

POSTERS 1 THROUGH 46 WILL PRESENT ON WEDNESDAY EVENING. POSTERS 47 THROUGH 86 WILL PRESENT ON THURSDAY EVENING

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| Poster #1 | Aerts | Hugo | ModelHub.AI: Dissemination Platform for Deep Learning Algorithms |
| Poster #2 | Antunes | Dinler | Conformational sampling of large ligands made possible by a parallelized incremental meta-docking approach |
| Poster #3 | Arnold | Corey | Classifying Prostate Cancer from Multiparametric Magnetic Resonance Imaging and Whole Slide Histology Imaging using Machine Learning |
| Poster #4 | Banerjee | Anjishnu | Stochastic covariance functions for understanding the histology and improving detection in solid tumors |
| Poster #5 | Boca | Simina | CGDNET: Cancer Gene Drug Network |
| Poster #6 | Broom | Bradley | Cloud-Enabled Sharing of Next-Generation Clustered Heat Maps |
| Poster #7 | Carey | Vincent | Opening Apps and Notebooks for Cloud-Scale Cancer Genomics with Bioconductor |
| Poster #8 | Carey | Vincent | Metadata Analysis Laboratory for Integrative Cancer Genomics: Methods and Resources |
| Poster #9 | Castanza | Anthony | MSigDB 7 and Beyond, a Scalable Resource for Transcriptome Interpretation |
| Poster #10 | Cerami | Ethan | The cBioPortal for Cancer Genomics |
| Poster #11 | Chen | Jin | STAN-CT: Standardization and Normalization of CT images for Lung Cancer Patients |
| Poster #12 | Chen | Mei-Ju | TCPA Pan-cancer Analytic Module: Protein-centric Analysis of Multi-omics Data in Human Cancer |
| Poster #13 | Chevalier | Aaron | Enhanced Deconvolution and Prediction of Mutational Signatures |
| Poster #14 | Conte | Nathalie | Implementing novel functionality for PDX Finder through collaborations with ITCR and other community resources |
| Poster #15 | Cooper | Lee | Cell Detection and Classification in Hematopathology |
| Poster #16 | Cooper | Lee | Using the Digital Slide Archive to Coordinate an International Digital Pathology Annotation Study |
| Poster #17 | Corrada Bravo | Hector | Computational steering of interactive exploratory analysis of cancer genomics data |
| Poster #18 | Craft | Brian | UCSC Xena for personal and public cancer genomics visualization and interpretation |
| Poster #19 | Davatzikos | Christos | The Cancer Imaging Phenomics Toolkit (CaPTk) |
| Poster #20 | Del Fiol | Guilherme | A Natural Language Processing Method to Extract Cancer Age of Onset from Unstructured Family History in the EHR |
| Poster #21 | Del Fiol | Guilherme | Using Standards-Based Clinical Decision Support Algorithms to Identify and Manage Patients who Meet Evidence-Based Criteria for Genetic Evaluation of Familial Cancer |

