

## Lee Zou, PhD



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Cancer is a complex disease driven by genetic and epigenetic alterations in the genome. To prevent these detrimental alterations, cells have evolved an intricate signaling network, called the DNA damage checkpoint, to detect and signal problems in the genome. During cancer development, the activation of oncogenes and loss of tumor suppressors leads to genomic instability, rendering cancer cells increasingly dependent upon specific DNA repair and checkpoint signaling proteins to survive. **The Zou laboratory** is particularly interested in understanding how the checkpoint detects DNA damage and genomic instability, and how the checkpoint can be targeted in cancer therapy. Our current studies are focused on the activation of ATR and ATM, the master sensor kinases of two major checkpoint pathways. Furthermore, we are developing new strategies to exploit the genomic instability and checkpoint addition of different cancer cells in targeted cancer therapy.

### Sensing of DNA Damage, Replication Stress, and Transcription Problems

ATM and ATR are two master checkpoint kinases in human cells. In particular, ATR is the key responder to a broad spectrum of DNA damage and DNA replication problems. To understand how ATR is activated, we sought to identify the key DNA structural elements and sensor proteins that activate ATR. We have developed unique biochemical and cell biological assays to dissect the process of ATR activation. Our recent studies have revealed that ATR is important not only for sensing DNA damage and replication stress, but also for problems associated with transcription. R loops, which arise from stable DNA:RNA hybrids during transcription, are a major source of genomic instability. We found that ATR is activated by R loops and plays a key role in suppressing R loop-induced genomic instability, thus, uncovering a new function of ATR in safeguarding the genome.

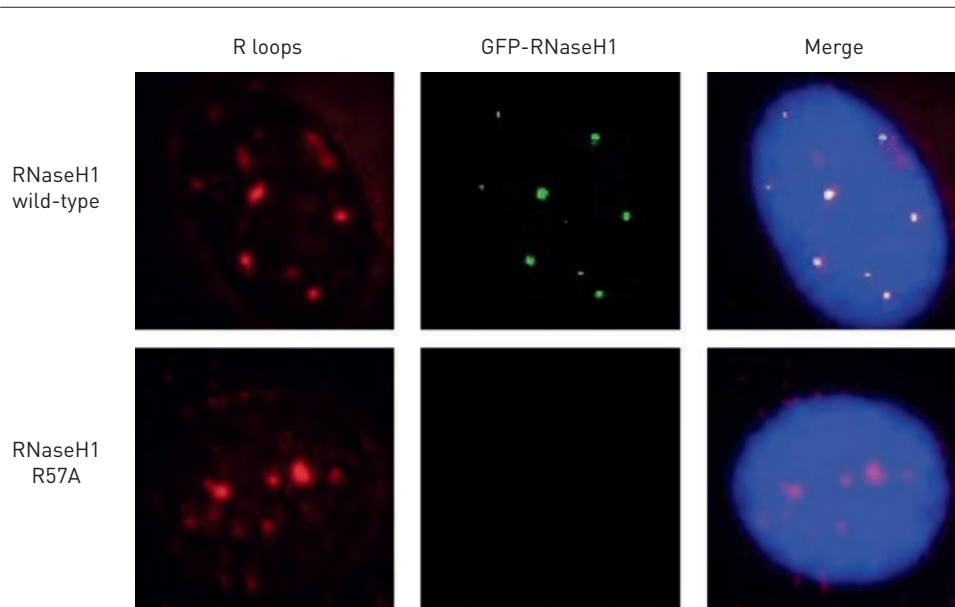
### Checkpoint, DNA Replication, DNA Repair, Telomeres, Centromeres and the Cell Cycle

The ATR checkpoint plays a key role in

regulating and coordinating DNA replication, DNA repair, and cell cycle transitions. During the past few years, our studies have identified a number of novel roles that ATR plays in protecting the genome, such as: suppressing single-stranded DNA (ssDNA) accumulation during DNA replication, regulating homologous recombination (HR), and promoting alternative lengthening of telomeres (ALT). Recently, we have discovered a surprising function of ATR in mitosis. We have shown that ATR is localized to centromeres in mitosis, where it is activated by centromeric R loops. The activation of ATR at centromeres is critical for faithful chromosome segregation, thus revealing the unexpected importance of ATR in suppressing chromosomal instability (CIN).

