

Posters alphabetical by first author. \*Presenting author

	<b>Authors</b>	<b>Title</b>
<b>1</b>	M.J. <b>BLOW*</b> (mjblow@lbl.gov), A.M. Deutschbauer, C.A. Hoover, M.N. Price, K.M. Wetmore, A.P. Arkin, and J. Bristow	A Functional Encyclopedia of Bacteria and Archaea
<b>2</b>	Alexander E. <b>BOYD*</b> (aebayd@lbl.gov), Christopher M. Sullivan, and Brett M. Tyler	Easy Terminal Alternative (ETA): An intuitive Web portal to simplify computational analysis, visualisation, and collaboration
<b>3</b>	Jason <b>CHIN*</b> (jchin@pacificbiosciences.com), Patrick Marks, David H. Alexander, Aaron Klammmer, Michael Brown, and Cheryl Heiner	Sequence consensus algorithms and hierarchical genome assembly process for effective <i>de novo</i> assembly with SMRT® sequencing
<b>4</b>	Scott <b>CLINGENPEEL*</b> (srclingenpeel@lbl.gov), Derek Lundberg, Tanja Woyke, Susannah Tringe, and Jeff Dangl	Investigating <i>Arabidopsis thaliana</i> root endophyte communities by single cell genomics
<b>5</b>	Devin <b>COLEMAN-DERR*</b> (DAColeman-Derr@lbl.gov), Stephen Gross, Tanja Woyke, Gretchen North, Laila Partida-Martinez, Kristen DeAngelis, Scott Clingenpeel, Susannah Tringe, and Axel Visel	Mining the <i>Agave</i> microbiome for adaptations to arid environments
<b>6</b>	Alex <b>COPELAND*</b> (accopeland@lbl.gov), George Vacek, Kirby Collins, Susannah Tringe, and Janet Jansson	Efficient assembly of Grand Challenge metagenome data sets on a hybrid-core architecture
<b>7</b>	Sam <b>DEUTSCH*</b> (sdeutsch@lbl.gov), Sarah Richardson, Angela Tarver, Matthew Hamilton, David Robinson, Sangeeta Nath, Matthew Bendall, Miranda Harmon-Smith, Lisa Simirenko, Nathan J. Hillson, and Jan-Fang Cheng* (jfcheng@lbl.gov)	DNA synthesis and assembly pipeline at the Joint Genome Institute
<b>8</b>	John <b>EID*</b> (jeid@pacificbiosciences.com), Paul Peluso, David Rank, Satwik Kamtekar, Erik Miller, Walter Lee, Phil Jiao, Colleen Cutcliffe, Paul Lundquist, Annette Grot, Michael Gandy, Jeremiah Hanes, Keith Bjornson, Lubomir Sebo, Louis Brogley, Regina Lam, Gene Shen, Honey Osuna, Anushweta Asthana, Arunashree Bhamidipati, Emilia Mollova, Alicia Yang, John Lyle, Joan Wilson, Kevin Travers, and Michael Phillips	Longer read length, higher throughput SMRT® sequencing
<b>9</b>	Celeste <b>GLAZER*</b> (cglazer@labcyte.com), Joe Barco, Brent Eaton, and Sammy Datwani	High throughput miniaturized PCR using the Echo® liquid handler
<b>10</b>	Igor <b>GRIGORIEV*</b> (ivgrigoriev@lbl.gov)	Fungal Genomics for Energy and Environment
<b>11</b>	Stephen M. <b>GROSS*</b> (smgross@lbl.gov), Jeffrey A. Martin, June Simpson, Zhong Wang, and Axel Visel	Transcriptome analysis of drought tolerant CAM plants, <i>Agave deserti</i> and <i>A. tequilana</i>
<b>12</b>	Jenny <b>GU*</b> (jgu@pacificbiosciences.com), Lawrence Hon, Jason Chin, David Alexander, Aaron Klammmer	Towards Finished Genome Assemblies using SMRT® Sequencing
