



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

	Authors	Abstract Title
1	Ahrendt, Steven R.* (sahrendt0@lbl.gov); Quandt Alisha C.; Ciobanu, Doina; Clum, Alicia; Salamov, Asaf; Cheng, Jan-Fang; Woyke, Tanja; James, Timothy; Grigoriev, Igor	Exploring Fungal Dark Matter Using Single-Cell Genomics
2	Bushnell, Brian* (bbushnell@lbl.gov)	Clumpify: Efficient, Lossless Fastq Compression
3	Browne, Daniel R.* (dbrowne.up@gmail.com); Jenkins, Jerry; Schmutz, Jeremy; Barry, Kerrie; Koppisch, Andrew T.; Devarenne, Timothy P.	Capturing the Complete Genome of Botryococcus braunii by Combining Illumina and PacBio Assemblies
4	Cardarelli, Emily L.* (ecardare@stanford.edu); Bargar, John; Francis, Christopher	Microbial Communities Involved in Subsurface Nitrogen Cycling across the Upper Colorado River Basin and Potential Implications for Uranium Release
5	Carlson, Joseph W.* (JWCarlson@lbl.gov); Davidson, Patrick; Goodstein, David; Rokhsar, Daniel	Pathway Visualization Tools in Phytozome
6	Carver, Akiko A.* (acarver@lbl.gov); Stillman, Kyra; Liu, Haley; Branco, Sara; Kuo, Alan J.; Bruns, Tom; Grigoriev, Igor	Comparative Genomic Analyses of Two Pyrophilous Fungi
7	Chen, Jay* (chenj@ornl.gov); Yang, Yongil; Muchero, Wellington; Ranjan, Priya; Weston, David J.; Yang, Xiaohan; Jawdy, Sara; Gunter, Lee; Lipzen, Anna; Lindquist, Erika; Barry, Kerrie; Schmutz, Jeremy; Tuskan, Gerald A.	eQTL Mapping in Populus (Short Talk)



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

8	Cole, Benjamin J.* (bjcole@lbl.gov); Feltcher, Meghan E.; Waters, Robert J.; Wetmore, Kelly M.; Mucyn, Tatiana S.; Ryan, Elizabeth M.; Wang, Gaoyan; Ul-Hasan, Sabah; McDonald, Meredith; Yoshikuni, Yasuo; Malmstrom, Rex R.; Deutschbauer, Adam; Dangl, Jeffery L.; Visel, Axel	Genome-Wide Identification of Bacterial Plant Colonization Genes
9	Crump, Byron C.* (bcrump@coas.oregonstate.edu); Fine, Lindy M.; Herfort, Lydie; Smith, Maria W.; Payet, Jérôme P.; Simon, Holly M.	The Estuarine Metagenome of Microbial Communities in the Columbia River estuary
10	Dippel, Andrew B.* (adippel@berkeley.edu); Evans, Robert; Deutsch, Samuel; Hammond, Ming	Development of Luminescent Biosensors for Analysis of Bacterial Cyclic-di-GMP
11	Edwards, Joseph A.* (edwards@ucdavis.edu); Kilmer, John; Santos, Christian; Liechty, Zachary; Nguyen, Bao; Phillips, Gregory; Sundaresan, Venkatesan	The Plant Root-Associated Microbiome Viewed across Diverse Plant Species and Developmental Stages
12	Egan, Rob* (rsegan@lbl.gov); E. Georganas, A. Buluç, S. Hofmeyr, R. Egan, L. Olikier, D. Rokhsar, K. Yelick, P. Chai, n P. Senin, R. Egan, N. Ivanova, N. Kyrpides, T. Neilson, D. Rokhsar	ExaBiome: Exascale Solutions to Microbiome Analysis
13	Floge, Sheri A.* (floge.1@osu.edu); Roux, Simon; Bowen, Benjamin P.; Northen, Trent R.; Woyke, Tanja; Sullivan, Matthew B.	Under Attack: How a Marine Cyanobacterium Responds to Virus Infection and Grazer Predation
14	Francis, Christopher A.* (caf@stanford.edu); Rasmussen, Anna; Damashek, Julian; Lee, Jessica; Baker, Brett	Spatiotemporal Characterization of Microbial Communities Controlling Estuarine Nitrogen Cycling in the San Francisco Bay-Delta
15	Fritts, Ryan K.* (rkfritts@indiana.edu); Gliessman, Jennifer R.; Behringer, Megan G.; Lynch, Michael; McKinlay, James B.	Evolution of Mutualistic Cross-Feeding in a Synthetic Bacterial Coculture



