

# Michael K Deyholos

## List of Publications by Year in descending order

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76  
papers

8,351  
citations

66343

42  
h-index

74163

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.   | 1.4 | 5         |
| 2  | Mammalian Melatonin Agonist Pharmaceuticals Stimulate Rhomboid Proteins in Plants. <i>Biomolecules</i> , 2022, 12, 882.  | 4.0 | 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.                  | 5.7 | 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.                                    | 1.7 | 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.   | 2.1 | 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. | 5.2 | 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.   | 5.7 | 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.  | 2.1 | 15        |
| 9  | VvWRKY30, a grape WRKY transcription factor, plays a positive regulatory role under salinity stress. <i>Plant Science</i> , 2019, 280, 132-142.  | 3.6 | 104       |
| 10 | Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.  | 5.7 | 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.   | 3.1 | 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.   | 5.2 | 13        |
| 13 | Transcriptome Assembly of the Bast Fiber Crop, Ramie, <i>Boehmeria nivea</i> (L.) Gaud. (Urticaceae). <i>Fibers</i> , 2018, 6, 8.  | 4.0 | 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.  | 5.2 | 46        |
| 15 | LTR-retrotransposons in plants: Engines of evolution. <i>Gene</i> , 2017, 626, 14-25.  | 2.2 | 177       |
| 16 | Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.   | 4.8 | 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.   | 3.7 | 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.   | 3.6 | 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.  | 3.6 | 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.   | 3.6 | 36        |
| 21 | Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.  | 3.3 | 91        |
| 22 | Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax ( <i>Linum</i> ) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 622  | 2.8 | 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.                   | 3.9 | 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. | 1.3 | 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.  | 5.7 | 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.   | 1.9 | 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.  | 2.9 | 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.   | 1.8 | 13        |
| 29 | The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.  | 1.7 | 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.   | 3.5 | 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.   | 5.7 | 62        |
| 32 | Multiple Polyploidy Events in the Early Radiation of Nodulating and Nonnodulating Legumes. <i>Molecular Biology and Evolution</i> , 2015, 32, 193-210.  | 8.9 | 223       |
| 33 | A Plant-Produced Bacteriophage Tailspike Protein for the Control of <i>Salmonella</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 1221.  | 3.6 | 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.   | 2.5 | 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.   | 2.5 | 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.   | 4.8 | 70        |

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|----|--|-----|-----------|
| 37 | Data access for the 1,000 Plants (1KP) project. GigaScience, 2014, 3, 17.  | 6.4 | 582       |
| 38 | Phylogenetic pinpointing of a paleopolyploidy event within the flax genus ( <i>Linum</i> ) using transcriptomics. Annals of Botany, 2014, 113, 753-761.                                    | 2.9 | 47        |
| 39 | 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. | 7.1 | 1,123     |
| 40 | Engineering bast fiber feedstocks for use in composite materials. Biocatalysis and Agricultural Biotechnology, 2014, 3, 53-57.   | 3.1 | 18        |
| 41 | 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. | 7.1 | 146       |
| 42 | Pectinmethylesterases (PME) and Pectinmethylesterase Inhibitors (PMEI) Enriched during Phloem Fiber Development in Flax ( <i>Linum usitatissimum</i> ). PLoS ONE, 2014, 9, e105386.        | 2.5 | 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  | 5.6 | 9         |
| 44 | The genome of flax ( <i>Linum usitatissimum</i> ) assembled <i>de novo</i> from short shotgun sequence reads. Plant Journal, 2012, 72, 461-473.  | 5.7 | 415       |
| 45 | Over-expression of a novel JAZ family gene from Glycine soja, increases salt and alkali stress tolerance. Biochemical and Biophysical Research Communications, 2012, 426, 273-279.         | 2.1 | 69        |
| 46 | Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. PLoS ONE, 2012, 7, e50226.                              | 2.5 | 172       |
| 47 | Plant Fiber Formation: State of the Art, Recent and Expected Progress, and Open Questions. Critical Reviews in Plant Sciences, 2012, 31, 201-228.  | 5.7 | 132       |
| 48 | Modeling the Yew Tree Tubulin and a Comparison of its Interaction with Paclitaxel to Human Tubulin. Pharmaceutical Research, 2012, 29, 3007-3021.  | 3.5 | 20        |
| 49 | Two Wheat ( <i>Triticum aestivum</i> ) Pathogenesis-Related 10 (PR-10) Transcripts with Distinct Patterns of Abundance in Different Organs. Molecular Biotechnology, 2012, 51, 103-108.    | 2.4 | 11        |
| 50 | Development of Cellulosic Secondary Walls in Flax Fibers Requires Î²-Galactosidase. Plant Physiology, 2011, 156, 1351-1363.  | 4.8 | 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                                     | 5.2 | 19        |
| 52 | PELPK1 (At5g09530) contains a unique pentapeptide repeat and is a positive regulator of germination in <i>Arabidopsis thaliana</i> . Plant Cell Reports, 2011, 30, 1735-1745.              | 5.6 | 20        |
| 53 | Transcriptome analysis of secondary-wall-enriched seed coat tissues of canola ( <i>Brassica napus</i> L.). Plant Cell Reports, 2010, 29, 327-342.  | 5.6 | 28        |
| 54 | Exploration of inhibitors for diaminopimelate aminotransferase. Bioorganic and Medicinal Chemistry, 2010, 18, 2141-2151.   | 3.0 | 32        |

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|----|--|-----|-----------|
| 55 | Making the most of drought and salinity transcriptomics. <i>Plant, Cell and Environment</i> , 2010, 33, 648-654.   | 5.7 | 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.  | 3.9 | 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.   | 3.9 | 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.  | 2.2 | 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.   | 3.6 | 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.  | 2.9 | 48        |
| 61 | High-Throughput, High-Sensitivity Analysis of Gene Expression in Arabidopsis. <i>Plant Physiology</i> , 2007, 144, 1256-1266.  | 4.8 | 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.  | 3.6 | 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. | 4.2 | 42        |
| 64 | Comparative proteomic analysis of NaCl stress-responsive proteins in Arabidopsis roots. <i>Journal of Experimental Botany</i> , 2007, 58, 3591-3607.   | 4.8 | 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.  | 5.7 | 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.   | 2.1 | 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.  | 2.3 | 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.  | 3.2 | 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.   | 8.3 | 58        |
| 70 | Vascular development: the long and winding road. <i>Current Opinion in Plant Biology</i> , 2006, 9, 48-54.   | 7.1 | 82        |
| 71 | Temporal progression of gene expression responses to salt shock in maize roots. <i>Plant Molecular Biology</i> , 2003, 52, 873-891.  | 3.9 | 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.  | 5.7 | 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.       | 3.9 | 503       |
| 74 | A genomics approach towards salt stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 295-311.                                       | 5.8 | 176       |
| 75 | Gene Expression Profiles during the Initial Phase of Salt Stress in Rice. <i>Plant Cell</i> , 2001, 13, 889-905.                                       | 6.6 | 850       |
| 76 | Separable Whorl-Specific Expression and Negative Regulation by Enhancer Elements within the AGAMOUS Second Intron. <i>Plant Cell</i> , 2000, 12, 1799. | 6.6 | 13        |