Patrick J Gulick

List of Publications by Year
in descending order

27 papers	1,185 citations	471509 17 h-index	552781 26 g-index
27 all docs	27 docs citations	27 times ranked	1372 citing authors

#	Article	IF	Citations
1	Characterization of the heterotrimeric G protein gene families in Triticum aestivum and related species. 3 Biotech, 2022, 12, 99.	2.2	3
2	Characterization and expression of the <i>Pirin</i> gene family in <i>Triticum aestivum</i>. Genome, 2022, 65, 349-362.	2.0	6
3	Duplicated antagonistic EPF peptides optimize grass stomatal initiation. Development (Cambridge), 2021, 148, .	2.5	6
4	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	19
5	The stress induced caleosin, RD20/CLO3, acts as a negative regulator of GPA1 in Arabidopsis. Plant Molecular Biology, 2021, 107, 159-175.	3.9	7
6	<i>Aegilops tauschii</i>Genome Sequence: A Framework for Meta-analysis of Wheat QTLs. G3: Genes, Genomes, Genetics, 2019, 9, 841-853.	1.8	1
7	Characterization of the Esi3/RCI2/PMP3 gene family in the Triticeae. BMC Genomics, 2018, 19, 898.	2.8	14
8	Structural variation and rates of genome evolution in the grass family seen through comparison of sequences of genomes greatly differing in size. Plant Journal, 2018, 95, 487-503.	5.7	31
9	Genetic combining ability of coriander genotypes for agronomic and phytochemical traits in response to contrasting irrigation regimes. PLoS ONE, 2018, 13, e0199630.	2.5	14
10	Identification and characterization of rye genes not expressed in allohexaploid triticale. BMC Genomics, 2015, 16, 281.	2.8	43
11	Characterization of the caleosin gene family in the Triticeae. BMC Genomics, 2014, 15, 239.	2.8	21
12	Gene expression analysis in the roots of salt-stressed wheat and the cytogenetic derivatives of wheat combined with the salt-tolerant wheatgrass, Lophopyrum elongatum. Plant Cell Reports, 2014, 33, 189-201.	5.6	7
13	Heterotrimeric GÎ± subunit from wheat (Triticum aestivum), GA3, interacts with the calcium-binding protein, Clo3, and the phosphoinositide-specific phospholipase C, PI-PLC1. Plant Molecular Biology, 2011, 77, 145-158.	3.9	48
14	Data mining for miRNAs and their targets in the Triticeae. Genome, 2008, 51, 433-443.	2.0	56
15	The Î±-tubulin gene family in wheat (Triticum aestivum L.) and differential gene expression during cold acclimation. Genome, 2007, 50, 502-510.	2.0	36
16	Interaction network of proteins associated with abiotic stress response and development in wheat. Plant Molecular Biology, 2007, 63, 703-718.	3.9	126
17	Regulatory gene candidates and gene expression analysis of cold acclimation in winter and spring wheat. Plant Molecular Biology, 2007, 64, 409-423.	3.9	96
18	Wheat EST resources for functional genomics of abiotic stress. BMC Genomics, 2006, 7, 149.	2.8	100

#	Article	IF	Citations
19	Transcriptome comparison of winter and spring wheat responding to low temperature. Genome, 2005, 48, 913-923.	2.0	95
20	The Salt Stress-Inducible Protein Kinase Gene, Esi47, from the Salt-Tolerant WheatgrassLophopyrum elongatum Is Involved in Plant Hormone Signaling. Plant Physiology, 2001, 125, 1429-1441.	4.8	55
21	Direct evidence for ribonucleolytic activity of a PR-10-like protein from white lupin roots. Plant Molecular Biology, 2000, 42, 871-881.	3.9	161
22	Characterization of Two cDNA Clones Which EncodeO-Methyltransferases for the Methylation of both Flavonoid and Phenylpropanoid Compounds. Archives of Biochemistry and Biophysics, 1998, 351, 243-249.	3.0	75
23	cDNA cloning and characterization of a 3?/5?-O-methyltransferase for partially methylated flavonols from Chrysosplenium americanum. Plant Molecular Biology, 1996, 32, 1163-1169.	3.9	45
24	Molecular and biochemical characterization of two nucleoside diphosphate kinase cDNA clones from Flaveria bidentis. Genome, 1996, 39, 404-409.	2.0	0
25	Enzymatic prenylation of isoflavones in white lupin. Phytochemistry, 1993, 34, 147-151.	2.9	47
26	Coordinate Gene Response to Salt Stress in Lophopyrum elongatum. Plant Physiology, 1992, 100, 1384-1388.	4.8	46
27	Selective enrichment of cDNAs from salt-stress-induced genes in the wheatgrass, Lophopyrum elongatum, by the formamide-phenol emulsion reassociation technique. Gene, 1990, 95, 173-177.	2.2	27