AACR Special Conference in Cancer Research

ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING

July 10-12, 2025 | Montreal, QC, Canada

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Current as of June 10, 2025

Poster Session A (July 10, 2025, 7:30-9 p.m.)

A001 **Harnessing machine learning for the virtual screening of natural compounds as both EGFR and HER2 inhibitors in colorectal Cancer: A novel therapeutic approach**. Deli-Bright Oku. University of South Africa, Roodepoort, South Africa

A002 **A Bayesian Machine Learning Approach for Estimating Treatment Effects in Decentralized Clinical Trials**. Ying Yuan. University of Texas MD Anderson Cancer Center, Bellaire, TX, United States

A003 **An active learning platform for predictive oncology in rare cancers**. Wesley Tansey. Memorial Sloan Kettering Cancer Center, New York, NY, United States

A004 **Integrating high-throughput screening with ligand-based pharmacophore modeling and virtual screening strategies to optimize exonuclease 1 inhibitor design**. Jessica Hess. City of Hope, Duarte, CA, United States

A005 **Monotherapy cancer drug-blind response prediction is limited to intraclass generalization**. William Herbert. Mayo Clinic, Rochester, MN, United States

A006 **Data Curation and Knowledge Integration Pipeline for Biomarker Discovery**. Samantha Majoros. Ontario Institute for Cancer Research, Toronto, ON, Canada

A007 **Bayesian Counterfactual Machine Learning Individualizes Radiation Modality Selection to Mitigate Immunosuppression**. Michael Kane. Yale School of Public Health, New Haven, CT, United States

A008 **AI-Predict: Artificial intelligence-mediated drug synergy prediction and validation in cancer models**. Alicia Pliego. University of Zurich, Zurich, Switzerland

A009 **AI-driven metabolomics and synthetic drug design for targeting CNS metastases**. Rajvi Babaria. Johns Hopkins University, Baltimore, MD, United States

A010 **Benchmarking 3D against 2D deep learning-driven image-based profiling for predicting biological relationships amongst genes**. Matt De Vries. Sentinal4D, London, United Kingdom

A011 **Interpretable machine learning for discovery, evaluation and clinical translation of context-specific dependencies**. Timothy Sterne-Weiler. Genentech, South San Francisco, CA, United States

A012 **AI-assisted Design of Novel NRF2^{Mut} Inhibitors**. Xiaoxin Chen. Cooper University Health Care, Camden, NJ, United States

A013 **Facilitating AI-Based Hit Discovery through the Development of the AIRCHECK Platform**. Shaghayegh Reza. University of Toronto, Toronto, ON, Canada

A014 **Machine Learning-Guided Discovery of Drug Combinations Targeting PI3K and mTOR Pathways Using Cell Line and PDX Data**. Yuan-Hung Chien. Certis Oncology, San Diego, CA, United States

A015 **Precision medicine approach to melanoma immunotherapy: Predicting response, adverse events, and hospital admissions using machine learning and explainable artificial intelligence**. Lakshya Sharma. University College London, London, United Kingdom

A016 **A computational chemistry and AI-driven framework for structure-based drug design informed by underlying factors of mutation-induced drug resistance: A study of KRAS**. Katarzyna Mizgalska. Moffitt Cancer Center, Tampa, FL, United States

A017 **Personalizing treatment selection for prostate cancer using causal machine learning**. Emma Graham Linck. UW-Madison School of Medicine and Public Health, Madison, WI, United States

A018 **Accelerating drug discovery at an HBCU with AI/ML: Text mining, computational modeling, and drug repurposing approaches**. Kevin Williams. North Carolina Central University, Durham, NC, United States

A019 **A fully transparent and automatable form of AI for biomarker and new target discovery using diverse multi-omics data**. Jedidiah Gaetz. Plex Research, Cambridge, MA, United States

A020 **Machine learning models of RNA expression landscapes help predict overall tumor response to chemotherapy in cholangiocarcinoma**. Ellen Larson. Mayo Clinic, Rochester, MN, United States

A021 **Improving cardiotoxicity prediction for oncology drugs via domain-specific adaptation**. Daniel Nguyen. University of Virginia, Charlottesville, VA, United States

A022 **Deep Learning Meets Transcriptomics: CNN-1D Powered Interpretation of probe based transcriptome array in Prostate Cancer**. Neetu Singh. King George's Medical University, Lucknow, India

