Genomic Sciences Program - List of Awards
Genome-Enabled Plant Biology for Determination of Gene Function
Funding Opportunity Number: DE-FOA-00002060

Title	Lead PI	Institution	Location
Functional Analysis of Candidate Genes Involved in Oil Storage and Stability in Pennycress	Alonso, Ana	University of North Texas	Denton, TX
Coupling metabolic source isotopic pair labeling and genome wide association for metabolite and gene annotation in plants	Chapple, Clint	Purdue University	West Lafayette, IN
Discovering innovations in stress tolerance through comparative gene regulatory network analysis and cell-type specific expression maps	Dinneny, José	Stanford University	Redwood City, CA
Elucidating the molecular mechanisms underlying drought resilience in sorghum	Eveland, Andrea	Donald Danforth Plant Science Center	St. Louis, MO
Creation of an Acyltransferase Toolbox for Plant Biomass Engineering	Fox, Brian	University of Wisconsin	Madison, WI
Transforming our understanding of chloroplast-associated genes through comprehensive characterization of protein localizations and protein-protein interactions	Jonikas, Martin	Princeton University	Princeton, NJ
Constructing the Nitrogen Flux Maps (NFMs) of Plants	Maeda, Hiroshi	University of Wisconsin	Madison, WI
Constructing the Nitrogen Flux Maps (NFMs) of Plants	Yoshikuni, Yasuo	Collaborating Lab: Lawrence Berkeley National Lab	Berkeley, CA
High-throughput determination of a subcellular metabolic network map of plants	Rhee, Seung	Carnegie Institution of Washington	Washington, DC
High-throughput determination of a subcellular metabolic network map of plants	Mortimer, Jennifer	Collaborating Lab: Lawrence Berkeley National Lab	Berkeley, CA
TGCM: (T)rait, (G)ene, and (C)rop Growth (M)odel directed targeted gene characterization in sorghum	Schnable, James	University of Nebraska	Lincoln, NE
Combining genome-wide association studies and expression quantitative trait nucleotide mapping with molecular and genetic validations to identify transcriptional networks regulating drought tolerance	Taylor, Gail	University of California, Davis	Davis, CA
Combining genome-wide association studies and expression quantitative trait nucleotide mapping with molecular and genetic validations to identify transcriptional networks regulating drought tolerance	Chen, Jin-Gui	Collaborating Lab: Oak Ridge National Lab	Oak Ridge, TN
Deep Green: Structural and Functional Genomic Characterization of Conserved Unannotated Green Lineage Proteins	Umen, James	Donald Danforth Plant Science Center	St. Louis, MO
Deep Green: Structural and Functional Genomic Characterization of Conserved Unannotated Green Lineage Proteins	Knoshaug, Eric	Collaborating Lab: National Renewable Energy Lab	Golden, CO
Infer Net: Gene function inference by leveraging large, organ-specific expression datasets and validation of non-redundant regulators	Varala, Kranthi	Purdue University	West Lafayette, IN
Infer Net: Gene function inference by leveraging large, organ-specific expression datasets and validation of non-redundant regulators	Hudson, Karen	Collaborator: USDA-ARS-MWA-CPPCRU	West Lafayette, IN