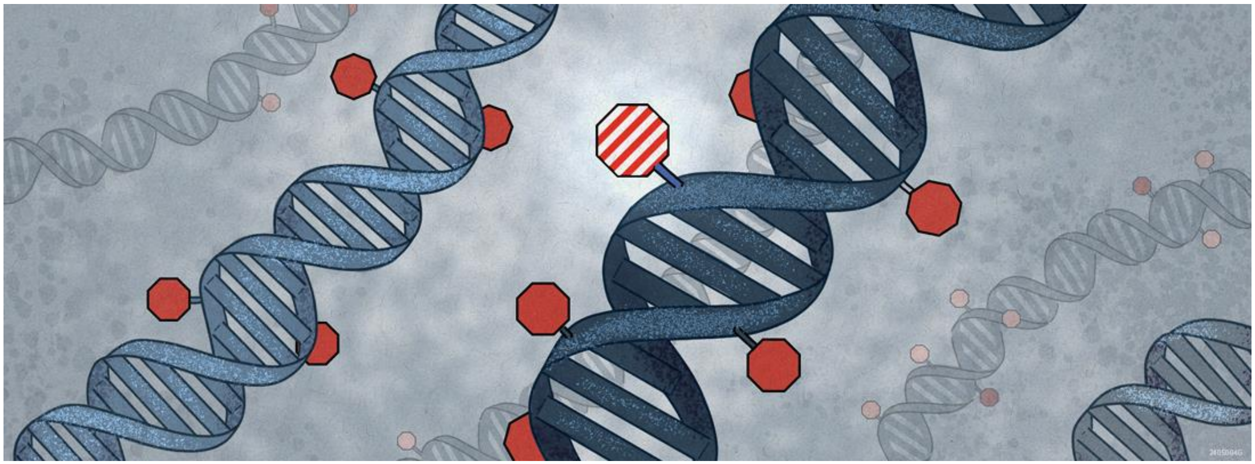
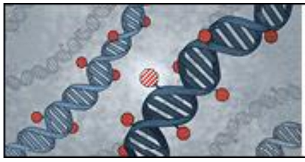




AACR Special Conference on

DNA Methylation, Clonal Hematopoiesis, and Cancer

February 1-4, 2025 | San Diego, CA

AACR
American Association for Cancer Research®

2405004E

POSTER LISTING

**Current as of December 31, 2024*

PROFFERED PRESENTATIONS

POSTER SESSION A

POSTER SESSION B

Proffered Presentations

PR001, A001 ZNFX1 is a master regulator and tumor suppressor in epigenetically-induced pathogen mimicry, mitochondrial dysfunction and STING-dependent signaling in cancer. Feyruz V. Rassool, University of Maryland, Baltimore, Maryland.

PR002, A017 Characteristics of methylation heritability in human somatic cells. Lori D. Kregar, Wellcome Sanger Institute, Cambridge, United Kingdom.

PR003, A003 DNA methylation reveals metastatic colonization routes in ovarian cancer. Alexandra Lahtinen, University of Helsinki, Helsinki, Finland.

PR004, A005 Interplay between histone modifications and DNA methylation in cancer. Chao Lu, Columbia University, New York, New York.

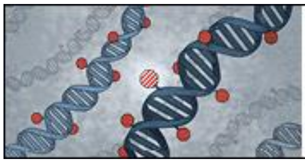
PR005, B009 Forced accumulation of R-loops through inhibiton of RNase H impairs the proliferation of TET-deficient cancer cells. Isaac F. López-Moyado, La Jolla Institute for Immunology, La Jolla, California.

PR006 An AML-associated mutation in DNMT3A gives rise to hyperactive T cells with alloimmune and anti-leukemic activity. LaShanale Wallace, St. Jude Children's Research Hospital, Memphis, Tennessee.

PR007, A011 High-throughput CRISPR screens uncover selective EZH2 inhibitor EPZ-6438 driving expansion of preleukemic hematopoietic stem cell with mutation in Asxl1. Ieva Budriunaite, University of Dundee, Dundee, United Kingdom.

PR008 Epigenetic regulation of transposable elements to reverse cancer immune evasion. Katherine B. Chiappinelli, The George Washington University, Washington, District of Columbia.

PR009 Decitabine/venetoclax reduced-toxicity induction: A very effective bridge-to-transplant in older AML patients with non-favorable genetics. Michael Lübbert, University of Freiburg Medical Center, Freiburg, Germany.