<b>13</b>	Cheryl <b>HEINER*</b> (cheiner@pacificbiosciences.com), Primo Baybayan, Susana Wang, Meredith Ashby, Yan Guo, and Jason Underwood	Greater than 10 kb read lengths routine when sequencing with Pacific Biosciences' XL release
<b>14</b>	Cindi A. <b>HOOVER*</b> (cahoover@lbl.gov), Kevin S. Eng, Hui Sun, Jeff Froula, and Feng Chen	Assessment of Nextera™ long mate-pair libraries: A rapid, low-input method for mate-pair library construction yields improved assemblies
<b>15</b>	K. <b>LaButti*</b> (klabutti@lbl.gov), A. Copeland, A. Clum, and H. Sun	Genome assembly improvement with Pacific Biosciences RS long-read sequencing technology
<b>16</b>	Dominique <b>LOQUÉ*</b> (dloque@lbl.gov)	Use of synthetic biology to redesign plant secondary cell wall deposition
<b>17</b>	Khai <b>LUONG*</b> (kluong@pacificbiosciences.com), Tyson A. Clark, Matthew Boitano, Yi Song, Stephen W. Turner, Jonas Korlach, Lukas Chavez, Patricia J. Pukkila, Yun Huang, Virginia K. Hench, William Pastor, Lakshminarayan M. Iyer, Suneet Agarwal, L. Aravind Iyer, and Anjana Rao	Single molecule, real-time sequencing for base modification detection in eukaryotic organisms: <i>Coprinopsis cinerea</i>
<b>18</b>	Yujie <b>MEN*</b> (menyj@berkeley.edu), Julien Tremblay, Emmanuel Prestat, Jacob Baelum, Susannah G. Tringe, Janet R. Jansson, and Lisa Alvarez-Cohen	Metagenomic and metatranscriptomic analysis on TCE-dechlorinating microbial communities enriched under different exogenous cobalamin conditions

<b>19</b>	Supratim <b>MUKHERJEE*</b> (supratimmukherjee@lbl.gov), Neha Varghese* (njvarghese@lbl.gov), Aydin Buluc, Nikos C. Kyrpides, Amrita Pati, and Konstantinos Mavromatis	Pangenome: A new perspective to study microbial genomes
<b>20</b>	Robin A. <b>OHM*</b> (raohm@lbl.gov), Nicolas Feau, Bernard Henrissat, Conrad L. Schoch, Benjamin A. Horwitz, Kerrie W. Barry, Bradford J. Condon, Alex C. Copeland, Braham Dhillon, Fabian Glaser, Cedar N. Hesse, Idit Kosti, Kurt LaButti, Erika A. Lindquist, Susan Lucas, Asaf A. Salamov, Rosie E. Bradshaw, Lynda Ciuffetti, Richard C. Hamelin, Gert H. J. Kema, Christopher Lawrence, James A. Scott, Joseph W. Spatafora, B. Gillian Turgeon, Pierre J.G.M. de Wit, Shaobin Zhong, Stephen B. Goodwin, and Igor V. Grigoriev	Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen <i>Dothideomycetes</i>
<b>21</b>	Robin A. <b>OHM*</b> (raohm@lbl.gov), Martin Tegelaar, Bernard Henrissat, Heather M. Brewer, Samuel O. Purvine, Scott Baker, Han A. B. Wösten, Igor V. Grigoriev, and Luis G. Lugones	Functional genomics of lignocellulose degradation in the Basidiomycete white rot <i>Schizophyllum commune</i>
<b>22</b>	Ze <b>PENG*</b> (zpeng@lbl.gov), Nandita Nath, Andrew Tritt, Shoudan Liang, James Han, Chia-Lin Wei, Len Pennacchio, and Feng Chen	Comparison of three Cre-loxP based paired-end library construction methods
<b>23</b>	Emmanuel <b>PRESTAT*</b> (EPrestat@lbl.gov), Maude M. David, Konstantinos Mavromatis, and Janet R. Jansson	A custom database for functional annotation of soil omics datasets using Hidden Markov Models
