CURRICULUM VITA

Name: Seung Yon (Sue) Rhee (She/Her) 이승연 李烝涓
Website: https://www.rheelab.org/
Address: Michigan State University, 1066 Bogue St Rm A283, East Lansing, MI 48824
E-mail: **rheeseu6@msu.edu**

Education:
Ph.D. (biology), Stanford University, Molecular genetic analysis of cell separation during *Arabidopsis thaliana* pollen development, 1998
B.A. (biology), Swarthmore College, 1992

Employment:
Director, Plant Resilience Institute, Michigan State University, 2023-present
MSU Foundation Professor, Biochemistry and Molecular Biology, Plant Biology, and Plant, Soil, and Microbial Sciences, Michigan State University, 2023-present
Founding Director, Water and Life Interface Institute (WALII), 2022-present
Senior Staff Scientist, Department of Plant Biology, Carnegie Institution for Science, 2018-2023
Acting Director, Department of Plant Biology, Carnegie Institution for Science, 2016-2018
Staff Scientist, Department of Plant Biology, Carnegie Institution for Science, 2005-2016
Staff Associate, Department of Plant Biology, Carnegie Institution for Science, 1999-2005
Founding Director, the *Arabidopsis* Information Resource (TAIR), Department of Plant Biology, Carnegie Institution for Science, 1999-2005
Database Curator, *Arabidopsis thaliana* Database (AtDB), Dept of Genetics, Stanford University, 1998-1999
Independent Science Education Film Producer, Celadon Films, 1998-1999
Research Associate, Department of Plant Biology, Carnegie Institution for Science, 1994-1998
Research Associate, Department of Biochemistry, Stanford University, 1993-1994
Research Assistant, Biology Department, Swarthmore College, 1990-1992
Research Intern, Johns Hopkins University School of Medicine, 1990 (summer)

Professional Services:
Scientific Advisory or Assessment Boards: 24. Senior Scientific Advisor, JR Biotek Foundation (2022-present); 23. Evaluator, European Research Council (ERC) Impact on Scientific Progress in Crop Production - Biological basis, genetic engineering (2022); 22. Member, DOE Biological and Environmental Research Advisory Committee's Subcommittee Working Group on Biodesign (2021-2022); 21. Committee of Visitors, DOE Biological Systems Science Division (2021); 20. Chair, Steering Committee, Plant Cell Atlas (2021-2026); 19. Advisory Committee, DOE Joint Genome Institute (2020-present); 18. Advisory Committee, Gene Ontology Consortium (2019-present); 17. Scientific Advisory Board, Phylos, Inc. (2018-present); 16. ASPB Award Nominations Committee (2018-2021); 15. Advisory Committee, IPMB conference (2018); 14. Scientific Advisory Board, VIB Department of Plant Systems Biology, Belgium (2016-present); 13. Scientific Advisory Committee, Joint Genome Institute's Plant Group (2015-present); 12. Scientific Advisor Board, Protein Data Bank (2009-present); 11. Advisor, Program for International Consortia and Collaboration on Agribioinformatics in National Agricultural Genome Program (PICCAN) in Korea (2016-2017); 10. Advisor, NSF C3-C4 Photosynthesis Project (2012-2013); 9. Member, Nominating Committee for the International Society of Biocuration's Executive Committee (2009-2010); 8. Member, Nominating Committee for Plant Cyberinfrastructure Board of Directors (2007); 7. Scientific Advisory Committee, Value-directed Evolutionary Genomics Initiative (VEGI) (2010-2014); 6. Scientific Advisory Committee, CropLink Global Database (2006-2009); 5.

Steering Committee Member, International Solanaceae Genome Initiative (2004-2008); 4. Scientific Advisory Board, Saccharomyces Genome Database (SGD) (2003-2006); 3. Scientific Advisory Board, GrainGenes (2003-2006); 2. Scientific Advisory Board, Cornell Genomics (2002-2006); 1. Scientific Advisory Committee, ChromDB (2001-2004)

Grant Review Boards: DOE (2018); NSF (2021, 2020, 2018, 2016, 2015, 2014, 2012, 2011, 2008, 2006); USDA-ARS (2002); NHGRI (2002)

International Conference Organization Boards: Lead organizer, Gordon Research Conference on Single-Cell Approaches in Plant Biology (2023, 2025); A Plenary session organizer, ASPB 2023 Conference (2023); Co-organizer, Phytochemical Society of North America Conference, East Lansing, MI (2023); Co-organizer, 20th National Plant Biochemistry and Molecular Biology Congress, Mexico (2023); Co-organizer, Second Plant Cell Atlas Consortium (2022); Lead organizer, First Plant Cell Atlas Symposium (2021); Scientific Organizing Committee, VIB conference Plant Science for Climate Emergency (2021); Lead organizer, First Plant Cell Atlas Workshop (2020); Co-organizer, 2nd Plant Systems Biology Conference (2020); Co-organizer, Plant Genomes, Systems Biology, and Engineering Conference at Cold Spring Harbor Laboratory (2017, 2019, 2021); Co-organizer, Fourth Conference of International Society for Biocuration (2010); Lead organizer, Second International Biocurators meeting (2007); Co-organizer, Solanaceae Genomics meeting (2007); Lead organizer, First International Biocurators Conference (2005); Co-organizer, NSF sponsored workshop on 'National Plant Synthesis Center' (2005)

Scientific Journal Editorial Boards: Guest Editor, Focus Issue on Plant Cell Atlas, Plant Physiology (2021); Advisory Editor, Plant & Cell Physiology (2020-2023); *In silico* Plants Editorial Board (2018-present); Associate Editor, Molecular Plant (2014-2019); Monitoring Editor, Plant Physiology (2002-2008, 2013-2016, 2021)

Carnegie Institution for Science Services: Pasadena Life Science Division Building Committee (2020-2021); Deputy Organizer for Carnegie Workshop on Genomes to Ecosystems (2019); Faculty Advisor for Intrinsically Disordered Proteins Scientific Interest Group (2018-present); Faculty Advisor for DPB Website (2019); Carnegie's Center for Scientific Computation Committee (2014-2016); Carnegie Summer Internship Program Coordination (2013-2016); DPB IT Committee (2012-2016); Departmental Website Design (2010); Carnegie Seminar Organization (2008-2010); Departmental Website Design (2002); Internal Seminar Series Initiation and Organization (2000-2001)

Michigan State University Services: Chair of PRI Faculty Search Committee (2023); MSU Plant Science Training Ecosystem Group Organizer (2023-present); Executive Committee Member, NIH Plant Biotechnology for Health and Sustainability (PBHS) Training Program (2023-present)

Teaching:
Fundamentals and Frontiers in Plant Biology (BIO129/229) (2020, 2022); Career Exploration & Planning (BIO380) (2019); Carnegie Writing Workshop (2018, 2019); Networks in Biology (Freshman Seminar) (2010, 2012)

Awards:
NSF Predoctoral Fellowship (1993-1996); NSF/DOE/USDA Plant Training Grant Fellowship (1992-1993); Sigma Xi National Society (1991-1992); Howard Hughes Undergraduate Research Fellowship (1990-1991); National Honors Society (1988)

Scientific Society Memberships:
American Indian Science and Engineering Society (2022-present); SACNAS (2022-lifetime); American Society of Plant Biologists (2010-present); International Society of Biocuration (2010-present); American Chemical Society (2014-present); Society for the Study of Evolution (2014-present); Society of Molecular Biology and Evolution (2014-present); Genetics Society of America (2014-present); International Society for Computational Biology (2015-present); California Native Plant Society (2015-present); Northern California Science Writers Association (2016-present); American Society of Cell Biologists (2016-present); American Geophysical Union (2019-present)

Outreach:
San Francisco Dept of Children, Youth and their Families Summer Camp Program –Tardigrade Hunting (2022-present); Science on the Screen (2021-present); Plant Science and Art Exhibit (2021-present); Plant Science Lesson Plans for Middle School (2021); Popular Science Essays (2018-present); Chemical Ecology Journal Club with Faulty, Students, and Local Citizens (2015-present)

Contribution to Science:
1. **From discovering cell separation mechanisms to centromere mapping:** My early work in graduate school focused on understanding how plant cells separate, which is rare in plants because cells are connected by walls. However, cell separation occurs during male gametogenesis in many plants to create individual pollen grains. Through molecular genetics, cell biological, and biochemical approaches, I identified a class of mutants called *quartet,* which are required for cell separation, and subsequently determined the molecular nature of the defects through gene cloning and molecular and biochemical characterization. Using immunolocalization and biochemical analyses, I showed that the phenotype resulted from defects in degrading the temporary cell wall before the secondary cell wall is deposited from the maternal tissue. I then cloned one of the genes, which encoded a pectin methylesterase, the first cell wall degrading enzyme with a demonstrated function *in vivo*. The *quartet* strains are still the *de facto* lines for plant scientists to study a variety of topics including gametophytic function, meiotic drive, genome stability, and centromere mapping. The strains have been used to map Arabidopsis centromeres, which was instrumental in refining the physical map and completing the genome sequencing. In the future, these strains could enable the creation of artificial plant chromosomes.

Preuss D, Rhee SY, and Davis RW. (1994) Tetrad analysis possible in Arabidopsis with mutation of the QUARTET (QRT) genes. **Science** 264(5164):1458-60.
Rhee SY and Somerville CR. (1998) Tetrad pollen formation in quartet mutants of *Arabidopsis thaliana* is associated with persistence of pectic polysaccharides of the pollen mother cell wall. **Plant Journal** 15(1):79-88.
Rhee SY, Osborne E, Poindexter P, and Somerville, CR (2003) Microspore separation in the *quartet 3* mutants of Arabidopsis is impaired by a defect in a developmentally regulated pectinase required for pollen mother cell degradation. **Plant Physiology** 133(3):1170-80.

2. **Establishing and enabling systems and omics biology:** As genome sequencing became feasible towards the end of my graduate work, I became interested in the possibility of genome-enabled biology to understand the functions of all genes and pathways encoded in a genome and elucidate how organisms are hard- and soft-wired. As an early career investigator at Carnegie, I led a team of biologists and software engineers to create a computational infrastructure called the Arabidopsis Information Resource (TAIR) to collect and encode all

available genomic and literature data to be computable by algorithms and easily accessible by researchers. TAIR has been a primer for revolutionizing plant research by enabling systematic and quantitative analyses of biological functions and pathways. Over time, TAIR has been used by 6.8 million people. Some 20,000 scientists around the world are still actively using it. In addition, my group was one of the early developers of the Gene Ontology (GO) system where we contributed to making the system work for plant genomes. GO is a shared, controlled and structured vocabulary for describing gene attributes. GO has been instrumental in analyzing and interpreting genomic and post-genomic data across many organisms, including many studies of various human diseases. GO has been mentioned in more than 26,000 articles, which have been cited over 580,000 times without self-citations.

The Gene Ontology Consortium (2001) Creating the Gene Ontology Resource: Design and Implementation. **Genome Research** 11(8):1425-1433.

Rhee SY, Beavis W, Berardini TZ, Chen G, Dixon D, Doyle A, Garcia-Hernandez M, Huala E, Lander G, Montoya M, Miller N, Mueller LA, Mundodi S, Reiser L, Tacklind J, Weems DC, Wu Y, Xu I, Yoo D, Yoon J, Zhang P. (2003) The Arabidopsis Information Resource (TAIR): a model organism database providing a centralized, curated gateway to Arabidopsis biology, research materials and community. **Nucleic Acids Research** 31(1):224-228.

Howe D, Costanzo M, Fey P, Gojobori T, Hannick L, Hide W, Hill DP, Kania R, Schaeffer M, St. Pierre S, Twigger S, White O, and Rhee SY (2008) The future of biocuration. **Nature** 455:47-50.

3. **Revealing functions of unknown genes:** One of the biggest problems facing biology in the post-genome era is that we still do not know the functions of many genes (25%-75% of protein-encoding genes are not even predictable for their function based on sequence similarity), even for intensively studied organisms such as *E. coli*, yeast, and human. We developed several systematic approaches to determine functions of unknown genes in the model plant *Arabidopsis thaliana*. First, to systematically infer functions of genes and group them into pathways, my group collaborated with Dr. Ed Marcotte's group to create the first plant genome-wide co-function network called AraNet, which has been used to systematically identify new genes in pathways and infer functions of uncharacterized genes based on the functions of their network neighbors. Second, we collaborated with Dr. Wolf Frommer's group to develop high-throughput experimental and computational pipelines to systematically identify interactions between membrane proteins and signaling proteins, testing over 6 million binary interactions between 3000 proteins. To date, this is still the largest eukaryotic membrane protein interaction network (such a network previously existed only for yeast, at ~10% of the scale). The vast majority of the membrane protein interactions we found had never before been identified. Third, we developed a computational pipeline to identify novel transcriptional regulators using non-sequence similarity approaches, and discovered a novel water sensor that is required for seed germination, FLOE1, and a gene family that controls the transition between proliferation and differentiation in leaves, CHIQUITA. We continue to explore systematic ways to accelerate gene function discovery.

