

	Authors	Abstract Title
1	ANANTHARAMAN* Karthik Anantharaman (karthik.a@berkeley.edu) Christopher T. Brown, Laura A. Hug, Itai Sharon, Cindy J. Castelle, Alexander J. Probst, Brian C. Thomas, Andrea Singh, Michael J. Wilkins, Ulas Karoaz, Eoin L. Brodie, Kenneth H. Williams, Susan S. Hubbard, Jillian Banfield	Extensive genomic reconstructions provide insights into biogeochemical cycling in a complex terrestrial subsurface environment
2	ARMANHI* Jaderson Armanhi, (Jader.armanhi@gmail.com) Rafael Souza, Laura Araujo, Vagner Okura, Piotr Mieczkowski, Juan Imperial, Paulo Arruda	Construction and annotation of a representative community-based culture collection of sugarcane
3	AZNAR* Aude Aznar (aaznar@lbl.gov) Camille Chalvin, Patrick Shih, Devon Birdseye, Dominique Loque, Henrik V. Scheller	Development of Plants with Multiple Traits for High Yield of Fermentable Sugars
4	BELIAEV* Alex S. Beliaev (alex.beliaev@pnnl.gov) Ryan S. McClure	Engineering RNA Aptamer-Based Gene Circuits for Control of Microbial Interactions
5	BLAINEY* Paul C. Blainey (pblainey@broadinstitute.org)	Microfluidic integration for genomic analysis
6	BLANCHARD* Jeffrey L. Blanchard (jeffb@bio.umass.edu) Kelly Haas, Eric Gann, Shane Lawson, Ava Bakhtyari, Fauzia Iqbal, Nadia Klanfar, Nicholas Mucci, Jaice Rottenberg, Amy Biddle	Insights into the functions and evolution of bacterial microcompartment prompted by new bacterial genomes sequenced by the Joint Genome Institute
7	BROWN* Steven D. Brown, (brownsd@ornl.gov) Sagar M. Utturkar, Dawn M. Klingeman, Richard A. Hurt, Marcel Huntemann, Manoj Pillay, Krishnaveni Palaniappan, Neha Varghese, Natalia Mikhailova, Dimitrios Stamatias, T.B.K. Reddy, Chew Yee Ngan, Chris Daun, Nicole Shapiro, Markowitz, Victor, Ivanova, Natalia, Kyripides, Nikos, Woyke, Tanja, 3	Evaluation of unassembled DNA regions from Illumina and PacBio technologies and finishing microbial genomes
8	BROWNE* Daniel R. Browne (dbrowne.up@gmail.com) Timothy P. Devarenne	Supercomputing and Genome Assembly: Improved Reconstruction of Illumina Sequencing Data

TUESDAY EVENING POSTER SESSION

March 22, 2016 – Marriott Hotel, Walnut Creek



9	BRUM* Jennifer R. Brum (brum.11@osu.edu) Simon Roux, Matthew B. Sullivan	Global Ecology and Ecosystem Effects of Marine Viruses
10	BUTTERFIELD* Cristina N. Butterfield (butterfc@berkeley.edu) Zhou Li, Peter Andeer, Susan Spaulding, David Burstein, Susannah G. Tringe, Brian C. Thomas, Robert Hettich, Trent Northen, Chongle Pan, Jillian F. Banfield	Multi-'Omic' Analyses of the Dynamics, Mechanisms, and Pathways for Carbon Turnover in Grassland Soil
11	CAMPBELL* Barbara J. Campbell (bcampb7@clermson.edu) Emily Castelloe, Joseph Painter, Jean S. Lim, Michael Gonsior, David L. Kirchman	Effects of Size, Season and Salinity on Composition and Function of Estuarine Communities
12	CARDARELLI* Emily L. Cardarelli (ecardare@stanford.edu) John R. Bargar, Christopher A. Francis	Metagenomic Characterization of Nitrogen-Cycling Microbial Communities Impacting Uranium Release in the Upper Colorado River Basin
13	CASTRUITA* Madeli Castruita (madeli.c@gmail.com) Thomas Leya, Sabeeha Merchant	Comparative genomics of snow algae <i>Chlamydomonas cribrum</i> and <i>Chloromonas nivalis</i>
14	CHAFEE* Meghan Chafee (mchafee@mpi-bremen.de) Karen Kruger, Lennart Kappelmann, Jost Waldman, Greta Reintjes, Judith Lucas, Antje Wichels, Gunnar Gerdts, Karen Wiltshire, F.O. Glockner, Bernhard M. Fuchs, Hanno Teeling,	Oligotyping and metagenome analyses reveal a high-resolution recurrence that frames potential ecological strategies of North Sea bacterioplankton
15	CHAKRABORTY* Romy Chakraborty (rchakraborty@lbl.gov) Marcus Schicklberger, Masuno Duy, Jenny Pang, Stefan Jenkins, Trent R. Northen, Dominique Loque, Nicole Shapiro, Tanja Woyke	Diazotrophic Endophytes in Bioenergy Crops
16	CHEN* Jay Chen (chenj@ornl.gov) Yongil Yang, Wellington Muchero, Priya Ranjan, David Weston, Xiaohan Yang, Sara Jawdy, Lee Gunter, Anna Lipzen, Erika Lindquist, Kerrie Barry, Jeremy Schmutz, Gerald Tuskan	eQTL Mapping in Populus

