

# David F Marshall

## List of Publications by Year in descending order

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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	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
2	Using Tablet for visual exploration of second-generation sequencing data. <i>Briefings in Bioinformatics</i> , 2013, 14, 193-202.	6.5	836
3	Tablet—next generation sequence assembly visualization. <i>Bioinformatics</i> , 2010, 26, 401-402.	4.1	590
4	TOPALi v2: a rich graphical interface for evolutionary analyses of multiple alignments on HPC clusters and multi-core desktops. <i>Bioinformatics</i> , 2009, 25, 126-127.	4.1	578
5	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	2.8	570
6	Natural variation in a homolog of <i>Antirrhinum CENTRORADIALIS</i> contributed to spring growth habit and environmental adaptation in cultivated barley. <i>Nature Genetics</i> , 2012, 44, 1388-1392.	21.4	477
7	TOPALi: software for automatic identification of recombinant sequences within DNA multiple alignments. <i>Bioinformatics</i> , 2004, 20, 1806-1807.	4.1	372
8	A structured mutant population for forward and reverse genetics in Barley ( <i>Hordeum vulgare</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf .	9.7	339
9	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18656-18661.	7.1	309
10	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene <i>TEOSINTE BRANCHED 1</i> . <i>Nature Genetics</i> , 2011, 43, 169-172.	21.4	302
11	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21611-21616.	7.1	259
12	Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. <i>Molecular Genetics and Genomics</i> , 2005, 274, 515-527.	2.1	250
13	Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2031-2047.	1.8	244
14	A Century of Evolution in <i>Spartina anglica</i> . <i>Advances in Ecological Research</i> , 1991, 21, 1-62.	2.7	169
15	The genetic diversity and evolution of field pea ( <i>Pisum</i> ) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. <i>BMC Evolutionary Biology</i> , 2010, 10, 44.	3.2	169
16	Flapjack—graphical genotype visualization. <i>Bioinformatics</i> , 2010, 26, 3133-3134.	4.1	168
17	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	3.5	138
18	An integrated AFLP and RFLP <i>Brassica oleracea</i> linkage map from two morphologically distinct doubled-haploid mapping populations. <i>Theoretical and Applied Genetics</i> , 2000, 100, 75-81.	3.6	130

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19	Single-feature polymorphism discovery in the barley transcriptome. <i>Genome Biology</i> , 2005, 6, R54.	9.6	130
20	Intronic noncoding RNAs and splicing. <i>Trends in Plant Science</i> , 2008, 13, 335-342.	8.8	129
21	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	12.8	129
22	Identification and Characterization of miRNA Transcriptome in Potato by High-Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e57233.	2.5	119
23	Genetics of genetic conservation. I. Sample size when collecting germplasm. <i>Euphytica</i> , 1995, 84, 89-99.	1.2	101
24	The evolution of <i>Spartina anglica</i> C.E. Hubbard (Gramineae): origin and genetic variability. <i>Biological Journal of the Linnean Society</i> , 1991, 43, 111-126.	1.6	88
25	Relocalization of Nuclear ALY Proteins to the Cytoplasm by the Tomato Bushy Stunt Virus P19 Pathogenicity Protein. <i>Plant Physiology</i> , 2004, 135, 2411-2423.	4.8	88
26	Changes in gene expression during meristem activation processes in <i>Solanum tuberosum</i> with a focus on the regulation of an auxin response factor gene*. <i>Journal of Experimental Botany</i> , 2004, 55, 613-622.	4.8	78
27	Polymorphism for outcrossing frequency at the ray floret locus in <i>Senecio vulgaris</i> L. I. Evidence. <i>Heredity</i> , 1982, 48, 227-235.	2.6	77
28	An eQTL Analysis of Partial Resistance to <i>Puccinia hordei</i> in Barley. <i>PLoS ONE</i> , 2010, 5, e8598.	2.5	77
29	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	8.8	70
30	<i>Arabidopsis</i> nucleolar protein database (AtNoPDB). <i>Nucleic Acids Research</i> , 2004, 33, D633-D636.	14.5	68
31	Helium: visualization of large scale plant pedigrees. <i>BMC Bioinformatics</i> , 2014, 15, 259.	2.6	67
32	Physical mapping of DNA repetitive sequences to mitotic and meiotic chromosomes of <i>Brassica oleracea</i> var. <i>alboglabra</i> by fluorescence in situ hybridization. <i>Heredity</i> , 1998, 81, 666-673.	2.6	60
33	Evolutionary Dynamics of the Cellulose Synthase Gene Superfamily in Grasses. <i>Plant Physiology</i> , 2015, 168, 968-983.	4.8	55
34	Polymorphism for outcrossing frequency at the ray floret locus in <i>Senecio vulgaris</i> L. II. Confirmation. <i>Heredity</i> , 1984, 52, 331-336.	2.6	54
35	The use of genotyping by sequencing in blackcurrant ( <i>Ribes nigrum</i> ): developing high-resolution linkage maps in species without reference genome sequences. <i>Molecular Breeding</i> , 2014, 33, 835-849.	2.1	53
36	Tablet: Visualizing Next-Generation Sequence Assemblies and Mappings. <i>Methods in Molecular Biology</i> , 2016, 1374, 253-268.	0.9	48

