David F Marshall

List of Publications by Year
in descending order

73 papers	10,198 citations	81900 39 h-index	79698 73 g-index
75 all docs	75 docs citations	75 times ranked	13183 citing authors

#	Article	IF	Citations
1	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
2	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. Nature Communications, 2020, 11, 4572.	12.8	129
3	<scp>RNA</scp>iâ€suppression of barley caffeic acid <i>O</i>â€methyltransferase modifies lignin despite redundancy in the gene family. Plant Biotechnology Journal, 2019, 17, 594-607.	8.3	37
4	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
5	An ultra-high density genetic linkage map of perennial ryegrass (<i>Lolium perenne</i>) using genotyping by sequencing (GBS) based on a reference shotgun genome assembly. Annals of Botany, 2016, 118, 71-87.	2.9	31
6	Analytical and Decision Support Tools for Genomics-Assisted Breeding. Trends in Plant Science, 2016, 21, 354-363.	8.8	70
7	Tablet: Visualizing Next-Generation Sequence Assemblies and Mappings. Methods in Molecular Biology, 2016, 1374, 253-268.	0.9	48
8	An investigation of causes of false positive single nucleotide polymorphisms using simulated reads from a small eukaryote genome. BMC Bioinformatics, 2015, 16, 382.	2.6	42
9	Evolutionary Dynamics of the Cellulose Synthase Gene Superfamily in Grasses. Plant Physiology, 2015, 168, 968-983.	4.8	55
10	The lowâ€recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. Plant Journal, 2014, 79, 981-992.	5.7	30
11	The use of genotyping by sequencing in blackcurrant (Ribes nigrum): developing high-resolution linkage maps in species without reference genome sequences. Molecular Breeding, 2014, 33, 835-849.	2.1	53
12	In silico identification and characterization of conserved plant microRNAs in barley. Open Life Sciences, 2014, 9, 841-852.	1.4	1
13	Helium: visualization of large scale plant pedigrees. BMC Bioinformatics, 2014, 15, 259.	2.6	67
14	Genome-Tagged Amplification (GTA): a PCR-based method to prepare sample-tagged amplicons from hundreds of individuals for next generation sequencing. Molecular Breeding, 2014, 34, 977-988.	2.1	7
15	The Barley Genome Sequence Assembly Reveals Three Additional Members of the CslF (1,3;1,4)-Î²-Glucan Synthase Gene Family. PLoS ONE, 2014, 9, e90888.	2.5	39
16	Using Tablet for visual exploration of second-generation sequencing data. Briefings in Bioinformatics, 2013, 14, 193-202.	6.5	836
17	Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. G3: Genes, Genomes, Genetics, 2013, 3, 2031-2047.	1.8	244
18	Identification and Characterization of miRNA Transcriptome in Potato by High-Throughput Sequencing. PLoS ONE, 2013, 8, e57233.	2.5	119

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19	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
20	Genome sequence and analysis of the tuber crop potato. Nature, 2011, 475, 189-195.	27.8	1,912
21	Highly parallel gene-to-BAC addressing using microarrays. BioTechniques, 2011, 50, 165-174.	1.8	8
22	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. Nature Genetics, 2011, 43, 169-172.	21.4	302
23	Syringyl Lignin Is Unaltered by Severe Sinapyl Alcohol Dehydrogenase Suppression in Tobacco. Plant Cell, 2011, 23, 4492-4506.	6.6	34
24	Comparative visualization of genetic and physical maps with Strudel. Bioinformatics, 2011, 27, 1307-1308.	4.1	33
25	A Robust Statistical Method for Association-Based eQTL Analysis. PLoS ONE, 2011, 6, e23192.	2.5	5
26	Exploiting induced variation to dissect quantitative traits in barley. Biochemical Society Transactions, 2010, 38, 683-688.	3.4	11
27	Cereal variety identification using MALDI-TOF mass spectrometry SNP genotyping. Journal of Cereal Science, 2010, 52, 356-361.	3.7	14
28	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
29	An eQTL Analysis of Partial Resistance to Puccinia hordei in Barley. PLoS ONE, 2010, 5, e8598.	2.5	77
30	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
31	Flapjackâ€"graphical genotype visualization. Bioinformatics, 2010, 26, 3133-3134.	4.1	168
32	Tabletâ€"next generation sequence assembly visualization. Bioinformatics, 2010, 26, 401-402.	4.1	590
33	Whole-genome association mapping in elite inbred crop varietiesThis article is one of a selection of papers from the conference â€œExploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farmingâ€. Genome, 2010, 53, 967-972.	2.0	22
34	Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582.	2.8	570
35	The 172-kb genomic DNA region of the O. rufipogon yld1.1 locus: comparative sequence analysis with O. sativa ssp. japonica and O. sativa ssp. indica. Functional and Integrative Genomics, 2009, 9, 97-108.	3.5	3
36	TOPALi v2: a rich graphical interface for evolutionary analyses of multiple alignments on HPC clusters and multi-core desktops. Bioinformatics, 2009, 25, 126-127.	4.1	578