### RNA, DNA repair and Genomic Integrity

Non-coding RNAs are important components and regulators of chromatin. We are interested in understanding how non-coding RNAs affect DNA repair and genomic stability in specific chromosomal regions.



This image shows that GFP-tagged RNaseH1 (green) localizes to sites of R loops (red) through binding to RPA. R loops are transcription intermediates that contain RNA:DNA hybrids and single-stranded DNA (ssDNA). RPA is a protein complex that recognizes ssDNA. RNaseH1 is an enzyme that suppresses R loops by cleaving the RNA in RNA:DNA hybrids. Wild-type RNaseH1 recognizes R loops through binding to RPA, but the R57A mutant of RNaseH1, which is defective for RPA binding, fails to recognize R loops.

For example, the telomere non-coding RNA TERRA is upregulated in ALT-positive tumors, and may regulate the lengthening of telomeres through a unique DNA repair pathway. Moreover, centromeric RNAs form R loops in mitotic cells, promoting ATR activation and accurate chromosome segregation. In addition to non-coding RNAs, our recent studies also suggest that even coding RNA transcripts may directly participate in the repair of DNA breaks, revealing another function of RNA in the regulation of genomic integrity.

### Cancer Genomics, Tumor evolution and Targeted Cancer Therapy

During the evolution of tumors, cancer cells acquire mutations through a variety of mechanisms. We recently discovered that APOBEC3A/B proteins, two cytidine deaminases that are aberrantly expressed in multiple types of cancers, induce DNA replication stress and render cancer cells

susceptible to ATR inhibition. Working with the team of Dr. Michael Lawrence, we find that APOBEC3A prefers substrate sites in DNA hairpins, leading to the discovery of passenger hotspot mutations in cancer. Furthermore, in collaboration with Dr. Tim Graubert, we find that the splicing factor mutations associated with myelodysplastic syndromes (MDS) and acute myeloid leukemia (AML) induce R loops and trigger an ATR response. Cells that express these splicing factor mutants are sensitive to ATR inhibitors, providing a new strategy for the treatment of MDS and possibly other malignancies associated with RNA splicing defects.

### Selected Publications:

Buisson R, Langenbucher A, Bowen D, Kwan EE, Benes CH, Zou L\*, and Lawrence SM\*. (2019) Passenger Hotspot Mutations in Cancer Driven by APOBEC3A and Mesoscale Genomic Features. *Science* 364:eaaw2872.

Moquin MD, Buisson R, Genois MM, Ouyang J, Yadav T, Boukhali M., Morris R, Haas W, and Zou L. (2019) Localized Protein Biotinylation Identifies ZPET, a Repressor of Homologous Recombination. *Genes & Dev.* 33:75-89.

Nguyen HD, Leong WY, Li W, Walter M, Zou L\*, and Graubert T\*. (2018) Spliceosome mutations in myelodysplastic syndrome induce R loop-associated sensitivity to ATR inhibition. *Cancer Res.* 78:5363-5374.

Kabeche L, Nguyen HD, Buisson R, and Zou L. (2018) A mitosis-specific and R loop-driven ATR pathway promotes faithful chromosome segregation. *Science* 359:108-114.

Buisson R, Lawrence MS, Benes CH, and Zou L. (2017) APOBEC3A and APOBEC3B activities render cancer cells susceptible to ATR inhibition. *Cancer Res.* 77:4567-4578.

Nguyen HD, Yadav T, Giri S, Saez B, Graubert TA, and Zou L. (2017) Functions of RPA as a Sensor of R Loops and a Regulator of RNaseH1. *Mol. Cell* 65:832-847.

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