17	CHISTOSERDOVA* Ludmila Chistoserdova (milachis@uw.edu) Maria E. Hernandez, Janet B. Matsen, David A. Beck	Sequencing microcosm communities active in methane oxidation: new insights into the physiology and activities of major players
18	COLEMAN* Maureen L. Coleman (mlcoleman@uchicago.edu) Sara F. Paver, Gabriel Vargas, Ryan J. Newton	Drivers of diversity in the Laurentian Great Lakes
19	COSTA* Kyle C. Costa (costak@caltech.edu) Nathaniel R. Glasser, Elena K. Perry, Stuart J. Conway, Dianne K. Newman	A novel phenazine-reducing pyocyanin demethylase disrupts <i>Pseudomonas aeruginosa</i> biofilms
20	CRNOVIC* Ivana Crnovcic (icrnovci@scripps.edu) Jan-Fang Cheng, Jeffrey D. Rudolf, Hindra, Xiaohui Yan, Chin-Yuan Chang, Yasuo Yoshikuni, Samuel Deutsch, Ben Shen	Construction of BAC vector library for comparative genomics, elucidation of gene functions and heterologous expression of targeted genes
21	DIFAZIO* Stephen P. DiFazio (spdifazio@mail.wvu.edu) Ran Zhou, Craig Carlson, Fred Gouker, Haibao Tang, Vivek Krishnakumar, Christopher Town, Luke Evans, Eli Rodgers-Melnick, Jeremy Schmutz, Jerry Jenkins, Lawrence B. Smart, Gerald A. Tuskan	Comparative Genomics in the Salicaceae: The Case of Sex Determination
22	DOLLHOFER* Veronika Dollhofer (veronika.dollhofer@lfl.bayern.de) Tony M. Callaghan, Isabella Kinker, Johann Bauer, Gareth W. Griffith, Alexander Sczyrba, Michael Lebuhn	Novel anaerobic fungi for lignocellulose degradation
23	DORN* Kevin M. Dorn (dorn@ksu.edu) Traci Kantarski, Shuwen Wang, Xiaofei Zhang, Jim Anderson, Steve Larson, Chris Plott, Jerry Jenkins, Jane Grimwood, Jeremy Schmutz, Lee DeHaan, Jesse Poland	The Intermediate Wheatgrass Genome: A resource for understanding mechanisms of perenniality and accelerating the development of perennial crops
24	DOTY* Sharon L. Doty (sldoty@uw.edu) Zareen Khan, Soo-Hyung Kim	Nitrogen fixation in <i>Populus</i> : Identification and localization of the key diazotrophs in planta