Poster Session A

Sunday, February 2

6:15-8:45 P.M.

A002 Epigenetic aging as a predictive biomarker of genetic and pharmacological vulnerabilities in cancer cells. Irene Fernández-Rebollo, Human Technopole, Milano, Italy.

A004 Blood DNA methylation in association with immune checkpoint inhibitor related outcomes among patients with head and neck squamous cell carcinoma. Gyeyoon Yim, Geisel School of Medicine at Dartmouth, Lebanon, New Hampshire.

A006 Copy number analysis of single-cell methylomes reveal distinct subclone methylation in early breast cancer. Ryan M. Mulqueen, MD Anderson Cancer Center, Houston, Texas.

A007 Regulation of DNA methylation and gene expression in T-cell acute lymphoblastic leukemia by IKAROS tumor suppressor. Sinisa Dovat, Penn State University College of Medicine, Hershey, Pennsylvania.

A008 Epigenetic dynamics in KMT2A-amplified leukemia. Jayme Ogino, Children's Hospital Los Angeles, Los Angeles, California.

A009 Direct multi-omics for the masses: Linking DNA methylation to chromatin targets via CUT&RUN-EM. Vishnu Sunitha Kumary, EpiCypher, Durham, North Carolina.

A010 Dnmt3a2 ensures proper enhancer DNA methylation during embryonic development. Guillermo A. Urrutia, Van Andel Institute, Grand Rapids, Michigan.

A012 Divergent impacts of DNMT3A and TET2 mutant clonal hematopoiesis on COVID-19 related outcomes. Jenna A. Fernandez, Mayo Clinic, Rochester, Minnesota.

A013 Clonal hematopoiesis as biomarker for 10-year risk of coronary heart disease in men with prostate cancer. Caroline Himbert, University of Utah/Huntsman Cancer Institute, Salt Lake City, Utah.

A014 Tet2 deficiency mitigates epigenetic aging in clonal hematopoiesis. Sheng Li, University of Southern California, Los Angeles, California.

A015 A prospective cohort study of biological aging and epigenetic age acceleration in 106 patients with age and therapy-related clonal hematopoiesis. Marissa Li, Mayo Clinic, Rochester, Minnesota.

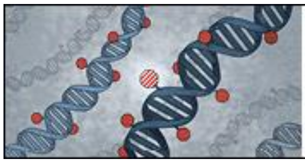
A016 DNA methylation variability in aging and Clonal Hematopoiesis. Anthony J. Pompetti, Coriell Institute for Medical Research, Camden, New Jersey.

A018 Association of clonal hematopoiesis and diabetes with mortality after autologous hematopoietic cell transplantation. June-Wha Rhee, City of Hope, Duarte, California.

A019 CRISPR-based investigation of CHIP mutations reveals their role in CAR-T therapy-related inflammatory toxicities. Xiuli Wang, City of Hope, Duarte, California.

A020 Clonal hematopoiesis is associated with acute kidney injury in the context of breast, endometrial, and ovarian cancers. Neil Ruthen, Computational Oncology Service, Memorial Sloan Kettering Cancer Center, New York, New York.

A021 Evolutionary trajectories and single cell methylation analysis of DNMT3A and TET2 mutant acute myeloid leukemia. Nisargbhai Shah, University of Pennsylvania, Philadelphia, Pennsylvania.



Poster Session B

Monday, February 3

6:45-9:15 P.M.

B001 A mutant ASXL1-EHMT complex contributes to heterochromatin dysfunction in clonal hematopoiesis and chronic monomyelocytic leukemia. Zhen Dong, La Jolla Institute for Immunology, La Jolla, California.

B002 DNA methylation protects cancer cells against senescence. Xiaoying Chen, Université Paris Cité, CNRS, Epigenetics and Cell Fate, Paris, France.

B003 BRAFV600E is essential for maintenance of the CpG island methylator phenotype and DNA methylation of PRC2 target genes in colon cancer. Layla El Bouazzaoui, UMC Utrecht, Utrecht, Netherlands.

B004 Promoter methylation gains in aging and cancer are independent of replication. Sara-Jayne Thursby, The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, Baltimore, Maryland.

B005 The functional role of transposable element-oncogene chimeric transcript during cancer progression. Wesley N. Saintilnord, Washington University School of Medicine in St. Louis, St. Louis, Missouri.