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

16	Georganas, E.* Egan, Rob S. (rsegan@lbl.gov); Buluc, A.; Hofmeyr, S.; Olikier, L; Rokhsar, Daniel; Yelick, Kathy.; Chain, P.; Senin, P.; Ivanova, N.; Kyrpides, Nikos; Neilson, T.	ExaBiome: Exascale Solutions to Microbiome Analysis
17	Gordon, Sean* (seangordon07@gmail.com); Session, Adam; Jenkins, Jerry; Shu, Shengqiang; Schmutz, Jeremy; Barry, Kerrie; Catalan, Pilar; Contreras, Bruno; Levy, Joshua; Katz, Andrew; Phillips, Jeremy; Grimwood, Jane; Hasterok, Robert; Doonan, John; Mur, Luis; Dinh-Thi, Vinh-Ha; Chalhoub, Boulos; Rokhsar, Dan; Vogel, John	The genus <i>Brachypodium</i> as a tool to study polyploidy
18	Greenspan, Alex* (greenspan@ucdavis.edu); Alford, Betsy; Chang, Peter; Von Wettberg, Eric; Kahraman, Abdullah; Bükün, Bekir; Mohammed, Zehara; Fikre, Asnake; Sarma, Birinchi; Cook, Douglas R.	Quantifying Genomic Exchange in Chickpea-Nodulating Mesorhizobium (Short Talk)
19	Griessemer, Marc* ; D'haeseleer, Patrik M. (dhaeseleer2@llnl.gov); Kimbrel, Jeffrey; Navid, Ali	Combining Multiple Functional Annotation Tools Increases Completeness of Metabolic Annotation
20	Hartman, Wyatt H.* (whhartman@lbl.gov); Ye, Rongzhong; Horwath, William R.; Tringe, Susannah G	A Genomic Perspective on Stoichiometric Regulation of Soil Carbon Cycling
21	Hayes, Richard D.* (rdhayes@lbl.gov); Carlson, Joseph W.; Goodstein, David M.; Rokhsar, Daniel S.	Efficient Integration of Phytosome Population Diversity and Expression Data with JBrowse
22	Inskeep, William P.* ; Inskeep, Dylan J. (dilly@live.com); Jay, Zackary J.; Beam, Jacob P.; Dlakic, Mensur; Rusch, Douglas B.; Kozubal, Mark A.	Novel Microbial Lineages Endemic to Geothermal Iron-Oxide Mats Fill Important Gaps in the Evolutionary History of Archaea



