

	Authors	Abstract Title
1	AHRENDT* Steven R. Ahrendt (sahrendt0@lbl.gov) C. A. Quandt, Doina Ciobanu, Alicia Clum, Asaf A. Salamov, Jan-Fang Chang, Tanja Woyke, Timmothy Y. James, Igor V. Grigoriev,	Exploring "Dark Matter Fungi" Using Single-Cell Genomics
2	CHIN* Jason Chin (jchin@pacificbiosciences.com) Paul Peluso, David Rank, Maria Nattestad, Fritz J. Sedlazeck, Michael Schatz, Alicia Clum, Kerrie Barry, Alex Copeland, Ronan O'Malley, Chongyuan Luo, Joseph Ecker	Un-zipping Diploid Genomes - Revealing All Kinds of Heterozygous Variants from Comprehensive Haplotig Assembly
3	CHOWDHURY* Priya Roy Chowdhury (roychowdhury@umass.edu) Grace Pold, William Rodriguez, Jeff Blanchard, Kristen DeAngelis	Does long-term soil warming affect the rate of horizontal gene transfer in bacterial communities?
4	COLE* Benjamin Cole (bjcole@lbl.gov) Meghan Feltcher, Jordon Waters, Kelly Wetmore, Elizabeth Ryan, Natalie Wang, Sabah Ul-Hasan, Yasuo Yoshikuni, Rex Malmstrom, Adam Deutschbauer, Jeff Dangl, Axel Visel	Genome-wide Identification of Bacterial Plant Colonization Genes
5	GACH* Philip C. Gach (pcgach@lbl.gov) Steve C. C. Shih, Jess Sustarich, Jay D. Keasling, Nathan J. Hillson, Paul D. Adams, Anup K. Singh	A Droplet Microfluidic Platform for Automating Genetic Engineering
6	GORDON* Sean Gordon (sgordon@lbl.gov) Bruno Contreras-Moreira, David L. Des Marais, Diane Burgess, Wendy Schackwitz, Ludmila Tyler, Joel Martin, Daniel Woods, Anna Lipzen, Shengquang Shu, Jeremy Phillips, Kerrie Barry, Richard Amasino, Ana Caicedo, Luis Mur, Michael Freeling, Pilar Catalan, John Vogel	The pan-genome of <i>Brachypodium distachyon</i> , capturing the full genetic complement of a plant species
7	GREEN* Elizabeth Green (green74@llnl.gov) Erin Nuccio, Jessica Wollard, Daniel Nilson, Kate Heckman, Ashley Campbell, Tana Wood, Jennifer Pett-Ridge	Tropical microbial soil diversity and carbon turnover across a depth profile

8	GRIESEMER* Marc Griesemer (griesemer1@lbl.gov) Jeffrey Kimbrel, Patrik D'haeseleer, Carol Zhou, Ali Navid	Improving the Completeness of Metabolic Networks used for Automatic Generation of Genomic-Scale Constraint-Based Models
9	GU* Jenny Gu (jgu@pacb.com) Kevin Eng, Anand Sethuraman, Denise Raterman, Todd Richmond, Steve Kujawa	Targeted Sequencing of Genes from Soybean using NimbleGen SeqCap EZ and PacBio SMRT Sequencing
10	GUNTER* Lee E. Gunter (gunterle@ornl.gov) Kerrie Barry, Jeremy Schmutz, Christopher Plott, Jerry W. Jenkins, Gerald A. Tuskan	Populus deltoides de novo assembly
11	HALL* Richard J. Hall (rhall@pacificbiosciences.com) Cheryl Heiner, Chris Stanley, Matt Hamilton, Alexander Khoruts, Michael Sadowsky	Profiling the Microbiome in Fecal Microbiota Transplantation using Circular Consensus and Single Molecule, Real-Time Sequencing
12	HARTMAN* Wyatt H. Hartman (whhartman@lbl.gov) Rongzhong Ye, William R. Horwath, Susannah G. Tringe	Coupling of Belowground Carbon Cycling and Stoichiometry from Organisms to Ecosystems along a Soil C Gradient Under Rice Cultivation
13	HEINER* Cheryl Heiner (cheiner@pacificbiosciences.com) Steve Oh, Richard Hall, Lawrence Hon	Minimization of Chimeras and Substitution Errors in Full-Length 16S PCR Amplification
14	HIGGINS* Steven A. Higgins (shiggin8@vols.utk.edu) Christopher W. Schadt, Frank A. Loffler	Comparative genomics of N ₂ O-producing fungi reveals extensive denitrification gene modularity and cryptic nitrate utilization genotypes
15	IWAI* Kosuke Iwai (KosukeIwai@lbl.gov) Peter W. Kim, Manasi Raje, Todd A. Duncombe, Joshua 'Deng Kai Heinemann, Paul D. Adams, Anup K. Singh	Automated Analog-Digital Optofluidic Platform to Detect and Sort Microdroplets for High-Throughput Genetic Engineering
16	JUENGER* Thomas E. Juenger (tjuenger@austin.utexas.edu) John Lovell, Billie Gould, David Lowry, Jerry Jenkins, Jeremy Schmutz	Genetic and genomic studies of local adaptation in <i>Panicum hallii</i>