A023 **Spatially resolved drug response predictions reveal fibroblast-associated resistances in in situ lung cancer samples**. Robert Gruener. University of Minnesota, Minneapolis, MN, United States

A024 **AI-Integrated Framework for Predicting ADME and Toxicological Profiles: A Hybrid Data- and Physics-Driven Approach**. Md Ataul Islam. SilicoScientia Pvt Ltd, Bengaluru, India

A025 **PicoGen: A structure-grounded generative AI model for drugging undruggable targets, including the TEAD–YAP axis**. Nicholas Hamilton. Pledge Therapeutics, LLC, Canton, MA, United States

A026 **GenAI and Physics Assisted Methods for the Design and Development of USP1 Inhibitors**. Appaji Mandhare. VeGen Labs LLP, Hyderabad, India

A027 **Multiscale systems approach to target tumor ecosystem responses for therapeutic benefit**. Laura Heiser. OHSU, Portland, OR, United States

A028 **Automated Rule Synthesis from Literature for Agent-Based Modeling of the Tumor Microenvironment**. Zachary Sims. Oregon Health & Science University, Portland, OR, United States

A029 **Validation of a Deep Learning Serial Computed Tomography Response Biomarker for Predicting Overall Survival in Metastatic Kidney Cancer Treated with Immune Checkpoint Inhibitors**. Chiharu Sako. Onc.AI, San Carlos, CA, United States

A030 **Advancing Pharmacogenomic Modeling: Robust Dose-Response Curve Fitting and Drug Combination Analytics in the Next-Generation PharmacoGx Framework**. Nikta Feizi. University of Toronto, Toronto, ON, Canada

A031 **Unsupervised graph-based visualization of variational autoencoder latent spaces reveals hidden multiple myeloma subtypes**. Anish Simhal. Memorial Sloan Kettering Cancer Center, New York, NY, United States

A032 **Using machine learning to tackle tumor heterogeneity**. Jennifer Neumaier. TRON gGmbH, Mainz, Germany

A033 **Utilizing machine learning algorithms to identify methylation regions predictive of outcome in ICI-treated patients: Insights from the longitudinal RADIOHEAD study**. Christopher Pretz. Guardant Health, Castle Rock, CO, United States

A034 **A robust ensemble-feature selection and machine learning approach to identify true somatic variants**. YunTe Lin. Memorial Sloan Kettering Cancer Center, New York, NY, United States

A035 **Denoising Models Enhance Detection of Tumor-Derived cfDNA fragments and Cancer Tissue signal in Liquid Biopsy**. Shiva Farashahi. Harbinger Health, Boston, MA, United States

A036 **Genomic alterations associate with distinct tumor dynamics in NSCLC: A genomics-informed Bayesian hierarchical modeling approach**. Nikolaos Dimitriou. Memorial Sloan Kettering Cancer Center, New York, NY, United States

A037 **Survival-based subtyping of lung cancer through integrated genomic and methylation signatures**. Aaron Hardin. Guardant Health, Palo Alto, CA, United States

A038 **Unmasking hidden mutational footprints of therapy in pediatric tumors** . Mehdi Layeghifard. The Hospital for Sick Children, Toronto, ON, Canada

A039 **Pediatric pan-cancer characterization of transposable elements and their modulation by germline TP53 variants**. Brianne Laverty. The University of Toronto, Toronto, Ontario, Canada

A040 **Digital Controls: An Efficient, Robust, and Privacy-Preserving Bayesian Tool for Adaptive Information Borrowing from External Data**. Ruitao Lin. The University of Texas MD Anderson Cancer Center, Houston, United States

A041 **A Hybrid Active Learning (AL) Random Forest Model with KNN Imputation to Predict Recurrence in Ductal Carcinoma In Situ (DCIS) of the Breast**. Kai Chan. Queen Mary University London, London, United Kingdom

A042 **Real-world clinical multi-omics and AI/ML analyses reveal bifurcation of drug resistance mechanisms to CDK4/6 inhibitors**. Zhengyan Kan. Pfizer, San Diego, CA, United States

A043 **Mutational profiling and machine learning for risk stratification and biomarker identification in intraductal papillary mucinous neoplasms progressing to pancreatic cancer**. Aleksandra Karolak. Moffitt Cancer Center, Tampa, FL, United States