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

23	<p>Jing, Beibei*; Mortimer, Jenny C. (jcmortimer@lbl.gov); Ishikawa, Toshiki; Lao, Jeemeng; Pidatala, Ramana; Anderbehan, Fekadu; Yu, Xiaolan; Baidoo, Edward; Kawai-Yamada, Maki; Li, Guotian; Ronald, Pamela; Dupree, Paul</p>	<p>Using Whole-Genome Sequencing to Identify the Components in GIPC-Related Plant Immunity Pathway</p>
24	<p>Kim, Peter W.* (pwkim@sandia.gov); Arlow, Dan; Palluk, Sebastian; Bector, Rathin; Kang, Justine; Hillson, Nathan; Singh, Anup; Keasling, Jay D.</p>	<p>Automated DNA Synthesis in a Microfluidic Chip</p>
25	<p>Kimbrel, Jeffrey* (kimbrel1@llnl.gov); Samo, Ty; Ligeti, Jorge; Thelen, Michael; Weber, Peter; Siccardi, Anthony; Lane, Todd; Mayali, Xavier</p>	<p>Isotope Tracing and Phylogenetic Composition of Simplified Bacterial Communities Conferring Growth and Biomass Enhancements to Biofuel-Producing Microalgae</p>
26	<p>Kuo, Alan J.* (akuo@lbl.gov); Riley, Robert; Mondo, Stephen J.; Haridas, Sajeet; Salamov, Asaf; Korzeniewski, Frank; Simmons, Blake; Baker, Scott; Andersen, Mikael; Grigoriev, Igor</p>	<p>Genomics of the First 100 Aspergilli</p>
27	<p>Lawrence, Jennifer E.* (jelawrence@berkeley.edu); Zhou, Lijie; Antell, Edmund; Keren, Ray; Yu, Ke; Alvarez-Cohen, Lisa</p>	<p>Nitrogen flows in an Autotrophic, Anaerobic Ammonium Oxidation (Anammox) Community</p>
28	<p>Levy, Asaf* (alevy@lbl.gov); Clingenpeel, Scott; Gonzalez, Isai S.; Paredes, Sur H.; Stillman, Kyra; Monteiro, Freddy; Alvarez, Bryan R.; Lundberg, Derek S.; Lu, Tse-Yuan; Sarah, Lebeis; Jin, Zhao; McDonald, Meredith; Feltcher, Meghan E., del Rio, Tijana G., Grant, Sarah R, Doty, Sharon L., Ley, Ruth E., Pelletier, Dale A., Tringe, Susannah G., Woyke, Tanja, Dangl, Jeffery L.</p>	<p>Genetic Determinants of Bacterial Adaptation to Plants</p>



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

29	Li, Guotian* (guotianli@lbl.gov); Jain, Rashmi; Chern, Mawsheng; Pham, Nikki; Martin, Joel; Wei, Tong; Schackwitz, Wendy; Lipzen, Anna; Duong, Phat; Poster Presentations Posters alphabetical by presenting author* Jones, Kyle; Jiang, Liangrong; Ruan, Deling; Bauer, Diane; Barry, Kerrie; Schmutz, Jeremy; Ronald, Pamela	The Sequence of 1504 Mutants in the Model Rice Variety Kitaake Facilitates Rapid Functional Genomic Studies
30	Liu, Lifeng* (lifeng.liu@lbl.gov); Lin, Junyan; Tolkunov, Denis; Singan, Vasanth; Blow, Matthew; Yuko, Yoshinaga; O'Malley, Ronan; Vogel, John P.	Epigenetics of cold acclimation and vernalization in <i>Brachypodium distachyon</i>
31	MacGregor, Barbara J.* (bmaccgreg@unc.edu); Flood, Beverly; Bailey, Jake; Kanke, Matthew	Multiplication Is Vexation: A Genomic Perspective on Cell Division and DNA Replication in the Large Sulfur Bacteria
32	Matheus Carnevali, Paula B.* (pmatheus@berkeley.edu); Williams, Kenneth H.; Dong, Wenming; Thomas, Brian C.; Hubbard, Susan; Banfield, Jillian F.	Genome-Resolved Metagenomic and Geochemical Analysis of East River Riparian Zone Soils Supports the 'Systems within Systems' Approach for Watershed Analysis
33	McKay, Luke J.* (mcgucas@gmail.com); Hatzenpichler, Roland; Fields, Matthew W.; Inskeep, William P	Methane Cycling by Novel Archaea in Yellowstone National Park Hot Springs
34	Montoya, Liliam A.* (liliam_m007@berkeley.edu); Catcheside, David; Ellison, Chris; Freitag, Michael; Gladieux, Pierre; Daskalov, Asen; Brem, Rachel; Schackwitz, Wendy; Hann-Soden, Christopher; Glass, Lousie N; Taylor, John	Interpopulation Mating to Associate the Phenotype of Growth at Low Temperature With Specific Genes in <i>Neurospora crassa</i> Populations
35	Mukherjee, Supratim* (supratimmukherjee@lbl.gov); Stamatis, Dimitrios; Bertsch, Jon; Ovchinnikova, Galina; Kyrpides, Nikos; Reddy T.B.K.	Genomes OnLine Database (GOLD): A Curated Catalogue of Genome and Metagenome Sequencing and Analysis Projects