17	KIMBREL* Jeffrey A. Kimbrel (kimbrel1@lbl.gov) Ty J. Samo, Daniel J. Nilson, Erin E. Nuccio, Jennifer Pete-Ridge, Anthony Siccardi, Todd W. Lane, Xavier Mayali	Simplified Bacterial Communities Conferring Productivity Enhancements to Biofuels-Producing Algae
18	KNELMAN* Joseph Knelman (jknelman@lbl.gov) Andrew Katz, Gelsomina Manganiello, Amy Cartwright, Ulrich Mueller, Jeff Dangl, Lorito Matteo, Katherine Louie, Trent Northn, John P. Vogel	Exploring the underpinnings of plant-microbial community interactions: a defined microbiome for <i>Brachypodium</i>
19	KUO* Alan Kuo (akuo@lbl.gov) Stephen Mondo, Asaf Salamov, Kurt LaButti, John Henske, Kevin Solomon, Sean Gilmore, Michelle O'Malley, Igor Grigoriev	Genomics of anaerobic cellulose-degrading fungal symbionts of the herbivore gut
20	KWAK* Yunyoung Kwak (yun@knu.ac.kr) Jae-Ho Shin	Metagenomic insights into the response of microbial communities to polycyclic aromatic hydrocarbons in soil
21	LA REAU* Alex J. La Reau (alareau@wisc.edu) Melissa R. Christopherson, John A. Dawson, David M. Stevenson, Paul J. Weimer, Christina Kendzioriski, Garret Suen	Insights into Fiber Degradation by <i>Ruminococcus albus</i> 7 Revealed by Growth in Continuous-Culture Chemostat Using Transcriptomic and Physiological Analyses
22	LAMBERT* Christine Lambert (clambert@pacb.com) John Harting, Walter Lee, Primo Baybayan	Multiplexing Strategies for Microbial Whole Genome SMRT® Sequencing
23	LEVY* Asaf Levy (alevy@lbl.gov) Scott Yourstone, Scott Clingenpeel, Bryan Rangel Alvarez, Sur Herrera Paredes, Derek Lundberg, Sarah Lebeis, Dale Pelletier, Susannah Tringe, Jeffery Dangl, Tanja Woyke	Genetic determinants of bacterial adaptation to plants
24	LI* Rachel A. Li (rachel@berkeley.edu) Yasuo Yoshikuni, Jay D. Keasling	Characterization of the <i>Eucalyptus grandis</i> terpenome using engineered yeast strains
25	LIU* Lifeng Liu (lifeng.liu@lbl.gov) Nir Sade, Sean Gordon, Amy Cartwright, Maria del Mar Rubio-Wilhelmi, Jeremy Schmutz, Jerry Jenkins, Christian Tobias, Roger Thilminy, Eduardo Blumwald, John Vogel	Genome sequence of the model perennial grass <i>Brachypodium sylvaticum</i> and the identification of transgene combinations conferring tolerance to multiple abiotic stresses

