

## REGISTRATION FORM

|  |   |
|--|---|
| <b>First Name</b>                              |   |
| <b>Last Name</b>                               |   |
| <b>Institution</b>                             |   |
| <b>Current Status</b>                          | <input type="checkbox"/> Master or bachelor student <input type="checkbox"/> PhD student<br><input type="checkbox"/> Post-doc <input type="checkbox"/> Others, please specify:_____                       |
| <b>Academic Discipline</b>                     | <input type="checkbox"/> Medicine <input type="checkbox"/> Pharmacology<br><input type="checkbox"/> Biology <input type="checkbox"/> Agriculture<br><input type="checkbox"/> Others, please specify:_____ |
| <b>Phone</b>                                   |   |
| <b>Email</b>                                   |   |
| <b>Attending Opening Ceremony &amp; Dinner</b> | <input type="checkbox"/> Yes <input type="checkbox"/> No  |
| <b>Accommodations</b>                          | Participants are responsible for their own accommodations for the day 5 <sup>th</sup> November.   |

**ABSTRACT**

**Tumor Genome Project: From Sequence to Function**

Author (s)

Affiliation/Institution Name

City, Country

Tumor genomes can be highly rearranged and non colinear with the host genome. Recurrent genome rearrangements involve genes that are increasingly targeted by anti-tumor therapeutics. Current technologies for studying tumor genomes do not determine their structure and relate it to the underlying sequence. Thus, the role of translocations and inversions in solid tumors is poorly understood. Even the structural organization of amplicons remains largely enigmatic. End Sequence Profiling (ESP) is a sequence-based method for directly determining the structure of tumor genomes, and for cloning all types of rearrangements en masse. **(Times New Roman, 12 pt, normal)**

**Keywords: (provide 3 keywords, Times New Roman, 12 pt, bold)**

**Tables (if any)**

**Figures (if any)**