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| Poster #22 | Dingerdisen | Haley | OncoMX: a web resource for exploring integrated cancer biomarker data in the context of mutation, differential expression, evolutionarily conserved expression patterns, and automatically mined literature evidence |
| Poster #23 | Fedorov | Andrey | Quantitative Image Informatics for Cancer Research (QIICR) |
| Poster #24 | Fitzgerald | Paul | Introducing a new open-source tool: XCIST (X-ray-based Cancer Imaging Simulation Toolkit) |
| Poster #25 | Furman | Samantha | THRIVE 1.0: A Computational Pathology Platform for Quantifying Spatial Intratumoral Heterogeneity in Multi to Hyperplexed Fluorescence Images |
| Poster #26 | Goecks | Jeremy | Galaxy Workflows for the Human Tumor Atlas Network |
| Poster #27 | Goecks | Jeremy | Galaxy Integration with the NCI Cancer Research Data Commons |
| Poster #28 | Griffin | Tim | A resource for complete proteogenomic informatics in cancer research: Built on ITCR Tools |
| Poster #29 | Griffith | Obi | Aggregating evidence to determine the clinical significance of cancer variants in the CIViC knowledgebase |
| Poster #30 | Griffith | Malachi | Expansion of the CIViC data model to incorporate emerging standards for variant |
| Poster #31 | Gutman | David | The Digital Slide Archive 2.0: MultiChannel Image Support and Dockerized Algorithm Support |
| Poster #32 | Ha | Min Jim | Personalized Integrated Network Modeling of the Cancer Proteome Atlas |
| Poster #33 | Haas | Brian | Latest Developments in the Trinity Cancer Transcriptome Analysis Toolkit |
| Poster #34 | Hanauer | David | EMERSE: The Electronic Medical Record Search Engine |
| Poster #35 | Harris | Gordon | Precision Imaging Metrics: All-in-One Cloud-Hosted Quantitative Imaging Assessment and Workflow Management System for Cancer Centers |
| Poster #36 | He | Bing | Diverse noncoding mutations contribute to deregulation of cis-regulatory landscape in pediatric cancers |
| Poster #37 | Holmes | Ian | The JBrowse Cancer Genome Browser |
| Poster #38 | Huang | Xiaomeng | Subclone analysis in CLL patients receiving ibrutinib vs acalabrutinib treatment reveal differential patterns of drug-induced cancer evolution |
| Poster #39 | Jagtap | Pratik | Developing multi-omic informatics workflows within the Galaxy platform to uncover cancer-microbiome interactions |
| Poster #40 | Janowczyk | Andrew | HistoQC: A quality control pipeline for digital pathology slides |
| Poster #41 | Johnson | Evan | Interactive single cell RNA-Seq analysis with the Single Cell Toolkit (SCTK) |
| Poster #42 | Juarez | Edwin | Patient Specific Drug Recommendations Using GenePattern Notebooks |
| Poster #43 | Kalpathy-Cramer | Jayashree | Automated Response Assessment in Brain Tumors |
| Poster #44 | Karchin | Rachel | Informatics Tools for High-Throughput Analysis of Cancer Mutations |

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| Poster #45 | Kontos | Despina | The Cancer Imaging Phenomics Toolkit (CaPTk) |
| Poster #46 | Kurc | Tahsin | Actionable Pathomics |
| Poster #47 | LaViolette | Peter | The Effects of Pathologist Specific Ground Truth Variance on Radio-Pathomic Mapping in Prostate Cancer |
| Poster #48 | Li | Jianyun | Classifying Prostate Cancer from Multiparametric Magnetic Resonance Imaging and Whole Slide Histology Imaging using Machine Learning |
| Poster #49 | Liang | Han | Systematic Identification of Cancer Therapeutic Liabilities Through Adaptive Functional Proteomics |
| Poster #50 | Liang | Han | Eagle Nebula: an easy platform for bioinformatics tool sharing and commercialization |
| Poster #51 | Madduri | Ravi | Applying ConVarCal, A High Performance Consensus Variant Calling, for Discovery of Prevalance of Inherited Mutations in Breast Cancer Predisposition Genes among Ugnada and Cameroon Women |
| Poster #52 | Marjoram | Paul | Conservation and Functional-Charcterization of Tumor Methylation Sites |
| Poster #53 | Martel | Anne | Pathology Image Informatics Platform forVisualization, Analysis and Management (PIIP): Application to assessment of residual cellularity in WSIs |
| Poster #54 | Meyer | Clifford | Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis |
| Poster #55 | Morgan | Martin | Cancer Genomics: Integrative and Salable Solutions in R / Bioconductor |
| Poster #56 | Naegle | Kristen | Inferring Kinase Activity Profiles from Phosphoproteomic Data |
| Poster #57 | Narzisi | Guiseppe | Somatic variant analysis of linked-reads sequencing data with Lancet |
| Poster #58 | Nicholas | Thomas | Expanding GEMINI to annotate and prioritize subclonal mutations in heterogeneous tumors |
| Poster #59 | Perl | Joseph | The TOPAS Tool for Particle Simulation, a Monte Carlo Simulation Tool for Physics, Biology and Clinical Research |
| Poster #60 | Pochet | Nathalie | The *AMARETTO Framework: Multimodal and Multiscale Network Inferencefor Driver and Drug Discovery in Cancer |
| Poster #61 | Pratt | Dexter | NDEx in 2019: Workflows and Application Integration |
| Poster #62 | Pratt | Dexter | How to Integrate your Web App with NDEx and the Cytoscape Ecosystem |
| Poster #63 | Prior | Fred | Semantic Integration of Neuroinformatics Data in the Arkansas Image Enterprise System (ARIES) |
| Poster #64 | Qiao | Yi | scBayes: a computational method to study tumor subclone-specific gene expression and chromatin accessibility using single cell RNA sequencing and single cell ATAC sequencing in combination of bulk DNA sequencing |
| Poster #65 | Qin | Li-Xuan | Statistical Evaluation and Selection of Normalization Methods for microRNA Sequencing Data in Cancer Biomarker Studies |

