

****All Posters Need to be Removed by 1:30pm Friday - Posters Left Will be Recycled**

**13th Annual DOE Joint Genome Institute
Genomics of Energy & Environment Meeting
Poster Sessions**

Wednesday, March 14, 2018 / 6:00pm - 9:00pm Continental 1-3 & 7-9

Thursday, March 15, 2018 / 12:00pm - 1:30pm Continental 1-3 & 7-9

	METAGENOME	CONTINENTAL 1 - 3
1	ALTEIO , Lauren laiteio@umass.edu	Broadening the Scope of Soil Biodiversity Using Mini-Metagenomics
2	BARNETT , Samuel seb369@cornell.edu	Exploring microbial metabolic capacity and its role in soil carbon cycling
3	BELLER , Harry hrbeller@lbl.gov	Omics-enabled discovery from microbial communities of a novel glycy radical enzyme enabling bio-based toluene production
4	BEMAN , Michael mbeman@ucmerced.edu	Metagenomics of methane production and consumption in high elevation lakes of the Sierra Nevada, California
5	BERRY , Timothy tdberry@wisc.edu	Pyrogenic Organic Matter Effects on Soil Microbial Communities and Carbon Cycling: A Metagenomic Approach
6	CHINIQUY , Dawn dmchinquy@lbl.gov	Diverse sorghum microbiome discovery and characterization in nitrogen- and water-limited soils for improved biomass production
7	CHOI , Jinlyung jinchoi@iastate.edu	Microbial drivers of cellulose decomposition in agricultural soils: linking genes to carbon metabolism
8	COLATRIANO , David d_colat@live.concordia.ca	Genomic evidence for the degradation of terrestrial organic matter by Arctic Ocean bacteria
9	CHOI , Jinlyung jinchoi@iastate.edu	Microbial drivers of cellulose decomposition in agricultural soils: linking genes to carbon metabolism
10	SINGER , Esther esinger@lbl.gov	Seasonality affects switchgrass microbiomes more than planting site
11	REJI , Linta linta@stanford.edu	Exploring thaumarchaeal ecotype diversification in the coastal ocean using metagenomic, metatranscriptomic, and modeling approaches
12	FRANK , Carolin cfrank3@ucmerced.edu	Nitrogen fixation by the foliar conifer microbiome
13	FREEDMAN , Zachary zachary.freedman@mail.wvu.edu	Mine reclamation using bioenergy crops: An investigation into plant-microbe interactions of switchgrass (<i>Panicum virgatum</i>)
14	GARCIA COSTAS , Amaya garciaostas.amaya@gmail.com	The dark side of the mushroom spring microbial mat: life in the shadow of phototrophs. Ecophysiological patterns deciphered through diel metatranscriptomic analyses
15	KIM , DaeHyun danielkim617@kaist.ac.kr	Microbial community analyses of produced waters from high-temperature oil reservoirs reveal extraordinary similarity between geographically distant oil reservoirs: implications in microbial enhanced oil recovery

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16	UL-HASAN , Sabah cnidariancubozoa@gmail.com	Small-scale coastal microbial ecosystem patterns: Putting Puerto Nuevo, Baja California on the microbial biodiversity map
17	LEMOS , Leandro llemos@usp.br	Assembly of new alternative state of Archaea microbiota associated with methane production in Amazon soils
18	LIN , Jonathan johlin@ucdavis.edu	Contribution of ureolytic bacteria to nitrogen recycling in the termite gut
19	MATHEUS CARNEVALI , Paula pmatheus@berkeley.edu	Microbial community structure of meander-associated riparian zone topsoil resembles that of a hillslope floodplain site, but differs from deeper samples
20	MAYALI , Xavier mayali1@llnl.gov	Nanoscale Stable Isotope Tracing to Investigate Interactions between Bacteria and Biofuel-producing Algae
21	NOBU , Masaru ranmei2@illinois.edu	Metabolic partitioning among microbial dark matter across anaerobic digesters
22	NAUGHTON , Hannah hnaught@stanford.edu	Microbial metabolic constraints on carbon cycling in upland soils
23	NOGUERA , Daniel noguera@engr.wisc.edu	Production of medium-chain fatty acids from the residues of lignocellulosic biomass biorefining
24	NOVOTNIK , Breda breda.novotnik@ucalgary.ca	Biological, metal dependent oxidation of hydrocarbons, for generation of electricity.
25	BALDRIAN , Petr baldrian@biomed.cas.cz	Transcription profiles of dominant microbes in the forest topsoil show distinct activity, ecology and seasonality
26	PODOWSKI , Justin jpodowski@uchicago.edu	Metabolic and Phylogenetic Diversity across the Laurentian Great Lakes
27	POLACCO , Ben bpolacco@gmail.com	Profiling the Enzymatic Capacity of Metagenomes
28	PYLRO , Victor victor.pylro@gmail.com	Enrichment of methanogenic archaea in Amazonian soils under land use changes
29	RASMUSSEN , Anna arasmuss@stanford.edu	Spatiotemporal Characterization of the San Francisco Estuary Bottom Water Microbiome
30	ROITMAN , Sofia sofiaroitman@gmail.com	Characterization of microbial communities between healthy and diseased Caribbean corals
31	ROSADO , Alexandre asrosado@micro.ufrj.br	Chasing novel Carbon Assimilation and Nitrogen Fixation Systems in a Thermophilic and Autotrophic Bacterial Consortium
32	HEALEY , Adam ahealey@hudsonalpha.org	The Sphagnum Microbiome: Describing the seasonal variations between Sphagnum and their symbiotic bacteria
33	SORENSEN , Patrick posorensen@lbl.gov	The synchronization of microbial and plant phenology in a mountainous watershed and its importance for nutrient retention under changing hydrologic regimes
34	STEVENS , Sarah	Evolutionary Genomics of Freshwater Lake Bacterial Populations

