

# Michael K Deyholos

## List of Publications by Year in descending order

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76  
papers

8,351  
citations

66234

42  
h-index

74018

75  
g-index

76  
all docs

76  
docs citations

76  
times ranked

10324  
citing authors

#	ARTICLE	IF	CITATIONS
1	An Overview of Databases and Bioinformatics Tools for Plant Antimicrobial Peptides. <i>Current Protein and Peptide Science</i> , 2022, 23, 6-19.	0.7	5
2	Mammalian Melatonin Agonist Pharmaceuticals Stimulate Rhomboid Proteins in Plants. <i>Biomolecules</i> , 2022, 12, 882.	1.8	0
3	Ectopic overexpression of a membrane-anchored transcription factor gene <i>NAC60</i> from oilseed rape positively modulates programmed cell death and age-triggered leaf senescence. <i>Plant Journal</i> , 2021, 105, 600-618.	2.8	21
4	Organellomic data sets confirm a cryptic consensus on (unrooted) land-plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	0.8	38
5	Impact of betacyanins on responses to ultraviolet radiation in <i>Amaranthus tricolor</i> L.. <i>Journal of Plant Interactions</i> , 2020, 15, 117-126.	1.0	5
6	A Rapeseed WRKY Transcription Factor Phosphorylated by CPK Modulates Cell Death and Leaf Senescence by Regulating the Expression of ROS and SA-Synthesis-Related Genes. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7348-7359.	2.4	32
7	WRKY42 transcription factor positively regulates leaf senescence through modulating SA and ROS synthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2020, 104, 171-184.	2.8	73
8	A virus-induced gene silencing system for functional genetics in a betalainic species, <i>Amaranthus tricolor</i> (Amaranthaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e01221.	0.8	15
9	VvWRKY30, a grape WRKY transcription factor, plays a positive regulatory role under salinity stress. <i>Plant Science</i> , 2019, 280, 132-142.	1.7	104
10	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.	2.8	119
11	A Novel NAC-Type Transcription Factor, NAC87, from Oilseed Rape Modulates Reactive Oxygen Species Accumulation and Cell Death. <i>Plant and Cell Physiology</i> , 2018, 59, 290-303.	1.5	46
12	Sucrose synthase gene expression analysis in the fibre nettle ( <i>Urtica dioica</i> L.) cultivar 'clone 13'. <i>Industrial Crops and Products</i> , 2018, 123, 315-322.	2.5	13
13	Transcriptome Assembly of the Bast Fiber Crop, Ramie, <i>Boehmeria nivea</i> (L.) Gaud. (Urticaceae). <i>Fibers</i> , 2018, 6, 8.	1.8	3
14	Influence of flax fibre variety and year-to-year variability on composite properties. <i>Industrial Crops and Products</i> , 2017, 98, 1-9.	2.5	46
15	LTR-retrotransposons in plants: Engines of evolution. <i>Gene</i> , 2017, 626, 14-25.	1.0	177
16	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	2.3	62
17	Impact of Low-Intensity Pulsed Ultrasound on Transcript and Metabolite Abundance in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2017, 16, 2975-2982.	1.8	7
18	RNASeq Analysis of the Shoot Apex of Flax ( <i>Linum usitatissimum</i> ) to Identify Phloem Fiber Specification Genes. <i>Frontiers in Plant Science</i> , 2016, 7, 950.	1.7	44