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37	Exploiting regulatory variation to identify genes underlying quantitative resistance to the wheat stem rust pathogen Puccinia graminis f. sp. tritici in barley. Theoretical and Applied Genetics, 2008, 117, 261-272.	3.6	43
38	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. BMC Genetics, 2008, 9, 73.	2.7	26
39	Intronic noncoding RNAs and splicing. Trends in Plant Science, 2008, 13, 335-342.	8.8	129
40	Molecular barley breeding. Euphytica, 2007, 158, 295-303.	1.2	29
41	A hAT superfamily transposase recruited by the cereal grass genome. Molecular Genetics and Genomics, 2006, 275, 553-563.	2.1	35
42	An atlas of gene expression from seed to seed through barley development. Functional and Integrative Genomics, 2006, 6, 202-211.	3.5	138
43	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18656-18661.	7.1	309
44	Characterisation and functional analysis of two barley caleosins expressed during barley caryopsis development. Planta, 2005, 221, 513-522.	3.2	27
45	Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. Molecular Genetics and Genomics, 2005, 274, 515-527.	2.1	250
46	A comparative analysis of transcript abundance using SAGE and Affymetrix arrays. Functional and Integrative Genomics, 2005, 5, 163-174.	3.5	36
47	GERMINATE. A Generic Database for Integrating Genotypic and Phenotypic Information for Plant Genetic Resource Collections. Plant Physiology, 2005, 139, 619-631.	4.8	35
48	Single-feature polymorphism discovery in the barley transcriptome. Genome Biology, 2005, 6, R54.	9.6	130
49	TOPALi: software for automatic identification of recombinant sequences within DNA multiple alignments. Bioinformatics, 2004, 20, 1806-1807.	4.1	372
50	Relocalization of Nuclear ALY Proteins to the Cytoplasm by the Tomato Bushy Stunt Virus P19 Pathogenicity Protein. Plant Physiology, 2004, 135, 2411-2423.	4.8	88
51	A structured mutant population for forward and reverse genetics in Barley (<i>Hordeum vulgare</i>) Tj ETQq1 1 0.784314 rgBT /Over	5.7	339
52	Changes in gene expression during meristem activation processes in Solanum tuberosum with a focus on the regulation of an auxin response factor gene*. Journal of Experimental Botany, 2004, 55, 613-622.	4.8	78
53	Arabidopsis nucleolar protein database (AtNoPDB). Nucleic Acids Research, 2004, 33, D633-D636.	14.5	68
54	Sufficient Conditions for Coordination of Coupled Nonlinear Biochemical Systems: Analysis of a Simple, Representative Example. Journal of Biological Systems, 2003, 11, 275-291.	1.4	1

#	ARTICLE	IF	CITATIONS
55	Title is missing!. Genetic Resources and Crop Evolution, 2002, 49, 59-66.	1.6	11
56	Morphological differentiation in four species of the genus Lolium. Genetic Resources and Crop Evolution, 2000, 47, 247-255.	1.6	21
57	An integrated AFLP and RFLP Brassica oleracea linkage map from two morphologically distinct doubled-haploid mapping populations. Theoretical and Applied Genetics, 2000, 100, 75-81.	3.6	130
58	Analysis of Arabidopsis genome sequence reveals a large new gene family in plants. Plant Molecular Biology, 1999, 39, 927-932.	3.9	47
59	Physical mapping of DNA repetitive sequences to mitotic and meiotic chromosomes of Brassica oleracea var. alboglabra by fluorescence in situ hybridization. Heredity, 1998, 81, 666-673.	2.6	60
60	Higher recombination frequencies in female compared to male meioses in Brassica oleracea. Theoretical and Applied Genetics, 1996, 92-92, 363-367.	3.6	42
61	The genetic control of maturity and seed characters in sunflower crosses. Journal of Agricultural Science, 1995, 125, 69-78.	1.3	2
62	Genetics of genetic conservation. I. Sample size when collecting germplasm. Euphytica, 1995, 84, 89-99.	1.2	101
63	Genetics of genetic conservation. II. Sample size when collecting seed of cross-pollinating species and the information that can be obtained from the evaluation of material held in gene banks. Euphytica, 1995, 84, 101-107.	1.2	25
64	The population genetics of the self-incompatibility polymorphism in Papaver rhoeas. VIII. Sampling effects as a possible cause of unequal allele frequencies. Heredity, 1994, 72, 345-352.	2.6	10
65	A Century of Evolution in Spartina anglica. Advances in Ecological Research, 1991, 21, 1-62.	2.7	169
66	The evolution of Spartina anglica C.E. Hubbard (Gramineae): origin and genetic variability. Biological Journal of the Linnean Society, 1991, 43, 111-126.	1.6	88
67	The evolution of Spartina anglica C. E. Hubbard (Gramineae): genetic variation and status of the parental species in Britain. Biological Journal of the Linnean Society, 1991, 44, 369-380.	1.6	41
68	Morph differences in seed output and the maintenance of the polymorphism for capitulum type and outcrossing rate in <i>Senecio vulgaris</i> L. Transactions of the Botanical Society of Edinburgh, 1987, 45, 107-119.	0.1	8
69	Gametophytic self-incompatibility re-examined: a reply. Heredity, 1985, 54, 131-138.	2.6	27
70	Polymorphism for outcrossing frequency at the ray floret locus in Senecio vulgaris L. II. Confirmation. Heredity, 1984, 52, 331-336.	2.6	54
71	Polymorphism for outcrossing frequency at the ray floret locus in senecio vulgaris L. III. causes. Heredity, 1984, 53, 145-149.	2.6	46
72	Polymorphism for outcrossing frequency at the ray floret locus in Senecio vulgaris L. I. Evidence. Heredity, 1982, 48, 227-235.	2.6	77

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73	On the frequency of introgression of the radiate (Tr) allele from Senecio squalidus L. into Senecio vulgaris L.. Heredity, 1980, 45, 133-135.	2.6	25