

## CURRICULUM VITA

**Name:** Seung Yon (Sue) Rhee  
**Website:** <https://dpb.carnegiescience.edu/labs/rhee-lab/>  
**Address:** Carnegie Institution, Department of Plant Biology, 260 Panama Street,  
Stanford, CA 94305 USA.  
**E-mail:** [srhee@carnegiescience.edu](mailto:srhee@carnegiescience.edu)

### *Education:*

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

### *Employment:*

Director, Department of Plant Biology, Carnegie Institution for Science, 2016-present  
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, 1999-2004  
Database Curator, *Arabidopsis thaliana* Database (AtDB), Department 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, Swarthmore College, 1990-1992  
Research Intern, Johns Hopkins University School of Medicine, 1990 (summer)

### *Professional Services:*

#### **Scientific Advisory Boards:**

Joint Genome Institute's Plant Group (2015-present); NSF's small RNAs in maize anther development (2014-present); NSF C3-C4 Photosynthesis Project (2012-2013); Value-directed Evolutionary Genomics Initiative (VEGI) (2010-2014); Protein Data Bank (2009-present); CropLink Global Database (2006-2009); *Saccharomyces* Genome Database (SGD) (2003-2006); GrainGenes (2003-2006); Cornell Genomics (2002-2006); ChromDB (2001-2004)

#### **Grant Review Boards:**

NSF panel for MCB (2016, 2015, 2011); NSF panel for IOS (2014, 2012); NSF Review Panel for Protein Data Bank (2008); PDB site visit (Chair) (2006); USDA-ARS Federal Support for Bioinformatics (2002); NHGRI Federal Support for Central Database of Protein Sequence and Function (2002)

#### **International Conference and Scientific Community Organization Boards:**

Co-organizer, 11<sup>th</sup> Plant Genome Conference at Cold Spring Harbor Laboratory (2017); Co-organizer, Forth Conference of International Society for Biocuration (2010); Member, Nominating Committee for the International Society of Biocuration's Executive Committee (2009-2010); Member, Nominating Committee for Plant Cyberinfrastructure Board of Directors (2007); 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); Steering Committee Member, International Solanaceae Genome Initiative (2004-2008)

#### **Scientific Journal Editorial Boards:**

Associate Editor, *Molecular Plant* (2014-present); Monitoring Editor, *Plant Physiology* (2002-2008, 2013-present)

**Carnegie Institution for Science Services:**

Carnegie Institution for Science's Center for Scientific Computation Committee (2014-present); Carnegie Summer Internship Program Coordination (2013-2014); DPB IT Committee (2012-present); Departmental Website Design (2010); Carnegie Seminar Organization (2008-2010); Departmental Website Design (2002); Internal Seminar Series Initiation and Organization (2000-2001)

*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 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)

*Contribution to Science:*

1. My early work in graduate school focused on understanding how plant cells separate, which is very rare because plant cells are connected by cell 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. 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. 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 to 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 and has been used to analyze data in thousands of research articles, including many studies of various human diseases.

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. 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. 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. It can be used to systematically identify new genes in pathways and infer functions of uncharacterized genes based on the functions of their network neighbors. In addition to contributing to the design and analysis of the network, my group demonstrated that AraNet could be used successfully to guide the functional identification of novel genes. Using molecular genetic approaches, we discovered novel regulators of drought resistance and lateral root development, traits that are essential in engineering drought resistance in plants.

Membrane proteins are perhaps the darkest matter in the pool of uncharacterized proteins because of the difficulty of working with them biochemically and expressing them heterologously. To better understand how proteins function across and within membranes, my group 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). I led the bioinformatics component of the project where we created a computational pipeline to enable the large-scale experimental pipeline (primer design, sequence validation, and image and statistical analyses of the interactions) and analyzed the resulting protein interaction network. This is a foundational resource for generating many new hypotheses. The vast majority of the membrane protein interactions we found had never before been identified. In addition, the methods we developed for generating high-throughput membrane protein interactions are applicable to any species and the datasets will be useful in identifying patterns of signaling and regulation in plants.