A044 **Developing a digital twin framework for colorectal cancer outcome prediction and robust clinical trial simulation**. Ian Ruchlin. ConcertAI, Cambridge, MA, United States

A045 **Unlocking deep learning for cell-free DNA-based early colorectal cancer detection**. Michael Widrich. Freenome, Brisbane, CA, United States

A046 **Cell states and neighborhoods in distinct clinical stages of primary and metastatic esophageal adenocarcinoma**. Josephine Yates. Broad Institute, Boston, MA, United States

A047 **Building clinically relevant and interpretable multi-modal machine learning algorithms to predict glioblastoma disease progression**. Shreya Chappidi. National Institutes of Health & University of Cambridge, Bethesda, MD, United States

A048 **Weakly supervised prediction of EGFR mutation status and early metastasis of lung adenocarcinoma whole slide histopathology images using artificial intelligence**. Chi-Long Chen. Taipei Medical University and Taipei Medical University Hospital, Taipei, Taiwan (Greater China)

A049 **Development of a tri-modal contrast learning model integrating pathology-text and CT-text for clinical oncology tasks**. Zhicheng Du. Tsinghua Shenzhen International Graduate School, Shenzhen, Taiwan (Greater China)

A050 **Multimodal integration of H&E slides and matched targeted DNA sequencing data for enhanced cancer subtype identification**. Madison Darmofal. Memorial Sloan Kettering Cancer Center, New York, NY, United States

A051 **Multi-omic explainable machine learning improves cancer treatment outcome prediction**. Khoa Tran*. Cancer Program, QIMR Berghofer Medical Research Institute; School of Biomedical Sciences, Queensland University of Technology (QUT), Brisbane, Australia

A052 **The S-RACE Platform: Empowering Healthcare Real-World Data with Artificial Intelligence (AI) Using a Cloud-Based Approach**. Alberto Traverso. Università Vita-Salute San Raffaele, Milan, Italy

A053 **A pre-operative Artificial Intelligence-based model to estimate the risk of cancer specific mortality in patients with non-metastatic kidney cancer**. Alberto Traverso. Università Vita-Salute San Raffaele, Milan, Italy

A054 **Multimodal LLM-Driven Intervention for Precision Risk Prediction in Lung Cancer Surgery**. Kenneth Seastedt. Roswell Park Comprehensive Cancer Center, Buffalo, NY, United States

A055 **Inferring genomic properties and histologic subtypes of solid tumors from H&E whole-slide images**. Kevin Boehm. MSKCC, New York, NY, United States

A056 **Integrative Machine Learning Approaches for Predicting Prostate Cancer Risk Using Multi-Omics Data**. Zhanwei Wang. University of Hawaii John A. Burns School of Medicine, Honolulu, HI, United States

A057 **Multimodal AI Modeling of Clinical Panel-Based Sequencing for HRD Detection in Ovarian Cancer**. Areej Alsaafin. Memorial Sloan Kettering Cancer Center, New York, NY, United States

A058 **Multimodal generative AI jointly learns pathology and clinical data to synthesize a multinational lung cancer cohort**. Samantha Riesenfeld. Department of Medicine, University of Chicago, Chicago, IL, United States

A059 **CP-Fuse: A Comprehensive Assessment of Clinico-Pathological Fusion in TCGA Survival Prediction**. Juan Duran. McGill University, Montreal, QC, Canada

A060 **OncoMindPro: An AI-augmented assistant to oncologists**. Samuel Ding. Lexington High School, Lexington, United States

A061 **Machine Learning and Causal Inference-Based Predictive Risk Modeling of Unplanned Radiation Treatment Interruption**. David Schwartz. College of Medicine, The University of Tennessee Health Science Center, Memphis, TN, United States

A062 **Uncovering Social and Clinical Determinants of Baseline Distress Prior to Radiation Therapy: An Explainable Machine Learning Approach**. David Schwartz. College of Medicine, University of Tennessee Health Science Center, Memphis, TN, United States

A063 **Artificial Intelligence in Cytopathology and Histopathology of Cancer: The Evolution to Precision Pathology** . Priya Hays. Hays Documentation Specialists, LLC, San Mateo, CA, United States

A064 **Dynamics in automatic CT based body composition and blood biomarkers in predicting mortality on immune therapy treated solid malignancy patients**. Hilla Vardi Behar. The Samueli Institute at the Davidoff Center, Petah Tikva, Israel

Poster Session B (July 11, 2025, 7-9 p.m.)