Lee I, Ambaru B, Thakkar P, Marcotte E, and Rhee SY (2010) Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. **Nature Biotechnology** 2(28):149-156.

Jones AM, Xuan Y, Xu M, Wang R-S, Ho C-H, Lalonde S, You CH, Sardi MI, Parsa SA, Smith-Valle E, Su T, Frazer KA, Pilot G, Pratelli R, Grossmann G, Acharya BR, Hu HC, Engineer C, Villiers F, Ju C, Takeda K, Su Z, Dong Q, Assmann SM, Chen J, Kwak JM, Schroeder JI, Albert R, Rhee SY, and Frommer WB (2014) Border control – a membrane-linked interactome of Arabidopsis. (2014) **Science** 344:711-716.

Bossi F, Fan J, Xiao J, Chandra L, Shen M, Dorone Y, Wagner D, Rhee SY (2017) Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. **BMC Genomics** 18(1):480

Dorone Y, Boeynaems S, Jin B, Bossi F, Flores E, Lazarus E, Michiels E, De Decker M, Baatsen P, Holehouse AS, Sukenik S, Gitler AD, Rhee SY (2021) Hydration-dependent phase separation of a prion-like protein regulates seed germination during water stress. **Cell** 184(16), 4284-4298.e27. bioRViv 2020.08.07.242172; doi: https://doi.org/10.1101/2020.08.07.242172

Bossi F, Jin B, Lazarus E, Cartwright H, Dorone Y, Rhee SY (2021) *CHIQUITA1* maintains temporal transition between proliferation and differentiation in *Arabidopsis thaliana* **Development** 149(11):dev200565. doi: 10.1242/dev.200565 BioRXiv 2021.11.24.469926; doi:10.1101/2021.11.24.469926

4. **Systems biology of plant metabolism and enabling metabolic engineering:** Plant metabolism plays a vital role in the health and well-being of our society. Despite our dependence on plants for energy, nutrition, and medicine, plant metabolism remains a surprisingly understudied field. For example, more than 30% of all pharmaceuticals are based on plant natural products, yet our knowledge of plant metabolic pathways accounts for less than 0.1% of the metabolites thought to exist in flowering plants. Understanding how plants evolved this prodigious chemical vocabulary has been a longstanding goal in plant biology. Our group developed computational pipelines that systematically annotate enzyme function on the genome-scale. Using this system, we created a unique, unified resource of plant metabolic networks and discovered several properties that illustrate the differential evolution of secondary metabolism, permitting elucidation of novel secondary metabolic pathways. This opportunity is particularly relevant because secondary metabolites often confer upon plants the ability to survive major biotic and abiotic threats, and are the major sources of medicine, fragrance, and flavor. Thus, the molecular components involved in the production of secondary metabolites are a source of great interest across many fields of research, including agricultural biotechnology, synthetic biology, and biomedical and pharmaceutical research.

Mueller LA, Zhang P, and Rhee SY (2003) AraCyc. A Biochemical Pathway Database for Arabidopsis. **Plant Physiology** 132(2):453-60.

Zhang P, Dreher K, Karthikeyan A, Chi A, Pujar A, Caspi R, Karp P, Kirkup V, Latendresse M, Lee C, Mueller LA, Muller R, and Rhee SY (2010) Creation of a Genome-Wide Metabolic Pathway Database for Populus trichocarpa Using a New Approach for Reconstruction and Curation of Metabolic Pathways for Plants. **Plant Physiology** 153(4):1479-91.

Chae L, Kim T, Dreher K, and Rhee SY (2014) Genomic signatures of specialized metabolism in plants. **Science** 344:510-513

Schalpfer P, Zhang P, Chuan W, Kim T, Banf M, Chae L, Dreher K, Arvind C, Nilo-Poyanco R, Bernard T, Kahn D, and Rhee SY (2017) Genome-wide prediction of metabolic enzymes, pathways, and gene clusters in plants. **Plant Physiology** 173(4):2041-2059

Kang S-H, Pandey RP, Lee C-M, Jeong J-T, Choi B-S, Sim JS, Jung M, Won SY, Oh T-J, Yu Y, Lee OK, Kim HH, Lee T-H, Kim N-H, Bashyal P, Kim T-S, Kim C-K, Kim J-S, Ahn B-O, Rhee SY, Sohng JK (2020) Genome-enabled discovery of anthraquinone biosynthesis in *Senna tora*. **Nature Communications** 11, 5875.

Hawkins C, Ginzburg D, Zhao K, Dwyer W, Xue B, Xu A, Rice S, Cole B, Paley S, Karp P, and Rhee SY (2021) Plant Metabolic Network: A comprehensive resource of plant metabolic information. **Journal of Integrated Plant Biology**. https://doi.org/10.1111/jipb.13163

5. **Transcriptional regulation and bioengineering:** Transcriptional regulation is fundamental in biology and has been the subject of an intensive study. However, molecular, genetic, and

evolutionary studies suggest that there must be additional layers of control that have not been discovered. To investigate one of such layers, we used an integrated approach (computer science, genetics, genomics, proteomics, molecular evolution, development, and stress physiology) to uncover new layers of transcriptional regulation. First, we discovered a widespread occurrence of transcription factor-like proteins without a DNA binding domain, coined microProteins (miPs), which regulate evolutionarily related transcription factors. We found over 400 putative miPs in Arabidopsis along with their putative target transcription factors and their respective biological pathways. In collaboration with experimental biologists at Carnegie and Stanford, we experimentally validated two novel miPs and their predicted target transcription factors using genetic, molecular, and biochemical experiments as a proof-of-concept. Second, we discovered a new type of bivalent chromatin that we coined 'kairostat', which regulates the timing of gene expression for defense compound biosynthesis in response to pathogen attack. Third, we developed condition-specific genome-scale gene regulatory networks, which led to the discovery of several master regulators that control both growth and defense (manuscript in prep.).

Magnani E, De Klein N, Nam H-I, Kim J-G, Pham KL, Fiume E, Mudgett MB, and **Rhee SY** (2014) A comprehensive analysis of microProteins reveals their potentially widespread mechanism of transcriptional regulation. **Plant Physiology** 165(1):149-15.

Banf M and **Rhee SY** (2017) Enhancing gene regulatory network inference through data integration with markov random fields. **Nature Scientific Reports 7**:41174

Zhao K, Kong D, Jin B, Smolke CD, Rhee SY (2021) A Novel Form of Bivalent Chromatin Associates with Rapid Induction of Camalexin Biosynthesis Genes in Response to a Pathogen Signal in Arabidopsis. **eLife** https://elifesciences.org/articles/69508

6. **Single-Cell Plant Biology:** To supercharge our ability to understand how plants work, we need to quantitatively understand the dynamic molecular organization of plant cells and their functions at the level of individual cells. For this, we need a solid infrastructure that can incorporate and codify the theoretical and empirical data of plant cells, a task too big to tackle for a single group. Therefore, we want to create a community that includes scientists from plant biology, data science, AI, imaging, proteomics, single cell profiling and nanotechnology to lay the groundwork for creating a comprehensive understanding of the dynamic molecular organization of plant cells, an initiative we are calling the Plant Cell Atlas (PCA). We have successfully kickstarted the PCA community-building activities in 2020 with three digital workshops on the vision, technologies and broader impacts of the PCA. Because of COVID-19, our original plan for an in-person gathering of 70 scientists, mostly senior faculty, turned into three virtual workshops, each of which drew over 400 scientists (70% early career) participating from around the world. The PCA community currently has over 800 members with over 150 scientists actively collaborating in SLACK.

Rhee SY, Birnbaum KD, Ehrhardt DW (2019) Towards Building a Plant Cell Atlas. **Trends in Plant Science** 24(4):303-310

Rice S, Fryer E, Ghosh Jha S, Malkovskiy A, Meyer H, Thomas J, Weizbauer R, Zhao K, Birnbaum KD, Ehrhardt DW, Wang Z, Rhee SY, and The Plant Cell Atlas Consortium (2020) First Plant Cell Atlas Workshop Report. **Plant Direct** 00: 1– 10. https://doi.org/10.1002/pld3.271

Plant Cell Atlas Consortium, Ghosh Jha S, Borowsky AT, Cole BJ, Fahlgren N, Farmer A, Huang SC, Karia P, Libault M, Provart NJ, Rice SL, Saura-Sanchez M, Agarwal P, Ahkami AH, Anderton CR, Briggs SP, Brophy JAN, Denolf P, Di Costanzo LF, Exposito-Alonso M, Giacomello S, Gomez-Cano F, Kaufmann K, Ko DK, Kumar S, Malkovskiy AV, Nakayama N, Obata T, Otegui MS, Palfalvi G, Quezada-Rodríguez EH, Singh R, Uhrig RG, Waese J, Van

Wijk K, Wright RC, Ehrhardt DW, Birnbaum KD, Rhee SY (2021) Vision, challenges and opportunities for a Plant Cell Atlas. **eLife** DOI: 10.7554/eLife.66877

Eckelbarger M, Rice S, Osano A, Peng J, Ullah H, Rhee SY (2021) Recognizing Pioneering Black Plant Biologists in Our Schools and Society. **Trends in Plant Science** http://doi.org/10.1016/j.tplants.2021.07.021

Invited Seminars and Symposia:

1. Agricultural Genomics Conference, San Diego, CA (1999); 2. Advances in Genomic Research, Potentials and Applications, San Francisco State University, SF, CA (1999); 3. Genomic *Arabidopsis* Resource Network Workshop, York, UK (2000); 4. NSF Workshop on U.S.-Australia Interactions, Washington D.C. (2000); 5. York University, York, UK (2000); 6. The Institute for Genome Research (2000); 7. Oxford University, Oxford, UK (2000); 8. Lorne Genome Conference, Melbourne, Australia (2001); 9. University of Arizona, Tucson, AZ (2001); 10. Plant Gene Expression Center, Albany, CA (2001); 11. Entigen, Sydney, Australia (2001); 12. Cornell University, Ithaca, NY (2001); 13. Seoul National University, Seoul, South Korea (2001); 14. AAAS Annual Meeting, San Francisco, CA (2001); 15. Plant & Animal Genome IX Conference, San Diego, CA (2001); 16. Mini-symposium on Plant Bioinformatics, KRIBB, Daejon, South Korea (2001); 17. Plant Genome Awardees Meeting, San Diego, CA (2002); 18. Future of the National Plant Genome Initiative, National Academy of Sciences, Washington DC (2002); 19. National Science Foundation Managing Plant Genomic Resources Workshop, Asilomar, CA (2002); 20. International Horticultural Congress, Toronto, Canada (2002); 21. University of California at Riverside, Riverside, CA (2002); 22. University of Guelf, Guelf, Canada (2002); 23. VIB, University of Gent, Gent, Belgium (2003); 24. 2nd International Conference on Plant Metabolomics, Postsdam, Germany (2003); 25. Digital Archives for Science & Engineering Resources (DASER) Symposium (2003); 26. Crop Functional Genomics (2004); 27. 7th International Plant Cold Hardiness Symposium (2004); 28. Seoul National University, Seoul, South Korea (2004); 29. University of Missouri, Columbia (2004); 30. Plant Gene Expression Center, Albany, CA (2004); 31. Iowa State University (2007); 32. U.C. Riverside (2007); 33. University of Calgary, Canada (2007); 34. National Research Center-Plant Biotechnology Institute, Saskatoon, Canada (2007); 35. Danforth Center, MO (2007); 36. Solanaceae Genomics Meeting, Jeju Island, S. Korea (2007); 37. Korea Genome Organization Meeting, Seoul, S. Korea (2007); 38. iPlant Kick-off Conference, Cold Spring Harbor Labs, NY (2008); 39. American Society of Plant Biologists Conference, Merida, Mexico (2008); 40. Banff Plant Metabolism Conference, Banff, Canada (2008); 41. Dow Agrosciences (2010); 42. U.C. Riverside (2010); 43. International Conference on *Arabidopsis* Research (2010); 44. A Current Opinion Conference on Plant Genome Research, Amsterdam, the Netherlands (2011); 45. Alliance of Independent Plant Institutes Meeting, St. Louis, MO (2011); 46. ASMS Asilomar Conference on Mass Spectrometry, Asilomar, CA (2011); 47. U. Florida (2011); 48. Michigan State U. (2011); 49. Phenotype Ontology RCN, NASCent, Durham, NC (2012); 50. Plant Genomics in China XIII, Tai'an, China (2012); 51. Microbial and Plant Genomics Institute (MPGI) Symposium on Systems Biology of Genetic Regulation, St. Paul, MN (2012); 52. International Symposium on Root Systems Biology, Taipei, Taiwan (2012); 53. Danforth Center (2012); 54. National Cheng Kung U., Taiwan (2012); 55. Evolution of Metabolic Diversity, Banbury, NY (March 2013); 56. Washington State U. (April 2013); 57. UC Davis (May 2013); 58. Alliance of Independent Plant Institutes Meeting, Ithaca, NY (May 2013); 59. Plants and People Conference, Berlin, Germany (June 2013); 60. University of Missouri-Columbia (Oct 22, 2013); 61. Meeting on the Genetic Basis of Unintended Effects in Modified Plants, Ottawa, Canada (Jan 14-15, 2014); 62. JGI DOE Conference: "Genomics of Energy and the Environment" (March 24-25, 2015); 63. San Francisco State University (April 23, 2015); 64. Penn State Plant Biology Symposium: "Plant Stress-omics in a Changing Climate" (May 13-16, 2015); 65. Molecular Plant Symposium, Beijing, China (Aug 5-8, 2015); 66. Second Genome (Nov 9,