26	LOVEJOY* Connie Lovejoy (connie.lovejoy@bio.ulaval.ca) David Walsh	Metagenomics of western Arctic Ocean microbial communities
27	MAYALI* Xavier Mayali (mayali1@llnl.gov) Ty Samo, Daniel Nilson, Anthony Siccardi, Todd Lane, Jeffrey Kimbrel, Jennifer Pett-Ridge, Peter Weber	NanoSIMS Isotope Imaging to Investigate Algal-Bacterial Interactions in Biofuel-Producing Communities
28	MCCLURE* Ryan S. McClure (Ryan.Mcclure@pnnl.gov) Christopher C. Overall, Eric A. Hill, Hans Bernstein, Jason E. McDermott, Alex S. Beliaev	Studying Coordination of Microbial Community Behavior via Context-Based Mutual Information Networks
29	MCCORMICK* Ryan F. McCormick (ryanabashbash@tamu.edu) Sandra K. Truong, Jerry W. Jenkins, Daryl T. Morishige, Avinash Sreedasyam, Shengqiang Shu, Brock D. Weers, Brian A. McKinley, Ashley J. Mattison, Megan Kennedy, Mojgan Amirebrahimi, Jane Grimwood, Jeremy Schmutz, John Mullet	Genomic resources and 3D phenotyping to accelerate sorghum improvement
30	MEREDITH* Laura K. Meredith (laurameredith@email.arizona.edu) Esther Singer, Kristin Boye, Mary Whelan, Christian von Sperber, Erin Pang, Lisa Wingate, Lisa Ogee, Joseph A. Berry, Paula V. Welander	: Microbial, physical and chemical drivers of COS and 18O-CO ₂ exchange in soils
31	MONDO* Stephen J. Mondo (sjmondo@lbl.gov) Richard O. Dannebaum, Govindarajan K. Ramamoorthy, Andrii Gryganskyi, Timothy James, Michelle O'Malley, Jason Stajich, Igor V. Grigoriev	N ⁶ -methyladenine marks active gene expression in early diverged fungi
32	MUKHERJEE* Supratim Mukherjee (supratimmukherjee@lbl.gov) T.B.K. Reddy, Dimitrios Stamatis, Jonathon Bertsch, Galina Ovchinnikova, Michelle Isbandi, Olena Verezemskaya, Nikos C. Kyrpides	Genomes OnLine Database (GOLD): A curated catalogue of genome and metagenome sequencing and analysis projects
33	NEUMANN* Antony P. Neumann (apneumann2@wisc.edu) Caroline A. McCormick, Garret Suen	Isolation of novel mammal-associated Fibrobacter spp.

34	NOBU* Masaru K. Nobu (masarunobu@gmail.com) Takashi Narihiro, Miaomiao Liu, Kyohei Kuroda, Ran Mei, Wen-Tso Liu	Diverse syntrophic catabolism for escaping thermodynamic limitations
35	NUCCIO* Erin E. Nuccio (nuccio1@llnl.gov) Shengjing Shi, Jason Shi, Ulas Karaoz, Amy Boaro, Carrie Nicora, Rhona Stuart, Peter Weber, Zhili He, Eoin Brodie, Mary Lipton, Jizhong Zhou, Mary Firestone, Jennifer Pett-Ridge	The interconnected rhizosphere: Roots stimulate high microbial network complexity and alter the expression of enzymes related to organic matter decomposition in soil
36	OBERTORTNER* Ernst Oberortner (eoberortner@lbl.gov) Jan-Fang Cheng, Nathan J. Hillson, Samuel Deutsch	Automating the Design for Synthesis and Assembly Process using the Sequence Polishing Library (SPL)
37	OKATSU* Yuki Okatsu (yokatsu@ucdavis.edu) Casey Dykier, Robert D. Sainz, Matthias Hess	Effects of rumen microbiome composition on methane emission from enteric fermentation
38	PAEZ-ESPINO* David Paez-Espino (adpaezespino@lbl.gov) Emiley Eloé-Fadrosch, Alexander D. Thomas, Marcel Huntemann, Amrita Pati, Edward Rubin, Natalia N. Ivanova, Nikos C. Kyrpides	Uncovering Earth's Virome
39	PENG* Xuefeng Peng (xpeng@engineering.ucsb.edu) Sean P. Gilmore, John K. Henske, Michael K. Theodorou, Michelle A. O'Malley	Understanding the genomic basis of syntrophic relationships between rumen anaerobes
40	RAMAN* Srivatsan M. Raman (sraman4@wisc.edu)	Designer small molecule biosensors for high-throughput phenotyping of genomes and genes
41	RILEY* Robert Riley (rwiley@lbl.gov) Sajeet Haridas, Kenneth H. Wolfe, Mariana R. Lopes, Chris T. Hittinger, Markus Goker, Asaf Salamov, Jen Wisecaver, Tanja M. Long, Andrea L. Aerts, Kerrie Barry, Cindy Choi, Alica Clum, Aisling Coughlan, Shweta Deshpande, Alexander Douglass, Sara Hanson, Peter Hans-Klenk	Comparative genomics of biotechnologically important yeasts
42	RUPPERT* Noel Ruppert (nruppert@labcyte.com) Carl Jarman, Aurore Lejeune, Linda Orren, John Lesnick	Establishing a method for high precision cell dispensing with the Echo® 500 Series of Liquid Handlers