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	sstevens2@wisc.edu	
35	SUGDEN, Scott ssugden@ualberta.ca	Exploring the interplay between diet, gut microbiome, and behavior in urban-exploiting coyotes
36	TEACHEY, Morgan mteachey@uga.edu	Pelagic bacterial community dynamics in a temperate, urban stream
37	TOM, Lauren ltom@lbl.gov	Alteration of lignin biosynthetic pathways in sorghum enhances its deconstruction by adapted microbial consortia
38	JUNGBLUTH, Sean sjungbluth@lbl.gov	Illuminating global microbial diversity metabolic potential with thousands of metagenome-assembled genomes
39	COURADEAU, Estelle ecouradeau@lbl.gov	Probing metabolically active cells in soils using BONCAT
40	WANG, Kai kwang12@kent.edu	Contribution of Terrestrial Organic Carbon to the Sediment Bacterial Composition in Two China Marginal Seas
41	WANG, Shi ShiWang@lbl.gov	Microbial phosphorous mobilization strategies across a natural nutrient limitation gradient
42	WILHELM, Roland rwilhelm@cornell.edu	Evaluating the Metabolic Dependencies of a Cellulose-degrading Soil Consortium with Deep Metagenomic Sequencing and Stable Isotope Probing
43	WU, Dongying dongyingwu@lbl.gov	A reference database for metagenome-derived SSU rRNA genes
44	HARTMAN, Wyatt whhartman@lbl.gov	Multiple microbial guilds mediate soil methane cycling along a wetland salinity gradient spanning the San Francisco Bay – Delta region
45	CARDARELLI, Emily ecardare@stanford.edu	Historic hydrologic perturbations support niche partitioning and the occurrence of new phyla in the terrestrial subsurface
46	GOMEZ, Oscar ogomez@sdsu.edu	Desert Survivors: A Tale of Plants and Methanotrophs
47	FERNANDEZ BAYO, Jesus jdfbayo@ucdavis.edu	Methane production during thermophilic anaerobic digestion of green and food wastes and the impact on the microbial structure of the digestates
48	HESS, Nancy nancy.hess@pnnl.gov	Inference of microbial metabolic pathways from soil organic matter
49	DYKES, Gretchen gdykes@udel.edu	Silicon addition to rice paddy soils impacts arsenic biogeochemical cycling: implications for global food security.
50	LEBEIS, Sarah slebeis@utk.edu	Identifying mechanisms of duckweed protection from abiotic stress using PAM fluorescence image screening
51	BLANC-MATHIEU, Romain roblanc@kuicr.kyoto-u.ac.jp	Uncovering the diversity of marine large DNA viruses infecting protists and fingering out the ones involved in carbon export.