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.

4. 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. My 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

5. Transcriptional regulation is a fundamental process 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 into one of such layers, we used an integrated approach (applying concepts, data, and tools from computer science, genetics, genomics, proteomics, molecular evolution, development, and stress physiology) to uncover a new layer of transcriptional regulation across many domains of life. There are a handful of anecdotal examples of transcription factor-like proteins without a DNA binding domain, coined microProteins (miPs), which regulate evolutionarily related transcription factors. To test the prevalence of this mechanism, my group developed a genome-scale platform to discover, classify, and validate microProteins in *Arabidopsis*. 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. Given the prevalence of miPs in *Arabidopsis*, we applied the same strategy to predict miPs from 19 species, ranging from microbes to plants and metazoans. We detected putative miPs in all organisms examined and paired them with potential targets in almost all known transcription

factor families. Our analysis suggests a potential ubiquitous layer of transcriptional regulation by miPs and provides a systematic framework for their future study. The potential universality of miP function may offer new tools to modulate transcription factor function in practical applications ranging from gene therapy to bioengineering.

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.

de Klein N, Magnani E, and Rhee SY (2015) microProtein Prediction Program (miP3): a software for predicting microProteins and their target transcription factors. **International Journal of Genomics** Article ID 734147. 1-4.

*Invited Seminars:*

1. York University, York, UK (2000); 2. The Institute for Genome Research (2000); 3. Oxford University, Oxford, UK (2000); 4. Lorne Genome Conference, Melbourne, Australia (2001); 5. University of Arizona, Tucson, AZ (2001); 6. Plant Gene Expression Center, Albany, CA (2001); 7. Entigen, Sydney, Australia (2001); 8. Cornell University, Ithaca, NY (2001); 9. Seoul National University, Seoul, South Korea (2001); 10. University of California at Riverside, Riverside, CA (2002); 11. University of Guelph, Guelph, Canada (2002); 12. VIB, University of Gent, Gent, Belgium (2003); 13. Seoul National University, Seoul, South Korea (2004); 14. University of Missouri, Columbia (2004); 15. Plant Gene Expression Center, Albany, CA (2004); 16. Iowa State University (2007); 17. U.C. Riverside (2007); 18. University of Calgary, Canada (2007); 19. National Research Center-Plant Biotechnology Institute, Saskatoon, Canada (2007); 20. Danforth Center, MO (2007); 21. Dow Agrosiences (2010); 22. U.C. Riverside (2010); 23. U. Florida (2011); 24. Michigan State U. (2011); 25. Danforth Center (2012); 26. National Cheng Kung U., Taiwan (2012); 27. UC Davis (May 2013); 28. Washington State U. (April 2013); 29. University of Missouri-Columbia (Oct 22, 2013); 30. San Francisco State University (April 23, 2015); 31. Second Genome (Nov 9, 2015); 32. Louisiana State U. (Feb 22, 2016); 33. Plant Gene Expression Center, Albany CA (March 10, 2016); 34. Langebio, the National Laboratory of Genomics for Biodiversity, Mexico (May 10, 2016)

