

# Michael K Deyholos

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9194730/publications.pdf>

Version: 2024-02-01

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	Phylotranscriptomic analysis of the origin and early diversification of land plants. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4859-68.	3.3	1,123
2	Gene Expression Profiles during the Initial Phase of Salt Stress in Rice. Plant Cell, 2001, 13, 889-905.	3.1	850
3	Data access for the 1,000 Plants (1KP) project. GigaScience, 2014, 3, 17.	3.3	582
4	Functional characterization of Arabidopsis NaCl-inducible WRKY25 and WRKY33 transcription factors in abiotic stresses. Plant Molecular Biology, 2009, 69, 91-105.	2.0	554
5	Monitoring large-scale changes in transcript abundance in drought- and salt-stressed barley. Plant Molecular Biology, 2002, 48, 551-573.	2.0	503
6	Comparative proteomic analysis of NaCl stress-responsive proteins in Arabidopsis roots. Journal of Experimental Botany, 2007, 58, 3591-3607.	2.4	456
7	The genome of flax ( <i>Linum usitatissimum</i> ) assembled <i>de novo</i> from short shotgun sequence reads. Plant Journal, 2012, 72, 461-473.	2.8	415
8	Multiple Polyploidy Events in the Early Radiation of Nodulating and Nonnodulating Legumes. Molecular Biology and Evolution, 2015, 32, 193-210.	3.5	223
9	LTR-retrotransposons in plants: Engines of evolution. Gene, 2017, 626, 14-25.	1.0	177
10	A genomics approach towards salt stress tolerance. Plant Physiology and Biochemistry, 2001, 39, 295-311.	2.8	176
11	Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. PLoS ONE, 2012, 7, e50226.	1.1	172
12	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. American Journal of Botany, 2015, 102, 1089-1107.	0.8	157
13	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6672-6677.	3.3	146
14	Plant Fiber Formation: State of the Art, Recent and Expected Progress, and Open Questions. Critical Reviews in Plant Sciences, 2012, 31, 201-228.	2.7	132
15	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. Plant Journal, 2018, 95, 371-384.	2.8	119
16	Development of Cellulosic Secondary Walls in Flax Fibers Requires Î²-Galactosidase. Plant Physiology, 2011, 156, 1351-1363.	2.3	114
17	Making the most of drought and salinity transcriptomics. Plant, Cell and Environment, 2010, 33, 648-654.	2.8	113
18	VvWRKY30, a grape WRKY transcription factor, plays a positive regulatory role under salinity stress. Plant Science, 2019, 280, 132-142.	1.7	104

