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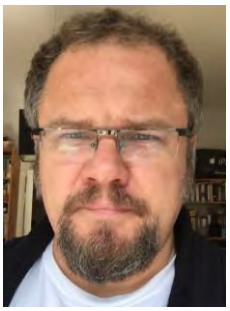
MART LOOG

CV

PARTICIPANT AT:



SYNTHETIC BIOLOGY.
FROM STANDARD BIOLOGICAL PARTS TO ARTIFICIAL LIFE

September, 17th-18th, 2015, Barcelona

Mart Loog, Professor of Molecular Systems Biology, Institute of Technology, University of Tartu, Tartu, Estonia

Mart Loog is professor of molecular systems biology and head of a research group at the Institute of Technology, University of Tartu. Mart received PhD in medicinal biochemistry from Uppsala University, Sweden in 2002, followed by postdoctoral training at University of California, San Francisco. In 2006 Mart established his laboratory at the newly established Institute of Technology. He has received several international fellowships and awards including The Welcome Trust Senior International Fellowship and a startup research grant from European Molecular Biology Organization (EMBO) and Howard Hughes Medical Institute (HHMI). In 2012 he received Estonian National Science Prize in chemistry and molecular biology. In 2015 he was awarded the ERC Consolidator Grant and became a principal coordinator of a H2020 ERA Chair project SynBioTEC to establish the multidisciplinary Centre of Synthetic Biology. Mart's research directions include regulation of eukaryotic cell cycle, synthetic circuit design and systems biology of regulatory networks.

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ABSTRACT

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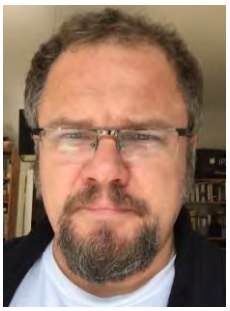

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Multisite Phosphorylation Networks as Tunable Circuit Elements for Synthetic Biology Applications

Multisite phosphorylation of proteins is a powerful signal processing mechanism playing crucial roles in cell division and differentiation as well as in disease. We recently demonstrated a novel phenomenon of multisite phosphorylation in cell cycle regulation. We showed that cyclin-dependent kinase (CDK)-dependent multisite phosphorylation of a crucial substrate is performed semiprocessively in the N-to-C terminal direction along the disordered protein. The process is controlled by key parameters including the distance between phosphorylation sites, the distribution of serines and threonines in sites, and the position of docking motifs. According to our model, linear patterns of phosphorylation networks along the disordered protein segments determine the net phosphorylation rate of the protein. Additionally, by introducing diversional phosphorylation sites for multiple kinase inputs three-branched switches can be designed. Similar principles of sequential signal processing via multisite phosphorylation can be applied to synthetic circuit design. A toolbox of synthetic parts based on multisite phosphorylation would revolutionize the field because of the fast time scales and wide combinatorial possibilities.

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