43	SAMO* TY J. Samo (samo1@llnl.gov) Jeffrey A. Kimbrel, Daniel J. Nilson, Erin E. Nuccio, Anthony Siccardi, Todd W. Lane, Jennifer Pett-Ridge, Xavier Mayali	Correlating taxonomic composition of algal-associated bacterial communities with productivity in biofuel-producing algal species
44	SHELLER* Henrik V. Scheller (hshell@lbl.gov) Solomon H. Stonebloom, Berit Ebert, Kerrie Barry	Identification of glycosyltransferases involved in biosynthesis of arabinogalactans via RNA-seq and virus-induced gene silencing
45	SEONG* Hoon Je Seong (s4645@naver.com) Chung Yeon Hwang, Hong Hee Won, Woo Jun Sul	Measuring Patterns by Geographical Locations in Marine Metagenome Data using Newly Adopted Genotyping by Sequencing
46	SHULSE* Christine N. Shulse (cshulse@lbl.gov) Mansi Chovatia, Yan Lei, Adam Deutschbauer, Matthew J. Blow	Discovery and transfer of novel pathways for phosphate solubilization
47	SIEBER* Christian MK Sieber (csieber@lbl.gov) Alexander J. Probst, Itai Sharon, Brian C. Thomas, Susannah G. Tringe, Jillian F. Banfield	Improving genome-resolved metagenomics by combining binning predictions
48	SINGER* Esther Singer (singer@lbl.gov) Thomas E. Juenger, Tanja Woyke	Towards understanding the Panicum virgatum microbiome - switchgrass geno-/ecotype and treatment practices influence the microbial community
49	SREEDASYAM* Avinash Sreedasyam (asreedasyam@hudsonalpha.org) Christopher Plott, Morgan Qualls, Jerry Jenkins, Jane Grimwood, Joseph Carlson, David Goodstein, Tom Juenger, Yuhong Tang, Gerald A. Tuskan, Tom Brutnell, Sabeeha S. Merchant, Stefan A. Rensing, John Mullet, Todd Mockler, Gary Stacey, Jeremy Schmutz"	JGI Plant Gene Atlas: Improving functional annotations of JGI Plants using transcriptional data
50	STUART* Rhona K. Stuart (stuart25@llnl.gov) Xavier Mayali, Amy Boaro, Craig Everroad, Daniel Nilson, Peter K. Weber, Mary Lipton, Brad M. Bebout, Jennifer Pett-Ridge, Michael P. Thelen	Linking microbial identity and function in phototrophic mats and biofilms

51	TOLAR* Bradley B. Tolar (btolar1@stanford.edu) Christopher A. Francis	Monitoring the transcriptional response of a representative low-salinity ammonia-oxidizing thaumarchaeote to shifts in environmental conditions
52	TSENG* Elizabeth Tseng (etseng@pacb.com) Hamid Ashrafi, Amanda M. Hulse-Kemp, Allen Van Deynze,	De novo reconstruction of the spinach coding genome using full-length transcriptome
53	WHITMAN* William B. Whitman (Whitman@uga.edu) Tanja Woyke, Nikos C. Kyrpides, Klenk Hans-Peter, Zhou Yuguang	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains
54	WU* Yu-Wei Wu (ywwei@lbl.gov) Brendan Higgins, Chaowei Yu, Amitha P. Reddy, Shannon Ceballos, Larry D. Joh, Blake A. Simmons, Steven W. Singer, Jean S. VanderGheynst	Integrating metagenomics and metatranscriptomics to analyze the impact of ionic liquids on the bioenergy feedstock degrading microbiome and transcription of enzymes relevant to polysaccharide hydrolysis
55	WU* Dongying Wu (dygwu@ucdavis.edu) Jonathan A. Eisen	The Development of a Bioinformatic Pipeline for ssu-rRNA Novelty Measurement
56	ZHANG* Ying Zhang (yingzhang@uri.edu) Jon Lund Steffensen, Keith Dufault-Thompson	Genome-scale Metabolic Modeling with the PSAMM Software