Open Ph.D. projects

1.

Announcer: Lajos Haracska

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Bioinformatic developments for the analysis of next-generation sequencing data

Description of the research topic: One of the fastest evolving fields of biology is next-generation sequencing (NGS). NGS procedures are capable of generating a significant amount of genomic data in a cost-efficient way. Though general bioinformatic methods have already been implemented, the adaptation of these to different sample preparation methods requires new development. Such a development is the introduction of unique molecular counters via which every single original piece of DNA is linked with a unique molecular counter, thus, by identifying these, later the original amount of templates can be determined precisely, independently of the amplification steps. Molecular counters help reduce faults during library preparation. The topic involves working on developments related to all currently available NGS methods (ChIP-Seq, RNA seq, Metagenom, Single cell techniques).

2.

Announcer: Lajos Haracska

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Studying genes that have a role in maintaining genome stability via Crisper/Cas9 and RNA-interference-based gene silencing

Description of the research topic: To study genes that participate in maintaining genome stability, we employ Crisper/Cas9 and RNA-interference-based gene silencing and analyse the role of proteins affecting the speed of DNA replication, via special confocal microscopy, in the presence of different agents (tumour therapeutic drugs, DNA-damaging agents, replication inhibitors). We study DNA-damage tolerance and repair processes using special fluorescent labelling and microscopic techniques. We implement state-of-the-art technology (live-cell microscopy, single-cell qualitative and quantitative analyses) in our laboratory.

Our research tools include human tissue culture-based reporter systems, next-generation sequencing, and reconstituted in vivo systems using purified proteins. Our investigations will provide deeper insight into the molecular processes of genome instability and carcinogenesis, and by identifying new tumour markers and drug targets, we will be able to contribute to the prevention of resistance to tumortherapeutic drugs and the development of personalised tumour therapy.

3.

Announcer: Lajos Haracska

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Studying DNA repair

Description of the research topic: DNA-repair pathways and genes are known to be essential for the maintenance of genome stability. Damage to the functioning of these genes, e.g., due to mutation-induced inactivation, may lead to genome instability and cancer. We have begun the identification and characterization of new small-molecule modulators of DNA repair. Our approach involves chemical biology, and we perform high-throughput screens utilizing the state-of-the-art Alpha assay technology.

4.

Announcer: Lajos Haracska

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Drug development via the identification of small molecule inhibitors of mutagenesis and carcinogenesis

Description of the research topic: It is known that the main driving force of carcinogenesis is the development of mutations and the acceleration of this process. Our project involves the identification and characterization of small molecule inhibitors that affect the development of new mutations by binding to DNA repair proteins and thus inhibiting their activity. The identified small molecule inhibitors are tested both in vitro (their physical relationships with the target protein, their inhibitory effect on enzyme activity) and in vivo in tissue culture models to determine their impact on cell growth and genome stability. Our final goal is to identify inhibitors that will lead to the development of new drugs with which we can inhibit the increase of genetic instability and the development of drug resistance in tumours.

5.

Announcer: Lajos Haracska

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Molecular analysis of carcinogenesis and mutagenesis

Description of the research topic: In cells, DNA is damaged by several endogenous and exogenous factors. If the damage is not repaired, the replication machinery stalls during DNA doubling. Different mechanisms have

evolved to rescue stalled replication forks; these help replication proceed over damaged DNA in an error-free or error-prone way. Error-prone processes, which cause mutations, increase the risk of carcinogenesis, while error-free replication protects genome stability and thus fulfils a tumour suppressor function.

Our research group investigates the causes and mechanisms of mutagenesis and carcinogenesis and strives to answer the questions of what the common roots of evolution and carcinogenesis are and how point mutations and chromosome rearrangements are generated.

6.

Announcer: Lajos Haracska

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Next-generation DNA and RNA sequencing and their employment in the molecular diagnostics of diseases

Description of the research topic: Non-invasive genetic diagnostics, or liquid biopsy, is based on the analysis of DNA or RNA isolated from the cell-free fraction of the blood. The term includes molecular diagnostic procedures that monitor different changes in the organism by sequencing and quantitating circulating cell-free nucleic acids. Currently, these types of methods represent the fastest evolving field in the precise diagnostics and characterisation of tumorous diseases and foetal genetic disorders. From a diagnostic point of view, the common characteristic of these two conditions is that the wild-type background derived from the tumour or the foetus is in great excess in the otherwise very limited amount of genetic material in the blood plasma.

Our research group works on developing panels with which the most frequent alterations found in certain diseases can be analysed via the next-generation sequencing of specific targeted regions.