### **TUESDAY, MAY 16**

5:00 p.m. - 6:00 p.m. Welcome and Opening Keynote

**Grand Ballroom** 

SWI/SNF (BAF) complex mutations in cancer: Mechanisms and vulnerabilities Charles W. M. Roberts, St. Jude Children's Research Hospital, Memphis, TN

6:00 p.m. - 8:30 p.m. Welcome Reception

Columbus Ballroom

### **WEDNESDAY, MAY 17**

7:00 a.m. - 8:00 a.m. Breakfast

Columbus Ballroom

8:00 a.m. – 10:00 a.m. Plenary Session 1: Genomics

Grand Ballroom

Session Chair: David Malkin, The Hospital for Sick Children, Toronto, ON, Canada

Modeling sarcoma susceptibility: The Li-Fraumeni syndrome paradigm

David Malkin

Translating genomic risk into an early detection strategy for sarcoma

David M. Thomas, Garvan Institute of Medical Research, Darlinghurst, NSW, Australia

Targeting the expression of EWS-FLI1

Natasha J. Caplen, National Cancer Institute, Bethesda, MD

A DNA methylation-based classifier for accurate molecular diagnosis of bone sarcomas\*

Shengyang Wu, NYU School of Medicine, New York, NY

Lnc-ing Ewing sarcoma susceptibility to translational stress response\* Heinrich Kovar, Children´s Cancer Research Institute, Vienna, Austria

10:00 a.m. - 10:30 a.m. Break

Grand Ballroom Foyer

10:30 a.m. – 12:30 p.m. Plenary Session 2: 'Omics

Grand Ballroom

Session Chair: Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA

Genomic approaches to drug discovery

Todd R. Golub

Targeting ATP-dependent chromatin remodeling complexes in human sarcomas

Cigall Kadoch, Dana-Farber Cancer Institute, Boston, MA

<sup>\*</sup>Short talk from proffered abstract

Cancer drug target identification using domain-focused CRISPR screening Christopher R. Vakoc, Cold Spring Harbor Laboratory Cancer Center, Cold Spring Harbor, NY

Enhancer reprogramming mediates metastatic competence in osteosarcoma\* James J. Morrow, Case Western Reserve University School of Medicine, Cleveland, OH

Progress towards development of an exosome-based biomarker assay in Ewing sarcoma\* Glenson Samuel, The Children's Mercy Hospital, Kansas City, MO

12:30 p.m. – 2:30 p.m. Lunch on own

2:30 p.m. - 4:30 p.m. Plenary Session 3: Novel Model Systems

**Grand Ballroom** 

Session Chair: David M. Langenau, Massachusetts General Hospital/

Harvard Medical School, Charlestown, MA

Analysis of a histiocytic carcinoma in the dog: The canine's utility in fetching disease genes

Elaine A. Ostrander, National Human Genome Research Institute, Bethesda, MD

A dog in the fight: How pet dogs with cancer can inform clinical research

William C. Eward, Duke University, Durham, NC

Vangl2 regulates stem cell self-renewal programs and growth in rhabdomyosarcoma David M. Langenau

Familial cancer patient specific iPSCs based study of a potential oncogenic factor, sFRP2, in osteosarcoma\*

Huen Suk Kim, Icahn School of Medicine, New York, NY

Functional genomics of CIC-DUX4 fusions in zebrafish recapitulates the spectrum of human CIC-rearranged cancers\*

James F. Amatruda, UT Southwestern Medical Center, Dallas, TX

4:30 p.m. – 7:00 p.m. Reception and Poster Session A

Columbus Ballroom

#### **THURSDAY, MAY 18**

7:00 a.m. - 8:00 a.m. Breakfast

Columbus Ballroom

8:00 a.m. - 10:00 a.m. Plenary Session 4: Signaling Perturbations and Targeted Therapeutics

Grand Ballroom

Session Chair: Benjamin A. Alman, Duke University, Durham, NC

CDK4 inhibition and senescence: Pathway understanding leads to rational drug combinations Andrew Koff, Memorial Sloan Kettering Cancer Center, New York, NY

<sup>\*</sup>Short talk from proffered abstract

Epigenetic deregulation of the Hippo pathway mediates NF-κB driven sarcomagenesis T. S. Karin Eisinger, University of Pennsylvania School of Medicine, Philadelphia, PA

Dynamic cell populations are responsible for sarcoma propagating potential Benjamin A. Alman

Stress-associated selective mRNA translation and sarcoma metastasis\*

Amal M. EL-Naggar, British Columbia Cancer Research Centre, Vancouver, BC, Canada

Ubiquitin-specific protease 6 (USP6) oncogene confers sensitivity of Ewing sarcoma to interferon cytotoxicity\*

lan Henrich, University of Pennsylvania, Philadelphia, PA

10:00 a.m. - 10:30 a.m.

**Break** 

Grand Ballroom Foyer

10:30 a.m. - 12:45 p.m.

