

Poster Session II: October 18, 2022  
 Secret Ingredient, Microbial Chatter & Pipe Dreams

Control Number	Poster Board No.	Presentation Start	Presentation End	Duration	Title	Author Block
<a href="#">2022-A-49-NGS</a>	101	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Antimicrobial resistance trends among <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> at Ethiopian Public Health Institute, Addis Ababa, Ethiopia: Retrospective analysis (2017-2021)	<b>A. Abdeta</b> , G. Guma, A. Negeri, S. Fentaw, D. Beyene; Ethiopian Public Health Institute, Addis Ababa, ETHIOPIA.
<a href="#">2022-A-47-NGS</a>	102	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Microbial Community Distribution and Core Microbiome in Graded Buruli Ulcer and Chronic Tropical Wounds	<b>M. Frimpong</b> <sup>1</sup> , A. Kreitman <sup>1</sup> , B. Agbavor <sup>2</sup> , O. Dornu <sup>2</sup> , R. Phillips <sup>2</sup> , E. Ghedin <sup>1</sup> ; <sup>1</sup> National Institutes of Health, Bethesda, MD, <sup>2</sup> Kumasi Centre for Collaborative Research, Kumasi, GHANA.
<a href="#">2022-A-77-NGS</a>	103	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	MftP is a Multi-Drug Efflux Pump with a Vital Role in Regulating Cellular Homeostasis in <i>Burkholderia thailandensis</i>	<b>A. Al-Tohamy</b> , F. Donnarumma, A. Grove; LSU, Baton Rouge, LA.
<a href="#">2022-A-106-NGS</a>	104	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Validation and Implementation of a High Throughput 16S V3-V4 rDNA Sequencing Assay for Clinical Testing and Research	<b>J. Williams</b> , H. Brochu, A. Bray, J. Crawford, L. Lyer, A. Suchanik; Labcorp, Burlington, NC.
<a href="#">2022-A-157-NGS</a>	105	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Metagenomic insight into <i>Chrysophyllum</i>	<b>V. Ezebuoro</b> , A. E. Ataga, N. G. Ogbuji, U. C. Nwosu;

					albidum spoilage implicates respective decline and increase in Pseudomonas and Acetobacter abundance	University of Port Harcourt, Port Harcourt, NIGERIA.
<a href="#">2022-A-165-NGS</a>	106	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Metagenomic Analysis Reveals Seasonal Patterns for DNA and RNA viruses in Urban Aquatic Environments Influenced by Anthropogenic Activities.	<b>J. D. Francis, M. Uyaguari;</b> University of Manitoba, Winnipeg, MB, CANADA.
<a href="#">2022-A-158-NGS</a>	107	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Characterization of Mock Fungal Organisms by 3 Bioinformatics Pipelines	<b>N. Mok</b> <sup>1</sup> , G. Van Domselaar <sup>2</sup> , A. Bar-Or <sup>3</sup> , C. N. Bernstein <sup>1</sup> , J. D. Forbes <sup>4</sup> , M. Grahm <sup>2</sup> , C. Bonner <sup>2</sup> , J. Hart <sup>5</sup> , R. A. Marrie <sup>1</sup> , J. O'Mahony <sup>6</sup> , E. A. Yeh <sup>4</sup> , F. Zhu <sup>7</sup> , M. Bakker <sup>1</sup> , B. Banwell <sup>8</sup> , E. Waubant <sup>5</sup> , H. Tremlett <sup>7</sup> , N. Knox <sup>2</sup> ; <sup>1</sup> University of Manitoba, Winnipeg, MB, CANADA, <sup>2</sup> Public Health Agency of Canada, Winnipeg, MB, CANADA, <sup>3</sup> University of Pennsylvania, Philadelphia, PA, <sup>4</sup> University of Toronto, Toronto, ON, CANADA, <sup>5</sup> University of California San Francisco, San Francisco, CA, <sup>6</sup> Hospital for Sick Children, Toronto, ON, CANADA, <sup>7</sup> University of British Columbia,