25	EGERTON-WARBURTON* Louise Egerton-Warburton (lwarburton@chicagobotanic.org) Kathryn M. Schreiner, Benjamin S.T. Morgan, Jeremy Schultz, Neal E. Blair	Coupled Metagenomic and Chemical Analyses of Degrading Fungal Necromass and Implications for Microbial Contributions to Stable Soil Organic Carbon
26	FERNANDEZ-BAYO* Jesus D. Fernandez-Bayo (jdfbayo@ucdavis.edu) Ygal Achmon, Duff R. Harrold, Dlinka G. McCurry, Katie Hernandez, Ruth M. Dahlquist-Willard, James J. Stapleton, Ramin Yazdani, Jean S. VanderGheynst, Christopher W. Simmons	Changes in soil microbial diversity following amendment with mesophilic and thermophilic digestates during soil solarization
27	FRANCIS* Christopher A. Francis (caf@stanford.edu) Bradley B. Tolar, Jason M. Smith, Francisco P. Chavez	Combining Molecular, Genomic, and Isotopic Techniques to Examine the Diversity and Activity of Marine Thaumarchaeota in Monterey Bay and the California Current System
28	GAO* Difeng, DG Gao (difengg@gmail.com) Murri Hussain, Jeremy Fowler, Mark Blenner	Expression of lignin-degrading enzymes in yeast <i>Yarrowia lipolytica</i>
29	GIBBONS* Jaimie Gibbons (jaimie.gibbons@jacks.sdstate.edu) Liping Gu, Ruanbao Zhou	Identification of Two Genes Required for Long-Chain Alkane Production in Cyanobacteria
30	GILMORE* Sean P. Gilmore (SeanGilmore@umail.ucsb.edu) Charles H. Haitjema, John K. Henske, Jessica A. Sexton, Kevin V. Solomon, Heather M. Brewer, Samuel O. Purvine, Aaron T. Wright, Alan Kuo, Stephen Mondo, Asaf Salamov, Kurt LaButti, Michael Theodorou, Igor Grigoriev, Michelle O'Malley	Engineering Synthetic Systems Inspired by Anaerobic Gut Fungi
31	GREEN* Richard E. Green (ed@soe.ucsc.edu) N. Putman, P. Havlak, B. O'Connell, M. Blanchette, J. Stites, R. Calef, E. Min	A fast, efficient approach for genome assembly from metagenomic data
32	GU* Liping Gu (ruanbao.zhou@sdstate.edu) Aldon Myrllie, Charles Halfmann, William Gibbons, Ruanbao Zhou	Biosolar Synthesis of Myrcene Using CO ₂ and H ₂ O via Engineered N ₂ -fixing Cyanobacteria
33	HAHN* Aria A. Hahn (hahnaria@gmail.com) Sarah E.I. Perez, Niels W. Hanson, Sangwon Lee, Melanie Scofield, Evan W. Durno, William W. Mohn, Steven J. Hallam	Probing the depths of microbial community structure in soil

34	HAITJEMA* Charles H. Haitjema (haitjema@engineering.ucsb.edu) Sean P. Gilmore, John K. Henske, Randall de Groot, Alan Kuo, Stephen Mondo, Asaf A. Salamov, Igor V. Grigoriev, Heather M. Brewer, Samuel O. Purvine, Aaron T. Wright, Michelle A. O'Malley	Cellulosomes from anaerobic fungi assemble on large non-catalytic scaffoldins
35	HAWLEY* Alyse K. Hawley (alysekh@mail.ubc.ca) Masaru K. Nobu, Jody J. Wright, Brent Sage, Patrick Schwientek, Brandon Swan, Christian Rinke, Wen-Tso Liu, Ramunas Stepanauskas, Tanja Woyke, Steven J. Hallam	Single-cell genomics reveals co-metabolic interactions within uncultivated Marine Group A bacteria
36	HENSKE* John K. Henske (johnhenske@engineering.ucsb.edu) Sean P. Gilmore, Kevin V. Solomon, Michael K. Theodorou, Heather M. Brewer, Samuel O. Purvine, Aaron T. Wright, Alan Kuo, Stephen Mondo, Asaf Salamov, Kurt LaButti, Dawn Thompson, Aviv Regev, Igor Grigoriev, Michelle O'Malley	Engineering Anaerobic Gut Fungi for Lignocellulose Breakdown
37	HERIN* Sayer Y. Herin (herin@ucdavis.edu)	JBrowse and GrainGenes
38	HERRERA PAREDES* Sur Herrera Paredes (sur@email.unc.edu) Gabriel Castrillo Malina, Sarah L. Lebeis, Jose Macalino Esteban, Paulo Jose Pereira Lima Teixeira, Corbin D. Jones, Jeffery L. Dangl	A complex system for a complex phenotype: synthetic communities and the plant microbiome
39	HITTINGER* Chris Todd Hittinger (cthittinger@wisc.edu) William G. Alexander, Nikolay Rovinskiy, Mariana Lopes, David Peris, Jin Kang, Angela Tarver, Miranda Harmon-Smith, Jan-Fang Cheng, Samuel Deutsch, Jeff S. Piotrowski, Trey K. Sato, Audrey P. Gasch	The Yeast Biodesign Library: leveraging DNA synthesis to assess and harness genes from diverse organisms
40	HO* Joe C.H. Ho (joeho776@gmail.com) Sandip V. Pawar, Cameron R. Strachan, Vikramaditya G. Yadav, Steven J. Hallam	Building better biosensors for biocatalyst discovery from metagenomic libraries

