

Peter A Crisp

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

2,918
citations

394421

19
h-index

289244

40
g-index

56
all docs

56
docs citations

56
times ranked

4120
citing authors

#	ARTICLE	IF	CITATIONS
1	Reconsidering plant memory: Intersections between stress recovery, RNA turnover, and epigenetics. <i>Science Advances</i> , 2016, 2, e1501340.	10.3	477
2	Evidence for a SAL1-PAP Chloroplast Retrograde Pathway That Functions in Drought and High Light Signaling in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011, 23, 3992-4012.	6.6	473
3	Learning the Languages of the Chloroplast: Retrograde Signaling and Beyond. <i>Annual Review of Plant Biology</i> , 2016, 67, 25-53.	18.7	455
4	Regulation of Carotenoid Composition and Shoot Branching in <i>Arabidopsis</i> by a Chromatin Modifying Histone Methyltransferase, SDG8. <i>Plant Cell</i> , 2009, 21, 39-53.	6.6	207
5	A chloroplast retrograde signal, 3 ^{â€™} -phosphoadenosine 5 ^{â€™} -phosphate, acts as a secondary messenger in abscisic acid signaling in stomatal closure and germination. <i>ELife</i> , 2017, 6, .	6.0	132
6	Subset of heat-shock transcription factors required for the early response of <i>Arabidopsis</i> to excess light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14474-14479.	7.1	123
7	The <i>Arabidopsis</i> DNA Methylome Is Stable under Transgenerational Drought Stress. <i>Plant Physiology</i> , 2017, 175, 1893-1912.	4.8	112
8	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2017, 29, 1836-1863.	6.6	90
9	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23991-24000.	7.1	67
10	Population-level analysis reveals the widespread occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. <i>Genome Biology</i> , 2019, 20, 243.	8.8	65
11	A Novel <i>fry1</i> Allele Reveals the Existence of a Mutant Phenotype Unrelated to 5 ^{â€²} ->3 ^{â€²} Exoribonuclease (XRN) Activities in <i>Arabidopsis thaliana</i> Roots. <i>PLoS ONE</i> , 2011, 6, e16724.	2.5	64
12	Chloroplast-to-nucleus communication. <i>Plant Signaling and Behavior</i> , 2010, 5, 1575-1582.	2.4	63
13	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	6.6	60
14	Uncoupling High Light Responses from Singlet Oxygen Retrograde Signaling and Spatial-Temporal Systemic Acquired Acclimation. <i>Plant Physiology</i> , 2016, 171, 1734-1749.	4.8	59
15	Heritable Epigenomic Changes to the Maize Methylome Resulting from Tissue Culture. <i>Genetics</i> , 2018, 209, 983-995.	2.9	57
16	Monitoring the interplay between transposable element families and DNA methylation in maize. <i>PLoS Genetics</i> , 2019, 15, e1008291.	3.5	56
17	Optimization of multiplexed CRISPR/Cas9 system for highly efficient genome editing in <i>Setaria viridis</i> . <i>Plant Journal</i> , 2020, 104, 828-838.	5.7	48
18	Maintenance of pre-existing DNA methylation states through recurring excess-light stress. <i>Plant, Cell and Environment</i> , 2018, 41, 1657-1672.	5.7	33

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19	Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. <i>Plant Cell</i> , 2022, 34, 514-534.	6.6	30
20	Epigenetic features drastically impact CRISPR-Cas9 efficacy in plants. <i>Plant Physiology</i> , 2022, 190, 1153-1164.	4.8	25
21	RNA Polymerase II Read-Through Promotes Expression of Neighboring Genes in SAL1-PAP-XRN Retrograde Signaling. <i>Plant Physiology</i> , 2018, 178, 1614-1630.	4.8	23
22	Molecular and physiological responses during thermal acclimation of leaf photosynthesis and respiration in rice. <i>Plant, Cell and Environment</i> , 2020, 43, 594-610.	5.7	23
23	Epigenetic Regulation of ABA-Induced Transcriptional Responses in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1727-1743.	1.8	18
24	Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize. <i>Plant Physiology</i> , 2021, 186, 420-433.	4.8	16
25	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020, 182, 318-331.	4.8	14
26	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , 2021, 217, 1-13.	2.9	14
27	Beyond the gene: epigenetic and cis-regulatory targets offer new breeding potential for the future. <i>Current Opinion in Biotechnology</i> , 2022, 73, 88-94.	6.6	13
28	Opportunities to Use DNA Methylation to Distil Functional Elements in Large Crop Genomes. <i>Molecular Plant</i> , 2019, 12, 282-284.	8.3	12
29	A community-led initiative for training in reproducible research. <i>ELife</i> , 2021, 10, .	6.0	10
30	Current status and prospects of plant genome editing in Australia. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2021, 57, 574-583.	2.1	8
31	Grafting in Arabidopsis. <i>Methods in Molecular Biology</i> , 2014, 1062, 155-163.	0.9	8
32	Hybrid Decay: A Transgenerational Epigenetic Decline in Vigor and Viability Triggered in Backcross Populations of Teosinte with Maize. <i>Genetics</i> , 2019, 213, 143-160.	2.9	7
33	Enzymes degraded under high light maintain proteostasis by transcriptional regulation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121362119.	7.1	6
34	Genetic suppression of plant development and chloroplast biogenesis via the Snowy Cotyledon 3 and Phytochrome B pathways. <i>Functional Plant Biology</i> , 2015, 42, 676.	2.1	5
35	Epigenome guided crop improvement: current progress and future opportunities. <i>Emerging Topics in Life Sciences</i> , 2022, 6, 141-151.	2.6	5
36	The Maize Methyloome. <i>Compendium of Plant Genomes</i> , 2018, , 81-96.	0.5	3

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37	Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. <i>C3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
38	Harnessing genetic variation at regulatory regions to fine-tune traits for climate-resilient crops. <i>Molecular Plant</i> , 2022, 15, 222-224.	8.3	2
39	Decoding the sorghum methylome: understanding epigenetic contributions to agronomic traits. <i>Biochemical Society Transactions</i> , 2022, 50, 583-596.	3.4	2
40	Genome-wide loss of CHH methylation with limited transcriptome changes in <i>Setaria viridis</i> DOMAINS REARRANGED METHYLTRANSFERASE (DRM) mutants. <i>Plant Journal</i> , 2022, 111, 103-116.	5.7	2