#	ARTICLE	IF	CITATIONS
19	Temporal progression of gene expression responses to salt shock in maize roots. <i>Plant Molecular Biology</i> , 2003, 52, 873-891.	2.0	102
20	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
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	The <i>sfr6</i> mutant of <i>Arabidopsis</i> 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
23	Vascular development: the long and winding road. <i>Current Opinion in Plant Biology</i> , 2006, 9, 48-54.	3.5	82
24	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
25	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
26	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
27	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
28	Over-expression of a novel JAZ family gene from <i>Glycine soja</i> , increases salt and alkali stress tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2012, 426, 273-279.	1.0	69
29	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
30	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
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	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	2.3	62
33	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
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Differential Expression of miRNAs in Brassica napus Root following Infection with Plasmodiophora brassicae. PLoS ONE, 2014, 9, e86648.	1.1	50
38	Microarray Analysis of Developing Flax Hypocotyls Identifies Novel Transcripts Correlated with Specific Stages of Phloem Fibre Differentiation. Annals of Botany, 2008, 102, 317-330.	1.4	48
39	Phylogenetic pinpointing of a paleopolyploidy event within the flax genus (Linum) using transcriptomics. Annals of Botany, 2014, 113, 753-761.	1.4	47
40	Influence of flax fibre variety and year-to-year variability on composite properties. Industrial Crops and Products, 2017, 98, 1-9.	2.5	46
41	A Novel NAC-Type Transcription Factor, NAC87, from Oilseed Rape Modulates Reactive Oxygen Species Accumulation and Cell Death. Plant and Cell Physiology, 2018, 59, 290-303.	1.5	46
42	Analysis of Arabidopsis arginase gene transcription patterns indicates specific biological functions for recently diverged paralogs. Plant Molecular Biology, 2008, 67, 429-440.	2.0	45
43	RNASeq Analysis of the Shoot Apex of Flax (Linum usitatissimum) to Identify Phloem Fiber Specification Genes. Frontiers in Plant Science, 2016, 7, 950.	1.7	44
44	Crystal Structure of II-Diaminopimelate Aminotransferase from Arabidopsis thaliana: A Recently Discovered Enzyme in the Biosynthesis of L-Lysine by Plants and Chlamydia. Journal of Molecular Biology, 2007, 371, 685-702.	2.0	42
45	Functional characterization of NAC55 transcription factor from oilseed rape (Brassica napus L.) as a novel transcriptional activator modulating reactive oxygen species accumulation and cell death. Plant Molecular Biology, 2016, 92, 89-104.	2.0	39
46	Organellomic data sets confirm a cryptic consensus on (unrooted) landâ€­plant relationships and provide new insights into bryophyte molecular evolution. American Journal of Botany, 2020, 107, 91-115.	0.8	38
47	Nutrient foraging behaviour of four coâ€­occurring perennial grassland plant species alone does not predict behaviour with neighbours. Functional Ecology, 2016, 30, 420-430.	1.7	36
48	Exploration of inhibitors for diaminopimelate aminotransferase. Bioorganic and Medicinal Chemistry, 2010, 18, 2141-2151.	1.4	32
49	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. Journal of Agricultural and Food Chemistry, 2020, 68, 7348-7359.	2.4	32
50	Towards identifying <b><i>Brassica</i></b> proteins involved in mediating resistance to <b><i>Leptosphaeria maculans</i></b>: A proteomicsâ€­based approach. Proteomics, 2008, 8, 3516-3535.	1.3	30
51	Transcriptome analysis of secondary-wall-enriched seed coat tissues of canola (Brassica napus L.). Plant Cell Reports, 2010, 29, 327-342.	2.8	28
52	Patterns of storage protein and triacylglycerol accumulation during loblolly pine somatic embryo maturation. Plant Cell, Tissue and Organ Culture, 2007, 88, 217-223.	1.2	25
53	Microarray analysis of bast fibre producing tissues of Cannabis sativa identifies transcripts associated with conserved and specialised processes of secondary wall development. Functional Plant Biology, 2007, 34, 737.	1.1	22
54	Calcium Mobilization in Salicylic Acid-Induced Salvia miltiorrhiza Cell Cultures and Its Effect on the Accumulation of Rosmarinic Acid. Applied Biochemistry and Biotechnology, 2015, 175, 2689-2702.	1.4	21

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	Effects of plant growth regulator treatments on stem vascular tissue development in linseed ( <i>Linum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 19	2.5	19
59	Engineering bast fiber feedstocks for use in composite materials. <i>Biocatalysis and Agricultural Biotechnology</i> , 2014, 3, 53-57.	1.5	18
60	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
61	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
62	A Plant-Produced Bacteriophage Tailspike Protein for the Control of Salmonella. <i>Frontiers in Plant Science</i> , 2015, 6, 1221.	1.7	14
63	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
64	High-Throughput, High-Sensitivity Analysis of Gene Expression in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2007, 144, 1256-1266.	2.3	13
65	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
66	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
67	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
68	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
69	LuFLA1PRO and LuBGAL1PRO promote gene expression in the phloem fibres of flax ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	2.8	10
70	Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax ( <i>Linum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	1.2	9
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Transcriptome Assembly of the Bast Fiber Crop, Ramie, <i>Boehmeria nivea</i> (L.) Gaud. (Urticaceae). <i>Fibers</i> , 2018, 6, 8.	1.8	3
76	Mammalian Melatonin Agonist Pharmaceuticals Stimulate Rhomboid Proteins in Plants. <i>Biomolecules</i> , 2022, 12, 882.	1.8	0