						Vancouver, BC, CANADA, <sup>8</sup> Perelman School of Medicine University of Pennsylvania, Philadelphia, PA.
<a href="#">2022-A-159-NGS</a>	108	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Using Microbial Communities and Machine Learning to Detect Oil Contamination in the Great Lakes	<b>I. Bigcraft</b> , A. Kuntzleman, E. Byrne, S. Techtmann; Michigan Technological University, Houghton, MI.
<a href="#">2022-A-168-NGS</a>	109	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Does Microbial Dark Matter matter?	<b>H. Barak</b> , N. Fuchs, A. Sivan, A. Kushmaro; Ben Gurion University, Beer Sheva, ISRAEL.
<a href="#">2022-A-149-NGS</a>	110	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Maximizing MAGs from long-read metagenomic assemblies: a new post-assembly pipeline with circular-aware binning	<b>D. Portik</b> , J. Wilkinson; PacBio, Menlo Park, CA.
<a href="#">2022-A-127-NGS</a>	111	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Use of recombinant bacteria with unique tags as spike-in controls for the quantification of microbiome content	<b>L. Papazisi</b> <sup>1</sup> , R. Chuang <sup>1</sup> , B. Tang <sup>1</sup> , M. Hunter <sup>2</sup> , S. J. Green <sup>3</sup> , J. Lopera <sup>2</sup> , B. Benton <sup>2</sup> ; <sup>1</sup> American Type Culture Collection (ATCC), Gaithersburg, MD, <sup>2</sup> American Type Culture Collection (ATCC), Manassas, VA, <sup>3</sup> University of Illinois at Chicago, Chicago, IL.
<a href="#">2022-A-80-NGS</a>	112	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Metagenomic Antimicrobial Susceptibility Testing from Simulated Native Patient Samples	L. Lüttinger <sup>1</sup> , A. Materna <sup>1</sup> , T. Rattei <sup>2</sup> , <b>S. Beisken</b> <sup>1</sup> ; <sup>1</sup> Ares Genetics GmbH, Vienna, AUSTRIA, <sup>2</sup> University of

						Vienna, Vienna, AUSTRIA.
<a href="#">2022-A-193-NGS</a>	113	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	An Interactive Metagenomics Analysis Platform with Increased Accuracy and Precision at the Strain Level	M. Narvaez, D. M. Walsh, K. Moffat, M. Dadlani, <b>N. Khan</b> ; CosmosID, Germantown, MD.
<a href="#">2022-A-199-NGS</a>	114	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Assessment of Differential Abundance Tools for NGS Microbiome Data: Towards Reproducibility and Robustness	B. Ozdinc, K. Arogyaswamy, M. Dadlani, <b>D. M. Walsh</b> ; CosmosID, Germantown, MD.
<a href="#">2022-A-128-NGS</a>	115	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Microbial cooperation and competition in polyethylene terephthalate degrading consortia	<b>L. Schaerer</b> , R. Wu, L. Putman, R. Ong, S. Techtmann; Michigan Technological University, Houghton, MI.
<a href="#">2022-A-180-NGS</a>	116	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Bioinformatic and Metabolomic Tools for Analysis of Toxicity of Single Cell Protein	<b>S. M. Techtmann</b> <sup>1</sup> , P. Kokate <sup>1</sup> , L. Putman <sup>1</sup> , L. Schaerer <sup>1</sup> , T. K. Meyer <sup>1</sup> , J. M. Pearce <sup>2</sup> ; <sup>1</sup> Michigan Technological University, Houghton, MI, <sup>2</sup> Western University, London, ON, CANADA.
<a href="#">2022-A-183-NGS</a>	117	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Exploring the Role of Bacterial Motility in Evolutionary Mechanisms for Antimicrobial Resistance	<b>L. Stabryla</b> , I. Keenum, J. Dootz, S. Servetas, J. Kralj; NIST, Gaithersburg, MD.
<a href="#">2022-A-154-NGS</a>	118	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Investigation of Changes in the Resistome and Phageome of Lab-scale Moving Bed	<b>K. Yanac</b> , Q. Yuan, M. Uyaguari; University of Manitoba, Winnipeg, MB, CANADA.