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19	RNA-seq Transcriptome Response of Flax ( <i>Linum usitatissimum</i> L.) to the Pathogenic Fungus <i>Fusarium oxysporum</i> f. sp. lini. <i>Frontiers in Plant Science</i> , 2016, 7, 1766.	1.7	67
20	Nutrient foraging behaviour of four co-occurring perennial grassland plant species alone does not predict behaviour with neighbours. <i>Functional Ecology</i> , 2016, 30, 420-430.	1.7	36
21	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	1.7	91
22	Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax ( <i>Linum</i> ) Tj ETQq0 0 0 rgBT /Oyrllock 10 Tf 50 622	1.2	9
23	Functional characterization of NAC55 transcription factor from oilseed rape ( <i>Brassica napus</i> L.) as a novel transcriptional activator modulating reactive oxygen species accumulation and cell death. <i>Plant Molecular Biology</i> , 2016, 92, 89-104.	2.0	39
24	Wild <i>Panax vietnamensis</i> and <i>Panax stipuleanatus</i> markedly increase the genetic diversity of <i>Panax notoginseng</i> (Araliaceae) revealed by start codon targeted (SCoT) markers and ITS DNA barcode. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 37-42.	0.6	11
25	Optimal fertilizer application for <i>Panax notoginseng</i> and effect of soil water on root rot disease and saponin contents. <i>Journal of Ginseng Research</i> , 2016, 40, 38-46.	3.0	52
26	Development of Microsatellite Markers Derived from Expressed Sequence Tags of Polyporales for Genetic Diversity Analysis of Endangered <i>Polyporus umbellatus</i> . <i>BioMed Research International</i> , 2015, 2015, 1-11.	0.9	3
27	Calcium Mobilization in Salicylic Acid-Induced <i>Salvia miltiorrhiza</i> Cell Cultures and Its Effect on the Accumulation of Rosmarinic Acid. <i>Applied Biochemistry and Biotechnology</i> , 2015, 175, 2689-2702.	1.4	21
28	The Amaranthin-Like Lectin (LuALL) Genes of Flax: a Unique Gene Family with Members Inducible by Defence Hormones. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 731-741.	1.0	13
29	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.	0.8	157
30	Wild soybean roots depend on specific transcription factors and oxidation reduction related genes in response to alkaline stress. <i>Functional and Integrative Genomics</i> , 2015, 15, 651-660.	1.4	51
31	Elucidating steroid alkaloid biosynthesis in <i>Veratrum californicum</i> : production of verazine in Sf9 cells. <i>Plant Journal</i> , 2015, 82, 991-1003.	2.8	62
32	Multiple Polyploidy Events in the Early Radiation of Nodulating and Nonnodulating Legumes. <i>Molecular Biology and Evolution</i> , 2015, 32, 193-210.	3.5	223
33	A Plant-Produced Bacteriophage Tailspike Protein for the Control of <i>Salmonella</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 1221.	1.7	14
34	Differential Expression of miRNAs in <i>Brassica napus</i> Root following Infection with <i>Plasmodiophora brassicae</i> . <i>PLoS ONE</i> , 2014, 9, e86648.	1.1	50
35	Chitinase-Like (CTL) and Cellulose Synthase (CESA) Gene Expression in Gelatinous-Type Cellulosic Walls of Flax ( <i>Linum usitatissimum</i> L.) Bast Fibers. <i>PLoS ONE</i> , 2014, 9, e97949.	1.1	59
36	Identification and functional analysis of mitogen-activated protein kinase kinase kinase (MAPKKK) genes in canola ( <i>Brassica napus</i> L.). <i>Journal of Experimental Botany</i> , 2014, 65, 2171-2188.	2.4	70

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37	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	3.3	582
38	Phylogenetic pinpointing of a paleopolyploidy event within the flax genus ( <i>Linum</i> ) using transcriptomics. <i>Annals of Botany</i> , 2014, 113, 753-761.	1.4	47
39	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4859-68.	3.3	1,123
40	Engineering bast fiber feedstocks for use in composite materials. <i>Biocatalysis and Agricultural Biotechnology</i> , 2014, 3, 53-57.	1.5	18
41	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6672-6677.	3.3	146
42	Pectinmethylesterases (PME) and Pectinmethylesterase Inhibitors (PMEI) Enriched during Phloem Fiber Development in Flax ( <i>Linum usitatissimum</i> ). <i>PLoS ONE</i> , 2014, 9, e105386.	1.1	16
43	LuFLA1PRO and LuBGA1PRO promote gene expression in the phloem fibres of flax ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	2.8	9
44	The genome of flax ( <i>Linum usitatissimum</i> ) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	2.8	415
45	Over-expression of a novel JAZ family gene from Glycine soja, increases salt and alkali stress tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2012, 426, 273-279.	1.0	69
46	Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. <i>PLoS ONE</i> , 2012, 7, e50226.	1.1	172
47	Plant Fiber Formation: State of the Art, Recent and Expected Progress, and Open Questions. <i>Critical Reviews in Plant Sciences</i> , 2012, 31, 201-228.	2.7	132
48	Modeling the Yew Tree Tubulin and a Comparison of its Interaction with Paclitaxel to Human Tubulin. <i>Pharmaceutical Research</i> , 2012, 29, 3007-3021.	1.7	20
49	Two Wheat ( <i>Triticum aestivum</i> ) Pathogenesis-Related 10 (PR-10) Transcripts with Distinct Patterns of Abundance in Different Organs. <i>Molecular Biotechnology</i> , 2012, 51, 103-108.	1.3	11
50	Development of Cellulosic Secondary Walls in Flax Fibers Requires Î²-Galactosidase. <i>Plant Physiology</i> , 2011, 156, 1351-1363.	2.3	114
51	Effects of plant growth regulator treatments on stem vascular tissue development in linseed ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	2.5	19
52	PELPK1 (At5g09530) contains a unique pentapeptide repeat and is a positive regulator of germination in <i>Arabidopsis thaliana</i> . <i>Plant Cell Reports</i> , 2011, 30, 1735-1745.	2.8	20
53	Transcriptome analysis of secondary-wall-enriched seed coat tissues of canola ( <i>Brassica napus</i> L.). <i>Plant Cell Reports</i> , 2010, 29, 327-342.	2.8	28
54	Exploration of inhibitors for diaminopimelate aminotransferase. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 2141-2151.	1.4	32

