Institute of Molecular Biology

IMB TechTalk

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"Quantitative DNA breakome analysis in low-input samples"

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Venue: IMB Auditorium, Ground Floor

Institute of Molecular Biology (IMB)

Johannes Gutenberg University Campus Mainz

All are welcome to attend

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Abstract:

Quantitative DNA breakome analysis in low-input samples

We have recently described a method for DNA double-strand breaks (DSBs) genome-wide mapping based on Breaks Labeling, Enrichment on Streptavidin and Sequencing (BLESS). Using BLESS, we mapped the genomic landscape of DSBs – breakome – induced by replication stress, and identified specific repetitive element classes that are highly fragile in response to replication stress. We are currently evolving the BLESS method with two goals i) achieving robust quantification of breakomes in low-input samples, such as rare or difficult to grow cell populations and tissue sections; ii) scale up the number of samples that can be processed in parallel in an efficient manner. Our aim is to provide the DNA damage and repair community with powerful tools to study DNA fragility at both nucleotide resolution and genome-wide scale.