David Grant

List of Publications by Year
in descending order

27 papers	6,517 citations	471509 17 h-index	610901 24 g-index
27 all docs	27 docs citations	27 times ranked	6540 citing authors

#	ARTICLE	IF	CITATIONS
1	A new decade and new data at SoyBase, the USDA-ARS soybean genetics and genomics database. Nucleic Acids Research, 2021, 49, D1496-D1501.	14.5	49
2	Using Crop Databases to Explore Phenotypes: From QTL to Candidate Genes. Plants, 2021, 10, 2494.	3.5	4
3	Ten quick tips for sharing open genomic data. PLoS Computational Biology, 2018, 14, e1006472.	3.2	8
4	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	52
5	SoyBase: A Comprehensive Database for Soybean Genetic and Genomic Data. Compendium of Plant Genomes, 2017, , 193-211.	0.5	2
6	The endogenous transposable element Tgm9 is suitable for generating knockout mutants for functional analyses of soybean genes and genetic improvement in soybean. PLoS ONE, 2017, 12, e0180732.	2.5	7
7	SoyBase and the Legume Information System: Accessing Information about the Soybean and Other Legume Genomes. , 2012, , 53-66.		3
8	Gene expression patterns are correlated with genomic and genic structure in soybean. Genome, 2011, 54, 10-18.	2.0	23
9	Changes in Twelve Homoeologous Genomic Regions in Soybean following Three Rounds of Polyploidy. Plant Cell, 2011, 23, 3129-3136.	6.6	66
10	Phenotypic and Genomic Analyses of a Fast Neutron Mutant Population Resource in Soybean Â Â. Plant Physiology, 2011, 156, 240-253.	4.8	175
11	SoyTEdb: a comprehensive database of transposable elements in the soybean genome. BMC Genomics, 2010, 11, 113.	2.8	122
12	RNA-Seq Atlas of Glycine max: A guide to the soybean transcriptome. BMC Plant Biology, 2010, 10, 160.	3.6	634
13	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	27.8	3,854
14	Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. Crop Science, 2010, 50, 1950-1960.	1.8	282
15	SoyBase, the USDA-ARS soybean genetics and genomics database. Nucleic Acids Research, 2010, 38, D843-D846.	14.5	553
16	An Integrative Approach to Genomic Introgression Mapping Â Â. Plant Physiology, 2010, 154, 3-12.	4.8	45
17	Molecular Mapping of Quantitative Trait Loci. , 2010, , 91-121.		1
18	Integrating microarray analysis and the soybean genome to understand the soybeans iron deficiency response. BMC Genomics, 2009, 10, 376.	2.8	56

#	ARTICLE	IF	CITATIONS
19	Identification of candidate signaling genes including regulators of chromosome condensation 1 protein family differentially expressed in the soybean–Phytophthora sojae interaction. Theoretical and Applied Genetics, 2009, 118, 399-412.	3.6	13
20	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. Genome, 2008, 51, 294-302.	2.0	50
21	Bioinformatic Resources for Soybean Genetic and Genomic Research. , 2008, , 141-159.		1
22	ESTminer: a suite of programs for gene and allele identification. Bioinformatics, 2005, 21, 691-693.	4.1	10
23	Mining EST databases to resolve evolutionary events in major crop species. Genome, 2004, 47, 868-876.	2.0	310
24	Soybean genomic survey: BAC-end sequences near RFLP and SSR markers. Genome, 2001, 44, 572-581.	2.0	66
25	RFLP map of soybean. Advances in Cellular and Molecular Biology of Plants, 2001, , 357-378.	0.2	3
26	Molecular characterization of iron deficiency chlorosis in soybean. Journal of Plant Nutrition, 2000, 23, 1929-1939.	1.9	55
27	Simple Sequence Repeat Diversity among Soybean Plant Introductions and Elite Genotypes. Crop Science, 2000, 40, 1452-1458.	1.8	73