2015); 67. Plant Genomes & Biotechnology: From Genes to Networks, CSHL, NY (Dec 2-5, 2015); 68. Louisiana State U. (Feb 22, 2016); 69. Plant Gene Expression Center, Albany CA (March 10, 2016); 70. Langebio, the National Laboratory of Genomics for Biodiversity, Mexico (May 10, 2016); 71. NAASC RCN: Arabidopsis Research and Training for the 21st century (May 13-15, 2016); 72. ASPB Conference, Plant Cell Symposium: New Biological Insights from Large-Scale Biology, Austin TX (July 9-13, 2016); 73. MSU - Plant Biotechnology for Health and Sustainability Annual Symposium (Oct 26-27, 2017), East Lansing, MI; 74. First International Plant Systems Biology Conference (Sept 10-14, 2018), Roscoff, France; 75. VIB, Ghent, Belgium (Sept 17, 2018); 76. U. Maryland at College Park (Nov 15, 2018); 77. UC Davis Plant Symposium (April 8, 2019); 78. Danforth Center (May 2019); 79. Plants of the Future, NYU NY (June 13-14, 2019); 80. 2019 Plant Science Symposium on Plant Metabolism and Engineering, UNL, NB (Oct 17-19, 2019); 81. LBNL Single Cell Solutions for Energy and Environment (Jan 23, 2020); 82. DOE BER Genome Science Program Meeting (Feb 23-26, 2020); 83. ASPB / Plantae Global Virtual Plant Research Seminar Series (June 16, 2020); 84. ASPB 2020 (Jul 25-29, 2020); 85. U. Kentucky (Nov 12, 2020); 86. Australian Bioinformatics and Computational Biology Society Conference 2020 (Keynote, Nov 24-26, 2020); 87. Washington State U. (Dec 17, 2020); 88. Williams College (April 9, 2021); 89. Cornell University Plant Breeding Symposium (April 23, 2021); 90. Cell Atlas workshop at EMBL-EBI Industry Programme (May 12-13, 2021); 91. EMSL (Aug 17, 2021); 92. UC Riverside (Nov 10, 2021); 93. Bowie State University (Nov 17, 2021); 94. CalTech-Carnegie Joint Research Workshop on Life Sciences and Ecology (Nov 19, 2021); 95. Western Regional Seed Physiology Research Group Annual Symposium, Virtual (Jan 25, 2022); 96. Digital Carnegie Science Program, Virtual (Jan 25, 2022); 97. Washington State U, Virtual (Feb 7, 2022); 98. U. Georgia's Plant Center Spring Symposium, Virtual (Feb 21, 2022); 99. DOE BER Genome Science Meeting, Virtual (Feb 28-Mar 2, 2022); 100. 31st Western Photosynthesis Conference (Mar 24-25, 2022); 101. MSU NRT-IMPACTS Symposium, Virtual (Apr 11-12, 2022); 102. UC Riverside (Apr 15, 2022); 103. U. Wisconsin-Madison, Virtual (Apr 21, 2022); 104. K-BioX Global Class Seminar, Virtual (Aug 23, 2022); 105. Gregor Mendel Institute, Virtual (Oct 7, 2022); 106. EMSL Seminar (Oct 22, 2022); 107. UNL Plant Sciences Retreat (keynote, Nov 10-11, 2022); 108. 2023 William F. Hanna Memorial Lecture, U. Manitoba, Canada (Feb 16-17, 2023); 109. U. Kentucky Biology Graduate Student Association Seminar (Mar 9, 2023); 110. Maize Genetics Conference (plenary, St. Louis, MO, Mar 16-19, 2023); 111. Norwich Single Cell Consortium (keynote, May 3, 2023); 112. The Sainsbury Laboratory Student Colloquium (May 4, 2023); 113. Biodiversity Cell Atlas Workshop, Barcelona, Spain (May 15-16, 2023); 114. AG2PI Conference: Mapping the Future of Agricultural Genome to Phenome Research, Kansas City, MO (June 15-16, 2023); 115. Seoul National University, Korea (July 3, 2023); 116. IPGSA2023, Korea (July 4-8. 2023); 117. National Institute of Agricultural Sciences, Korea (July 12, 2023); 118. The 62nd annual meeting of the Phytochemical Society of North America (plenary, July 16-20, 2023); 119. ASPB Concurrent Symposium on Plant Resilience and Climate Change, Savannah, GA (Aug 5-8, 2023); 120. UNAM, Mexico (Aug 21, 2023); 121. Lengebio, Irapuato, Mexico (Aug 25, 2023); 122. Center for Plant Biology Annual Symposium, Purdue University (keynote, Sept 8, 2023); 123. The Weill Institute Symposium at Cornell University (Oct 10, 2023); 124. Cell and Molecular Biology Program at MSU Annual Research Symposium, MSU (Oct 13, 2023); 125. The Future of Plant-Environment Interactions: Challenges and Opportunities in a Changing Climate, Banbury, CSHL, NY (Oct 29-Nov 1, 2023); 126. The Biophysical Society 2024 Conference (Feb 10-14, 2024); 127. Condensate Colloquium Series Season 3 (Feb 20, 2024, virtual); 128. EMBO|EMBL Symposium "Diversity of plants: from genomes to metabolism (plenary, Apr 9-12, 2024); 129. Copenhagen Plant Science Conference (keynote, Aug 21-23, 2024)

PEER REVIEWED PUBLICATIONS

1. Karine Prado, Bo Xue, Jennifer E Johnson, Sterling Field, Matt Stata, Charles Lynn Hawkins, Ru-Ching Hsia, Hongbing Liu, Shifeng Cheng, Seung Y. Rhee (2023) Photosynthetic acclimation mediates exponential growth of a desert plant in Death Valley summer bioRxiv 2023.06.23.546155; doi: https://doi.org/10.1101/2023.06.23.546155

2. Fryer E, Guha S, Rogel-Hernandez L, Logan-Garbisch T, Farah HN, Rezaei E, Mollhoff I, Nekimken AL, Xu A, Fechner S, Druckmann S, Clandinin TR, Rhee SY, and Goodman MB (2023) An efficient behavioral screening platform classifies natural products and other chemical cues according to their chemosensory valence in *C. elegans* bioRxiv 2023.06.02.542933; doi: https://doi.org/10.1101/2023.06.02.542933

3. Cho H, Banf M, Shahzad Z, Bossi F, Ruffel S, Van Leene J, Krouk G, Brandizzi F, De Jaeger G, Lacombe B, Rhee SY, and Rouached H (2023) ARSK1 activates TOR signaling to adjust growth to phosphate availability in Arabidopsis **Current Biology** Mar 20:S0960-9822(23)00291-9. PMID: 36963384. https://doi.org/10.1016/j.cub.2023.03.005

4. Field S, Jang G-J, Dean C, Strader L, Rhee SY (2023) Plants use molecular mechanisms mediated by biomolecular condensates to integrate environmental cues with development **The Plant Cell** https://doi.org/10.1093/plcell/koad062

5. Zhao K and Rhee SY (2023) Enzyme and pathway enrichment analyses using omics data. **Trends in Genetics** https://doi.org/10.1016/j.tig.2023.01.003

6. Ginzburg D and Rhee SY (2023) Evaluating drought resistance with a Raspberry Pi and time-lapse photography. **Bio-protocol** 13(2): e4593. DOI: 10.21769/BioProtoc.4593

7. Xue, B., & Rhee, S. Y. (2023). Status of genome function annotation in model organisms and crops. Plant Direct, 7(7), e499. https://doi.org/10.1002/pld3.499 **BioRXiv** (2022) https://biorxiv.org/cgi/content/short/2022.07.03.498619v1

8. Dwyer W, Ibe C, and Rhee SY (2022) Renaming Indigenous crops and addressing colonial bias in scientific language. **Trends in Plant Science** 27(12): 1189-1192 https://doi.org/10.1016/j.tplants.2022.08.022

9. BERAC (2022) U.S. Scientific Leadership Addressing Energy, Ecosystems, Climate, and Sustainable Prosperity: Report from the BERAC Subcommittee on International Benchmarking, DOE/SC-0208. M. McCann and P. Reed, eds. Biological and Environmental Research Advisory Committee. DOI:10.2172/1895129.

10. Rice S, Lazarus E, Anderton C, Birnbaum K, Brophy J, Cole B, Dickel D, Ehrhardt D, Fahlgren N, Frank M, Haswell E, Huang S-S, Leiboff S, Libault M, Otegui M, Provart N, Uhrig GR, and Rhee SY (2022) First Plant Cell Atlas Symposium Report **Plant Direct** 6(6):e406 doi: https://doi.org/10.1002/pld3.406

11. Zhao K, Rhee SY (2022) Omics-guided functional discovery of plant metabolic pathways. **Current Opinion in Plant Biology** 67:102222. doi: https://doi.org/10.1016/j.pbi.2022.102222

12. Ginzburg D, Bossi F, and Rhee SY (2022) Uncoupling differential water usage from drought resistance in a dwarf Arabidopsis mutant. **Plant Physiology** 190(4):2115–2121 **BioRXiv** (2021) https://www.biorxiv.org/content/10.1101/2021.11.25.470014v1

13. Bossi F, Jin B, Lazarus E, Cartwright H, Dorone Y, Rhee SY (2022) *CHIQUITA1* maintains temporal transition between proliferation and differentiation in *Arabidopsis thaliana* **Development** 149(11):dev200565. doi: 10.1242/dev.200565 **BioRXiv** (2021) 2021.11.24.469926; doi: https://doi.org/10.1101/2021.11.24.469926

14. Birnbaum KD, Otegui MS, Bailey-Serres J, Rhee SY (2022) The Plant Cell Atlas: Focusing New Technologies on the Kingdom that Nourishes the Planet. **Plant Physiology** 188(2):675–679. doi: 10.1093/plphys/kiab584. Epub ahead of print (2021) PMID: 34935969.

