

IMEG Seminar Series

The road to global science



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July 24th, 2023, 16:00-17:00

Non-canonical functions of UHRF1 maintain DNA methylation in cancer cells

This seminar series is open to all students and researchers in Kumamoto University.

The Zoom ID and passcode were sent via email. Check your inbox!

DNA methylation regulates gene expression and genome stability, and it is altered in various human diseases including cancer. The DNA methylome is shaped by the de novo methyltransferases DNMT3A and DNMT3B, and by the TET demethylases. In addition, at every round of DNA replication, the enzyme DNMT1, aided by its regulator UHRF1, reproduces the parental methylome. It is yet unclear if DNMT1 and UHRF1 are fully necessary for cancer cell survival, and whether their role is limited to maintenance DNA methylation. Using degron alleles, we show that, while their removal causes a strong proliferation defect, neither protein is strictly necessary for cell cycle progression or survival. Molecularly, bioinformatics, proteomics and genetics establish that UHRF1, besides regulating DNMT1, modulates DNMT3A, DNMT3B, and TET2 activity. Our results advance our understanding of epigenetic homeostasis in health and disease, and the tools we developed are valuable for future research on key chromatin regulators.