Plenary Session 5: Neurofibromatosis and MPNST

**Grand Ballroom** 

Session Chair: Ping Chi, Memorial Sloan Kettering Cancer Center, New York, NY

Molecular pathogenesis of malignant peripheral nerve sheath tumor Ping Chi

Using gene expression analyses to identify MPNST therapeutics

Nancy Ratner, Cincinnati Children's Hospital Medical Center, Cincinnati, OH

Natural history of peripheral nerve sheath tumors in NF1: Identification and characterization of malignant precursor lesions

Brigitte C. Widemann, National Cancer Institute, Bethesda, MD

Molecular pathogenesis and drug synergy in a zebrafish model of NF1-associated MPNST A. Thomas Look, Dana-Farber Cancer Institute, Boston, MA

Modeling the tumor microenvironment in sarcoma: The impact on MPNST biology and chemotherapeutic response\*

Rebecca Dodd, University of Iowa, Iowa City, IA

Development and characterization of novel/genetically defined mouse models of malignant peripheral nerve sheath tumor for preclinical therapeutics testing\*

Amish J. Patel, Memorial Sloan Kettering Cancer Center, New York, NY

12:45 p.m. - 3:15 p.m.

**Lunch and Poster Session B** 

Columbus Ballroom

3:15 p.m. - 5:15 p.m.

**Plenary Session 6: Novel Biologic Mechanisms** 

Grand Ballroom

Session Chair: Cristina K. Antonescu, Memorial Sloan Kettering Cancer Center,

New York, NY

Integrin-alpha 10 signaling pathway drives sarcomagenesis in mxyofibrosarcoma and undifferentiated pleomorphic sarcoma

Samuel Singer, Memorial Sloan Kettering Cancer Center, New York, NY

Emerging genetic mechanisms in undifferentiated round cell sarcomas

Cristina K. Antonescu

<sup>\*</sup>Short talk from proffered abstract

Autophagy in alveolar soft part sarcomagenesis

Kevin B. Jones, University of Utah Huntsman Cancer Institute, Salt Lake City, UT

SSX-mediated chromatin engagement and targeting of BAF complexes activates oncogenic transcription in synovial sarcoma\*

Matthew J. McBride, Dana-Farber Cancer Institute and Harvard Medical School, Boston, MA

Histone H3K36 mutations promote sarcomagenesis through altered histone methylation landscape\*

Chao Lu, The Rockefeller University, New York, NY

5:15 p.m. Evening off

#### FRIDAY, MAY 19

7:00 a.m. - 8:00 a.m. Breakfast

Columbus Ballroom

8:00 a.m. – 10:00 a.m. Plenary Session 7: Immune Modulation and Microenvironment

**Grand Ballroom** 

Session Chair: Irene L. Andrulis, University of Toronto Mount Sinai Hospital,

Toronto, ON, Canada

Immune mechanisms in gastrointestinal stromal tumor

Ronald P. DeMatteo, Memorial Sloan Kettering Cancer Center, New York, NY

Injury promotes sarcomagenesis

David G. Kirsch, Duke University Medical Center, Durham, NC

Variation in the immune cell infiltrate and expression of PD-L1 in sarcoma subtypes

Irene L. Andrulis

Pivotal role of Interleukin 23 in osteosarcoma development and its link with glutamate

metabotropic 4: Identification of novel therapeutic targets for osteosarcoma\*

Maya Kansara, Kinghorn Cancer Centre/Garvan Institute of Medical Research, Sydney,

NSW, Australia

Immune cell transcript levels, metastatic progression, and survival in osteosarcoma: A

comparative transcriptome analysis\*

Aaron Sarver, University of Minnesota, Minneapolis, MN

10:00 a.m. - 10:30 a.m. Break

Grand Ballroom Foyer

10:30 a.m. – 12:30 p.m. Plenary Session 8: Disease Progression

Grand Ballroom

Session Chair: Jonathan A. Fletcher, Brigham and Women's Hospital, Boston, MA

Identification of therapies for plexiform neurofibromas, a precursor of malignant peripheral nerve sheath tumors

D. Wade Clapp, Indiana University School of Medicine, Indianapolis, IN

<sup>\*</sup>Short talk from proffered abstract

TBD

Jonathan A. Fletcher

Cell plasticity and metastatic progression of Ewing sarcoma Elizabeth R. Lawlor, University of Michigan, Ann Arbor, MI

Hypoxia, polyploidy, neuropeptide Y, and Ewing sarcoma bone metastases: Is there a link?\* Akanksha Mahajan, Georgetown University, Washington, DC

Multiplatform analysis of paired primary and recurrent well- and dedifferentiated liposarcoma samples defines copy number alterations as dominant drivers of initiation and progression\*

Aimee M. Crago, Memorial Sloan Kettering Cancer Center, New York, NY

12:30 p.m. Closing Remarks

<sup>\*</sup>Short talk from proffered abstract