15. Dorone Y, Boeynaems S, Rhee SY (2021) Live imaging *Arabidopsis thaliana* embryos under different hydration conditions. **STAR Protocols** 2(4): 101025. https://doi.org/10.1016/j.xpro.2021.101025

16. Nam H-I, Shahzad Z, Dorone Y, Clowez S, Zhao K, Bouain N, Cho H, Rhee SY and Rouached H (2021) Interdependent nutrient availability controls photosynthesis through retrograde signaling. **Nature Communications** 12:7211 https://doi.org/10.1038/s41467-021-27548-2 **BioRXiv doi:** https://doi.org/10.1101/2021.02.11.430802

17. Therby-Vale R, Lacombe B, Rhee SY, Nussaume L, Rouached H (2021) Mineral Nutrient Signaling Controls Photosynthesis: A focus on iron-deficiency induced chlorosis. **Trends in Plant Science** https://doi.org/10.1016/j.tplants.2021.11.005

18. Silva TN, Thomas JB, Dahlberg J, Rhee SY, Mortimer JC (2021) Progress and Challenges in Sorghum Biotechnology, a Multi-Purpose Feedstock for the Bioeconomy. **Journal of Experimental Botany** 73(3): 646–664. https://doi.org/10.1093/jxb/erab450

19. Zhao K, Kong D, Jin B, Smolke CD, Rhee SY (2021) A Novel Form of Bivalent Chromatin Associates with Rapid Induction of Camalexin Biosynthesis Genes in Response to a Pathogen Signal in Arabidopsis. **eLife** https://elifesciences.org/articles/69508 **bioRxiv** doi: https://doi.org/10.1101/589036

20. Plant Cell Atlas Consortium, Ghosh Jha S, Borowsky AT, Cole BJ, Fahlgren N, Farmer A, Huang SC, Karia P, Libault M, Provart NJ, Rice SL, Saura-Sanchez M, Agarwal P, Ahkami AH, Anderton CR, Briggs SP, Brophy JAN, Denolf P, Di Costanzo LF, Exposito-Alonso M, Giacomello S, Gomez-Cano F, Kaufmann K, Ko DK, Kumar S, Malkovskiy AV, Nakayama N, Obata T, Otegui MS, Palfalvi G, Quezada-Rodríguez EH, Singh R, Uhrig RG, Waese J, Van Wijk K, Wright RC, Ehrhardt DW, Birnbaum KD, Rhee SY (2021) Vision, challenges and opportunities for a Plant Cell Atlas. **eLife** DOI: 10.7554/eLife.66877

21. Hawkins C, Ginzburg D, Zhao K, Dwyer W, Xue B, Xu A, Rice S, Cole B, Paley S, Karp P, and Rhee SY (2021) Plant Metabolic Network: A comprehensive resource of plant metabolic information. **Journal of Integrative Plant Biology**. https://doi.org/10.1111/jipb.13163

22. Eckelbarger M, Rice S, Osano A, Peng J, Ullah H, Rhee SY (2021) Recognizing Pioneering Black Plant Biologists in Our Schools and Society. **Trends in Plant Science** http://doi.org/10.1016/j.tplants.2021.07.021

23. Cole B, Bergmann D, Blaby-Haas C, Blaby I, Bouchard K, Brady S, Ciobanu D, Coleman-Derr D, Leiboff S, Mortimer J, Nobori T, Rhee SY, Schmutz J, Simmons BA Singh A, Sinha N, Vogel J, O'Malley R, Visel A (2021) Plant Single-Cell Solutions for Energy and the Environment. **Communications Biology** 4:962.

24. Dorone Y, Boeynaems S, Jin B, Bossi F, Flores E, Lazarus E, Michiels E, De Decker M, Baatsen P, Holehouse AS, Sukenik S, Gitler AD, Rhee SY (2021) Hydration-dependent phase separation of a prion-like protein regulates seed germination during water stress. **Cell** 184(16), 4284-4298.e27 **bioRxiv** 2020.08.07.242172; doi: https://doi.org/10.1101/2020.08.07.242172 [highlighted by Developmental Cell, PNAS, Nature Chemical Biology, F1000, Science]

25. Demirer GS, Silva TN, Thomas JB, Jackson CT, Ehrhardt DW, Rhee SY, Mortimer JC, and Landry MP (2021) Nanotechnology to advance CRISPR/Cas genetic engineering of plants. **Nature Nanotechnology 16**, 243–250.

26. Kang S-H, Pandey RP, Lee C-M, Jeong J-T, Choi B-S, Sim JS, Jung M, Won SY, Oh T-J, Yu Y, Lee OK, Kim HH, Lee T-H, Kim N-H, Bashyal P, Kim T-S, Kim C-K, Kim J-S, Ahn B-O, Rhee SY, Sohng JK (2020) Genome-enabled discovery of anthraquinone biosynthesis in *Senna tora.* **Nature Communications** 11, 5875. https://doi.org/10.1038/s41467-020-19681-1 **bioRxiv** doi: https://doi.org/10.1101/2020.04.27.063495

27. Rice S, Fryer E, Jha SG, Malkovskiy A, Meyer H, Thomas J, Weizbauer R, Zhao K, Birnbaum KD, Ehrhardt DW, Wang Z, Rhee SY, and The Plant Cell Atlas Consortium (2020) First Plant Cell Atlas Workshop Report. **Plant Direct** 00: 1– 10. https://doi.org/10.1002/pld3.271

28. Parry G, Provart NJ, Brady SM, Uzilday B, The Multinational Arabidopsis Steering Committee (2020) Current status of the multinational Arabidopsis community. **Plant Direct** 00:1-9.
29. Lin F, Lazarus E, Rhee SY (2020) QTG-Finder2: a generalized machine learning algorithm for prioritizing QTL causal genes in plants. **Genes|Genomes|Genetics** 10(7): 2411–2421. **bioRxiv** doi: https://doi.org/10.1101/2020.02.03.931444
30. Bouain N, Korte A, Satbhai SB, Rhee SY, Busch W, Rouached H (2019) Systems approaches provide new insights into *Arabidopsis thaliana* root growth under mineral nutrient limitation. **PLOS Genetics** 6;15(11):e1008392. **bioRxiv** 460360; doi: https://doi.org/10.1101/460360
31. Rhee SY, Birnbaum KD, Ehrhardt DW (2019) Towards Building a Plant Cell Atlas. **Trends in Plant Science** 24(4):303-310
32. Banf M, Zhao K, Rhee SY (2019) METACLUSTER - an R package for context-specific functionality analysis of metabolic gene clusters. **Bioinformatics** btz021, https://doi.org/10.1093/bioinformatics/btz021
33. Lin F, Fan J, Rhee SY (2018) QTG-Finder: a machine-learning algorithm to prioritize causal genes of quantitative trait loci in plants. **Genes|Genomes|Genetics** 9(10):3129-3138. **bioRxiv** doi: https://doi.org/10.1101/484204
34. Friesner J, Assmann SM, Bastow R, Bailey-Serres J, Beynon J, Brendel V, Buell CR, Bucksch A, Busch W, Demura T, Dinneny JR, Doherty CJ, Eveland AL, Falter-Braun P, Gehan MA, Gonzales M, Grotewold E, Gutierrez R, Kramer U, Krouk G, Ma S, Markelz RJC, Megraw M, Meyers BC, Murray JAH, Provart NJ, Rhee SY, Smith R, Spalding EP, Taylor C, Teal TK, Torii KU, Town C, Vaughn M, Vierstra R, Ware D, Wilkins O, Williams C, Brady SM (2017) The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. **Plant Physiology** 175(4):1499-1509. doi: 10.1104/pp.17.01490. PubMed PMID: 29208732; PubMed Central PMCID: PMC5717721.
35. Bossi F, Fan J, Xiao J, Chandra L, Shen M, Dorone Y, Wagner D, Rhee SY (2017) Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. **BMC Genomics** 18(1):480
36. Rouchard H and Rhee SY (2017) System-level understanding of plant mineral nutrition in the big data era. **Current Opinion in Systems Biology** 4:71-77
37. Schalpfer P, Zhang P, Chuan W, Kim T, Banf M, Chae L, Dreher K, Arvind C, Nilo-Poyanco R, Bernard T, Kahn D, and Rhee SY (2017) Genome-wide prediction of metabolic enzymes, pathways, and gene clusters in plants. **Plant Physiology** 173(4):2041-2059
38. Chavali A and Rhee SY (2017) Bioinformatics tools for the identification of gene clusters that biosynthesize specialized metabolites. **Briefings in Bioinformatics** bbx020. doi: 10.1093/bib/bbx020
39. Banf M and Rhee SY (2017) Enhancing gene regulatory network inference through data integration with markov random fields. **Nature Scientific Reports** 7:41174.
40. Banf M and Rhee SY (2016) Computational inference of gene regulatory networks: approaches, limitations and opportunities. **BBA Gene Regulatory Mechanisms** S1874-9399(16)30188-2.
41. Walsh JR, Schaeffer ML, Zhang, Rhee SY, Dickerson JA, Sen TZ (2016) The quality of metabolic pathway resources depends on initial enzymatic function assignments: a case for maize. **BMC Systems Biology** 10:129.
42. Zheng Y, Jiao C, Sun H, Rosli HG, Pombo MA, Zhang P, Banf M, Dai X, Martin GB, Giovannoni JJ, Zhao PX, Rhee SY, Fei Z (2016) iTAK: a program for genome-wide prediction and classification of plant transcription factors, transcriptional regulators, and protein kinases. **Molecular Plant** S1674-2052(16)30223-4.
43. Rhee SY, Parker J, and Mockler T (2016) A glimpse into the future of genome-enabled plant biology from the shores of Cold Spring Harbor. **Genome Biology** 17(1):3.

44. Fiume E, de Klein N, Rhee SY, and Magnani E (2015) A framework for discovering, designing, and testing microProteins to regulate synthetic transcriptional modules. **Methods in Molecular Biology** 1482:175-88.
45. Guo J, Fan J, Hauser B, and Rhee SY (2015) Target enrichment improves mapping of complex traits by deep sequencing. **Genes | Genomes | Genetics** 6(1):67-77.
46. Ladics G, Bartholomaeus A, Bregitzer P, Doerrer N, Gray A, Holzhauser T, Jordan M, Keese P, Kok E, Macdonald P, Parrott W, Privalle L, Raybould A, Rhee SY, Rice E, Romeis J, Vaughn J, Wal J-M, and Glenn K (2015) Genetic basis and detection of unintended effects in genetically modified crop plants. **Transgenic Research** 24(4):587-603.
47. Kim T, He K, Dreher K, Lee I, Moon S, Bais P, Dickerson J, Dixon P, Fiehn O, Lange BM, Sumner LW, Welti R, Wurtele ES, Nikolau BJ, and Rhee SY (2015) Patterns of metabolite changes from large-scale gene perturbations in *Arabidopsis thaliana* using genome-scale metabolic networks. **Plant Physiology** 167(4):1685-98.
48. de Klein N, Magnani E, and Rhee SY microProtein Prediction Program (miP3): a software for predicting microProteins and their target transcription factors. (2015) **International Journal of Genomics** Article ID 734147. 1-4.
49. Peng J, Uygun S, Kim T, Wang Y, Rhee SY, and Chen J (2015) Measuring genome-specific semantic similarities using Gene Ontology and Gene Co-Function networks. **BMC Bioinformatics** 16(1):44.
50. Xu M and Rhee SY (2014) Becoming data-savvy in a big-data world. **Trends in Plant Science** 19(10):619–622.
51. Jones AM, Xuan Y, Xu M, Wang R-S, Ho C-H, Lalonde S, You CH, Sardi MI, Parsa SA, Smith-Valle E, Su T, Frazer KA, Pilot G, Pratelli R, Grossmann G, Acharya BR, Hu HC, Engineer C, Villiers F, Ju C, Takeda K, Su Z, Dong Q, Assmann SM, Chen J, Kwak JM, Schroeder JI, Albert R, Rhee SY, and Frommer WB (2014) Border control – a membrane-linked interactome of *Arabidopsis*. **Science** 344:711-716. **[highlighted in F1000]**
52. Chae L, Kim T, Nilo-Poyanco R, and Rhee SY Genomic signatures of specialized metabolism in plants. (2014) **Science** 344:510-513. **[highlighted in F1000]**
53. Magnani E, De Klein N, Nam H-I, Kim J-G, Pham KL, Fiume E, Mudgett MB, and Rhee SY (2014) A comprehensive analysis of microProteins reveals their potentially widespread mechanism of transcriptional regulation. **Plant Physiology** 165(1):149-159.
54. Rhee SY and Mutwil M (2014) Towards revealing the functions of all genes in plants. **Trends in Plant Science** 19(4):212-221.
55. Bassel GW, Gaudinier A, Brady SM, Hennig L, Rhee SY, and Smet ID (2012) Systems analysis of plant functional, transcriptional, physical interaction, and metabolic networks. **Plant Cell** 24(10):3859-75.
56. Chen J, Lalonde S, Obrdlik P, Noorani Vatani A, Parsa SA, Vilariño C, Revuelta JL, Frommer WB, and Rhee SY (2012) Uncovering *Arabidopsis* membrane protein interactome enriched in transporters using mating-based split ubiquitin assays and classification models. **Frontiers in Plant Science** 3(124):1-14.
57. Moon S, He Kun, Bais P, Dickerson J, Dixon P, Rhee SY, Wohlgemuth G, Fiehn O, Barkan L, Lange I, Lange B, Cortes D, Shuman J, Shulaev V, Huhman D, Sumner L, Roth M, Welti R, Ilarslan H, Wurtele E, Brachova L, Campbell A, Perera A, and Nikolau B (2012) Metabolomics as a hypothesis-generating functional genomics tool for the annotation of *Arabidopsis thaliana* genes of "unknown function". **Frontiers in Plant Science** 3(15):1-12.
58. Chae L, Lee I, Shin J, and Rhee SY (2012) Towards an understanding of how molecular networks evolve in plants. **Current Opinion in Plant Biology** 15(2):177-184.
59. Hwang S, Rhee SY, Marcotte EM, and Lee I (2011) Systematic prediction of gene function using a probabilistic functional gene network for *Arabidopsis thaliana*. **Nature Protocols** 6(9):1429-1442.

