

## **Brian D. Keppler**

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Des Moines, Iowa 50309  
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### **PROFESSIONAL EXPERIENCE**

#### **McKee, Voorhees & Sease, PLC**

*Technology Specialist*

Des Moines, IA  
December 2016 – Present

#### **University of Wisconsin-Madison**

*Research Assistant*

Madison, WI  
August 2010 – December 2016

Investigated the regulation of pathogen induced plant cell wall reinforcement through chemical genetic and natural variation approaches

#### **Ohio University**

*Research Assistant*

Athens, OH  
January 2008 – March 2010

Utilized a reverse genetics approach to identify the function of two closely related enzymes involved in plant cell wall biosynthesis

*Teaching Assistant*

Taught the laboratory portion of courses including Principles of Biology, Foundations of Plant Biology, and Molecular and Cellular Biology

### **EDUCATION**

#### **University of Wisconsin-Madison**

PhD in Cellular and Molecular Biology

Madison, WI  
December 2016

#### **Ohio University**

MS in Plant Biology

Athens, OH  
March 2010

#### **Ohio University**

BS in Biochemistry

Athens, OH  
August 2007

Awards and Honors: Phi Beta Kappa, *magna cum laude*

### **RESEARCH PRESENTATIONS**

- Congress on Molecular Plant-Microbe Interactions, Portland, OR, July 2016 (Poster)
- International Conference on Arabidopsis Research, Vancouver, BC, July 2014 (Poster)
- American Society of Plant Biologists, Providence, RI, July 2013 (Poster)
- Congress on Molecular Plant-Microbe Interactions, Kyoto, Japan, July 2012 (Oral)
- American Society of Plant Biologists, Montreal, QC, July 2010 (Poster)

## SELECTED PUBLICATIONS

- Song J, **Keppler BD**, Wise RR, Bent AF (2015) PARP2 Is the Predominant Poly(ADP-Ribose) Polymerase in Arabidopsis DNA Damage and Immune Responses. *PLoS Genet* 11(5):e1005200.
- **Keppler BD**, Showalter AM (2010) IRX14 and IRX14-LIKE, two glycosyl transferases involved in glucuronoxylan biosynthesis and drought tolerance in Arabidopsis. *Mol Plant* 3(5): 834–841.
- Showalter AM, **Keppler BD**, Lichtenberg J, Gu D, Welch LR (2010) A bioinformatics approach to the identification, classification, and analysis of hydroxyproline-rich glycoproteins. *Plant Physiol* 153(2): 485–513.