<b>24</b>	Robert <b>RILEY*</b> (rwiley@lbl.gov), Asaf Salamov, Robert Otilar, Kirsten Fagnan, Bastien Boussau, Daren Brown, Bernard Henrissat, Anthony Levasseur, Benjamin Held, Laszlo Nagy, Dimitris Floudas, Emmanuelle Morin, Gerard Manning, Scott Baker, Francis Martin, Robert Blanchette, David Hibbett, and Igor V. Grigoriev	Comparative analysis of 35 basidiomycete genomes reveals diversity and uniqueness of the phylum
<b>25</b>	Christian <b>RINKE*</b> (crinke@lbl.gov), Patrick Schwientek, Alexander Sczyrba, Natalia N. Ivanova, Iain J. Anderson, Jan-Fang Cheng, Aaron Darling, Stephanie Malfatti, Brandon K. Swan, Esther A. Gies, Jeremy A. Dodsworth, Brian P. Hedlund, George Tsiamis, Stefan M. Sievert, Wen-Tso Liu, Jonathan A. Eisen, Steven Hallam, Nikos C. Kyrpides, Ramunas Stepanauskas, Edward M. Rubin, Philip Hugenholtz & Tanja Woyke	Single-Cell genomics at the JGI – Illuminating microbial dark matter
<b>26</b>	A. <b>SALAMOV*</b> (aasalamov@lbl.gov), R. Riley, A. Kuo, and I. Grigoriev	Comparative reannotation of 21 <i>Aspergillus</i> genomes
<b>27</b>	Wendy <b>SCHACKWITZ*</b> (wsschackwitz@lbl.gov), Joel Martin, Anna Lipzen, Len Pennacchio, Gerald Tuskan	Phasing variants in poplar trees using a hybrid of short and long read technologies
<b>28</b>	Kimmen <b>SJÖLANDER*</b> (kimmen@berkeley.edu), Cyrus Afrasiabi, Bushra Samad, and Dave Dineen	The PhyloFacts FAT-CAT Web server: Functional (and taxonomic) annotation of (meta)genomes across the Tree of Life
<b>29</b>	B. <b>STENUIT*</b> (bstenuit@berkeley.edu), J. Tremblay, X. Mao, Y. Men, S.G. Tringe, and L. Alvarez-Cohen	Molecular systems synecology of TCE-dechlorinating microbial communities using stable isotope probing combined with Illumina 16S rRNA-targeted and shotgun sequencing
<b>30</b>	Kankshita <b>SWAMINATHAN*</b> (kank@illinois.edu), Therese Mitros* (tmitros@gmail.com), Adam Barling, Won Byoung Chae, Brandon T. James, Jessica Kirkpatrick, Liang Xie, Katarzyna Glowacka, Magdy Alabady, Stanislaw Jezowski, John A. Juvik, Matthew Hudson, Daniel S. Rokhsar, and Stephen P. Moose	Genome organization and gene expression in <i>Miscanthus</i>
<b>31</b>	Susanna <b>THEROUX*</b> (stheroux@lbl.gov), Yongsong Huang, and Linda Amaral-Zettler	Diversity and ecology of Lacustrine haptophyte algae in Lake George, ND, USA: Implications for paleothermometry
<b>32</b>	Julien <b>TREMBLAY*</b> (jtremblay@lbl.gov), Kanwar Singh, Alison Fern, Edward S. Kirton, Feng Chen, Shaomei He, Tanja Woyke, Janey Lee, Robin A. Ohm, Matthias Hess, and Susannah G. Tringe	Evaluation of hypervariable 16S and ITS tag sequencing on Illumina MiSeq
<b>33</b>	Elizabeth <b>TSENG*</b> (etseng@pacificbiosciences.com) and Jason G. Underwood	Full length cDNA sequencing on the PacBio® RS
<b>34</b>	Dongying <b>WU*</b> (DYWu@lbl.gov) and Jonathan A. Eisen	Phylogenetic tree based taxonomic classification
<b>35</b>	Zhiying <b>ZHAO*</b> (zyzhao@lbl.gov), Yu-Chih Tsai, Alicia Clum, Katherine Munson, Chris Daum, Stephen W. Turner, Jonas Korfach, Len A. Pennacchio, and Feng Chen	PacBio only assembly with low genomic DNA input