41	HOYT* David W. Hoyt (david.hoyt@pnnl.gov) Paula Dalcin Martins, Michael D. Johnston, Malak Tfaily, Michael J. Wilkins	Rapid Sulfur Cycling in Prairie Pothole Lake Sediments Drives Extensive Carbon Mineralization
42	HUTCHINSON* Miriam I. Hutchinson (miramira@unm.edu) Amy J. Powell, Adrian Tsang, Nicholas O'Toole, Randy M. Berka, Igor V. Grigoriev, Kerrie Barry, Donald O. Natvig	Comparative genomic analyses of the Chaetomiaceae provide insights into evolution and inform the development of experimental genetic systems
43	GUO* Jiarong Guo (guojiaro@gmail.com) Aaron Garoutte, Adina Howe, Qiong Wang, Titus Brown, James Cole, James Tiedje	Rhizosphere metagenomics and metatranscriptomics of biofuel crops
44	KAMNEVA* Olga K. Kamneva (okamneva@stanford.edu)	Understanding mechanisms of microbe- microbe interactions using patterns of genome content evolution
45	KELLOGG* Elizabeth A. Kellogg (ekellogg@danforthcenter.org) Dustin Mayfield-Jones, Anthony J. Studer, Daniel Santana de Carvalho, James C. Schnable, Thomas P. Brutnell	Comparative genomics of C4 grasses
46	KOPAC* Sarah Kopac (Sarah.Kopac@uconn.edu) Kevin Lee, Jonathan Klassen	Genomic approaches to characterize fungus garden ecology and evolution
47	LAI* Ellen Lai (elai@ucdavis.edu) Yongjing Zhao, Matthias Hess, Frank M. Mitloehner	Assessing the environmental effect of biofiltration on greenhouse gas emissions from wastewater
48	LAMENDELLA* Regina Lamendella (lamendella@juniata.edu) Justin R. Wright, Maria Campa, Terry C. Hazen, Christopher McLimans, Nikea Ulrich	Community Science Project: Systems Biology Approach to Fracking for Environmental Monitoring
49	LAUDENCIA-CHINGCUANCO* Debbie Laudencia-Chingduanco (debbie.laudencia@ars.usda.gov) Richard Sibout, Fabienne Granier, Wendy Schackwitz, Joel Martin, Amy Cartwright, Colin Konishi, John Vogel	Genome-wide sequence-indexed collection of Brachypodium mutants