60. Sun Y, Fan X-Y, Cao D-M, He K, Tang W, Zhu J-Y, He J-X, Bai M-Y, Zhu S, Oh E, Patil S, Kim TW, Ji H, Wong WH, Rhee SY, and Wang J-Y (2010) Integration of Brassinosteroid Signal Transduction with the Transcription Network for Plant Growth Regulation in *Arabidopsis*. **Developmental Cell** 19(5):765-77.

61. Lalonde S, Sero A, Pratelli R, Pilot G, Chen J, Sardi MA, Parsa SA, Kim D-Y, Acharya BR, Stein EV, Hu H-C, Villiers F, Takeda K, Yang Y, Han YS, Schwacke R, Chiang W, Kato N, Loqué D, Assmann SM, Kwak JM, Schroeder J, Rhee SY, and Frommer WB (2010) A membrane protein / signaling protein interaction network for *Arabidopsis* version AMPv2. **Frontiers in Plant Science** 1(24):1-14.

62. Zhang P, Dreher K, Karthikeyan A, Chi A, Pujar A, Caspi R, Karp P, Kirkup V, Latendresse M, Lee C, Mueller LA, Muller R, and Rhee SY (2010) Creation of a Genome-Wide Metabolic Pathway Database for Populus trichocarpa Using a New Approach for Reconstruction and Curation of Metabolic Pathways for Plants. **Plant Physiology** 153(4):1479-91.

63. Bais P, Moon S, He K, Leitao R, Dreher K, Walk T, Sucaet Y, Barkan L, Wohlgemuth G, Wurtele ES, Dixon P, Fiehn O, Lange BM, Shulaev V, Sumner LW, Welti R, Nikolau B, Rhee SY, and Dickerson JA (2010) PlantMetabolomics.org: A web portal for Plant Metabolomics Experiments. **Plant Physiology** 152(4):1807-16.

64. Lee I, Ambaru B, Thakkar P, Marcotte E, and Rhee SY (2010) Rational association of genes with traits using a genome-scale gene network for *Arabidopsis thaliana*. **Nature Biotechnology** 2(28):149-156. **[highlighted in F1000]**

65. Reference Genome Group of the Gene Ontology Consortium (2009) The Gene Ontology's Reference Genome Project: a unified framework for functional annotation across species. **PLOS Computational Biology** 5(7): e1000431.

66. Chen J, Ji L, Hsu W, Tan K-L, and Rhee SY (2009) Exploiting Domain Knowledge to Improve Biological Significance of Biclusters with Key Missing Genes. **IEEE Technical Committee on Data Engineering Conference** ICED.2009.205: 1219-1222.

67. Aceituno FF, Moseyko N, Rhee SY, and Gutierrez RA (2008) The rules of gene expression in plants: Organ identity and gene body methylation are key factors for regulation of gene expression in *Arabidopsis thaliana*. **BMC Genomics** 9:438.

68. Howe D, Costanzo M, Fey P, Gojobori T, Hannick L, Hide W, Hill DP, Kania R, Schaeffer M, St. Pierre S, Twigger S, White O, and Rhee SY (2008) The future of biocuration. **Nature** 455:47-50.

69. Rhee SY, Wood V, Dolinski K, and Draghici S (2008) Use and Misuse of the Gene Ontology (GO) Annotations. **Nature Review Genetics** 9(7):509-15.

70. Pennycooke JC, Cheng H, Roberts SM, Yang Q, Rhee SY, and Stockinger E (2008) The low temperature-responsive, Solanum CBF1 genes maintain high identity in their upstream regions in a genomic environment undergoing gene duplications, deletions, and rearrangements. **Plant Molecular Biology** 67(5):483-97.

71. Lalonde S, Ehrhardt D, Loqué D, Chen J, Rhee SY, and Frommer WB (2008) Molecular and cellular approaches for the detection of protein-protein interactions and generation of protein interaction maps. **Plant Journal** 53(4):610-35.

72. Avraham S, Tung C-W, Ilic K, Jaiswal P, Kellogg EA, McCouch S, Pujar A, Reiser L, Rhee SY, Sachs MM, Schaeffer M, Stein L, Stevens P, Vincent L, Zapata F, and Ware D (2008) The Plant Ontology Database: a community resource for plant structure and developmental stages controlled vocabulary and annotations. **Nucleic Acids Research** 36:D449-D454.

73. Ilic K, Stevens PF, Kellogg EA, and Rhee SY (2008) Plant Structure Ontology –anatomical ontology of flowering plants. In: Anatomy Ontologies for Bioinformatics: Principles and Practice. A. Burger, D. Davidson and R. Baldock (Eds). Springer. 27-42. ISBN: 184628884.

74. Fiehn O, Sumner LW, Rhee SY, Ward J, Dickerson J, Lange BM, Lane G, Roessner U, Last R, and Nikolau B (2007) Minimum reporting standards for plant biology context information in metabolomic studies. **Metabolomics** 3(3):195-201.

75. Caspi R, Foerster H, Fulcher CA, Kaipa P, Krummenacker M, Latendresse M, Paley S, Rhee SY, Shearer AG, Tissier C, Walk TC, Zhang P, and Karp PD (2008) The MetaCyc Database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. **Nucleic Acids Research** 38(Database issue):D473-9.

76. The Gene Ontology Consortium (2008) The Gene Ontology project in 2008. **Nucleic Acids Research** 36(Database issue):D440-4.

77. Ilic K, Kellogg E, Jaiswal P, Zapata F, Stevens P, Vincent L, Pujar A, Avraham S, Reiser L, McCouch SR, Sachs S, Schaeffer M, Ware D, Stein L, and Rhee SY (2006) Plant Structure Ontology: A Unified Vocabulary for Flowering Plants. **Plant Physiology** 143(2):587-99.

78. Stein LD, Beavis WD, Gessler DD, Huala E, Lawrence CJ, Main D, Mueller LA, Rhee SY, and Rokhsar DS (2006) Save our data! **Scientist** 20(4):24-25.

79. Pujar A, Jaiswal P, Kellogg EA, Ilic K, Vincent L, Avraham S, Stevens P, Zapata F, Reiser R, Rhee SY, Sachs MM, Schaeffer M, Stein L, Ware D, and McCouch S (2006) Whole Plant Growth Stage Ontology: History, Development and Application. **Plant Physiology** 142(2):414-28.

80. Leebens-Mack J, Vision T, Brenner E, Bowers JE, Cannon S, Clement MJ, Cunningham CW, dePamphilis C, deSalle R, Doyle JJ, Eisen JA, Gu X, Harshman J, Kellogg EA, Koonin EV, Philippe H, Pires JC, Qiu YL, Rhee SY, Sjölander K, Soltis DE, Soltis PS, Stevens P, Stevenson DW, Warnow T, and Zmasek C. (2006) Taking the First Steps Towards a Standard for Reporting on Phylogenies: Minimal Information About a Phylogenetic Analysis (MIAPA). **OMICS** 10(2):231-237.

81. Rhee SY, Dickerson J, and Xu D (2006) Bioinformatics and its Applications in Plant Biology. **Annual Review of Plant Biology** 57:335-360.

82. Zimmermann P, Schildknecht B, Craigon D, Garcia-Hernandez M, Gruissem W, May S, Mukherjee G, Parkinson H, Rhee SY, Wagner U, and Hennig L. (2006) MIAME/Plant – adding value to plant microarrray experiments. **Plant Methods** 2:1-3.

83. Gene Ontology Consortium (2006) The Gene Ontology Project in 2006. **Nucleic Acids Research** 34(Database issue):D322-6.

84. Caspi R, Foerster H, Fulcher C, Hopkinson R, Ingraham J, Kaipa P, Krummenacker M, Paley S, Pick J, Rhee SY, Tissier C, Zhang P, and Karp P (2006) MetaCyc: A multiorganism database of metabolic pathways and enzymes. **Nucleic Acids Research** 34(Database issue):D511-6.

85. Li S, Ehrhardt D, and Rhee SY (2006) Systematic Analysis of *Arabidopsis* Protein Localization and Software Tools for Fluorescent Tagging of Full-Length *Arabidopsis* Proteins. **Plant Physiology** 141(2):527-39. **[highlighted in F1000]**

86. Jaiswal P, Avraham S, Ilic K, Kellogg EA, McCouch S, Pujar A, Reiser L, Rhee SY, Sachs MM, Schaeffer M, Stein L, Stevens P, Vincent L, Ware D, and Zapata F. (2005) Plant Ontology (PO): A controlled vocabulary of plant structures and growth stages. **Functional and Integrated Genomics** 6:388-397.

87. Rhee SY and Crosby W. (2005) Biological Databases for Plant Research. **Plant Physiology** 138(1):1-3.

88. Yoo D, Xu I, Berardini T, Rhee SY, Narayanasami V, and Twigger S (2005) PubSearch and PubFetch, a simple management system for semi-automated retrieval and annotation of biological information from the literature. In Current Protocols in Bioinformatics. John Wiley & Sons. Chapter 9. Unit 9.7

89. Reiser L and Rhee SY (2005) Using The *Arabidopsis* Information Resource (TAIR) to Find Information About *Arabidopsis* Genes. In Current Protocols in Bioinformatics. John Wiley & Sons. Chapter 1.11.

90. Rhee SY (2005) Bioinformatics: Current Limitations and Insights for the Future. **Plant Physiology** 138(2):569-70.

91. Yan T, Yoo D, Berardini T, Mueller L, Weems D, Weng S, Cherry JM, and Rhee SY (2005) PatMatch: a program for finding patterns in peptide and nucleotide sequences. **Nucleic Acids Research** 33(Web Server issue):W262-6.
92. Zhang P, Foerster H, Tissier CP, Mueller L, Paley S, Karp P, and Rhee SY (2005) MetaCyc and AraCyc: metabolic pathway databases for plant research. **Plant Physiology** 138(1):27-37.
93. Bard J, Rhee SY, and Ashburner M (2005) An ontology for cell types. **Genome Biology** 6:R21.
94. Schlueter SD, Wilkerson MD, Huala E, Rhee SY, and Brendel V (2005) Community-based gene structure annotation. **Trends in Plant Science** 10(1):9-14.
95. Rhee SY, Zhang P, and Foerster H, and Tissier C (2005) AraCyc: Overview of an *Arabidopsis* Metabolism Database and Its Applications for Plant Research. In Biotechnology in Agriculture and Forestry: Plant Metabolomics. K. Saito, R. Dixon and L. Willmitzer ed., Springer. Volume 57. pp. 141-153.
96. Jenkins H, Hardy N, Beckmann M, Draper J, Smith AR, Taylor J, Fiehn O, Goodacre R, Bino RJ, Hall R, Kopka K, Lange BM, Liu JR, Mendes P, Nikolau BJ, Oliver SG, Paton NW, Rhee SY, Roessner-Tunali U, Saito K, Smedsgaard J, Sumner LW, Wurtele ES, and Kell DB (2004) A proposed framework for the description of plant metabolomics experiments and their results. **Nature Biotechnology** 22(12):1601-6.
97. Zhang X, Fowler S, Cheng H, Lou Y, Rhee SY, Stockinger EJ, and Thomashow MF (2004) Freezing Sensitive Tomato has a Functional CBF Cold Response Pathway, but a CBF Regulon that Differs from that of Freezing Tolerant *Arabidopsis*. **Plant Journal** 39(6):905-19.
98. Berardini TZ, Mundodi S, Reiser R, Huala E, Garcia-Hernandez M, Zhang P, Mueller LM, Yoon J, Doyle A, Lander G, Moseyko N, Yoo D, Xu I, Zoeckler B, Montoya M, Miller N, Weems D, and Rhee SY (2004) Functional annotation of the *Arabidopsis* genome using controlled vocabularies. **Plant Physiology** 135(2):1-11.
99. Tian GW, Mohanty A, Chary SN, Li S, Paap B, Drakakis G, Kopec C, Li J, Ehrhardt E, Jackson D, Rhee SY, Raikhel N, and Citovsky V (2004) High-Throughput Fluorescent Tagging of Full-Length *Arabidopsis* Gene Products *in Planta*. **Plant Physiology** 135(1):25-38. **[highlighted in F1000]**
100.   Dolan EL, Soots BE, Lemaux PG, Rhee SY, and Reiser L (2004) Strategies to Avoid Reinventing the Pre-college Education and Outreach Wheel. **Genetics** 166:1601-1609.
101.   Weems D, Miller N, Garcia-Hernanzez M, Huala E, and Rhee SY (2004) Design, implementation, and maintenance of a model organism database for *Arabidopsis thaliana*. **Comparative and Functional Genomics** 5(4):362-369.
102.   Thimm O, Bläsing YG, Nagel, A, Meyer, S, Kruger, P, Selbig, J, Müller, L, Rhee, SY, and Stitt M (2004) MapMan: A User-Driven Tool to Display Genomics Data Sets onto Diagrams of Metabolic Pathways and other Biological Processes. **Plant Journal** 37(6):914-39. **[highlighted in F1000]**
103.   Bard JL and Rhee SY (2004) Ontologies in biology: design, applications and future challenges. **Nature Review Genetics** 5(3):213-22.
104.   Rhee SY (2004) Carpe Diem. Retooling the Publish or Perish Model into the Share and Survive Model. **Plant Physiology** 134(2):543-7.
105.   Krieger CJ, Zhang P, Mueller L, Wang A, Paley S, Arnaud M, Pick J, Rhee SY, and Karp P (2004) MetaCyc: Recent enhancements to a database of metabolic pathways and enzymes in microorganisms and plants. **Nucleic Acids Research** 32 Database issue:D438-42.
106.   Harris MA, Clark J, Ireland A, Lomax J, Ashburner M, Foulger R, Eilbeck K, Lewis S, Marshall B, Mungall C, Richter J, Rubin GM, Blake JA, Bult C, Dolan M, Drabkin H, Eppig JT, Hill DP, Ni L, Ringwald M, Balakrishnan R, Cherry JM, Christie KR, Costanzo MC, Dwight SS, Engel S, Fisk DG, Hirschman JE, Hong EL, Nash RS, Sethuraman A, Theesfeld CL,