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37	Analysis of Arabidopsis genome sequence reveals a large new gene family in plants. <i>Plant Molecular Biology</i> , 1999, 39, 927-932.	3.9	47
38	Polymorphism for outcrossing frequency at the ray floret locus in <i>senecio vulgaris</i> L. III. causes. <i>Heredity</i> , 1984, 53, 145-149.	2.6	46
39	Exploiting regulatory variation to identify genes underlying quantitative resistance to the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> in barley. <i>Theoretical and Applied Genetics</i> , 2008, 117, 261-272.	3.6	43
40	Higher recombination frequencies in female compared to male meioses in <i>Brassica oleracea</i> . <i>Theoretical and Applied Genetics</i> , 1996, 92-92, 363-367.	3.6	42
41	An investigation of causes of false positive single nucleotide polymorphisms using simulated reads from a small eukaryote genome. <i>BMC Bioinformatics</i> , 2015, 16, 382.	2.6	42
42	The evolution of <i>Spartina anglica</i> C. E. Hubbard (Gramineae): genetic variation and status of the parental species in Britain. <i>Biological Journal of the Linnean Society</i> , 1991, 44, 369-380.	1.6	41
43	The Barley Genome Sequence Assembly Reveals Three Additional Members of the CslF (1,3;1,4)- $\beta$ -Glucan Synthase Gene Family. <i>PLoS ONE</i> , 2014, 9, e90888.	2.5	39
44	RNAi suppression of barley caffeic acid O-methyltransferase modifies lignin despite redundancy in the gene family. <i>Plant Biotechnology Journal</i> , 2019, 17, 594-607.	8.3	37
45	A comparative analysis of transcript abundance using SAGE and Affymetrix arrays. <i>Functional and Integrative Genomics</i> , 2005, 5, 163-174.	3.5	36
46	GERMINATE. A Generic Database for Integrating Genotypic and Phenotypic Information for Plant Genetic Resource Collections. <i>Plant Physiology</i> , 2005, 139, 619-631.	4.8	35
47	A hAT superfamily transposase recruited by the cereal grass genome. <i>Molecular Genetics and Genomics</i> , 2006, 275, 553-563.	2.1	35
48	Syringyl Lignin Is Unaltered by Severe Sinapyl Alcohol Dehydrogenase Suppression in Tobacco. <i>Plant Cell</i> , 2011, 23, 4492-4506.	6.6	34
49	Comparative visualization of genetic and physical maps with Strudel. <i>Bioinformatics</i> , 2011, 27, 1307-1308.	4.1	33
50	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. <i>Annals of Botany</i> , 2016, 118, 71-87.	2.9	31
51	The low-recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. <i>Plant Journal</i> , 2014, 79, 981-992.	5.7	30
52	Molecular barley breeding. <i>Euphytica</i> , 2007, 158, 295-303.	1.2	29
53	Gametophytic self-incompatibility re-examined: a reply. <i>Heredity</i> , 1985, 54, 131-138.	2.6	27
54	Characterisation and functional analysis of two barley caleosins expressed during barley caryopsis development. <i>Planta</i> , 2005, 221, 513-522.	3.2	27