*Invited 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. AAAS Annual Meeting, San Francisco, CA (2001); 6. Plant & Animal Genome IX Conference, San Diego, CA (2001); 7. Mini-symposium on Plant Bioinformatics, KRIBB, Daejeon, South Korea (2001); 8. Plant Genome Awardees Meeting, San Diego, CA (2002); 9. Future of the National Plant Genome Initiative, National Academy of Sciences, Washington DC (2002); 10. National Science Foundation Managing Plant Genomic Resources Workshop, Asilomar, CA (2002); 11. International Horticultural Congress, Toronto, Canada (2002); 12. 2<sup>nd</sup> International Conference on Plant Metabolomics, Postdam, Germany (2003); 13. Digital Archives for Science & Engineering Resources (DASER) Symposium (2003); 14. Crop Functional Genomics (2004); 15. 7<sup>th</sup> International Plant Cold Hardiness Symposium (2004); 16. Solanaceae Genomics Meeting, Jeju Island, S. Korea (2007); 17. Korea Genome Organization Meeting, Seoul, S. Korea (2007); 18. iPlant Kick-off Conference, Cold Spring Harbor Labs, NY (2008); 19. American Society of Plant Biologists Conference, Merida, Mexico (2008); 20. Banff Plant Metabolism Conference, Banff, Canada (2008); 21. International Conference on *Arabidopsis* Research (2010); 22. A Current Opinion Conference on Plant Genome Research, Amsterdam, the Netherlands (2011); 23. Alliance of Independent Plant Institutes Meeting, St. Louis, MO (2011); 24. ASMS Asilomar

Conference on Mass Spectrometry, Asilomar, CA (2011); 25. Phenotype Ontology RCN, NASCent, Durham, NC (2012); 26. Plant Genomics in China XIII, Tai'an, China (2012); 27. Microbial and Plant Genomics Institute (MPGI) Symposium on Systems Biology of Genetic Regulation, St. Paul, MN (2012); 28. International Symposium on Root Systems Biology, Taipei, Taiwan (2012); 29. Evolution of Metabolic Diversity, Banbury, NY (March 2013); 30. Alliance of Independent Plant Institutes Meeting, Ithaca, NY (May 2013); 31. Plants and People Conference, Berlin, Germany (June 2013); 32. Meeting on the Genetic Basis of Unintended Effects in Modified Plants, Ottawa, Canada (Jan 14-15, 2014); 33. JGI DOE Conference: "Genomics of Energy and the Environment" (March 24-25, 2015); 34. Penn State Plant Biology Symposium: "Plant Stress-omics in a Changing Climate" (May 13-16, 2015); 35. Molecular Plant Symposium, Beijing, China (Aug 5-8, 2015); 36. Plant Genomes & Biotechnology: From Genes to Networks, CSHL, NY (Dec 2-5, 2015); 37. NAASC RCN: Arabidopsis Research and Training for the 21st century (May 13-15, 2016); 38. ASPB Conference, Plant Cell Symposium: New Biological Insights from Large-Scale Biology (July 9-13, 2016)

*People Trained:*

**Postdoctoral Researchers**

	First Name	Last Name	Start Date	End Date	Present Position
22	Kangmei	Zhang	7/1/16	Present	
21	Arvind	Chavali	1/4/16	Present	
20	Pascal	Schläpfer	8/1/14	Present	
19	Michael	Banf	1/6/14	Present	
18	Flavia	Bossi	2/16/10	Present	
17	Chuan	Wang	10/1/12	2/29/16	Bioinformatician, Hampton Creek Foods, Inc.
16	Taehyong	Kim	3/1/11	7/31/15	Staff bioinformatics scientist, Institute for Biomedical Informatics University of Pennsylvania
15	Jue	Fan	5/13/13	3/18/15	Bioinformatician, Cellular Research
14	Jim	Guo	7/16/12	3/31/15	Research scientist, Audentes therapeutics Inc.
13	Meng	Xu	11/22/11	8/29/14	Bioinformatics scientist, Hampton Creek Foods, Inc.
12	Ricardo	Nilo Poyanco	3/6/12	5/31/14	Research associate, FONDAP Center for Genome Regulation, Chile
11	Lee	Chae	7/14/08	5/2/2014	Director of bioinformatics, Hampton Creek Foods, Inc.
10	Chang	You	8/13/09	5/6/2011	Software developer, NetSeer, Inc.
9	Kun	He	9/6/07	12/21/09	Senior computational biologist, Monsanto
8	Ozgur	Ozturk	8/15/07	3/4/08	Unknown
7	Liping	Ji	5/1/07	5/31/08	Associate prof, Harbin Inst. Tech.
6	Jin	Chen	12/19/06	8/13/09	Assistant prof, MSU
5	Tom	Walk	1/9/06	9/31/07	Bioinformatics analyst, The Broad Institute
4	Dan	MacLean	5/1/05	6/30/06	Director of bioinformatics, Sainsbury labs, UK
3	Shijun	Li	10/21/02	10/16/05	QC analyst, ThermoFisher Scientific,

