Paul D Shaw

List of Publications by Year
in descending order

28 papers	4,111 citations	361413 20 h-index	501196 28 g-index
29 all docs	29 docs citations	29 times ranked	7032 citing authors

#	Article	IF	Citations
1	Using Tablet for visual exploration of second-generation sequencing data. Briefings in Bioinformatics, 2013, 14, 193-202.	6.5	836
2	Tablet—next generation sequence assembly visualization. Bioinformatics, 2010, 26, 401-402.	4.1	590
3	Natural variation in a homolog of Antirrhinum CENTRORADIALIS contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genetics, 2012, 44, 1388-1392.	21.4	477
4	A structured mutant population for forward and reverse genetics in Barley (<i>Hordeum vulgare</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	5.7	339
5	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21611-21616.	7.1	259
6	Development and Evaluation of a Barley 50k iSelect SNP Array. Frontiers in Plant Science, 2017, 8, 1792.	3.6	257
7	The genetic diversity and evolution of field pea (Pisum) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. BMC Evolutionary Biology, 2010, 10, 44.	3.2	169
8	Flapjack—graphical genotype visualization. Bioinformatics, 2010, 26, 3133-3134.	4.1	168
9	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. Nature Communications, 2020, 11, 4572.	12.8	129
10	An hnRNP-like RNA-binding protein affects alternative splicing by in vivo interaction with transcripts in Arabidopsis thaliana. Nucleic Acids Research, 2012, 40, 11240-11255.	14.5	124
11	Genome-wide association mapping of agronomic and morphologic traits in highly structured populations of barley cultivars. Theoretical and Applied Genetics, 2012, 124, 233-246.	3.6	122
12	Plant snoRNA database. Nucleic Acids Research, 2003, 31, 432-435.	14.5	82
13	BrAPI—an application programming interface for plant breeding applications. Bioinformatics, 2019, 35, 4147-4155.	4.1	82
14	Arabidopsis nucleolar protein database (AtNoPDB). Nucleic Acids Research, 2004, 33, D633-D636.	14.5	68
15	Helium: visualization of large scale plant pedigrees. BMC Bioinformatics, 2014, 15, 259.	2.6	67
16	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. Frontiers in Plant Science, 2019, 10, 544.	3.6	66
17	Mobilizing Crop Biodiversity. Molecular Plant, 2020, 13, 1341-1344.	8.3	50
18	Development and mapping of DArT markers within the Festuca - Lolium complex. BMC Genomics, 2009, 10, 473.	2.8	49

#	ARTICLE	IF	CITATIONS
19	Small changes in ambient temperature affect alternative splicing in *Arabidopsis thaliana*. Plant Signaling and Behavior, 2013, 8, e24638.	2.4	34
20	Comparative visualization of genetic and physical maps with Strudel. Bioinformatics, 2011, 27, 1307-1308.	4.1	33
21	From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. Crop Science, 2021, 61, 1538-1566.	1.8	26
22	Association mapping of malting quality traits in UK spring and winter barley cultivar collections. Theoretical and Applied Genetics, 2020, 133, 2567-2582.	3.6	23
23	Resistance to Rhynchosporium commune in a collection of European spring barley germplasm. Theoretical and Applied Genetics, 2018, 131, 2513-2528.	3.6	17
24	Arabidopsis PTB 1 and PTB 2 proteins negatively regulate splicing of a mini€exon splicing reporter and affect alternative splicing of endogenous genes differentially. New Phytologist, 2014, 203, 424-436.	7.3	15
25	Germinate 3: Development of a Common Platform to Support the Distribution of Experimental Data on Crop Wild Relatives. Crop Science, 2017, 57, 1259-1273.	1.8	15
26	An Induced Mutation in HvRECQL4 Increases the Overall Recombination and Restores Fertility in a Barley HvMLH3 Mutant Background. Frontiers in Plant Science, 2021, 12, 706560.	3.6	8
27	Development of High Yielding Cowpea [Vigna unguiculata (L.) Walp.] Lines with Improved Quality Seeds through Mutation and Pedigree Selection Methods. Horticulturae, 2021, 7, 271.	2.8	4
28	GridScore: a tool for accurate, cross-platform phenotypic data collection and visualization. BMC Bioinformatics, 2022, 23, .	2.6	2