Botstein D, Dolinski K, Feierbach B, Berardini T, Mundodi S, Rhee SY, Apweiler R, Barrell D, Camon E, Dimmer E, Lee V, Chisholm R, Gaudet P, Kibbe W, Kishore R, Schwarz EM, Sternberg P, Gwinn M, Hannick L, Wortman J, Berriman M, Wood V, de la Cruz N, Tonellato P, Jaiswal P, Seigfried T, and White R; Gene Ontology Consortium. (2004) The Gene Ontology (GO) database and informatics resource. **Nucleic Acids Research** 32 Database issue:D258-61.

107.   Berardini TA and Rhee SY (2004) *Arabidopsis thaliana*: Characteristics and Annotation of a Model Genome. In Encyclopedia of Plant & Crop Science. Marcel Dekker, Inc. 47-50*.*

108.   Rhee SY, Osborne E, Poindexter P, and Somerville CR (2003) Microspore separation in the quartet 3 mutants of *Arabidopsis* is impaired by a defect in a developmentally regulated pectinase required for pollen mother cell degradation. **Plant Physiology** 133(3):1170-80.

109.   Mueller LA, Zhang P, and Rhee SY (2003) AraCyc. A Biochemical Pathway Database for *Arabidopsis*. **Plant Physiology** 132(2):453-60.

110.   Rhee SY, Beavis W, Berardini TZ, Chen G, Dixon D, Doyle A, Garcia-Hernandez M, Huala E, Lander G, Montoya M, Miller N, Mueller LA, Mundodi S, Reiser L, Tacklind J, Weems DC, Wu Y, Xu I, Yoo D, Yoon J, and Zhang P (2003) The *Arabidopsis* Information Resource (TAIR): a model organism database providing a centralized, curated gateway to *Arabidopsis* biology, research materials and community. **Nucleic Acids Research** 31(1):224-228.

111.   Clarke BC, Lambrecht M, and Rhee SY (2003) *Arabidopsis* genomic information for interpreting wheat EST sequences. **Functional and Integrated Genomics** 3(1):33-38.

112.   Garcia-Hernandez M, Berardini TZ, Chen C, Crist D, Doyle A, Huala E, Knee E, Miller N, Mueller L, Mundodi S, Reiser L, Rhee SY, Scholl R, Tacklind J, Weems D, Wu Y, Xu I, Yoo D, Yoon J, and Zhang P (2002) **Functional and Integrated Genomics** 2(6):239-253.

113.   Reiser L, Mueller LA, and Rhee SY (2002) Surviving in a sea of data: a survey of plant genome data resources and issues in building data management systems. **Plant Molecular Biology** 48(1):59-74.

114.   The Gene Ontology Consortium (2001) Creating the Gene Ontology Resource: Design and Implementation. **Genome Research** 11(8):1425-1433.

115.   Huala E, Dickerman A, Garcia-Hernandez M, Weems D, Reiser L, LaFond F, Hanley D, Kiphart D, Zhuang J, Huang W, Mueller L, Bhattacharyya D, Bhaya D, Sobral B, Beavis B, Somerville C, and Rhee SY (2001) The *Arabidopsis* Information Resource (TAIR): A comprehensive database and web-based information retrieval, analysis, and visualization system for a model plant. **Nucleic Acids Research** 29(1):102-5.

116.   Rhee SY (2000) Bioinformatic resources, challenges, and opportunities using *Arabidopsis thaliana* as a model organism in post-genomic era. **Plant Physiology** 2000 124(4):1460-4.

117.   Rhee SY and Flanders DJ (2000) Web-based bioinformatic tools for *Arabidopsis* researchers. In *Arabidopsis*: A Practical Approach. pp. 225-265. Zoe Wilson ed., Oxford University Press, UK.

118.   Rhee SY, Weng S, Bongard-Pierce DK, Garcia-Hernandez M, Malekian A, Flanders, DJ, and Cherry JM (1999) Unified display of *Arabidopsis thaliana* physical maps from AtDB, the *A. thaliana* database. **Nucleic Acids Research** 27(1):79-84.

119.   Rhee SY, Weng S, Flanders D, Cherry JM, Dean C, Lister C, Anderson M, Koornneef M, Meinke DW, Nickle T, Smith K, and Rounsley SD (1998) Genome maps 9. *Arabidopsis thaliana*. Wall chart. **Science** 282(5389):663-7.

120.   Rhee SY and Somerville CR (1998) Tetrad pollen formation in quartet mutants of *Arabidopsis thaliana* is associated with persistence of pectic polysaccharides of the pollen mother cell wall. **Plant Journal** 15:79-88.

121.   Rhee SY and Somerville CR (1994) Flat-Surface Grafting in *Arabidopsis thaliana.* **Plant Molecular Biology Reporter** 13:118-123.

122. Preuss D, Rhee SY, Davis RW (1994) Tetrad analysis possible in *Arabidopsis* with mutation of the QUARTET (QRT) genes. **Science** 264:1458-60.
123. Ruan ZS, Anantharam V, Crawford IT, Ambudkar SV, Rhee SY, Allison MJ, and Maloney PC (1992) Identification, purification, and reconstitution of OxlT, the oxalate: formate antiport protein of *Oxalobacter formigenes*. **Journal of Biological Chemistry** 267:10537-43.

Other publications
124. Rhee SY (2014) An interview with Seung Yon (Sue) Rhee. **Trends in Plant Science** 19(4):198-199.
125. Rhee SY (2001) Extending the Frontiers of Plant Biology: Large scale biology, bioinformatics, and information management. **Plant Biotechnology Institute Bulletin** May Issue:10-12.

POPULAR SCIENCE ESSAYS
126. Rhee SY (1997) Gregor Mendel (1822-1884). Commissioned and originally published on Genetech. Reprinted at Access Excellence, a national educational program that provides high school biology teacher's access to their colleagues, scientists, and critical sources of new scientific information via the World Wide Web. Currently available at: http://www.cccbiotechnology.com/RC/AB/BC/Gregor_Mendel.php, http://www.math.usu.edu/rheal/stat1040/lecture_notes/Chapter_26.pdf, https://www.verslo.is/home/Raungreinar/lif/Itarefni/Erfdir/Gregor%20Mendel%28e%29.htm
127. Rhee SY (1997) Louis Pasteur (1822-1895). Commissioned and originally published on Genetech. Reprinted at Access Excellence, a national educational program that provides high school biology teacher's access to their colleagues, scientists, and critical sources of new scientific information via the World Wide Web. Currently available at: http://www.cccbiotechnology.com/RC/AB/BC/Louis_Pasteur.php
128. Rhee SY (1997) Linus Pauling (1901-1994). Commissioned and originally published on Genetech. Reprinted at Access Excellence, a national educational program that provides high school biology teacher's access to their colleagues, scientists, and critical sources of new scientific information via the World Wide Web. Currently available at: http://www.cccbiotechnology.com/RC/AB/BC/Linus_Pauling.php
129. Rhee SY (1997) Kary B. Mullis (1944 -). Commissioned and originally published on Genetech. Reprinted at Access Excellence, a national educational program that provides high school biology teacher's access to their colleagues, scientists, and critical sources of new scientific information via the World Wide Web. Currently available at: http://www.cccbiotechnology.com/RC/AB/BC/Kary_B_Mullis.php

People Trained:

	First Name	Last Name	Title	Start	End	Present Position
162	Bethany	Holland	Postdoc	6/23	-	
161	Danielle	Hoffmann	Postdoc	4/23	-	
160	Kristen	Yawitz	Communications manager	9/22	12/22	Unknown
159	Ava	Kloss-Schmidt	RA	8/22	-	
158	Elena	del Pup	Msc student	7/22	1/23	
157	Jac	Cox	RA	7/22	5/23	
156	Matt	Stata	Postdoc	7/22	-	
155	Ruby	Tebbutt	Intern	6/22	8/22	
154	Sandeep	Mangat	Intern	6/22	8/22	
153	Joanna	Feehan	Postdoc	5/22	-	

152	Julia	Gershon	Intern	3/22	-	
151	Maxine	Gutierrez	Intern MS student	4/22 9/22	8/22 -	
150	Nicole	Theberath	Intern	3/22	5/22	Stanford undergrad
149	Lara	Seyahi	Intern	3/22	5/22	Intern in Miriam Goodman's lab, Stanford U
148	Jacob	Dunlop	Intern	3/22	5/22	
147	Ryan	Vu	Intern	1/22	3/22	Stanford undergrad
146	Daniella	Morales	Intern	1/22	3/22	
145	Sterling	Field	Postdoc	9/21	-	
144	Evan	Saldivar	PhD student	6/21	-	
143	Maxwell	Eckelbarger	Intern RA	10/20 6/21	5/21 12/22	RA, Carnegie Science
142	Olivia	MacDonald	RA	9/20	3/22	Assistant Program Manager, Thermo Fisher
141	Megan	Ruffley	Postdoc	8/20	-	
140	Will	Dwyer	RA	6/20	6/23	PhD candidate, Stanford U
139	Selena	Rice	Biocurator	4/20	-	
138	Danny	Ginzburg	RA	4/20	8/22	PhD candidate, U. Cambridge, UK
137	Justin	Krupp	RA	3/20	8/21	RA, Takahashi Lab, UT Southwestern
136	Jason	Thomas	Postdoc	3/20	4/23	
135	Hodan	Farah	Intern	3/20	6/20	Intern in Miriam Goodman's lab
134	Elena	Lazarus	RA Assistant SC	7/19 11/21	10/21 -	Assistant Scientific Coordinator, Carnegie Science
133	David	Huang	Intern	6/19	8/19	Undergrad at UCSD
132	Suzie	Lee	Intern	6/19	8/19	Undergrad at Cal Poly
131	Emily	Fryer	RA	3/19	1/23	RA II at Stanford U
130	Navadeep	Boruah	Postdoc	10/18	7/21	Data Scientist, Bayer Corp
129	Karine	Prado	Postdoc Senior RA	10/18 11/21	10/21 -	Senior Research Associate, Carnegie Science
128	Cheng	Zhao	Postdoc	8/18	8/21	Principal Investigator, Agricultural Genomics Institute at Shenzhen, CAS
127	Charles	Hawkins	Curator	8/18	-	
126	Nienke	Besbrugge	Postdoc	8/18	4/19	Senior Consultant, Capgemini Invent
125	Angela	Xu	CA	6/18	3/20	PhD program at Johns Hopkins U
124	Kevin	Radja	RA	6/18	6/20	PhD program at Virginia Tech
123	Ankush	Bharadwaj	Intern	6/18	8/18	UCLA
122	Bharti	Parihar	Intern	6/18	8/18	CSU, East Bay
121	Lyn	Vakulenko	Intern	5/18	8/18	Carlton U, Canada
120	Benjamin	Jin	RA	11/17	7/20	PhD program at UC Santa Barbara