B001 **Jarvais: A modular framework to standardize machine learning workflows and accelerate reproducible AI in oncology – benchmarking against a human-developed model for predicting emergency department visits during cancer treatment**. Joshua Siraj. Cancer Digital Intelligence, University Health Network, Toronto, ON, Canada

B002 **Fairness by Design: End-to-End Bias Evaluation for LLM-Generated Data**. Melissa Estevez. Flatiron Health, Raleigh, NC, United States

B003 **Towards machine learning fairness in glioblastoma: An evaluation of protected attributes in publicly available clinical datasets**. Shreya Chappidi. National Institutes of Health; University of Cambridge, Bethesda, MD, United States

B004 **A practical framework for operationalizing responsible and equitable AI in healthcare: Tackling bias, inequity, and implementation challenges**. Benjamin Grant. Cancer Digital Intelligence, Princess Margaret Cancer Centre, Toronto, ON, Canada

B005 **Designing ethically aligned AI to support palliative care in hematologic malignancies: Ethical considerations for equity and patient-centered care**. Wamia Siddiqui. Icahn School of Medicine at Mount Sinai, New York, NY, United States

B006 **Using large language models for scalable extraction of real-world progression events across multiple cancer types**. Aaron Cohen. Flatiron Health, New York, NY, United States

B007 **TheBlueScrubs-v1: A Large-Scale Curated Dataset with ~11 Billion Oncology Tokens for AI-Driven Cancer Research**. Luis Felipe. Moffitt Cancer Center, Tampa, FL, United States

B008 **Fine-tuned large language model accurately estimates progression-free survival from radiology reports in immune checkpoint inhibitor–treated cancers**. Feyisope Eweje. Stanford University, Stanford, CA, United States

B009 **missense-kinase-toolkit: A toolkit to facilitate kinase sequence and structure-based modeling for property predictions**. Jessica White. Tri-Institutional PhD Program in Computational Biology and Medicine, New York, NY, United States

B010 **From RECIST to reality: A foundation model pipeline for scalable therapy response evaluation**. Caryn Geady. University of Toronto; University Health Network, Toronto, ON, Canada

B011 **Pan-cancer immunotherapy response prediction using the CURE AI large clinicogenomic foundation model**. Vitalay Fomin. Numenos, New York, NY, United States

B012 **Prompting Large Language Models to Predict Adverse Events during Cancer Treatment**. Wayne Isaac Uy. Division of Medical Oncology and Hematology, Princess Margaret Cancer Centre, University Health Network, Toronto, ON, Canada

B013 **Emotional tone classification as a tool for psychosocial risk detection in oncology: An AI-powered chatbot**. Nissim Frija-Gruman. McGill University, Montreal, QC, Canada

B014 **Are histopathology foundation models clinically ready for survival prediction?**. Vishwesh Ramanathan. University of Toronto, Toronto, ON, Canada

B015 **Large language models to predict cancer risk from free-text clinical notes**. Daniel Mau. ICES, Princess Margaret Cancer Centre, University Health Network, University of Toronto, Toronto, ON, Canada

B016 **Multi-Agent Framework for Deep Research in Cancer Immunogenomics via TCR Datasets and Scientific Literature Search**. Samuel Torres-Florez. Roche, Montreal, QC, Canada

B017 **Check: A hybrid continuous-learning framework for enhancing factual reliability in clinical language models.**. Carlos Garcia Fernandez. Moffitt Cancer Center, Tampa, FL, United States

B018 **Practical benchmarking of large language models for structuring synthetic prostate cancer histopathology statements in English and Finnish**. Teemu Laajala. University of Helsinki, Helsinki, Finland

B019 **Clinician-AI evaluation of prognostic information extraction in head and neck cancer using an on-premises LLM**. Yujing Zou. McGill University, Montreal, QC, Canada

B020 **Automated classification of thymic epithelial tumours. A novel deep learning approach**. Matteo Sacco. University of Chicago, Chicago, IL, United States

B021 **Current oncological large language model research lacks reproducibility, transparency, and long term support**. Tolou Shadbahr. University of Helsinki, Helsinki, Finland