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

36	Nowinski, Brent C.* (nowinski@uga.edu); Preston, Christina; Kiene, Ronald P.; Scholin, Christopher; Birch, James; Whitman, William B.; Moran, Mary Ann	Dimethylsulfoniopropionate Degradation in the Coastal Ocean: Gene- and Taxon-Centric Approaches
37	Perroud, Pierre-François* ; Haas, Fabian B. (fabian.haas@biologie.uni-marburg.de); Schmutz, Jeremy; Grimwood, Jane; Stacey, Gary; Sreedasyam, Avinash; Rensing, Stefan A.	DOE JGI Plant Flagship Gene Atlas: <i>Physcomitrella patens</i>
38	Redmond, Molly C.* (mcredmond@uncc.edu); Chan, Eric W.; Shiller, Alan M.; Kessler, John D.	Metagenomics of Methane-Oxidizing Mesocosms from the Gulf of Mexico and U.S. Atlantic Margin
39	Ruiz-Font, Angelica C.* (convenios22@hotmail.com); Melo-Perez, Flor M.; Betto-Sagahon, Janeli; Campos-Vazquez, Maria E.	Extremophile Microbial Bioprospecting for Biomass Production and Biorefinery
40	Samo, Ty* (samo1@llnl.gov); Kimbrel, Jeffrey; Nilson, Daniel J.; Siccardi, Anthony; Lane, Todd; Pett-Ridge, Jennifer; Weber, Peter K.; Mayali, Xavier	Enhanced Productivity of Biofuel-Producing Marine Microalgae Using Ecologically Engineered Bacteria—Examination Using Isotope Tracing and Marker Gene Sequencing
41	Santos-Medellin, Christian M.* (cmsantosm@ucdavis.edu); Liechty, Zachary; Edwards, Joseph; Nguyen, Bao; Sundaresan, Venkatesan	Drought Stress Alters the Structure of Microbial Communities Associated with Rice Roots
42	Shu, Shengqiang* (sqshu@lbl.gov); Herring, Robert; Jenkins, Jerry; Goodstein, David; Schmutz, Jeremy; Rokhsar, Daniel	JGI Plant Genome Re-Annotation Using NGS Sequences
43	Shulse, Christine N.* (cnshulse@lbl.gov); Chovatia, Mansi; Agosto, Carolyn; Wang, Gaoyan; Lei, Yan; Hamiton, Matthew; Deutsch, Samuel; Yoshikuni, Yasuo; Deutschbauer, Adam; Blow, Matthew J.	Discovery, Transfer, and Characterization of Novel Phytase Genes for Utilization of Recalcitrant Phosphate
44	Singer, Esther* (esinger@lbl.gov); Doud, Devin; Woyke, Tanja; Vogel, John	Assessing plant-microbe interactions at the molecular level