119	Jiun	Yen	Postdoc	10/17	10/19	Computational Biologist at BrightSeed, Inc.
118	Fan	Lin	Postdoc	9/17	2/20	Bioinformatician at Brightseed, Inc.
117	Kangmei	Zhao	Postdoc	7/16	-	
116	Hatem	Rouached	Visiting faculty	2016	2018	Assistant Professor, MSU
115	Sam	Craig	Intern	6/16	8/16	Undergrad at University of Chicago
114	Elena	Estrada	Intern	6/16	8/16	Product Manager, TriLink BioTechnologies
113	Nikhil	Kaimal	Intern	6/16 6/17	8/16 8/17	MS student at UC Irvine
112	JeaneAe	Kim	RA	2/16	7/17	PhD candidate, UC Riverside
111	Arvind	Chavali	Postdoc	1/16	3/18	Strategy consultant, ZS Associates
110	Bo	Xu	Intern RA Programmer	9/15 2/16 3/22	1/16 2/22 -	Programmer, Carnegie
109	Dylan	Koh	Intern	6/15	8/15	Stanford
108	Vivek	Sriram	Intern	6/15	8/15	PhD candidate, University of Pennsylvania
107	JeanAe	Kim	Intern	6/15	1/16	PhD candidate, UC Riverside
106	Luong	Mai	Intern	6/15	12/15	QC Specialist, Pendulum
105	Yanniv	Dorone	PhD student Postdoc	9/15 1/21	12/20 12/21	Senior Investment Associate - Fall Line Capital
104	Pascal	Schläpfer	Postdoc	8/14	12/17	Senior Assistant, ETH
103	In-Seob	Han	Visiting faculty	2014	2015	U Ulsan, Korea
102	Jenny	Guarino	Intern	5/14	8/14	Legal Assistant/Paralegal, Gordon Law Group PC
101	Phong	Nguyen	Intern RA	5/14 9/14	8/14 5/15	Developer at Parallax Volatility Advisers, LP
100	Michael	Banf	Postdoc	1/14	2/17	Head of Data Science and Algorithm Development, fabforce GmbHs
99	Catherine	Doyle	Intern	6/13	8/13	Postdoctoral Researcher, NC State
98	Jue	Fan	Postdoc	5/13	3/15	VP of Bioinformatics, Singleron Biotechnologies
97	Lessley	Peterson	Intern	1/13	10/13	U. Maryland
96	Bernie	Hauser	Visiting faculty	2013	2014	U Florida at Gainesville, USA
95	Chuan	Wang	Postdoc	10/12	2/16	Senior Bioinformatics Scientist, Brightseed
94	Lan	Jiang	Intern	10/12	2/13	Unknown
93	Lilyana	Chandra	Intern	6/12	12/12	QA Analyst at American Medical Systems

92	Varun	Dwaraka	Intern	7/12	9/12	Head of Bioinformatics, TruDiagnostic
91	Mohan	Avula	Intern	6/12	8/12	Unknown
90	Jim	Guo	Postdoc	7/12	3/15	Staff Scientist, Bioinformatics at the Clinical NGS group at Thermo Fisher
89	Ricardo	Nilo Poyanco	Postdoc	3/12	5/14	Lecturer at School of Biotechnology, Faculty of Science, U. Mayor, Chile
88	Meng	Xu	Postdoc	11/11	8/14	Director of Bioinformatics, Brightseed
87	Taehyong	Kim	Postdoc	3/11	7/15	Principal bioinformatician, Institute for Biomedical Informatics, University of Pennsylvania
86	Tam	Tran	Intern	11/11	8/12	Research associate, Mayo Clinic, Rochester, NY
85	Damian	Priamurskiy	Intern	6/11	3/12	Unknown
84	Caryn	Johansen	Intern Intern RA	6/11 7/12 10/12	9/11 9/12 7/14	PhD candidate at UC Davis
83	Flavia	Bossi	Postdoc Senior RA	2/10 3/18	2/18 -	Senior Research Associate, Carnegie
82	Hye-In	Nam	RA	1/10	5/19	Data Analyst, AXBIO
81	Niek	deKlein	Intern	9/10	1/11	Postdoc, Wellcome Sanger Institute
80	Kris	Sankaran	Intern	9/10	4/11	Assistant Professor, University of Wisconsin-Madison
79	Julian	Huang	Intern	6/10	12/10	Med student, Yale; MBA student, Harvard
78	Nathaniel	Leu	Intern	6/10	9/10	Physician, Alameda Health System
77	Kim	Pham	Intern	6/10	12/10	Resident Doctor at Creighton University School of Medicine
76	Chang	You	Postdoc	8/09	5/11	eCommerce Senior Data Engineer, PepsiCo
75	Rupa	Paduchuri	Intern	10/09	12/11	Principal Scientific Researcher, Genentech
74	Jon	Iloreta	Intern	6/09	12/10	Unknown
73	Purva	Karia	Intern Intern Postdoc	6/09 1/11 6/21	7/09 6/11 -	Postdoc, Carnegie Institution for Science
72	Cherise	Lau	Intern	6/09 7/10	8/09 9/10	Finance and Administration Assistant at SSH Communications Security
71	Vibhu	Bakshi	Intern	3/09	6/09	Business Immigration Analyst, Fragomen
70	Pranjali	Karia	Intern	3/09	11/09	Unknown

69	Azam	Noorani Vatani	RA	12/08	8/09	Associate Scientist, Cepheid
68	Sagaya	Arokiasamy	RA	10/08	12/08	Unknown
67	Lee	Chae	Postdoc	7/08	5/14	Cofounder and CTO, Brightseed
66	Ricardo	Leitão	Intern	7/08	1/09	Senior Scientific Researcher, Genentech
65	Michael	Ahn	Intern	7/08 8/09	8/08 8/09	Masters, Harvard Grad School of Design
64	Anjo	Chi	Programmer	1/08	1/10	Unknown
63	AS	Karthikyan	Curator	1/08	11/09	Unknown
62	Kun	He	Postdoc	9/07	12/09	Head of Data Systems, Bayer Crop Science
61	Ozgur	Ozturk	Postdoc	8/07	3/08	Adjunct Faculty at U. Maryland
60	Bindu	Ambaru	RA	7/07	4/10	Scientist, Institute of Bioinformatics and Applied Biotechnology
59	Joy	Zhang	Intern	6/07	8/07	Staff Software Engineer, Wayno
58	Liping	Ji	Postdoc	5/07	5/08	Associate prof, Harbin Inst. Tech.
57	Adeline	Wong	Intern	4/07	9/07	Software Engineer III, Waymo
56	Suzanne	Fleshman	CA	11/07	2/08	Office Administrator, Edward Jones
55	Kate	Dreher	Curator	11/07	11/13	Germplasm coordinator, CYMMIT
54	Cindy	Lee	Programmer	10/07	7/11	Software Developer at CardioDx
53	Raymond	Chetty	Programmer	10/07	5/10	Unknown
52	Larry	Ploetz	SA	3/07	5/13	Operations Engineer, Pinger
51	Jin	Chen	Postdoc	12/06	8/09	Associate prof, U. Kentucky
50	Phillipe	Lamesch	Curator	12/06	3/12	Head of Fundraising, U. Luxembourg
49	Vanessa	Swing	CA Webmaster	10/06 3/07	3/07 11/09	Horticultural Consultant
48	Donghui	Li	Curator	7/06	6/14	Technical Program Manager, Chan Zuckerberg Initiative
47	Shanker	Singh	DBA	7/06	3/13	Senior database administrator, Innovative Interfaces
46	John	McGee	Intern	6/06	8/06	Scientific Founder, FogPharma
45	Tom	Meyer	Programmer	6/06	5/10	Backend Engineer at DexaFit, Inc
44	Bob	Muller	IT	5/06	6/14	Retired
43	Tom	Walk	Postdoc	1/06	9/07	Large Plant Breeding Database Manager, North Dakoda State U.

42	Noah	Whitman	RA	1/06	4/07	Senior Data Scientist, Open City Labs, Inc
41	Natasha	Raikhel	Visiting faculty	2006	2006	Retired
40	Mohammed	Shaikh	Programmer	12/05	1/06	Unknown
39	David	Swarbreck	Curator	10/05	9/10	Group leader, Genome Analysis Team, The Genome Analysis Centre, UK
38	Ryan	Pham	Intern	6/05	8/05	Software Developer, IBM
37	Dan	MacLean	Postdoc	5/05	6/06	Head of Bioinformatics, Sainsbury labs, UK
36	Joe	Filla	SA	2/05	3/07	Director of Operations, QuinStreet
35	Christophe	Tissier	Curator	1/05	9/07	Project manager, CAVILAM
34	Hartmut	Foerster	Curator	8/04	8/07	Research Associate at Boyce Thompson Institute, Cornell
33	Chris	Wilks	Intern Programmer	6/04 6/05	5/05 1/11	Graduate student, UCSC
32	Jon	Slenk	Programmer	4/05	7/06	Software Engineer, Apple
31	Aleksey	Kleytman	CA	2/5	6/6	Senior Reliability Engineer, Akamai Technologies
30	Renee	Halbrook	Intern	6/04	8/04	Mom
29	Doug	Becker	Programmer	5/04	4/06	Technical Accountant Manager, NetApp
28	Katica	Ilic	Curator	1/04	10/06	Senior scientist, Fluidigm Corporation
27	Jessie	Zhang	Programmer	9/03	5/04	Unknown
26	Brandon	Zoeckler	CA	8/03	3/6	Research technician, UC Berkeley
25	Thomas	Yan	Intern	7/03	6/06	Senior Data Engineer, Tapjoy
24	Behzad	Mahini	Programmer	3/03	1/04	Strategic Business Development, EDLORE
23	Shijun	Li	Postdoc	10/02	10/05	Senior Software Testing Engineer, ThermoFisher
22	Yigong	Lou	Postdoc	9/02	10/04	Bioinformatics analyst, LBL
21	Nick	Moseyko	Curator	9/02	10/05	Director of DevOps, Direct Commerce
20	Gabriel	Lander	CA	8/02	3/03	Assistant professor, Scripps Institute
19	Peifen	Zhang	Curator	4/02	7/18	Project Scientist, Phoenix Bioinformatics
18	Suparna	Mundodi	Curator	3/02	5/06	Director, Clinical Mass Spectrometry at Agilent Technologies
17	Tanya	Berardini	Curator	1/02	6/14	Chief Scientific Officer, Phoenix Bioinformatics
16	Julie	Tacklind	Webmaster	12/01	2/07	Unknown
15	Chunxia	Xu	Programmer	10/01	1/06	Unknown
14	Danny	Yoo	Programmer	6/01	5/06	Software engineer, Google

13	Mark	Lambrecht	Postdoc	4/01	2/02	Director of the Health and Life Sciences Global Practice at SAS
12	Bryan	Murtha	Programmer	2/01	8/01	Manager of Programming and Databases, Intesa Sanpaolo
11	Holly	Nottage	Intern	2/01	7/01	Unknown
10	Jill	Larimore	Intern	1/01	4/02	Graduate student, Gladstone Institute, UCSF
9	Aisling	Doyle	CA	11/00	10/02	Biobank Technician, INFANT Center, ANU Lab, UCC
8	Jungwon	Yoon	CA	9/00	6/03	Unknown
7	Anell	Bengt	Visiting student	9/00	12/01	Freelance Consultant, Nordic Healthcare
6	Smita	Mitra	Visiting student	8/00	10/00	Director, Global Medical Data Science at Janssen
5	Debika	Bhattacharyya	Intern	7/00	8/00	Enterprise architect, Oracle
4	Lukas	Mueller	Curator	6/00	7/03	Adjunct Professor, Cornell University, BTI
3	Leonore	Reiser	Curator	12/99	3/06	Data Wrangler/Bio-Curator at Phoenix Bioinformatics
2	Margarita	Garcia-Hernandez	Curator	9/99	12/06	Associate Director of Health Analytics, Partnership HealthPlan of California
1	Eva	Huala	Curator	9/99	8/05	CEO, Phoenix Informatics

Patents Filed:

Title: PLANTS WITH IMPROVED PHOSPHORUS USE EFFICIENCY
MSUT Ref: TEC2021-0120
US Serial No. 63/362,155
MVS Ref: P13702US00
Filed: 03/30/2022
Inventor: ROUACHED, HATEM, et al.