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52	DALY, Rebecca daly.130@osu.edu	Top-down and bottom-up viral controls on Halanaerobium populations in the deep biosphere
53	DE LA HIGUERA, Ignacio ide@pdx.edu	From the Virome Back to the Environment: Understanding the Evolution and Biology of Cruciviruses
54	GULINO, Kristen kmg549@nyu.edu	Examining phage-host interactions in waste water
55	HARRISON, Amelia aoh@udel.edu	Ribonucleotide reductase as a marker for marine viroplankton communities
56	LANGENFELD, Kathryn klangenf@umich.edu	Quantitative Metagenomics to Determine the Role of Transduction in ARG Dissemination at Wastewater Treatment Plants
57	TRUBL, Gareth gtrubl@email.arizona.edu	Characterizing the soil virosphere: a comparison of viral and bulk soil metagenomes
58	AMGARTEN, Deyvid deyvidamgarten@gmail.com	MARVEL: Assessing phage genomes from metagenomics bins
59	BERG, Maureen mberg@lbl.gov	High-throughput methods to examine viral-host linkages
60	MORELLA, Norma morella@berkeley.edu	The impact of bacteriophages on phyllosphere bacterial abundance and composition
61	KALLIES, René rene.kallies@ufz.de	Preliminary results of the viral metagenome along an aquifer transect – comparison of three different viral DNA enrichment techniques
62	DŽUNKOVÁ, Mária p.hugenholtz@uq.edu.au	Phylogeny-based viral classification and single cell viral tagging
	PLANT	CONTINENTAL 1 - 3
63	AITKEN, Karen karen.aitken@csiro.au	Whole genome sequencing of sugarcane: building off the foundation of the single haplotype path
64	BARTLEY, Laura lbartley@ou.edu	A Novel Rice Genome-scale Network Reveals Transcriptional Regulators of Grass Cell Wall Synthesis
65	CATALAN, Pilar pcatalan@unizar.es	Integrative Genomic Characterization of the Brachypodium Polyploid Model to Unravel Bases of Success of Polyploidy in Flowering Plants
66	WING, Rod rwing@ag.arizona.edu	DOE JGI Emerging Technologies Opportunity Program – Plant Genomics Capabilities and Research & Development

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67	DONG, Chen dongchenchen@gmail.com	Deep sequencing and transcriptome analysis of guayule plant tissues reveals rubber biosynthesis pathways' response to drought stress
68	NIYOGI, Kris niyogi@berkeley.edu	Functional genomics of photosynthesis in Chlamydomonas, JGI's flagship alga PLANT/ALGAE
69	HUFFAKER, Alisa ahuffaker@ucsd.edu	Examination of metabolic traits and underlying genes in drought tolerant crops
70	JENKINS, Jerry jjenkins@hudsonalpha.org	Generation of High-Quality de novo Plant Genome Assemblies with PACBIO
71	LOVELL, John jlovell@hudsonalpha.org	Comparative and quantitative genomics in Panicum hallii and other C4 grasses
72	MAZAHERI, Mona mmazaheri@wisc.edu	New insights into the maize pan-genome and early flowering syndrome using genome-wide RNA-Seq analysis of an expanded diversity panel
73	OSCAR, Michelle arland@post.bgu.ac.il	Explaining salt tolerance in the tropical seagrass, Halophila stipulacea: A combined physiology, transcriptomic and metabolomic profiling approach
74	PINGAULT, Lise lise.pingault@ou.edu	Use of a single cell type model, the root hair cell, to advance our understanding of the soybean and sorghum transcriptomic and epigenomic responses to various environmental stresses
75	SREEDASYAM, Avinash asreedasyam@hudsonalpha.org	JGI Plant Gene Atlas: Long noncoding RNA landscape of JGI 'Flagship' Plants
76	YANG, Xiaohan yangx@ornl.gov	Establishing transcriptomic and genomic resources for crassulacean acid metabolism (CAM) species Kalanchoë fedtschenkoi and Agave tequilana
77	GREENWOLD, Matthew mjgreenwold@gmail.com	Unlocking the Photosynthetic and Genetic Diversity of Cryptophyte Algae through Whole-Genome Sequencing of a Diverse Assemblage of Species
78	RUFFING, Anne aruffin@sandia.gov	Expanding the Genetic Toolbox for Nannochloropsis Species
79	VALENZUELA, Jacob jvalenzu@systemsbiology.org	Genome-wide analysis of chromatin accessibility and miRNA-mediated transcriptional regulation dynamics of lipid accumulation in Chlamydomonas reinhardtii
80	BROWNE, Daniel dbrowne.up@gmail.com	Systems analyses of metabolism and physiology in the oil-producing green alga Botryococcus braunii
81	BEDRE, Renesh renesh.bedre@agnet.tamu.edu	A gene atlas of diverse grass-microbe interactions in Brachypodium and Setaria
82	FISHER, Brian bffisher@uchicago.edu	Genome Mining for New Halogenase Biocatalysts