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

45	<p>Sreedasyam, Avinash*; Schmutz, Jeremy (jschmutz@hudsonalpha.org); Plott, Christopher; Hossain, Shakhawat; Qualls, Morgan; Jenkins, Jerry; Grimwood, Jane; Carlson, Joseph; Goodstein, David; Kennedy, Megan; Wang, Mei; Johnson, Jenifer; Sandor, Laura; Amirebrahimi, Mojgan; Zane, Matthew, Chris, Daum, Torres-Jerez, Ivone, Udvardi, Michael; Jawdy, Sara S.; Tang, Yuhong; Tuskan, Gerald A.; Juenger, Tom; Brutnell, Tom; Merchant, Sabeeha S.; Rensing, Stefan A.; Mullet, John, Mockler, Todd, Stacey, Gary, Jeremy, Schmutz</p>	<p>JGI Plant Gene Atlas: An Updateable Transcriptome Resource for JGI 'Flagship' Plants</p>
46	<p>Swift, Candice L.* (cswift@umail.ucsb.edu); O'Malley, Michelle A.; Louie, Katherine; Northen, Trent R.</p>	<p>Identifying and Characterizing the Secondary Metabolites of Anaerobic Fungi</p>
47	<p>Taneja, Jyoti* (jyotitaneja@berkeley.edu); Andrew, Liu; Wildermuth, Mary</p>	<p>JGI CSP #1657: Genome Sequencing of Arabidopsis thaliana Powdery Mildew Pathogen Golovinomyces orontii Isolate MGH1</p>
48	<p>Tsang, Karen S. W.* (kswtsang@hotmail.com); Wong, Chong Kim; Kwan, Hoi Shan</p>	<p>Draft Genome Sequence of the Pathogenic White-Rot Fungus Phellinus noxius OVT-YTM/97</p>
49	<p>Ul-Hasan, Sabah* (sul-hasan@ucmerced.edu); Bowers, Robert M.; Woyke, Tanja; Sistrom, Mark</p>	<p>Searching for Microbes in the Uncharted Venomous Territories of Marine Cone Snails</p>
50	<p>Vogel, John* (jpvogel@lbl.gov); Gordon, Sean; Moreira, Contreras; Des Marais, David L.; Burgess, Diane; Schackwitz, Wendy; Tyler, Ludmila; Martin, Joel; Woods, Daniel; Lipzen, Anna; Shu, Shengqiang; Phillips, Jeremy; Barry, Kerrie; Amasino, Richard; Caicedo, Ana; Mur, Luis; Freeling, Michael; Catalan, Pilar</p>	<p>The pan-genome of Brachypodium distachyon, capturing the full genetic complement of a plant species</p>



2017 JGI User Meeting

WEDNESDAY EVENING POSTER SESSION

March 22, 2017 – Joint Genome Institute

51	Waldo, Nicholas B.* (nbwaldo@uw.edu); Fadely, Ella C.; Ardissono, Robert J.; Gough, Heidi L.; Chistoserdova, Ludmila; Beck, David; Neumann, Rebecca B.	A Rhizosphere-Scale Investigation of Root Effects on Wetland Methane Dynamics
52	Walsh, David A.* (david.walsh@concordia.ca); Lovejoy, Connie	Metagenome-Assembled Genomes from the Beaufort Sea Reveals a Unique Arctic Ocean Microbiome
53	Wheeldon, Ian R.* (iwheeldon@engr.ucr.edu); Schwartz, Cory; Frogue, Keith; Shabbir-Hussain, Murtaza; Blenner, Mark A.	CRISPR-Cas9 Genome Editing and Gene Regulation Tools for Rapid Engineering of <i>Yarrowia lipolytica</i>
54	Xie, Yichun* (xieyichun5050@gmail.com); Chang, Jinhui; Kwan, Hoi Shan	RNA-Editing in Model Mushroom <i>Coprinopsis cinerea</i>
55	Zeiner, Carolyn A.* (zeiner@bu.edu); Siletti, Cheta E.; Talbot, Jennifer M	Melanin Production across Species: A Fungal Comparative Genomics Case Study
56	Zhang, Qingpeng* (qingpeng@lbl.gov); Rivers, Adam; Tringe, Susannah G.	ViCA: Identifying Highly Divergent Viruses Using Supervised Learning across the Homology-Composition Spectrum