50	LEE* Kang Soo Lee (ks_lee@mit.edu) Marton Palatinszky, Jen Nguyen, Vicente I. Fernandez, Filippo Menolascina, Michael Wagner, Roman Stocker	Towards Raman-activated microbial cell sorting (RACS) in an automated microfluidic platform
51	LI* Goutian Li (gtli@ucdavis.edu) Rashmi Jain, Mawsheng Chern, Nhan T. Pham, Kyle Jones, Joel Martin, Wendy Schackwitz, Anna M. Lipzen, Liangrong Jiang, Kerri W. Barry, Jeremy Schmutz, Pamela C. Ronald	Use of KitBase to Facilitate Forward and Reverse Genetics Research in Rice
52	LI* Wei Li (liw9@miamioh.edu) Andor J. Kiss, Jenna M. Dolhi, Amber G. Teufel, Rachael M. Morgan-Kiss	Bacterial and Eukaryal Community Structures in Permanently Ice-Covered Antarctic Lakes
53	LIN* Chan-Shing Lin (shinlin@faculty.nsysu.edu.tw) Ying-Rong Lin	Transcriptomic analysis for a gorgonian coral and its associated organisms
54	LIU* Tong Liu (tongliu@berkeley.edu) Ke Yu, Max M. Hagblom	Identification of a Ruminococcaceae species that could mediate O-demethylation of methyl tert-butyl ether (MTBE) by metagenomics analysis of a methanogenic consortium
55	MANSOORI ZANGIR* Nasim Mansoori Zangir (NMansooriZangir@lbl.gov) Carlos Hernandez-Garcia, Fabrice Masson, Patrick Shih, Charlee Vuu, Garima Goyal, Sangeeta Nath, Nathan J. Hillson, Samuel Deutsch, Dominique Loque,	Universal expression tools to improve nutrient acquisition of energy crops
56	MAZAHERI* Mona Mazaheri (mmazaheri@wisc.edu) Brienne Vaillancourt, Joe Gage, Natalia de Leon, Manfred Mayer, Kerrie Barry, Robin C. Buell, Shawn Kaeppler	Expanding the Wisconsin diversity panel to improve GWAS of biofuel traits in maize
57	MEI* Ran Mei (ranmei2@illinois.edu) Takashi Narihiro, Masaru K. Nobu, Kyohei Kuroda, Julian S. Munoz, Patrick K.H. Lee, Po-Heng Lee, Jules van Lier, Yoichi Kamagata, Michael J. McInerney, Wen-Tso Liu	Microbiome of anaerobic digesters at 51 municipal wastewater reclamation plants
58	MICHENER* Joshua K. Michener (michenerjk@ornl.gov)	Construction and optimization of lignin degradation in Escherichia coli

59	MOBBERLEY* Jennifer Mobberley (jennifer.mobberley@pnnl.gov) Stephen Lindemann, Hans Bernstein, James Moran, Ryan Renslow, Jerome Babauta, Haluk Beyenal, William C. Nelson, Janet Jansson	How does a mat function? Organismal, metabolic, and geochemical microgradients in an epsomitic microbial mat ecosystem.
60	NALVEN* Sarah G. Nalven (sarahnalven@gmail.com) Byron C. Crump, Rose M. Cory, Collin P. Ward, George W. Kling	Decoding DOC degradation with metatranscriptomics: How is microbial metabolism altered when carbon source has been exposed to sunlight?
61	NELSON* William C. Nelson (william.nelson@pnnl.gov) Steven H. Wiley, Devin Fachko, Yukari Maezato, Jennifer M. Mobberley, Margaret F. Romine, Janet K. Jansson	Manifestations of Microdiversity in a Model Microbial Community
62	NICHOLSON* Wayne L. Nicholson (WLN@ufl.edu) Christina L. Davis, Nicole Shapiro, Marcel Huntemann, Alicia Clum, T.B.K. Reddy, Manoj Pillay, Vicotr Markowitz, Neha Varghese, Amrita Pati, Natalia Ivanova, Nikos Kyrpides, Tanja Woyke	Improved high-quality draft genome sequences for all Carnobacterium spp. type strains
63	NORTON* Jeanette M. Norton (Jeanette.norton@usu.edu) Yang Ouyang, John M. Stark, Nicole Shapiro	Agricultural nitrogen management affects microbial communities, enzyme activities and functional genes for nitrogen cycle processes
64	O'LEARY* Jade M. O'Leary (olearyJM@Cardiff.ac.uk) Dan Eastwood, Lynne Boddy, Jen Hiscox, Carten T. Muller, Galya Orr	Genomes to dynamic decay communities: Understanding fungal interactions during early decomposition events in natural lignocellulosic substrate
65	O'MALLEY* Michelle A. O'Malley (momalley@engineering.ucsb.edu) Kevin V. Solomon, Charles H. Haitjema, John K. Henske, Sean P. Gilmore, Diego Borges-Rivera, Anna Lipzen, Heather M. Brewer, Samuel O. Purvine, Aaron T. Wright, Michael K. Theodorou, Igor V. Grigoriev, Aviv Regev, Dawn A. Thompson	Deciphering the biomass-degrading abilities of anaerobic gut fungi

