

| | Authors | Abstract Title |
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| 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 | AZUAR* Aude Aznar (aazar@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 Stamatis, T.B.K. Reddy, Chew Yee Ngan, Chris Daun, Nicole Shapiro, Markowitz, Victor, Ivanova, Natalia, Kyrpides, 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 |

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| 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@clemsun.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 <i>Populus</i> |

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| 17 | CHITOSERDOVA* 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 | CRNOVCIC* 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 | DOLLHOFFER* 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 |

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| 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. Golmore (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 Myrlie, 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 |

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| 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 |

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| 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 |

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| 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. Haggblom | 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 |

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| 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 | 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 |
| 66 | 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 |

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| 67 | 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 |
| 68 | POLLEY* Tamsen Polley (tmpolley@ucdavis.edu) Matthias Hess | Identification of novel methane mitigation strategies using an in-vitro rumen system (RUSITEC) |
| 69 | 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 |
| 70 | 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 |
| 71 | RODIONOV* Dmitry Rodionov (rodionov@burnham.org) Matvei Khoroshkin, Semen Leyn | Metabolic and regulatory networks for carbohydrate utilization in human gut Clostridia |
| 72 | 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. |
| 73 | 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 |
| 74 | 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 |

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| 75 | SANCHEZ BARRIOS* Andrea Sanchez Barrios (asanchez-barrios@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 <i>Nicotiana benthamiana</i> plants |
| 76 | 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 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | 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 |
| 81 | 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 |
| 82 | 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 |
| 83 | SORENSEN* Jackson W. Sorensen (sorens75@msu.edu) Ashley Shade | Soil microbial community responses to a subterranean coal mine fire revealed by metagenome analysis |

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| 84 | 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 |
| 85 | 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. McMahon | Tracking distinct freshwater populations using single cell genomes and metagenomics |
| 86 | 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 |
| 87 | 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 |
| 88 | 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 |
| 89 | 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 |
| 90 | VAILLANCOURT* Brieanne Vaillancourt (vaillan6@msu.edu) Ian Beddows, Alex B. Brohammer, Cory D. Hirsch, Mei Wang, Kerrie Barry, Natalia de Leon, Shawn M. Kaepler, Candice N. Hirsch, Robin C. Buell | Diversity of transcriptome regulatory networks in maize and association with biomass and biofuel traits |

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| 91 | 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 |
| 92 | 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) |
| 93 | 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 |
| 94 | 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 |
| 95 | XUE* Liang-Jiao Xue (cjtsai@uga.edu) Scott A. Harding, Chung-Jui Tsai | Allele-specific transcriptome analysis of <i>Populus</i> hybrids |
| 96 | 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 |
| 97 | 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 <i>Arabidopsis thaliana</i> rhizosphere |
| 98 | 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 |

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| 99 | 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 |
| 100 | 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 |
| 101 | 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 |
| 102 | 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> |
| 103 | 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> |
| 104 | HSU* Suzie Hsu (hsuxx166@umn.edu) | Towards a mechanistic understanding of disease suppressive soils: Refactoring natural product gene clusters |