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55	Making the most of drought and salinity transcriptomics. <i>Plant, Cell and Environment</i> , 2010, 33, 648-654.	2.8	113
56	Functional characterization of Arabidopsis NaCl-inducible WRKY25 and WRKY33 transcription factors in abiotic stresses. <i>Plant Molecular Biology</i> , 2009, 69, 91-105.	2.0	554
57	Analysis of Arabidopsis arginase gene transcription patterns indicates specific biological functions for recently diverged paralogs. <i>Plant Molecular Biology</i> , 2008, 67, 429-440.	2.0	45
58	Towards identifying <i>Brassica</i> proteins involved in mediating resistance to <i>Leptosphaeria maculans</i> : A proteomics-based approach. <i>Proteomics</i> , 2008, 8, 3516-3535.	1.3	30
59	Proteome-level changes in the roots of <i>Brassica napus</i> as a result of <i>Plasmodiophora brassicae</i> infection. <i>Plant Science</i> , 2008, 174, 97-115.	1.7	82
60	Microarray Analysis of Developing Flax Hypocotyls Identifies Novel Transcripts Correlated with Specific Stages of Phloem Fibre Differentiation. <i>Annals of Botany</i> , 2008, 102, 317-330.	1.4	48
61	High-Throughput, High-Sensitivity Analysis of Gene Expression in Arabidopsis. <i>Plant Physiology</i> , 2007, 144, 1256-1266.	2.3	13
62	Transcriptional profiling of canola ( <i>Brassica napus</i> L.) responses to the fungal pathogen <i>Sclerotinia sclerotiorum</i> . <i>Plant Science</i> , 2007, 173, 156-171.	1.7	76
63	Crystal Structure of $\alpha$ -Diaminopimelate Aminotransferase from Arabidopsis thaliana: A Recently Discovered Enzyme in the Biosynthesis of L-Lysine by Plants and Chlamydia. <i>Journal of Molecular Biology</i> , 2007, 371, 685-702.	2.0	42
64	Comparative proteomic analysis of NaCl stress-responsive proteins in Arabidopsis roots. <i>Journal of Experimental Botany</i> , 2007, 58, 3591-3607.	2.4	456
65	Transcriptional profiling of hexaploid wheat ( <i>Triticum aestivum</i> L.) roots identifies novel, dehydration-responsive genes. <i>Plant, Cell and Environment</i> , 2007, 30, 630-645.	2.8	66
66	Microarray analysis of bast fibre producing tissues of <i>Cannabis sativa</i> identifies transcripts associated with conserved and specialised processes of secondary wall development. <i>Functional Plant Biology</i> , 2007, 34, 737.	1.1	22
67	Patterns of storage protein and triacylglycerol accumulation during loblolly pine somatic embryo maturation. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 88, 217-223.	1.2	25
68	Gene transcript and metabolite profiling of elicitor-induced opium poppy cell cultures reveals the coordinate regulation of primary and secondary metabolism. <i>Planta</i> , 2007, 225, 1085-1106.	1.6	98
69	A synthetic de-greening gene circuit provides a reporting system that is remotely detectable and has a re-set capacity. <i>Plant Biotechnology Journal</i> , 2006, 4, 605-622.	4.1	58
70	Vascular development: the long and winding road. <i>Current Opinion in Plant Biology</i> , 2006, 9, 48-54.	3.5	82
71	Temporal progression of gene expression responses to salt shock in maize roots. <i>Plant Molecular Biology</i> , 2003, 52, 873-891.	2.0	102
72	The <i>sfr6</i> mutant of Arabidopsis is defective in transcriptional activation via CBF/DREB1 and DREB2 and shows sensitivity to osmotic stress. <i>Plant Journal</i> , 2003, 34, 395-406.	2.8	86

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73	Monitoring large-scale changes in transcript abundance in drought- and salt-stressed barley. <i>Plant Molecular Biology</i> , 2002, 48, 551-573.	2.0	503
74	A genomics approach towards salt stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 295-311.	2.8	176
75	Gene Expression Profiles during the Initial Phase of Salt Stress in Rice. <i>Plant Cell</i> , 2001, 13, 889-905.	3.1	850
76	Separable Whorl-Specific Expression and Negative Regulation by Enhancer Elements within the AGAMOUS Second Intron. <i>Plant Cell</i> , 2000, 12, 1799.	3.1	13