66	FINKEL* Omri M. Finkel (ofinkel@live.unc.edu) Gabriel Castrillo, Isai Salas González, Jeff Dangl	Assessing the role of a-biotic stress in determining the community composition of the root microbiome
67	JENSEN* Paul Jensen (pjensen@ucsd.edu) Greg Amos, Anne-Catrin Letzel, Nadine Ziemert	The Ecology and Evolution of Secondary Metabolism in a Model Group of Marine Bacteria
68	PINGAULT* Lise Pingault (lise.pingault@ou.edu) Zhenzhen Qiao, Yuqi Ren, Marc Libault	Using a single cell type model to advance our understanding of the impact of the plant epigenome on gene transcription in response to environmental stresses
69	POLLEY* Tamsen Polley (tmpolley@ucdavis.edu) Matthias Hess	Identification of novel methane mitigation strategies using an in-vitro rumen system (RUSITEC)
70	PROBST* Alexander J. Probst (alexander.j.probst@gmail.com) Christian Sieber, Brian C. Thomas, Itai Sharon, Spencer Diamond, Jessica Jarett, Tijana G del Rio, Susannah G. Tringe, Tanja Woyke, Jillian F. Banfield	How to bin thousands of high quality genomes from an ecosystem with moderate complexity
71	RAPPE* Michael S. Rappe (rappe@hawaii.edu) Sean P. Jungbluth, Huei-Ting Lin, Olivia D. Nigro, Grieg F. Steward	The distribution, diversity, and function of microbial and viral communities inhabiting anoxic crustal fluids within deep seafloor basalt
72	RODIONOV* Dmitry Rodionov (rodionov@burnham.org) Matvei Khoroshkin, Semen Leyn	Metabolic and regulatory networks for carbohydrate utilization in human gut Clostridia
73	ROSSO* Marie-Noelle Rosso (marie-noelle.rosso@univ-amu.fr) Shingo Miyauchi, Elodie Drula, Marie-Pierre Forquin-Gomez, Francois Piumi, David Navarro, Anne Favel, Javier F. Ruiz-Duenas, Igor Grigoriev, Robert Riley, Anna Lipzen, Bernard Henrissat, Jean-Guy Berrin, Eric Record	Combined –omics approaches highlight functional diversity for lignocellulose breakdown within a single genus of the order Polyporales, Basidiomycetes.

74	RUIZ-FONT* Angelica Ruiz-Font (convenios22@hotmail.com) Isabel Ramos-Robles, Sugeyrol Villa-Ramirez, Gabriel Sanchez-Tozapantzi	Microbial Endophytes for Plant Biomass, biostimulant for Feedstock Biofuel Production
75	SALAS-GONZALEZ* Isai Salas-Gonzalez (isai@email.unc.edu) Omri Finkel, Gabriel Castrillo, Tianxiang Gao, Jeffery L. Dangl	Reconstruction of genome-scale metabolic networks and models from Arabidopsis thaliana root-associated bacterial isolates as probes to examine host-microbe interactions
76	SANCHEZ BARRIOS* Andrea Sanchez Barrios (asanchez-barrrios@uky.edu) Tom Shearin, Derek Lundberg, Laura De Lorenzo, Meera Nair, Seth Debolt	Effects of bacterial inoculants on the development and molecular response to changes in microbial communities in Nicotiana benthamiana plants
77	SHARRAR* Allison M. Sharrar, (asharrar@berkeley.edu) Evan P. Starr, Mary K. Firestone, Jillian F. Banfield	Metagenomic analysis shows phylogenetic and functional similarities across diverse soil microhabitats
78	SHEARMAN* Helen Shearman (helen@biomatters.com) Aaron Kennedy, Christian Olsen, Matt Kearse	The Geneious Sequence Classifier tool: Identifications of quarantine significant plant pathogenic fungi as an illustrated use case
79	SHEARMAN* Helen Shearman (helen@biomatters.com) Christian Olsen, Richard Moir, Matthew Cheung, Matt Kearse, Sebastian Dunn, Jonas Kuhn, Sidney Markowitz, Alex Cooper, Jo Smith	A User Friendly CRISPR Design Tool
80	SHRADER* Donna Grace Shrader (d.grace.shrader@gmail.com) Joshua Hamilton, Alexandra Linz, Katherine D. McMahon	Gene-centric and genome-centric approaches to understanding freshwater microbial communities
81	SIMISTER* Rachel L. Simister (rlsimister@gmail.com) Aurele Vuillemin, Jens Kallmeyer, Steven J. Hallam, Sean A. Crowe	Linking microbial genomic capacity to geochemical process in the deep terrestrial biosphere
82	SIMON* Holly M. Simon (simonh@ohsu.edu) Maria W. Smith, Lydie Herfort, Adam R. Rivers	Characterization of microbial "hotspots" of organic matter degradation in a fast-flowing estuary