					San Jose
2	Yigong	Lou	9/1/02	10/8/04	Bioinformatics analyst, LBL
1	Mark	Lambrech	4/1/01	2/28/02	Staff, Galápagos Genomics

**Graduate Students**

	First name	Last Name	Start Date	End Date	Present Position
1	Yanniv	Dorone	9/21/15	Present	

**Research Assistants**

	First name	Last Name	Start Date	End Date	Present Position
7	Bo	Xu	9/1/15	1/31/15	
6	Hye-In	Nam	1/6/2010	Present	
5	Caryn	Johansen	10/2/2012	7/31/14	Masters student, NYU
4	Bindu	Ambaru	7/24/07	4/23/10	Unknown
3	Azam	Noorani	12/11/08	8/28/09	Unknown
2	Sagaya	Arokiasamy	10/29/08	12/12/08	Unknown
1	Noah	Whitman	1/23/06	4/23/07	Unknown

**Visiting Graduate Students**

	First name	Last Name	Start Date	End Date	Present Position
2	Anell	Bengt	9/15/00	12/31/01	Software developer, AstraZeneca Inc.
1	Smita	Mitra	8/28/00	10/5/00	Software developer, IBM Life Sciences

**Visiting Professors**

	First name	Last Name	Start Date	End Date	Affiliation
4	Hatem	Rouached	2016	2018	INRA, France
3	In-Seob	Han	2014	2015	U Ulsan, Korea
2	Bernie	Hauser	2013	2014	U Floria @ Gainesville, USA
1	Natasha	Raikhel	2006	2006	UC Riverside, USA

**Interns**

	First name	Last Name	Start Date	End Date	School	Present position
39	Bo	Xu	9/1/15	1/31/15	U. Minn	
38	Dylan	Koh	6/1/15	8/15/15	Stanford	
37	Vivek	Sriram	6/1/15	8/15/15	High School	Duke U.
36	JeanAe	Kim	6/1/15	Present	UC Berkeley	
35	Luong	Mai	6/1/15	12/11/15	De Anza	Cornell U.
34	Jenny	Guarino	5/19/14	8/15/14	Cornell	
33	Phong	Nguyen	5/19/14		UC Berkeley	
32	Catherin e	Doyle	6/7/13	8/9/13	Davidson College	
31	Lessley	Peterson	1/2/13	10/4/13	U. Maryland	
30	Lan	Jiang	10/22/12	2/1/13		
29	Lilyana	Chandra	6/26/12	12/21/12	UC Berkeley	
28	Varun	Dwaraka	7/2/12	9/7/2012	Foothill College	PhD candidate, U.C. Santa Cruz