B022 **Prediction of radiotherapy-Induced esophagitis in non-small cell lung cancer using a 3D vision foundation model** . Chloe Min Seo Choi. Memorial Sloan Kettering Cancer Center, New York, NY, United States

B023 **Deep learning-based prediction of immune checkpoint inhibitor efficacy in brain metastases using brain MRI**. Christopher Bridge. Massachusetts General Hospital, Boston, MA, United States

B024 **Artificial intelligence enables the ethical reconstruction and social value realization of global cancer research: From technological innovation to humanistic care**. Zhicheng Du. Tsinghua Shenzhen International Graduate School, Shenzhen, Taiwan (Greater China)

B025 **Automated segmentation pipeline for radiological imaging using UniverSeg and similarity-guided support set retrieval**. Niket Patel. Drexel University College of Medicine, Philadelphia, PA, United States

B026 **Artificial Intelligence Apps for Medical Image Analysis using pyCERR and Cancer Genomics Cloud**. Aditya Apte. Memorial Sloan Kettering Cancer Center, New York, NY, United States

B027 **Multimodal prediction of pathological complete response in esophageal cancer using automated machine learning and variational autoencoder-based synthetic data augmentation**. Şefika Dinçer. Van Yüzüncü Yıl University, Van, Türkiye

B028 **Assessing variability in training deep models in delineating Prostate gland anatomy between clinical experts**. Yoganand Balagurunathan. Moffitt Cancer Center, Tampa, FL, United States

B029 **Confident Filtering in the context of primary Gleason pattern classification**. Yoganand Balagurunathan. Moffitt Cancer Center, Tampa, FL, United States

B030 **Multiple instance learning of large-scale DNA organization to characterize prostate cancer aggressiveness**. Fumiya Inaba. BC Cancer Research Institute, Vancouver, BC, Canada

B031 **Artificial Intelligence-Enhanced Image Analysis of Peripheral Blood Smears Supports the Diagnosis and Monitoring of Acute Promyelocytic Leukemia**. Xiaoping Sun. The University of Texas MD Anderson Cancer Center, Houston, TX, United States

B032 **Generative modeling (AI) for the analysis of Single-Cell RNA-seq data of radioresistant malignant pediatric brain tumors**. Chinar Salmanli. University of Strasbourg, STRASBOURG, France

B033 **Identifying triple-negative breast cancer patients at high risk of worse prognosis using molecular features derived from histology images**. Jung Hun Oh. Memorial Sloan Kettering Cancer Center, NEW YORK, NY, United States

B034 **Decoding the Leukocyte Effect: How Cell Retention Shapes ML Outcomes in Platelet RNA-based Cancer Detection**. Anna Supernat. Medical University of Gdansk, Gdansk, Poland

B035 **Deep learning-based spatially resolved immune clustering in the tumor microenvironment predicts distant metastasis risk in high-grade prostate cancer**. David Yang. Brigham and Women's Hospital/Dana-Farber Cancer Institute, Boston, MA, United States

B036 **Machine learning-based and marker-based combined strategy for circulating tumor cells candidates' detection**. Michał Sieczczyński. Medical University of Gdańsk, Gdańsk, Poland

B037 **AI-powered virtual tissues from spatial proteomics for clinical diagnostics and biomedical discovery**. Charlotte Bunne. EPFL, Lausanne, Switzerland

B038 **Machine learning used to validate neutrophil classification in Triple Negative Breast Cancer patients** . Krzysztof Pastuszak. 1 Department of Algorithms and System Modeling, Gdansk University of Technology, Gdańsk, Poland. 2 Laboratory of Translational Oncology, Intercollegiate Faculty of Biotechnology, University of Gdańsk and Medical University of Gdańsk, Gdańsk, Poland. 3 Cen, Gdańsk, Poland

B039 **Detecting obesity-associated histopathology characteristics in breast cancer using an AI foundation model**. Naim Matasci. Ellison Medical Institute, Los Angeles, CA, United States

B040 **Literature-scaled immunological gene set annotation using AI-powered immune cell knowledge graph (ICKG)**. Shan He. MD Anderson Cancer Center, Houston, TX, United States

B041 **A Cellular Network-Aware Foundation Model Improves Single-Cell Level Predictions**. Léo Dupire. Columbia University, New York, NY, United States

