap) in peach. <i>PLoS ONE</i> , 2022, 17, e0264543.	2.5	13
3	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
4	Characterization of metabolic responses, genetic variations, and microsatellite instability in ammonia-stressed CHO cells grown in fed-batch cultures. <i>BMC Biotechnology</i> , 2021, 21, 4.	3.3	10
5	Genetic Architecture of Maize Rind Strength Revealed by the Analysis of Divergently Selected Populations. <i>Plant and Cell Physiology</i> , 2021, 62, 1199-1214.	3.1	14
6	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
7	Comparative Transcriptomics of Non-Embryogenic and Embryogenic Callus in Semi-Recalcitrant and Non-Recalcitrant Upland Cotton Lines. <i>Plants</i> , 2021, 10, 1775.	3.5	10
8	Genome-wide identification, expression profiling, and network analysis of AT-hook gene family in maize. <i>Genomics</i> , 2020, 112, 1233-1244.	2.9	27
9	Homogeneity among glyphosate-resistant <i>Amaranthus palmeri</i> in geographically distant locations. <i>PLoS ONE</i> , 2020, 15, e0233813.	2.5	13
10	Autonomous replication sequences from the <i>Amaranthus palmeri</i> eccDNA replicon enable replication in yeast. <i>BMC Research Notes</i> , 2020, 13, 330.	1.4	14
11	Transcriptomic profiles of non-embryogenic and embryogenic callus cells in a highly regenerative upland cotton line ( <i>Gossypium hirsutum</i> L.). <i>BMC Developmental Biology</i> , 2020, 20, 25.	2.1	19
12	Quantitative Trait Loci Associated with <i>Rotylenchulus reniformis</i> Host Suitability in Soybean. <i>Phytopathology</i> , 2020, 110, 1511-1521.	2.2	8
13	A simple plant high-molecular-weight DNA extraction method suitable for single-molecule technologies. <i>Plant Methods</i> , 2020, 16, 38.	4.3	19
14	The eccDNA Replicon: A Heritable, Extranuclear Vehicle That Enables Gene Amplification and Glyphosate Resistance in <i>Amaranthus palmeri</i> . <i>Plant Cell</i> , 2020, 32, 2132-2140.	6.6	58
15	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
16	Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. <i>Plant Cell</i> , 2019, 31, 1968-1989.	6.6	63
17	Dissecting Resistance to <i>Phytophthora cinnamomi</i> in Interspecific Hybrid Chestnut Crosses Using Sequence-Based Genotyping and QTL Mapping. <i>Phytopathology</i> , 2019, 109, 1594-1604.	2.2	22
18	The Draft Genome of <i>Kochia scoparia</i> and the Mechanism of Glyphosate Resistance via Transposon-Mediated EPSPS Tandem Gene Duplication. <i>Genome Biology and Evolution</i> , 2019, 11, 2927-2940.	2.5	31

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19	A new reference genome for <i>Sorghum bicolor</i> reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. <i>BMC Genomics</i> , 2019, 20, 420.	2.8	73
20	Transcriptome Response of Female <i>Culicoides sonorensis</i> Biting Midges (Diptera: Ceratopogonidae) to Early Infection with Epizootic Hemorrhagic Disease Virus (EHDV-2). <i>Viruses</i> , 2019, 11, 473.	3.3	5
21	MicroRNA396-mediated alteration in plant development and salinity stress response in creeping bentgrass. <i>Horticulture Research</i> , 2019, 6, 48.	6.3	64
22	Omics Potential in Herbicide-Resistant Weed Management. <i>Plants</i> , 2019, 8, 607.	3.5	17
23	Genetic characterization of worldwide <i>Prunus domestica</i> (plum) germplasm using sequence-based genotyping. <i>Horticulture Research</i> , 2019, 6, 12.	6.3	58
24	DRMY1, a Myb-Like Protein, Regulates Cell Expansion and Seed Production in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 285-302.	3.1	15
25	Goosegrass Control and Turfgrass Injury Following Metribuzin and Topramezone Application with Immediate Irrigation. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2019, 54, 1621-1624.	1.0	2