83	SLONCZEWSKI* Joan L. Slonczewski (slonczewski@kenyon.edu) Wei Li, Sean P. Bush, Jeffrey Froula, Christopher Sedlacek, Darcy Blankenhorn, Racheal Morgain-Kiss	Antarctic Lake Metagenomes from Cyanobacterial Mats and Planktonic Microbes
84	SORENSEN* Jackson W. Sorensen (sorens75@msu.edu) Ashley Shade	Soil microbial community responses to a subterranean coal mine fire revealed by metagenome analysis
85	SOUZA* Rafael S. C. Souza (scs.rafael@gmail.com) Vagner K. Okura, Jaderson S. L. Armani, Natalia B. Damasceno, Beatriz Jorrin, Nuria Lozano, Marcio J. Silva, Manuel Gonzalez-Guerreiro, Laura M. Araujo, Natalia F. Verza, Homayoun Bagheri, Juan Imperial, Paulo Arruda	Accessing the potential of the core microbiome of a bioenergy crop in plant development and biomass accumulation
86	STEVENS* Sarah LR Stevens (sstevens2@wisc.edu) Sarahi L. Garcia, Benjamin Crary, Manuel Martinez-Garcia, Ramunas Stepanauskas, Tanja Woyke, Susannah G. Tringe, Siv Andersson, Stefan Bertilsson, Rex Malmstrom, Katherine D. McMahan	Tracking distinct freshwater populations using single cell genomes and metagenomics
87	STRENKERT* Daniela Strenkert (DanielaS@chem.ucla.edu) Sean D. Gallaher, Stefan Schmollinger, Matteo Pellegrini, James G. Umen, Sabeeha S. Merchant	A day in the life of Chlamydomonas
88	SUZUKI* Yo Suzuki (ysuzuki@jcv.org) Maxim Kostylev, Anne E. Otwell, Timothy J. Hanly	Synthetic Biology Pipeline for Constructing and Testing Combinatorics of Cellulose- and Lignin-Degrading Enzymes
89	TOBIAS* Christian M. Tobias (christian.tobias@ars.usda.gov) Sangwoong Yoon, Bradley Hernlem, Serge Edme, Gautam Sarath, Nathan Palmer	Generation of Octaploid Switchgrass by Seedling Treatment