27	Mohan	Avula	6/11/12	8/10/12	Los Altos HS	
26	Tam	Tran	11/1/11	8/24/12	UC Davis	Research associate, Mayo Clinic, Rochester, NY
25	Damian	Priamurskiy	6/15/11	3/30/12	Foothill College	
24	Caryn	Johansen	6/1/11, 7/6/12	9/1/11, 10/1/12	Humbolt State U.	Maters student, NYU
23	Niek	deKlein	9/1/10	1/14/11	Netherlands	PhD candidate, U. Groningen
22	Kris	Sankaran	9/17/10	4/25/11	Stanford U.	PhD candidate, Stanford U.
21	Julian	Huang	6/16/10	12/1/10	Lynbrook HS	Undergrad, Harvard
20	Nathanie l	Leu	6/16/10	9/17/10	UC Davis	Medical student, Eastern Virginia Medical School
19	Kim	Pham	6/16/10	12/1/10	Stanford U.	
18	Rupa	Paduchuri	10/1/09	12/31/20 11	Foothill College	
17	Jon	lloreta	6/23/09	12/31/10	UC. Berkeley, Ph.D.	
16	Purva	Karia	6/29/09	7/31/09, 1/3/11- 6/30-11	Padmashree Dr. D. Y. Patil University	Ph.D. student, McGill U.
15	Cherise	Lau	6/29/09 7/6/10	8/28/09 9/17/10	UCLA	
14	Vibhu	Bakshi	3/24/09	6/5/09	U. North Texas, Ph.D.	
13	Pranjali	Karia	3/23/09	11/1/09	Foothill college	
12	Ricardo	Leitão	7/1/08	1/26/09	San Jose State	Ph.D. candidate, UCSC
11	Michael	Ahn	7/1/08, 8/3/09	8/22/08, 8/28/09	Swarthmore College	
10	Joy	Zhang	6/11/07	8/17/07	Carlmont HS	
9	Adeline	Wong	4/23/07	9/6/07	Stanford	
8	John	McGee	6/19/06	8/26/06	Stanford	Postdoc, Harvard U.
7	Ryan	Pham	6/6/05	8/18/05	San Jose State	
6	Chris	Wilks	6/21/04	5/31/05	San Jose State	Graduate student, UCSC
5	Renee	Halbrook	6/1/04	8/31/04	San Jose State	
4	Thomas	Yan	7/1/03	6/23/06	San Jose State	Senior staff engineer at SanDisk
3	Holly	Nottage	2/1/01	7/15/01	Foothill College	unknown
2	Jill	Larimore	1/3/01	4/30/02	Foothill College	Graduate student, Gladstone Institute, UCSF
1	Debika	Bhattacharyya	7/1/00	8/31/00	RPI	Enterprise architect, Oracle Corporation



### Curator Assistants

	First name	Last Name	Start Date	End Date	Present Position
7	Suzanne	Fleshman	11/12/07	2/15/08	Unknown
6	Vanessa	Swing	10/18/06	3/14/07	Webmaster
5	Aisling	Doyle	11/1/00	10/10/02	Biosafety inspector, University College Cork
4	Gabriel	Lander	8/26/02	3/15/03	Assistant professor, Scripps Institute
3	Brandon	Zoeckler	8/11/03	3/3/06	Research technician, UC Berkeley
2	Aleksey	Kleytman	2/1/05	6/2/06	Tech support
1	Jungwon	Yoon	9/1/00	6/31/03	Unknown

### Scientific Curators

	First Name	Last Name	Start Date	End Date	Present Position
16	Peifen	Zhang	4/15/02	Present	
15	Kate	Dreher	11/1/07	11/31/13	Germplasm coordinator, CYMMIT
14	Donghui	Li	7/24/06	6/30/14	Curator, Phoenix Informatics
13	Tanya	Berardini	1/15/02	6/30/14	Curator, Phoenix Informatics
12	Eva	Huala	9/1/99	8/31/05	Executive director, Phoenix Informatics
11	Phillipe	Lamesch	12/1/06	3/7/12	Communication adviser, Luxembourg Centre for Systems Biomedicine, U. Luxembourg
10	David	Swarbreck	10/16/05	9/3/10	Group leader, Genome Analysis Team, The Genome Analysis Centre, UK
9	AS	Karthikyan	1/2/08	11/31/09	Unknown
8	Hartmut	Foerster	8/1/04	8/31/07	Database curator, SGN
7	Christophe	Tissier	1/1/05	9/6/07	Project manager, Learning in Motion, Inc.
6	Margarita	Garcia-Hernandez	9/1/99	12/15/06	Research scientist, California Department of Health Care Services
5	Katica	Ilic	1/5/04	10/31/06	Senior scientist, Fluidigm Corporation
4	Lukas	Mueller	6/19/00	7/1/03	Associate professor, Cornell University
3	Leonore	Reiser	12/01/99	3/31/06	Program manager at Breakout Labs, Thiel Foundation
2	Suparna	Mundodi	3/1/02	5/31/06	Bioinformatics analyst, Biorad Inc.
1	Nick	Moseyko	9/1/02	10/15/05	Bioinformatics analyst, UC Berkeley