26	Draft Genome Sequence of the 1,4-Dioxane-Degrading Bacterium <i>Pseudonocardia dioxanivorans</i> BERK-1. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
27	The power and potential of genomics in weed biology and management. <i>Pest Management Science</i> , 2018, 74, 2216-2225.	3.4	76
28	Extrachromosomal circular DNA-based amplification and transmission of herbicide resistance in crop weed <i>Amaranthus palmeri</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3332-3337.	7.1	159
29	An EST-SSR based genetic linkage map and identification of QTLs for anthracnose disease resistance in water yam ( <i>Dioscorea alata</i> L.). <i>PLoS ONE</i> , 2018, 13, e0197717.	2.5	28
30	The genome of the biting midge <i>Culicoides sonorensis</i> and gene expression analyses of vector competence for bluetongue virus. <i>BMC Genomics</i> , 2018, 19, 624.	2.8	19
31	Fixation and Laser Capture Microdissection of Plant Tissue for RNA Extraction and RNASeq Library Preparation. <i>Current Protocols in Plant Biology</i> , 2018, 3, 14-32.	2.8	3
32	RNA-Seq transcriptome analysis of <i>Amaranthus palmeri</i> with differential tolerance to glufosinate herbicide. <i>PLoS ONE</i> , 2018, 13, e0195488.	2.5	35
33	Genomic Sequencing of Japanese Plum ( <i>Prunus salicina</i> Lindl.) Mutants Provides a New Model for Rosaceae Fruit Ripening Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 21.	3.6	55
34	Bacterial and Viral Products Affect Differential Pattern Recognition Receptor Activation of Chicken Thrombocytes Evidenced through RNA Sequencing. <i>Journal of Immunology</i> , 2017, 199, 774-781.	0.8	13
35	Low glucose concentrations within typical industrial operating conditions have minimal effect on the transcriptome of recombinant CHO cells. <i>Biotechnology Progress</i> , 2017, 33, 771-785.	2.6	7
36	Complete gene sequence of spider attachment silk protein (PySp1) reveals novel linker regions and extreme repeat homogenization. <i>Insect Biochemistry and Molecular Biology</i> , 2017, 81, 80-90.	2.7	48

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37	Sub genome anchored physical frameworks of the allotetraploid Upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq1 17, 15274.	0.784314 3.3	rgBT /Over 23
38	The unique genomic landscape surrounding the EPSPS gene in glyphosate resistant <i>Amaranthus palmeri</i> : a repetitive path to resistance. <i>BMC Genomics</i> , 2017, 18, 91.	2.8	54
39	Transcriptome Profile of the Chicken Thrombocyte: New Implications as an Advanced Immune Effector Cell. <i>PLoS ONE</i> , 2016, 11, e0163890.	2.5	25
40	Developing expressed sequence tag libraries and the discovery of simple sequence repeat markers for two species of raspberry ( <i>Rubus</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 258.	3.6	13
41	<i>Entamoeba histolytica</i> Dmc1 Catalyzes Homologous DNA Pairing and Strand Exchange That Is Stimulated by Calcium and Hop2-Mnd1. <i>PLoS ONE</i> , 2015, 10, e0139399.	2.5	9
42	Sequence composition of BAC clones and SSR markers mapped to Upland cotton chromosomes 11 and 21 targeting resistance to soil-borne pathogens. <i>Frontiers in Plant Science</i> , 2015, 6, 791.	3.6	22
43	BAC-End Sequence-Based SNP Mining in Allotetraploid Cotton ( <i>Gossypium</i> ) Utilizing Resequencing Data, Phylogenetic Inferences, and Perspectives for Genetic Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1095-1105.	1.8	20
44	Making a chocolate chip: development and evaluation of a 6K SNP array for <i>Theobroma cacao</i> . <i>DNA Research</i> , 2015, 22, 279-291.	3.4	46
45	Sequencing of allotetraploid cotton ( <i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
46	BAC Sequencing Using Pooled Methods. <i>Methods in Molecular Biology</i> , 2015, 1227, 55-67.	0.9	6