					Biofilm (MBB) and Suspended Sludge (SS) Reactors under Tetracycline Exposure	
<a href="#">2022-A-62-NGS</a>	119	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	A strategy for screening broad-spectrum antiviral drugs against respiratory viruses	<b>O. Bajinka;</b> University of The Gambia, Banjul, GAMBIA.
<a href="#">2022-A-75-NGS</a>	120	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Subtyping Evaluation of <i>Salmonella</i> Enteritidis Using SNP and Core Genome MLST with Nanopore Reads	<b>Z. Xian</b> <sup>1</sup> , S. Li <sup>2</sup> , D. A. Mann <sup>1</sup> , Y. Huang <sup>1</sup> , F. Xu <sup>3</sup> , X. Wu <sup>3</sup> , S. Tang <sup>3</sup> , G. Zhang <sup>3</sup> , A. Stevenson <sup>4</sup> , C. Ge <sup>3</sup> , X. Deng <sup>1</sup> ; <sup>1</sup> Center for Food Safety, University of Georgia, Griffin, GA, <sup>2</sup> School of Biomedical and Pharmaceutical Sciences, Guangdong University of Technology, Guangzhou, CHINA, <sup>3</sup> Mars Global Food Safety Center, Beijing, CHINA, <sup>4</sup> Mars Advanced Research Institute, Mclean, VA.
<a href="#">2022-A-97-NGS</a>	121	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	A Bioinformatics Pipeline for Characterizing SARS-CoV-2 Viral Stocks	<b>F. Combs, N.</b> Puthuveetil, A. Reese, D. Yarmosh, M. Riojas; ATCC, Manassas, VA.
<a href="#">2022-A-108-NGS</a>	122	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Using Next Generation Sequences (NGS) to advance Identity (ID) Testing in the Biosafety Testing Field	<b>R. A. Bova;</b> MilliporeSigma, Rockville, MD.
<a href="#">2022-A-113-NGS</a>	123	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Combining Mash and NCBI Datasets via Nextflow for	<b>J. Hamlin, M. Willby, J.</b> Winchell; Centers for Disease

					a <i>Legionella</i> Species Identification Tool	Control and Prevention, National Center for Immunization and Respiratory Diseases, Respiratory Diseases Branch, Atlanta, GA.
<a href="#">2022-A-120-NGS</a>	124	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Species-Specific Subgrouping and Whole Genome-Based Identification of <i>Pseudomonas aeruginosa</i> Rectifies Taxonomy Assignment within the NCBI Database	<b>S. Park</b> <sup>1</sup> , N. A. Hasan <sup>2</sup> , J. Chun <sup>1</sup> ; <sup>1</sup> CJ Bioscience Inc., Seoul, KOREA, REPUBLIC OF, <sup>2</sup> EzBiome Inc., Gaithersburg, MD.
<a href="#">2022-A-129-NGS</a>	125	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Development and Evaluation of Bioinformatic Approach to Predict Antibiotic Susceptibility of <i>Mycobacterium tuberculosis</i>	M. Ezewudo, L. Cowan, <b>J. Posey</b> ; 1Division of Tuberculosis Elimination, National Center for HIV, Viral Hepatitis, STD, and TB Prevention, Centers for Disease Control and Prevention, Atlanta, GA.
<a href="#">2022-A-141-NGS</a>	126	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Long read genome assemblers are prone to missing small plasmids	<b>J. Johnson</b> , K. Jacob, M. Soehnen, H. Blankenship; Michigan Department of Health and Human Services, Bureau of Laboratories, Lansing, MI.
<a href="#">2022-A-171-NGS</a>	127	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Assemblies Matter: AMR Detection	<b>E. Litrup</b> , K. Loaiza; Statens Serum Institut, Copenhagen, DENMARK.
<a href="#">2022-A-174-NGS</a>	128	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	An End to End Pipeline for Characterization and Annotation of	<b>J. Bagnoli</b> , D. Yarmosh, N. Puthuveetil, F. Combs, A. Reese;