### Programmers

	First Name	Last Name	Start Date	End Date	Present Position
19	Larry	Ploetz	3/1/07	5/31/13	Systems admin
18	Bob	Muller	5/22/06	6/30/14	Tech lead, Phoenix Informatics
17	Shanker	Singh	7/17/06	3/31/13	Database admin

16	Cindy	Lee	10/15/07	7/15/11	Programmer
15	Chris	Wilks	6/1/05	1/28/11	Programmer
14	Raymond	Chetty	10/1/07	5/2010	Programmer
13	Tom	Meyer	6/16/06	5/2010	Programmer
12	Anjo	Chi	1/7/08	1/26/10	Programmer
11	Vanessa	Swing	3/14/07	11/31/09	Webmaster
10	Joe	Filla	2/16/05	3/14/07	Systems admin
9	Julie	Tacklind	12/5/01	2/14/07	Webmaster
8	Jon	Slenk	4/1/05	7/1/06	Senior programmer
7	Doug	Becker	5/1/04	4/7/06	Unknown
6	Chunxia	Xu	10/10/01	1/15/06	Unknown
5	Danny	Yoo	6/1/01	5/5/06	Software engineer, Google
4	Mohammed	Shaikh	12/1/05	1/1/06	Unknown
3	Jessie	Zhang	9/23/03	5/31/04	Unknown
2	Behzad	Mahini	3/28/03	1/15/04	Unknown
1	Bryan	Murtha	2/1/01	8/3/01	Unknown

#### PEER REVIEWED PUBLICATIONS

##### Peer reviewed publications (\* corresponding author)

- Guo J, Fan J, Hauser B, and Rhee SY\* (2015) Target enrichment improves mapping of complex traits by deep sequencing. **Genes | Genomes | Genetics** *in press*.
- Ladics G\*, Bartholomaeus A, Bregitzer P, Doerrner 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** [Epub ahead of print].
- 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.
- 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.
- 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.
- Xu M and Rhee SY\* (2014) Becoming data-savvy in a big-data world. **Trends in Plant Science** 19(10):619–622.
- 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]
- 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]
- 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.
- Rhee SY\* and Mutwil M\* (2014) Towards revealing the functions of all genes in plants. **Trends in Plant Science** 19(4):212-221.

- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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]
- 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.
- 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.**
- 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.
- 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.
- 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.

- 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.
- 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.
- 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.
- 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.
- 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.
- The Gene Ontology Consortium (2008) The Gene Ontology project in 2008. **Nucleic Acids Research** 36(Database issue):D440-4.
- 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.
- 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.
- 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.
- 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.
- Rhee SY\*, Dickerson J\*, and Xu D\* (2006) Bioinformatics and its Applications in Plant Biology. **Annual Review of Plant Biology** 57: 335-360.
- Zimmermann P\*, Schildknecht B, Craigon D, Garcia-Hernandez M, Grisse W, May S, Mukherjee G, Parkinson H, Rhee SY, Wagner U, and Hennig L. (2006) MIAME/Plant – adding value to plant microarray experiments. **Plant Methods** 2:1-3.
- Gene Ontology Consortium (2006) The Gene Ontology Project in 2006. **Nucleic Acids Research** 34(Database issue):D322-6.
- 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.
- 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]