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83	CARTWRIGHT , Amy acartwright@lbl.gov	A Genome-wide Sequence-indexed Collection of Grass Mutants
	SYNTHESIS	CONTINENTAL 7 - 9
84	GUAY , Lisa M. guayl@mit.edu	Assembly, screening, and functional characterization of glucaric acid pathway enzymes in model organisms E. coli and S. cerevisiae
85	OBERORTNER , Ernst eoberortner@lbl.gov	The Operon Refactoring and Construction Assistant (ORCA): An integrated workflow for refactoring biosynthetic gene clusters
86	RUIZ-FONT , Angelica convenios22@hotmail.com	Selection of microbial hosts for small hydrocarbons production and potential commodity chemicals
87	SKYRUD , Will skyrud@berkeley.edu	Combinatorial heterologous expression and pathway engineering of the neoantimycin depsipeptides
88	LIN , Yu-Ju superolulu@gmail.com	Constructing a Cellulosic Yeast Host with an Efficient Cellulase Cocktail
89	MARIMUTHU , Anandharaj anandharaj49@gmail.com	Engineering the Clostridium thermocellum scaffoldin protein along with dockerin fused fungal cellulases into Kluyveromyces marxianus genome for Consolidated Bioprocessing
90	PROTZKO , Ryan rprotzko@berkeley.edu	Identification of novel D-altronate dehydratases in the enolase superfamily enabling pectin utilization in S. cerevisiae
91	BLAKE-HEDGES , Jacquelyn jblakehedges@lbl.gov	Identifying and applying design rules to engineer polyketide synthases for production of biofuels and bioproducts

	FUNGAL	CONTINENTAL 7 - 9
92	AVERILL , Colin caverill@bu.edu	Scaling molecular mechanisms of mycorrhizal-decomposer interactions to emergent ecosystem carbon balance
93	BREM , Rachel rachel_brem@yahoo.com	The polygenic basis of an ancient divergence in yeast thermotolerance
94	CALHOUN , Sara secalhoun@lbl.gov	Genome-scale investigation of metabolism and regulation in filamentous fungus Neurospora crassa
95	CATCHESIDE , David David.Catcheside@flinders.edu.au	Acquisition of the truffle-like habit by basidiomycete macrofungi CSP1956.
96	DEL CERRO , Carlos carlos.delcerro@nrel.gov	Systematic identification of gene deletions that decrease barriers to cell lysis in Saccharomyces cerevisiae

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97	CHENTHAMARA , Komal komal.chenthamara@tuwien.ac.at	Decoding the expanded Ankyrin-Repeat gene family in Trichoderma
98	DEANER , Matt mhdeaner@gmail.com	Systematic Testing of Gene Sensitivities in Yeast via an sgRNA Library Approach
99	GABRIEL , Raphael raphaelgabriel@lbl.gov	Unraveling glycoside hydrolase induction in the thermophilic biomass-deconstructing fungus Thermoascus aurantiacus
100	GARRE , Victoriano vgarre@um.es	Exploring the role of DNA methylation in biofuel production, environmental sensing and development in basal fungi
101	AHRENDT , Steven sahrendt0@lbl.gov	Leveraging single-cell genomics to expand the Fungal Tree of Life
102	LOMAS , Johnathan jslomas@ucdavis.edu	CAZymes from Anaerobic Fungi - The Missing Link of Efficient Biomass Degradation?
103	HUBERMAN , Lori huberman@berkeley.edu	Transcriptional profiling of Neurospora crassa reveals secrets of plant cell wall degradation by filamentous fungi
104	KOMINEK , Jacek jkominek@wisc.edu	Eukaryotic acquisition of a bacterial operon identified through comprehensive comparative genomics in the yeast subphylum
105	KRAUSE , David dkrause2@wisc.edu	Genomic investigations of yeast species with biofuel-relevant traits
106	MONDO , Stephen sjmondo@lbl.gov	Evolutionary transitions in fungal epigenomics
107	PEAY , Kabir kpeay@stanford.edu	Coprhilous fungi as a model for community genomics
108	CARVER , Akiko aacarver@berkeley.edu	Comparative Genomic Analyses of Four Pyrophilous Fungi FUNGAL
109	PENNERMAN , Kayla k.pennerm@rutgers.edu	Genomic and transcriptomic analyses of atoxigenic Aspergillus flavus WRRL 1519
110	ROJAS , Alejandro alejo.rojas@duke.edu	Dissecting the compatibility and diversity of the mycobiome of Populus trichocarpa
111	SALVACHUA , Davinia davinia.salvachua@nrel.gov	Synergy between white-rot fungal enzymes and aromatic-catabolizing bacteria during lignin decay
112	TANEJA , Jyoti jyotitaneja@berkeley.edu	JGI CSP #1657: Genome of Arabidopsis thaliana powdery mildew pathogen Golovinomyces orontii isolate MGH1
113	NGUYEN , Nhu H. fungirv@gmail.com	A genome atlas of the ectomycorrhizal genus Suillus: Phylogenetic diversity and population genomics of a keystone guild of symbiotic forest fungi
114	WARD , Christopher ward56@llnl.gov	Towards an integrative understanding of chytrid parasitism and its drivers in mass algal culture
115	ZIMMERMAN , Naupaka nzimmerman@usfca.edu	Mechanisms of Interaction in the Foliar Fungal Microbiome of Populus trichocarpa