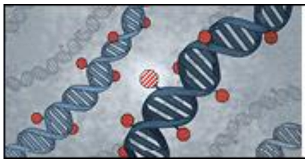
B006 Methylation variability and LINE-1 activation in plasmablastic multiple myleoma. Qianhui Wan, Department of Diabetes Complications and Metabolism, Beckman Research Institute, City of Hope, Duarte, California.

B007 Epigenetic reactivation of transposable elements as prognostic markers for PD1/PDL1 immunotherapy in cancer. Yixin Wu, Washington University in St. Louis, St. Louis, Missouri.

B008 Machine-learning modelling of lung cancer metastasis to the brain using alterations in DNA methylation. Jeffrey A. Zuccato, University of Toronto, Toronto, Ontario, Canada.

B010 Concurrent analysis of multiple methylated CpG sites using multiplex MethyLight assay for epithelial ovarian cancer detection. Deepa Bisht, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, India.

B011 Clinical correlation of PARP1, DNMT1 and GCS gene expression in ovarian cancer along with global methylation pattern (LINE1). Luxmi Devi, All India institute of medical sciences, New Delhi, India.



B012 The effect of a novel therapy on DNA methylation in Ewing Sarcoma. Emily Isenhart, Roswell Park Comprehensive Cancer Center, Buffalo, New York.

B013 Gene-body DNA methylation of ONECUT2 predicts its expression status and prostate cancer aggressiveness in clinic specimens. Gangning Liang, University of Southern California, Los Angeles, California.

B014 MCED - DNA methylation-based liquid biopsy for early detection of HPV-related cancers. Belinda Nedjai, Queen Mary University of London, West Drayton, United Kingdom.

B015 Collection and purification of microgram amounts of cfDNA from urine for methylation analysis. Floyd Taub, aiGENE, Inc., Golden, Colorado.

B016 Identify DNA methylation signatures to predict chemo-resistance retinoblastoma in aqueous humor liquid biopsy. Liya Xu, Children's Hospital Los Angeles, Los Angles, California.

B017 Detection of aberrant DNA methylation profiles in saliva samples as a potential screening method for Barrett's Esophagus and esophageal adenocarcinoma. Ying Yu, Cancer Early Detection Advanced Research Center (CEDAR), Knight Cancer Institute, Oregon Health & Science University, Portland, Oregon.

B019 Hypomethylating agents induce DNA methylation heterogeneity in AML cells and have persistent transcriptional and metabolic effects that are independent of global methylation loss. Heather J. Lee, The University of Newcastle, Callaghan, New South Wales, Australia.

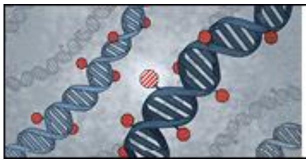
B020 Sensitization of acute myeloid leukemia cells to the antileukemic activity of all-trans retinoic acid (ATRA) by decitabine is p53-independent. Usama-Ur Rehman, ZTZ, Uniklinik Freiburg, Freiburg, Germany.

B021 Epigenetic reprogramming with DNA methylation inhibitors during CAR T cell manufacturing enhances anti-tumor activity, persistence, and cytotoxicity against solid and brain tumors. Elton L. VanNoy, Children's National Hospital, Washington, District of Columbia.

B022 TEDEdb: Transposable element differential expression database. Gennaro H. Calendo, Coriell Institute for Medical Research, Camden, New Jersey.

B023 Harnessing the dual therapeutic approach of CRISPR/CAS9 and CAR-T cell technologies in KRAS mutated solid tumors. Danish Kadir, South Dakota State University, Brookings, South Dakota.

B024 Transposable elements activation produces pan-cancer tumor-specific neoantigens. Yonghao Liang, Washington University in St. Louis, St. Louis.



B025 Inducible mouse models of cancer driver mutations as a powerful tool for in vivo and epigenetic studies of colorectal cancer. Mary Olesnavich, Van Andel Institute, Grand Rapids, Michigan.

B026 NEBNext® enzymatic solutions for DNA methylation profiling at picogram scale. Vaishnavi panchapakesa, New England Biolabs, Ipswich, Massachusetts.

B027 Modeling age-related DNA methylation changes with intestinal organoids. Himani Vaidya, Coriell Institute for Medical Research, Camden, New Jersey.

B028 Epigenetic landscape and gene regulations in embryonal brain tumors with multilayered rosettes (ETMR). Shanzheng Wang, Hopp Children´s Cancer Center (KiTZ),German Cancer Research Center (DKFZ) and German Cancer Consortium (DKTK), and Heidelberg University, Heidelberg, Germany.