B042 **Identifying single-cell transcriptomic signatures and changes underlying the evolution of fusion-negative rhabdomyosarcoma in Li-Fraumeni Syndrome mice.**. Ashby Kissoondoyal. The Hospital for Sick Children, Toronto, ON, Canada

B043 **Cellular localization as a prognostic indicator in invasive breast cancer** . Matthew McNeil. University of Toronto, Toronto, ON, Canada

B044 **Distributed Transcriptomic Modeling for Biomarker Discovery in Immuno-Oncology**. Farnoosh Abbas-Aghababazadeh. Princess Margaret Cancer Centre, University Health Network, Toronto, ON, Canada

B045 **Deep learning–guided spatial dissection of melanoma uncovers compartmentalized tumor states associated with response and resistance to immunotherapy and its combination with MAPK inhibitors**. Kalpit Shah. Genentech, South San Francisco, CA, United States

B046 **Enhancing the Diagnosis and Monitoring of Chronic Lymphocytic Leukemia with Artificial Intelligence-Driven Peripheral Blood Smear Image Analysis**. Yun Gong. The University of Texas MD Anderson Cancer Center, Houston, TX, United States

B047 **Path2Space: An AI approach for cancer biomarker discovery via histopathology inferred spatial transcriptomics**. Emma Campagnolo. National Cancer Institute (NIH), Bethesda, MD, United States

B048 **Large Scale, AI-Enabled, Spatial Signal Processing of Breast Cancer Pathology Identifies Consensus Tissue Structures Related to Biology and Outcomes**. Jordan Krull. The Ohio State University, Columbus, OH, United States

B049 **Deep Learning Enables Identification of Cell Types and Clusters (iCTC) in Immune Tumor Ecosystems for Prognostic Assessment in Cancer**. Andrew Hoffmann. Northwestern University, Chicago, IL, United States

B050 **Spatially aware transcriptomic topic modeling reveals novel signals of spatial organization in glioblastoma**. Joseph Sifakis. University of Chicago, Chicago, IL, United States

B051 **Elastic net discovery of DNA methylation biomarkers for non-invasive diagnosis and recurrence detection in head and neck cancer**. Alexander Sprague. University of Cincinnati, Cincinnati, OH, United States

B052 **Utilizing Dimensionality Reduction for Classification of Cell Senescence and Immune Synapse Formation via Imaging Flow Cytometry**. Mohamed Moustafa. AstraZeneca, Gaithersburg, MD, United States

B053 **Empowering AI-driven prediction of the tumor microenvironment from histopathology images via molecular annotation**. Siao-Han Wong. German Cancer Research Center (DKFZ), Heidelberg, Germany

B054 **Identification of spatial motifs linked to tumor genotype using graph attention networks**. Nicholas Ceglia. Memorial Sloan Kettering Cancer Center, New York, NY, United States

B055 **Analysis of pathologists' intraobserver, interobserver and AI agreement in breast cancer HER2 scoring: AI-assessed intra-sample tumor heterogeneity relates to lower agreement among pathologists and with AI**. Pedro S. S. M. Ferrari. D'Or Institute of Research & Education, São Paulo, Brazil

B056 **Deep Antigen Sets, a new deep-learning framework, enables in vivo modeling of patient neoantigens for effective targeted immunotherapy design**. Frank Zhang. Natera, Inc., Austin, TX, United States

B057 **DrBioRight: an AI chat assistant enabling scalable and flexible multi-omics analysis in cancer**. Jun Li. UT MD Anderson Cancer Center, Houston, TX, United States

B058 **An informed machine learning-based blood test for risk assessment of lethal and common cancers**. Ehsan Irajizad. University of Texas MD Anderson Cancer Center, Houston, TX, United States

B059 **Cancer Recurrence and Anxiety/Depression: High Accuracy Artificial Intelligence Predictive Modeling**. Nabil Adam. Rutgers University, Newark, NJ, United States

B060 **DIGIONE: From Fragmentation to Federation: Enabling Scalable Oncology RWE (Real World Evidence) through an international hospital based Cancer OMOP (Observational Medical Outcomes Partnership) Network**. Alberto Traverso. DIGICORE (Digital Institute For Cancer Outcome Research), Brussels, Belgium

B061 **Learning the Language of Somatic Mutations: A Large Language Model Approach to Precision Oncology**. John-William Sidhom. Weill Cornell Medicine, New York, NY, United States