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116	KUO, Alan akuo@lbl.gov	Gene families associated with the lichen lifestyle
117	BROWN, Jennifer jenniferbrown@umail.ucsb.edu	Engineering stable anaerobic consortia by understanding the genomic basis for syntrophic interactions
118	HARIDAS, Sajeet sharidas@lbl.gov	Dothideomycetes Genomics 101: Evolution and Adaptation

	MICROBIAL	CONTINENTAL 7 - 9
119	BRUCKBAUER, Steven steven.bruckbauer@gmail.com	Mechanisms of Experimentally-Evolved Ionizing Radiation Resistance in an E. coli Population after 50 Rounds of Selection
120	CHEWNING SLOAN, Sarah Stuart jgy618@vols.utk.edu	In soil and in silico: Outlining Streptomyces' ability to shape the plant root microbiome
121	COLLINS, David collins.david.andrew@gmail.com	Dissection of methanotrophy: a systems level approach in M. alcaliphilum 20Z
122	COX, Michael cox@biochem.wisc.edu	Ionizing Radiation Resistance in Experimentally Evolved Escherichia coli Populations
123	GILBERT, Sarah seg163@scarletmail.rutgers.edu	Characterization of Auxin Producing Bacteria Suggests Coevolution between Duckweed and Associated Endophytes
124	GRIEB, Anissa agrieb@mpi-bremen.de	Targeted sorting and genomic characterization of microbial clades using HCR-FISH and FACS
125	HEMPEL, Priscilla hempel@udel.edu	Cryptic Light-Enhanced Growth in Heterotrophic Bacteria
126	JARETT, Jessica jkjarett@lbl.gov	Single cell genomics of Nanoarchaeota and co-sorted, attached cells suggests rapid evolution and novel putative host associations
127	KIM, Kyoung Heon khekim03@gmail.com	Global profiling of metabolic response of a marine bacterium to 3,6-anhydro-L-galactose, a rare sugar from red macroalgae
128	KIMBREL, Jeffrey kimbrel1@llnl.gov	Combining multiple functional annotation tools increases completeness of metabolic annotation
129	LOWE-POWER, Tiffany tiff.lowe@gmail.com	Revisiting the acyl-homoserine lactone quorum sensing system in the bacterial wilt pathogen Ralstonia solanacearum.
130	SALAS-GONZALEZ, Isai isai@email.unc.edu	Untangling host-microbe and microbe-microbe interactions in plant-associated bacteria using genome-scale positive selection profiling
131	TOLAR, Bradley btolar1@stanford.edu	Impact of a changing environment on growth and transcription of a low-salinity ammonia-oxidizing thaumarchaeote