90	TRUONG* Sandra K. Truong (thkhavi@tamu.edu) Ryan F. McCormick, Avinash Sreedasyam, Shengqiang Shu, Brodk D. Weers, Brian A. McKinley, Ashely J. Mattison, Jerry W. Jenkins, Megan Kennedy, Mojgan Amirebrahimi, Jane Grimwood, Jeremy Schmutz, John Mullet	Functional genomics and plant modeling for sorghum improvement
91	VAILLANCOURT* Brienne Vaillancourt (vaillan6@msu.edu) Ian Beddows, Alex B. Brohammer, Cory D. Hirsch, Mei Wang, Kerrie Barry, Natalia de Leon, Shawn M. Kaeppler, Candice N. Hirsch, Robin C. Buell	Diversity of transcriptome regulatory networks in maize and association with biomass and biofuel traits
92	WARSHAN* Denis Warshan (denis.warshan@su.se) Josh L. Espinoza, R. Alexander Richter, Christopher L. Dupont, Philip D. Weyman, Ulla Rasmussen	Functional genomics of moss-cyanobacteria interactions in boreal forest ecosystems
93	WU* Chengcang C. Wu (cwu@intactgenomics.com) Kenneth D. Clevenger, Jin Woo Bok, Rosa Ye, Galen P. Miley, Thomas Velk, Cynthia Chen, KaHoua Yang, Peng Gao, Matthew Lamprecht, Paul M. Thomas, M. N. Islam, Nancy P. Keller, Neil L. Kelleher	Large scale discovery and deorphanization of natural products using fungal artificial chromosomes and untargeted metabolomics (FAC-MS)
94	WU* Guangxi Wu (guangxiwu@gmail.com) Guohua Yin, Jiujiang Yu, Wayne M. Jurick II, Joan W. Bennett, Daniel R. Shelton	Genome of blue mold causing fungus <i>Penicillium solitum</i> compared to related species to reveal genetic features likely involved in virulence
95	WU* Vincent Wu (vwu104@berkeley.edu) David Kowbel, Yi Xiong, Ann Lipzen, Vasanth Singan, Igor Gregoriev, Louise N. Glass	RNA Profiling of <i>Neurospora crassa</i> : Insights Into Plant Cell Wall Degradation by Filamentous Fungi
96	XUE* Liang-Jiao Xue (cjtsai@uga.edu) Scott A. Harding, Chung-Jui Tsai	Allele-specific transcriptome analysis of <i>Populus</i> hybrids
97	YAMAHARA* Kevan M. Yamahara (kyamahara@mbari.org) Christina M. Preston, Doug Pargett, Scott Jensen, Brent Roman, Anna Romano, John Cardwell, James Birch, Edward Delong, Christopher Scholin	Towards a Mobile Ecogenomic Sensor: Development and Applications of the 3rd Generation Environmental Sample Processor

98	YOURSTONE* Scott Yourstone (scott.yourstone81@gmail.com) Sur Herrera Paredes, Hunter Cameron, Omri Finkel, Isai Salas Gonzalez, Derek Lundberg, Sarah Lebeis, Scott Clingenpeel, Asaf Levy, Tanja Woyke, Susannah Tringe, Corbin Jones, Jeff Dangl	Functional selection of microbial genes in the Arabidopsis thaliana rhizosphere
99	ZALLOT* Remi Zallot (vcrecy@ufl.edu) Robert Ross, Wei-Hung Chen, Steven D. Bruner, Patrick A. Limbach, Valerie de Crecy-Lagard	Identification of missing enzymes and transporters involved in the synthesis and salvage of Queuosine by comparative genomics
100	ZHOU* Jinglie Zhou (jzz0026@auburn.edu) Scott Monsma, Alinne Pereira, Blaine Pfeifer, Scott R. Santos, Megan Niebauer, Erin Ferguson, Ron Godiska, ChengCang Wu, David Mead, Mark Liles	Recovery and expression of intact secondary metabolite biosynthetic pathways from a large-insert soil metagenomic library
101	ZON* Gerald Zon (gzon@trilinkbiotech.com) Sabrina Shore, Jordana M. Henderson, Anton P. McCaffrey, Richard I. Hogrefe	Improved MicroRNA Library Preparation Workflow for Next-Generation Sequencing Allows Ultra-Low Inputs and Eliminates Gel Purification
102	KUDRNA* David A. Kudrna (dkudrna@email.arizona.edu) Dario Copetti, Jianwei Zhang, Jayson Talag, Seunghee Lee, Rod A. Wing	ETOP: Resources and protocols for generating high-quality genome assemblies
103	JACOBSON* Daniel Jacobson (jacobsonda@ornl.gov) Deborah Weighill, Carissa Bleker, Gerald Tuskan, Wellington Muchero, Tim Tschaplinski	Pleiotropic and Epistatic Network-Based Discovery: Integrated SNP Correlation, Co-expression and Genome-Wide Association Networks for <i>Populus trichocarpa</i>
104	JACOBSON* Daniel Jacobson (jacobsonda@ornl.gov) Deborah Weighill, Carissa Bleker, Gerald Tuskan, Wellington Muchero, Timothy Tschaplinski	Pleiotropic and Epistatic Network-Based Discovery of Plant Functions involved in Microbial Interactions: Integrated SNP Correlation, Co-expression and Genome-Wide Association Networks for <i>Populus trichocarpa</i>
105	HSU* Suzie Hsu (hsuxx166@umn.edu)	Towards a mechanistic understanding of disease suppressive soils: Refactoring natural product gene clusters