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55	Towards systems genetic analyses in barley: Integration of phenotypic, expression and genotype data into GeneNetwork. <i>BMC Genetics</i> , 2008, 9, 73.	2.7	26
56	From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. <i>Crop Science</i> , 2021, 61, 1538-1566.	1.8	26
57	On the frequency of introgression of the radiate (Tr) allele from <i>Senecio squalidus</i> L. into <i>Senecio vulgaris</i> L. <i>Heredity</i> , 1980, 45, 133-135.	2.6	25
58	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. <i>Euphytica</i> , 1995, 84, 101-107.	1.2	25
59	Whole-genome association mapping in elite inbred crop varieties This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 967-972.	2.0	22
60	Morphological differentiation in four species of the genus <i>Lolium</i> . <i>Genetic Resources and Crop Evolution</i> , 2000, 47, 247-255.	1.6	21
61	Germinate 3: Development of a Common Platform to Support the Distribution of Experimental Data on Crop Wild Relatives. <i>Crop Science</i> , 2017, 57, 1259-1273.	1.8	15
62	Cereal variety identification using MALDI-TOF mass spectrometry SNP genotyping. <i>Journal of Cereal Science</i> , 2010, 52, 356-361.	3.7	14
63	Title is missing!. <i>Genetic Resources and Crop Evolution</i> , 2002, 49, 59-66.	1.6	11
64	Exploiting induced variation to dissect quantitative traits in barley. <i>Biochemical Society Transactions</i> , 2010, 38, 683-688.	3.4	11
65	The population genetics of the self-incompatibility polymorphism in <i>Papaver rhoeas</i> . VIII. Sampling effects as a possible cause of unequal allele frequencies. <i>Heredity</i> , 1994, 72, 345-352.	2.6	10
66	Morph differences in seed output and the maintenance of the polymorphism for capitulum type and outcrossing rate in <i>Senecio vulgaris</i> L. <i>Transactions of the Botanical Society of Edinburgh</i> , 1987, 45, 107-119.	0.1	8
67	Highly parallel gene-to-BAC addressing using microarrays. <i>BioTechniques</i> , 2011, 50, 165-174.	1.8	8
68	Genome-Tagged Amplification (GTA): a PCR-based method to prepare sample-tagged amplicons from hundreds of individuals for next generation sequencing. <i>Molecular Breeding</i> , 2014, 34, 977-988.	2.1	7
69	A Robust Statistical Method for Association-Based eQTL Analysis. <i>PLoS ONE</i> , 2011, 6, e23192.	2.5	5
70	The 172-kb genomic DNA region of the <i>O. rufipogon</i> yld1.1 locus: comparative sequence analysis with <i>O. sativa</i> ssp. <i>japonica</i> and <i>O. sativa</i> ssp. <i>indica</i> . <i>Functional and Integrative Genomics</i> , 2009, 9, 97-108.	3.5	3
71	The genetic control of maturity and seed characters in sunflower crosses. <i>Journal of Agricultural Science</i> , 1995, 125, 69-78.	1.3	2
72	Sufficient Conditions for Coordination of Coupled Nonlinear Biochemical Systems: Analysis of a Simple, Representative Example. <i>Journal of Biological Systems</i> , 2003, 11, 275-291.	1.4	1

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73	In silico identification and characterization of conserved plant microRNAs in barley. Open Life Sciences, 2014, 9, 841-852.	1.4	1