Title: Modulation of Iron- and Phosphate-Dependent Chlorophyll Accumulations

U.S. Provisional Application No. 63/143,366
Filing Date: January 29, 2021
Inventors: Seung Yoon RHEE, et al.
Your Ref: 5135
KT Ref: 107321-1219474-000100US

Title: FLOE1-MEDIATED MODULATION OF SEED LONGEVITY AND GERMINATION RATES
U.S. Provisional Patent Application No. 63/063,009
Filed: August 7, 2020
Stanford Ref.: S20-324
Carnegie Ref.: 5133
KTS Ref.: 079445-1204833-006800US

Research Funding:

(Cumulative to Carnegie: $59,516,888; Cumulative to MSU: $2,208,504; Cumulative Total: $154,812,448)

Current Research Grants:
Title: BII: Life without water: Protecting macromolecules, cells, and organisms during desiccation and rehydration across kingdoms of life
Funding Organization: NSF BII: 2213983
Dates of Project: 8/1/2022 - 7/31/2027
Award Amount: $12,500,000
PI: Sue Rhee

Title: Integrated engineering of whole plant water use efficiency in Sorghum and Setaria
Funding Organization: DOE Baxter *(11076)*
Dates of Project: 9/1/2022 - 8/31/2027
Total Award Amount: $16,000,000 Individual Subaward Amount: $1,940,908
PI: Ivan Baxter

Title: Creating and Fostering the Plant Cell Atlas Community
Funding Organization: NSF RCN *(11002)*
Dates of Project: 06/1/2021 -- 05/31/2026
Award Amount: $765,382
PI: Sue Rhee

Title: Interrogating pennycress natural and induced variation to improve abiotic stress tolerance and oilseed bioenergy crop resilience
Funding Organization: Illinois State (DoE): DE-FOA-0002214
Dates of Project: 09/01/20 – 08/31/25
Total Award Amount: $12,899,996 Individual Subaward Amount: $2,429,132
PI: John Sedbrook

Title: High-throughput determination of a subcellular metabolic network map of plants
Funding Organization: DOE BER *(10931)*
Dates of Project: 09/15/2019 -- 09/14/2023
Award Amount: $2,311,477
PI: Sue Rhee

Title: NeuroPlant PHASE 2: Leveraging a botanical armamentarium to manipulate the brain
Funding Organization: Stanford (11051)
Dates of Project: 01/01/22 – 12/31/23
Total Award Amount: $400,000   **Individual Subaward Amount: $169,740**
PI: Miriam Goodman

Past Research Grants:

Title: 1st Workshop on the Plant Cell Atlas Initiative
Funding Organization: NSF *(10913)*
Dates of Project: 06/01/2019 -- 05/31/2023
Award Amount: $82,861
PI: Sue Rhee

Title: Using Systems Approaches to Improve Photosynthesis and Water Use Efficiency in Sorghum
Funding Organization: Danforth (DOE DE-SC0018277). Subaward #: 23021-C   *(10797)*
Dates of Project: 09/15/2017 – 09/14/2023
Total Award Amount: $16,067,709   Individual Subaward Amount: $1,866,443
PI: Ivan Baxter

Title: TOOLS-PGR: Computational Infrastructure to Enable High-throughput, High-quality Annotations of Compartmentalized Metabolic Networks for Plant Genomes
Funding Organization: NSF: IOS-1546838 *(10708)*
Dates of Project: 08/15/16 – 07/31/22
Award Amount: $2,193,335
PI: Sue Rhee

Title: NeuroPlant: Leveraging a botanical armamentarium to manipulate the brain (10897)
Funding Organization: Stanford (NSF): # 62019381 - 140753
Dates of Project: 01/01/19 – 12/31/21
Total Award Amount: $700,000   **Individual Subaward Amount:** $208,000
PI: Miriam Goodman

Title: Deciphering Life Functions in Extreme Environment
Funding Organization: Venture Grant / Broccoli Charitable Fund.   *(10877)*
Dates of Project: 10/01/18 – 09/30/21
Award Amount: $60,000
PI: Sue Rhee

Title: BASF Participation in the Plant Cell Atlas Initiative
Funding Organization: BASF (BBCC Innovation Center, Belgium)   *(10952)*
Dates of Project: 02/14/20 – 02/13/21
Award Amount: $10,000
PI: Sue Rhee

Title: Thermo-adaptation of photosynthesis in extremophilic desert plants
Funding   Organization: Carnegie
       (10908)
Dates of Project: 06/01/2019 -- 5/31/2021
Award Amount: $150,000
PI: Sue Rhee

Title: Prediction and Discovery of Host Metabolites and Metabolic Pathways Required for Proliferation of an Obligate Fungal Biotroph
Funding Organization: UC Berkeley (NSF): MCB-1617020. Subaward #: 00009338 *(10722)*
Dates of Project: 09/15/2016 – 08/31/2020
Total Award Amount: $1,891,482   **Individual Subaward Amount:** $417,893
PI: Mary Wildermuth

Title: Discovery of new molecular pathways for regulating phosphate content in Arabidopsis thaliana and *Vitis vinifera* for sustainable food production
Funding Organization: Fondation de France   *(10649)*
Dates of Project: 09/08/2015 – 09/07/2020

Award Amount: $30,000
PI: Sue Rhee

Title: An Integrated Pipeline for Accelerated Plan Natural Product Discovery *(10643)*
Funding Organization: Stanford (NIH): 3U01GM110699-02S1. Subaward #: 61066255-112225
Dates of Project: 08/15/2015 – 04/30/2020
Total Award Amount: $4,491,520.00 **Individual Subaward Amount:** $924,810
PI: Christina Smolke

Title: A systems-level analysis of drought and density response in the model c4 grass *Setaria viridis*
Funding Organization: Danforth (DOE): DE-SC0008769; 23009-CI *(10412)*
Dates of Project: 09/01/2012 – 08/31/2018
Total Award Amount: $12,138,927 **Individual Subaward Amount:** $2,212,640
PI: Thomas Brutnell

Title: The membrane-based protein Interactome
Funding Organization: NSF: MCB-1052348. *(10274)*
Dates of Project: 04/15/2011 – 03/31/2016
Award Amount: $1,834,556
PI: Wolf Frommer

Title: Systematic identification of regulators of transcription factors using computational predictions and high-throughput yeast-one-hybrid assays
Funding Organization: Association of Independent Plant Research Institutes (AIPI) *(10383)*
Dates of Project: 07/01/2012 – 06/30/2015
Award Amount: $14,400
PI: Sue Rhee

Title: AIPI Plant Genome Annotation Group
Funding Organization: Association of Independent Plant Research Institutes (AIPI) *(10534)*
Dates of Project: 03/11/2014 – 02/28/2015
Award Amount: $25,000
PI: Sue Rhee

Title: *Arabidopsis* 2010: Towards a Comprehensive *Arabidopsis* Protein Interactome Map: Systems Biology of the Membrane Proteins and Signalosome
Funding Organization: NSF: MCB-0618402 *(2066)*
Dates of Project: 09/01/2006 – 08/31/2011
Award Amount: $4,799,186
PI: Wolf Frommer

Title: Building a Network of Plant Metabolic Pathway Databases and Communities
Funding Organization: NSF: DBI-0640769 *(2098)*
Dates of Project: 03/15/2008 – 02/28/2013
Award Amount: $1,477,869
PI: Sue Rhee

Title: Metabolomics: A Functional Genomics Tool for Deciphering Functions of *Arabidopsis* Genes in the Context of Metabolic and Regulatory Networks
Funding Organization: Iowa State University (NSF): 420-40-71A   (10079)
Dates of Project: 03/01/2009 – 02/28/2013
Total Award Amount: $2,925,398   **Individual   Subaward   Amount:** $269,862

PI: Basil Nikolau

Title: TAIR: The *Arabidopsis* Information Resource
Funding Organization: NSF: DBI-0850219   (10107)
Dates of Project: 09/01/2009 – 08/31/2014
Award Amount: $4,170,595
PI: Eva Huala

Title: TRPGR: Building a Highly Automated Metabolic Pathway Reconstruction Infrastructure for Plants
Funding Organization: NSF: IOS-1026003   (10204)
Dates of Project: 09/01/2010 – 08/31/2016
Award Amount: $1,825,569
PI: Sue Rhee

Title: The First International Biocurator Meeting
Funding Organization: Genetics Society of America   (5133)
Dates of Project: 5/22/2005 – 12/01/2008
Award Amount: $25,000
PI: Sue Rhee

Title: Enhancing the Quality and Quantity of *Arabidopsis* Metabolism Data in AraCyc and MetaCyc
Funding Organization: Pioneer Hi-Breed International   (5119)
Dates of Project: 02/18/2005 – 08/06/2006
Award Amount: $40,000
PI: Sue Rhee

Title: 2nd International Biocurator Meeting
Funding Organization: Villa Bosch   (5134)
Dates of Project: 02/13/2007 – 02/12/2008
Award Amount: $24,968
PI: Sue Rhee
Title: TAIR: The *Arabidopsis* Information Resource
Funding Organization: NSF: DBI-0417062   (2462)
Dates of Project: 09/01/2004 – 08/31/2009
Award Amount: $7,988,952
PI: Sue Rhee

Title: *Arabidopsis* 2010: Metabolomics: A Functional Genomics Tool for Deciphering Functions of *Arabidopsis* Genes in the Context of Metabolic and Regulatory Networks
Funding Organization: Iowa State Univ. (NSF): 420-40-17   (4306)
Dates of Project: 09/01/2005 – 08/31/2008
Total Award Amount: $1,000,000   **Individual Subaward Amount:** $64,875
PI: Basil Nikolau

Title: Low Temperature Regulatory Circuits and Gene Regulation in Higher Plants
Funding Organization: MSU (NSF): DBI-0110124   (4433)
Dates of Project: 09/01/2001 – 08/31/2008
Total Award Amount: $5,591,234   **Individual Subaward Amount:** $539,021
PI: Michael F. Thomashow

Title: First International Biocurator Meeting
Funding Organization: NSF: DBI-0551286   (2282)
Dates of Project: 01/01/2006 – 12/31/2007
Award Amount: $29,810
PI: Sue Rhee

Title: The Plant Ontology Consortium
Funding Organization: CSHL (NSF): 22130313   (4417)
Dates of Project: 09/01/2003 – 08/31/2007
Total Award Amount: $1,672,411   **Individual Subaward Amount:** $530,928
PI: Lincoln Stein

Title: The MetaCyc Metabolic Pathway Database
Funding Organization: SRI (NIH): 55-000650   (4441)
Dates of Project: 03/01/2004 – 02/28/2007
Total Award Amount: $3,337305   **Individual Subaward Amount:** $839,512
PI: Peter Karp

Title: Gene Ontology Consortium
Funding Organization: The Jackson Laboratory (NIH): 2P41HG002273-04   (4442)
Dates of Project: 03/09/2004 – 02/28/2007
Total Award Amount: $12,396,096   **Individual Subaward Amount:** $634,431
PI: Judith Blake
Title: First International Biocurator Meeting
Funding Organization: NIH: 1R13HG004030-01 (1403)
Dates of Project: 12/07/2005 – 11/30/2006
Award Amount: $12,000
PI: Sue Rhee

Title: The Arabidopsis Biological Resource Center at The Ohio State University
Funding Organization: OSURF (NSF): DBI-0091471   (4428)
Dates of Project: 02/01/2001 – 02/28/2006
Total Award Amount: $2,123,500   **Individual Subaward Amount:** $402,983
PI: Randy Scholl

Title: AtIR: An *Arabidopsis* Thaliana Information Resource
Funding Organization: NSF: DBI-9978564   (2665)
Dates of Project: 10/01/1999 – 09/30/2005
Award Amount: $5,728,633
PI: Chris Somerville

Title: A Literature Curation Tool for Organism Databases
Funding Organization: NIH: 1R01HG02728-01 (1092)
Dates of Project: 09/30/2002 – 08/31/2005

Award Amount: $896,386
PI: Sue Rhee

Title: Large-scale Fluorescent Tagging of Full-length Genes to Characterize Native Expression Patterns and Subcellular Targeting of *Arabidopsis* Proteins of Unknown Function
Funding Organization: SUNY at Stony Brook (NSF): 1027553   (4413)
Dates of Project: 09/01/2002 – 12/31/2004
Total Award Amount: $1,580,000   **Individual Subaward Amount:** $168,497
PI: Vitaly Citovsky

Title: Partnership for Research & Education in Plants
Funding Organization: Virginia Tech (NIH): CR-19501-431399   (4402)
Dates of Project: 09/30/2003 – 08/31/2004
Total Award Amount: $249,302   **Individual Subaward Amount:** $27,522
PI: Erin L. Dolan

Title: Gene Ontology Consortium
Funding Organization: The Jackson Laboratory (NIH)   (4435)
Dates of Project: 01/01/2002 – 03/08/2004
Total Award Amount: $5,784,994   **Individual Subaward Amount:** $536,045
PI: Judith Blake

Title: Development of the MetaCyc Metabolic Pathway Database
Funding Organization: SRI (NIH): P11833   (4437)
Dates of Project: 03/01/2002 – 02/28/2004
Total Award Amount: $1,842,466   **Individual Subaward Amount:** $238,999
PI: Peter Karp

Title: Sequencing of *Arabidopsis* Chromosome II and Beyond, and Development of Resources for *Arabidopsis* Genome Analysis
Funding Organization: TIGR (NSF): TIGR-00-007   (4432)
Dates of Project: 05/01/2001 – 12/31/2001
Total Award Amount: $15,806,875   **Individual Subaward Amount:** $105,824
PI: Claire Fraser