- 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.
- Rhee SY\* (2005) Bioinformatics: Current Limitations and Insights for the Future. **Plant Physiology** 138(2):569-70.
- 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.
- 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.
- Bard J, Rhee SY, and Ashburner M\* (2005) An ontology for cell types. **Genome Biology** 6:R21.
- 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.
- 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.
- 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.
- 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.
- 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]**
- 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.
- Weems D, Miller N, Garcia-Hernandez 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.
- 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]**
- Bard JL\* and Rhee SY\* (2004) Ontologies in biology: design, applications and future challenges. **Nature Review Genetics** 5(3):213-22.
- Rhee SY\* (2004) Carpe Diem. Retooling the Publish or Perish Model into the Share and Survive Model. **Plant Physiology** 134(2):543-7.
- 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.
- 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.
- 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.
- Mueller LA, Zhang P, and Rhee SY\* (2003) AraCyc. A Biochemical Pathway Database for *Arabidopsis*. **Plant Physiology** 132(2):453-60.
- 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.
- Clarke BC, Lambrecht M, and Rhee SY\* (2003) *Arabidopsis* genomic information for interpreting wheat EST sequences. **Functional and Integrated Genomics** 3(1):33-38.
- 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.
- 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.
- The Gene Ontology Consortium (2001) Creating the Gene Ontology Resource: Design and Implementation. **Genome Research** 11(8):1425-1433.
- 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.
- 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.
- 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.
- 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.
- 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.
- Rhee SY and Somerville CR\* (1994) Flat-Surface Grafting in *Arabidopsis thaliana*. **Plant Molecular Biology Reporter** 13:118-123.
- Preuss D\*, Rhee SY, Davis RW (1994) Tetrad analysis possible in *Arabidopsis* with mutation of the QUARTET (QRT) genes. **Science** 264:1458-60.
- Ruan ZS, Anantharam V, Crawford IT, Ambudkar SV, Rhee SY, Allison MJ, and Maloney PC\* (1992) Identification, purification, and reconstitution of OxIT, the oxalate: formate antiport protein of *Oxalobacter formigenes*. **Journal of Biological Chemistry** 267:10537-43.

### Book chapters and other publications

- Rhee SY (2014) An interview with Seung Yon (Sue) Rhee. **Trends in Plant Science** 19(4):198-199.
- 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.
- Rhee SY and Crosby W. (2005) Biological Databases for Plant Research. **Plant Physiology** 138(1):1-3.
- 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
- 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.
- 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.
- 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.
- Rhee SY (2001) Extending the Frontiers of Plant Biology: Large scale biology, bioinformatics, and information management. **Plant Biotechnology Institute Bulletin** May Issue:10-12.
- 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.

### POPULAR SCIENCE ESSAYS

- 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.cccbotechnology.com/RC/AB/BC/Gregor\\_Mendel.php](http://www.cccbotechnology.com/RC/AB/BC/Gregor_Mendel.php), [http://www.math.usu.edu/rheal/stat1040/lecture\\_notes/Chapter\\_26.pdf](http://www.math.usu.edu/rheal/stat1040/lecture_notes/Chapter_26.pdf), <https://www.verslo.is/home/Raungreinar/lif/ltarefni/Erfdir/Gregor%20Mendel%28e%29.htm>
- 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.cccbotechnology.com/RC/AB/BC/Louis\\_Pasteur.php](http://www.cccbotechnology.com/RC/AB/BC/Louis_Pasteur.php)
- 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.cccbotechnology.com/RC/AB/BC/Linus\\_Pauling.php](http://www.cccbotechnology.com/RC/AB/BC/Linus_Pauling.php)
- 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.cccbotechnology.com/RC/AB/BC/Kary\\_B\\_Mullis.php](http://www.cccbotechnology.com/RC/AB/BC/Kary_B_Mullis.php)