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| Poster #66 | Raumann | Brigitte | A new browser-based application to allow self-service exploration and visualization of cancer registry data by reseachers |
| Poster #67 | Reich | Michael | GenePattern Notebooks for Cancer Research |
| Poster #68 | Robinson | James | The Integrative Cancer Genomics Viewer (IGV): visualization supporting cancer research |
| Poster #69 | Rubinstein | Samuel | Compound somatic mutations in the GENIE cancer database: a descriptive analysis |
| Poster #70 | Savova | Guergana | Annotation and sources for clinical data |
| Poster #71 | Sekar | Shobana | Application of CNVnator to analyze copy number alterations in cancer |
| Poster #72 | Shapiro | Linda | A Unified Machine Learning Package for Cancer Diagnosis |
| Poster #73 | Sharma | Ashish | PRISM — Platforms for Quantitative Imaging Informatics in Precision Medicine |
| Poster #74 | Sigworth | Elizabeth | Real-world Investigation of Hypomagnesemia in the Setting of Platinum Exposure |
| Poster #75 | Song | Li | Bioinformatics Technology to Characterize Tumor Infiltrating Immune Repositories |
| Poster #76 | Tan | Kai | Diverse noncoding mutations contribute to deregulation of cis-regulatory landscape in pediatric cancers |
| Poster #77 | Urban | Trinity | Crowds Cure Cancer: Crowd-sourcing ground-truth measurements on publicly available imaging data |
| Poster #78 | Waller | Rosalie | Structured Interviews in Primary Care Reveal Extensive Variation in Family Health History Collection Strategies |
| Poster #79 | Warner | Jeremy | HemOnc: A New Standard Vocabulary for Chemotherapy Regimen Representation in the OMOP Common Data Model |
| Poster #80 | Weinstein | John | Next-Generation Clustered Heat Maps (NGCHMs) for Multiple User Communities |
| Poster #81 | Wu | Xiaodong | What does AI see? Deep segmentation networks discover biomarkers for lung cancer survival |
| Poster #82 | Xing | Fyuyong | Deep Pixel-to-pixel Learning for Single-stage Nucleus Recognition in Digital Pathology Images |
| Poster #83 | Xu | Hua | Developing customizable cancer information extraction modules for pathology reports using CLAMP |
| Poster #84 | Yang | Ei-Wen | Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA |
| Poster #85 | Zhang | GQ | An Ontology Driven Faceted Query Engine for the Kentucky Cancer Registry |
| Poster #86 | Zhu | Jing | Million-cell scale single-cell RNA-seq data visualization using UCSC Xena Visual Spreadsheet |