					Traceable Bacterial Material	ATCC, Gaithersburg, MD.
<a href="#">2022-A-178-NGS</a>	129	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Analysis of Complex Metagenomes with MetScale Workflows	<b>M. Scholz</b> <sup>1</sup> , N. Keplinger <sup>1</sup> , C. Grahlmann <sup>1</sup> , C. Hulme-Lowe <sup>1</sup> , M. Isbell <sup>1</sup> , T. Treangen <sup>2</sup> , K. Ternus <sup>1</sup> ; <sup>1</sup> Signature Science, LLC, Austin, TX, <sup>2</sup> Rice University, Houston, TX.
<a href="#">2022-A-184-NGS</a>	130	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	SeqScreen-LR: functional and taxonomic characterization of long read metagenomic data	A. Balaji <sup>1</sup> , <b>M. N. Nute</b> <sup>1</sup> , B. Hu <sup>1</sup> , A. D. Kappell <sup>2</sup> , G. D. Godbold <sup>3</sup> , K. L. Ternus <sup>2</sup> , T. J. Treangen <sup>1</sup> ; <sup>1</sup> Rice University, Houston, TX, <sup>2</sup> Signature Science, Austin, TX, <sup>3</sup> Signature Science, Charlottesville, VA.
<a href="#">2022-A-189-NGS</a>	131	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	TheiaProk: Species-Agnostic Bacterial Genome Analysis Workflows that Overcome Barriers to Bioinformatics for Public Health Laboratories	<b>M. R. Scribner</b> , K. G. Libuit, R. A. Petit III, S. M. Wright, F. J. Ambrosio, C. J. Kapsak, E. A. Smith, E. L. Doughty, J. Sevinsky; Theiagen Genomics, Highlands Ranch, CO.
<a href="#">2022-A-191-NGS</a>	132	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Performance of adaptor trimming algorithms and their effect on analysis of viral NGS data generated using Illumina iSeq and MiSeq platforms	<b>G. Nabakooza</b> , D. D. Wagner, N. Momin, R. Marine, W. Weldon; CDC, Atlanta, GA.
<a href="#">2022-A-18-NGS</a>	133	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	A general flexible framework to evaluate performance and provide guidelines for bioinformatics methods for	<b>A. Van Uffelen</b> , A. Posadas, N. H. Roosens, S. C. De Keersmaecker, K. Vanneste; Sciensano, Brussels, BELGIUM.

					taxonomic classification and resistance gene detection based on noisy long metagenomic reads	
<a href="#">2022-A-27-NGS</a>	134	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Supporting the bioinformatics community by supporting users of Bactopia	<b>R. A. Petit III</b> <sup>1</sup> , T. Fearing <sup>1</sup> , C. Rowley <sup>1</sup> , J. Mildenerger <sup>1</sup> , T. D. Read <sup>2</sup> ; <sup>1</sup> Wyoming Public Health Laboratory, Cheyenne, WY, <sup>2</sup> Emory University, Atlanta, GA.
<a href="#">2022-A-51-NGS</a>	135	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Antimicrobial Genes in Thermophilic <i>Bacillus paralicheniformis</i> Associated with Mobile Elements	<b>O. Elsakhawy</b> , M. Abouelkhair, S. Kania, R. Jones, S. Rajeev; University of Tennessee, Knoxville, KNOXVILLE, TN.
<a href="#">2022-A-43-NGS</a>	136	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Performance of bioinformatics tools for the detection of insecticidal protein-encoding genes in <i>Bacillus cereus sensu lato</i> biovar Thuringiensis genomes	<b>T. Chung</b> <sup>1</sup> , A. Salazar <sup>1</sup> , G. Harm <sup>1</sup> , S. Johler <sup>2</sup> , L. M. Carroll <sup>3</sup> , J. Kovac <sup>1</sup> ; <sup>1</sup> Department of Food Science, The Pennsylvania State University, University Park, PA, <sup>2</sup> Institute for Food Safety and Hygiene, University of Zurich, Zurich, SWITZERLAND, <sup>3</sup> Structural and Computational Biology Unit, EMBL, Heidelberg, GERMANY.
<a href="#">2022-A-144-NGS</a>	137	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Genome mining for bioactive secondary metabolites in surfactin producing <i>Bacillus</i>	<b>S. O. Akintayo</b> <sup>1</sup> , B. Neumann <sup>2</sup> , M. Vahidinasab <sup>1</sup> , M. Henkel <sup>1</sup> , L. Lilge <sup>1</sup> , R. Hausmann <sup>1</sup> ; <sup>1</sup> University of