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132	FLOYD, James james.floyd@ou.edu	Linking Microbiological Contamination to Biodiesel Degradation and Increased Corrosion Rates
133	AVILA, Viridiana vxa146@psu.edu	Coral holobiont dynamics with distinctive gene expression profiles and bacterial communities are associated to heat tolerance in Caribbean coral species
134	DEANGELIS, Kristen deangelis@microbio.umass.edu	Truth and (E. co)lies: expanding knowledge of genotype-phenotype linkages beyond the usual suspects
135	BOEUF, Dominique dboeuf@hawaii.edu	Analyses of bacterioplankton single cell amplified genomes (SAG) from the model Hawaii Ocean Time-series (HOT) site, Station ALOHA.
136	GILMORE, Sean SeanGilmore@umail.ucsb.edu	Selective enrichment of rumen microbial consortia enables rapid conversion of biomass
137	GRETTEMBERGER, Christen christygrettenberger@gmail.com	A new genus transitional between non-phototrophic Melainabacteria and crown group Cyanobacteria
138	LEVDOKYMENKO, Kateryna ocampo.jewel@gmail.com	Engineering enzyme networks for biomass deconstruction in synthetic microbial communities
139	LEVY, Asaf alevy@lbl.gov	Genomic features of bacterial adaptation to plants
140	LYMPEROPOULOU, Despoina dlympero@berkeley.edu	Determining the relative importance of immigration and emigration in the composition of epiphytic microbial communities in an agro-ecological context.
141	HUANG, Laibin w.martenshabbena@ufl.edu	Biogeochemistry of carbon and nitrogen cycling in subsiding subtropical soils
142	MCDANIEL, Elizabeth emcdaniel@wisc.edu	Comparative Genomics of Microbial Methylmercury Production
143	MOCK, Thomas t.mock@uea.ac.uk	Temperature drives the diversity of co-occurrence networks between micro-eukaryotes and prokaryotes in the surface ocean
144	MOREIRA, Julio jfornazier@usp.br	Host species identity and seasonality drive structure of the phyllosphere bacterial community in Amazon forest trees
145	MORRISON, Eric eric.morrison@uci.edu	Investigation of diel variation in microbial decomposition processes
146	NORTON, Jeanette jeanette.norton@usu.edu	Diversity in the functional genes encoding ammonification and mineralization of nitrogen in agricultural soils
147	PAYET, Jerome jerome.payet@gmail.com	Decoding metagenomic and metatranscriptomic signals of microbial carbon transformations in major U.S. rivers
148	PEDRINHO, Alexandre alpedrinho@usp.br	Land use change alters the denitrification process in the Amazon Rainforest

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149	MUSHINSKI, Ryan drusch@indiana.edu	Ammonia-oxidizing archaea are the dominate nitrifiers in two Midwestern (USA) forest types, but do not contribute to nitric oxide production
150	SAYRE, Jordan Jmsayre@ucdavis.edu	Dairy manure increases the abundance of methanogenic microbial communities in forage field soils
151	BUCHAN, Alison abuchan@utk.edu	Geo-metabolomics of a saltmarsh: Combining in situ, bulk, genomic, transcriptomic, and DOMEomic data streams to understand microbial transformations of terrestrially derived organic matter
152	KLEIN, Andrew andrewpklein@gmail.com	Synthetic bacterial communities to define mechanisms of root microbiome function
153	FRANCOEUR, Charlotte francoeur@wisc.edu	Microbial tolerance of plant defense compounds in the fungus-farming ant system
154	DIAZ-MUNOZ, Samuel samdiazmunoz@ucdavis.edu	Viral coinfection is shaped by host ecology and virus-virus interactions across diverse microbial taxa and environments
155	ADLER, Benjamin ba14@berkeley.edu	A High-Throughput Genetics Approach Reveals Underlying Complexity of Salmonella Phage-Host Interactions
156	DOVE, Nicholas ndove@lbl.gov	Soil microbial ecology of the Sierra Nevada: predictions for a warmer and fiery future
157	FRITTS, Ryan rkfritts@umail.iu.edu	Evolution of mutualistic cross-feeding in a synthetic bacterial coculture
	OTHER	CONTINENTAL 7 - 9
158	SUTER, Bernhard suter@nextinteractions.com	Next-Generation Sequencing for Revealing Binary Protein–Protein Interactions
159	CONG, Qian congqian1986@gmail.com	From metagenomic data to protein structures and beyond
160	COTTINGHAM, Bob cottinghamrw@ornl.gov	Learning to use KBase to accelerate your research
161	SHAKYA, Migun migun@lanl.gov	From Raw Reads to Trees: Whole Genome Single Nucleotide Polymorphisms Phylogenetics Across the Tree of Life
162	BROWN, Keith kbrown@igenomx.com	RipTide™ Ultra High-Throughput Rapid DNA Library Preparation for Next Generation Sequencing

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163	SWIFT, Joel joel.swift@slu.edu	Multifaceted DNA metabarcoding: validation of a non-invasive, next-generation approach to studying bat populations
164	BINGOL, Kerem kerem.bingol@pnnl.gov	Structure Elucidation of Unknown Metabolites in Metabolomics by Combined NMR and MS/MS Prediction
165	BUSHNELL, Brian bbushnell@lbl.gov	BBSketch - Estimate the Composition of your library in 2 seconds
166	CAMPBELL, Ashley Campbell87@llnl.gov	TBD

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