47	Impact of the blood meal on humoral immunity and microbiota in the gut of female <i>Culicoides sonorensis</i> . <i>Veterinaria Italiana</i> , 2015, 51, 385-92.	0.5	10
48	Genomic Resources for Water Yam ( <i>Dioscorea alata</i> L.): Analyses of EST-Sequences, De Novo Sequencing and GBS Libraries. <i>PLoS ONE</i> , 2015, 10, e0134031.	2.5	29
49	The Reference Transcriptome of the Adult Female Biting Midge ( <i>Culicoides sonorensis</i> ) and Differential Gene Expression Profiling during Teneral, Blood, and Sucrose Feeding Conditions. <i>PLoS ONE</i> , 2014, 9, e98123.	2.5	20
50	Gene discovery and differential expression analysis of humoral immune response elements in female <i>Culicoides sonorensis</i> (Diptera: Ceratopogonidae). <i>Parasites and Vectors</i> , 2014, 7, 388.	2.5	17
51	Studying <i>Culicoides</i> vectors of BTV in the post-genomic era: Resources, bottlenecks to progress and future directions. <i>Virus Research</i> , 2014, 182, 43-49.	2.2	49
52	A physical map of the Chinese chestnut ( <i>Castanea mollissima</i> ) genome and its integration with the genetic map. <i>Tree Genetics and Genomes</i> , 2013, 9, 525-537.	1.6	36
53	Choline Supplementation and DNA Methylation in the Hippocampus and Prefrontal Cortex of Rats Exposed to Alcohol During Development. <i>Alcoholism: Clinical and Experimental Research</i> , 2012, 36, 1701-1709.	2.4	121
54	Isolation and characterization of 12 microsatellites for the commercially important sablefish, <i>Anoplopoma fimbria</i> . <i>Conservation Genetics Resources</i> , 2012, 4, 415-417.	0.8	5

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55	A genetically anchored physical framework for <i>Theobroma cacao</i> cv. Matina 1-6. <i>BMC Genomics</i> , 2011, 12, 413.	2.8	13
56	Complete Plastid Genome Sequences of Three Rosids ( <i>Castanea</i> , <i>Prunus</i> , <i>Theobroma</i> ): Evidence for At Least Two Independent Transfers of <i>rpl22</i> to the Nucleus. <i>Molecular Biology and Evolution</i> , 2011, 28, 835-847.	8.9	203
57	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
58	Genomic tools development for <i>Aquilegia</i> : construction of a BAC-based physical map. <i>BMC Genomics</i> , 2010, 11, 621.	2.8	13
59	Divergence genetics analysis reveals historical population genetic processes leading to contrasting phylogeographic patterns in co-distributed species. <i>Molecular Ecology</i> , 2010, 19, 5043-5060.	3.9	47
60	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2009–30 November 2009. <i>Molecular Ecology Resources</i> , 2010, 10, 404-408.	4.8	84
61	The complete nucleotide sequence of the cassava ( <i>Manihot esculenta</i> ) chloroplast genome and the evolution of <i>atpF</i> in Malpighiales: RNA editing and multiple losses of a group II intron. <i>Theoretical and Applied Genetics</i> , 2008, 116, 723-37.	3.6	96
62	Complete chloroplast genome sequences of <i>Hordeum vulgare</i> , <i>Sorghum bicolor</i> and <i>Agrostis stolonifera</i> , and comparative analyses with other grass genomes. <i>Theoretical and Applied Genetics</i> , 2007, 115, 571-590.	3.6	194
63	Complete chloroplast genome sequences of <i>Solanum bulbocastanum</i> , <i>Solanum lycopersicum</i> and comparative analyses with other Solanaceae genomes. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1503-1518.	3.6	157
64	Involvement of Coenzyme M during Aerobic Biodegradation of Vinyl Chloride and Ethene by <i>Pseudomonas putida</i> Strain AJ and <i>Ochrobactrum</i> sp. Strain TD. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3756-3758.	3.1	33
65	Complete Chloroplast Genome Sequence of <i>Glycine max</i> and Comparative Analyses with other Legume Genomes. <i>Plant Molecular Biology</i> , 2005, 59, 309-322.	3.9	255