					<i>subtilis</i> strain E2-03	Hohenheim, Department of Bioprocess Engineering, Stuttgart, GERMANY, <sup>2</sup> Institute for Hospital Hygiene, Medical Microbiology and Clinical Infectiology, Paracelsus Medical University, Nuremberg General Hospital, Nuremberg, GERMANY.
<a href="#">2022-A-200-NGS</a>	138	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Genome Sequencing and Molecular Characterization of a Novel <i>Canine Distemper Virus</i> Strain, Isolated from a Fox ( <i>Otocyon megalotis</i> ) in the United States	<b>A. Roozitalab</b> , S. Kania, O. Elsakhawy, R. Donnell, M. Abouelkhair; The University of Tennessee, KNOXVILLE, TN.
<a href="#">2022-A-91-NGS</a>	139	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	GenomeTrakr Database and Network Updates 2022	<b>M. Allard</b> , R. Timme, M. Timme, S. Cianci, E. Stevens, M. Hoffmann, G. Kastanis, T. Muruvanda, J. Payne, A. Pightling, H. Rand, J. Pettengill, Y. Luo, N. Gonzalez-Escalona, D. Melka, P. Curry, Y. Chen, S. Tallent, E. Brown; FDA, South Hero, VT.
<a href="#">2022-A-92-NGS</a>	140	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Whole-Genome Sequence-Based Analysis of the <i>Bacillus</i> Sp. And <i>Corynebacterium</i> Sp., Two Metabolizing Bacteria Isolated from Two Major	<b>A. K. Ogunyemi</b> <sup>1</sup> , O. M. Buraimoh <sup>1</sup> , B. C. Ogunyemi <sup>2</sup> , S. K. Odetunde <sup>3</sup> , T. T. Oshin <sup>3</sup> , T. A. Samuel <sup>1</sup> , O. O. Amund <sup>4</sup> , M. O. Illori <sup>1</sup> , O. O. Amund <sup>4</sup> ; <sup>1</sup> University of Lagos, LAGOS, NIGERIA, <sup>2</sup> Yaba

					Landfills in Lagos, Nigeria	College of Technology, LAGOS, NIGERIA, <sup>3</sup> Lagos State University of Science and Technology, LAGOS, NIGERIA, <sup>4</sup> Elizade University, Ondo State, NIGERIA.
<a href="#">2022-A-21-NGS</a>	141	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Genome and transcriptome analysis of the microalgae <i>Desmodesmus abundans</i> used for flue gas mitigation and byproduct obtaining after 13 years under high-CO <sub>2</sub>	<b>S. Mora Godínez</b> , A. Pacheco; Tecnológico de Monterrey, Monterrey, MEXICO.
<a href="#">2022-A-29-NGS</a>	142	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Assessing the spatial and temporal variability of bacterial communities in two Bardenpho wastewater treatment systems via Illumina MiSeq sequencing	<b>s. sherchan</b> ; Morgan State University, Baltimore, MD.
<a href="#">2022-A-5-NGS</a>	144	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	<b>Bioaerosol Surveillance via Untargeted Nanopore Sequencing</b>	<b>R. Bernhardt</b> ; US Army, Baltimore, MD.
<a href="#">2022-A-12-NGS</a>	145	10/18/2022 5:00:00 PM	10/18/2022 7:00:00 PM	120	Online quality control of SARS-CoV-2 data with RonaQC	<b>N. Alikhan</b> , A. J. Page; Quadram Institute Bioscience, Norwich, UNITED KINGDOM.
<a href="#">2022-A-15-NGS</a>	146			120	Finding New and Unique Drug Targets against the Resistant Microbial Pathogens using	<b>R. Uddin</b> ; University of Karachi, Karachi, PAKISTAN.

					Bioinformatics Pipeline	
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Late Breakers:

**Poster board no. 147**

Kaylee Watson

Investigating the Role of Epitranscriptomics in Host-Microbe Interactions through Direct RNA Sequencing

**Poster board no. 148**

Julio Diaz Caballero

Pathogenwatch: a global platform for genomic surveillance

**Poster board no. 149**

Olabiyi Obayomi

A pipeline for paired-end, dual-indexed microbiome analysis using QIIME2 and PICRUSt2.

**Poster board no. 150**

Jill Hagey

PHoeNix: A Nextflow Pipeline for Reproducible Characterization of Healthcare-associated Bacterial Pathogens and Antibiotic Resistance Detection

**Poster board 151 no.**

Robin Bromley

Oxford Nanopore Direct RNA Sequencing: it's AAAAAAAAAAll in the de'TAILS