hexadecenal. The obtained results suggest the described mechanism of free radical fragmentation of sphingolipids may be implemented on cell culture under stress of reactive chlorinating species.

We demonstrated that 2-hexadecenal causes cytoskeletal reorganization during neutrophil adhesion which is revealed by increasing of both F-actin content and the cells' size. 2-Hexadecenal can regulate the redox state of neutrophils which stimulated by chemotactic peptide fMLP, redistributing contribution of myeloperoxidase, phospholipase A_2 and enzymes of arachidonic acid metabolism in the formation of reactive oxygen and halogen species.

These findings evidence the existence of non-enzymatic pathway of sphingolipid destruction leading to formation of 2-hexadecenal, which possesses a wide spectrum of biological activity. Therefore, any change in the sphingolipid/2-hexadecenal ratio in a cell should play an important role in the signaling way switchover mechanisms and, as a consequence, in functioning of the cell. Hence, realization of non-enzymatic reactions leading to formation of 2-hexadecenal in living organisms may influence functions of the latter.

Keywords: 2-hexadecenal, reactive chlorinating species, sphingolipids.

WED-029
How can we quantify ligand sensitivity for single-cell heterogenous dynamical responses?

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All biological organisms need to sense and response to their environment. At the level of single cells, surface receptors convert extracellular cues into activation of transcription factors that control cellular decisions.

A considerable unresolved issue is how information about ligand binding is encoded into nuclear activity of the transcription factors. A growing number of studies supports the hypothesis that this is achieved by temporal regulation of their activities. The current challenge is to recognise the features of temporal activity profile that represent information about a given stimulus.

A natural strategy to decipher this temporal coding is to scan cellular responses across a range of considered stimuli and identify most sensitive features of temporal profiles. Methods however to quantify sensitivity at the single cell level, where stochastic effects play a major role, are virtually missing. We have developed a statistical framework to measure sensitivity of cellular outcomes from time-resolved, single cell, heterogeneous responses. The method allow us to quantify changes in response to stimuli despite substantial heterogeneity of single cell behaviours.

We use the method to analyse nuclear translocation of the NF-kB transcription factor upon TNF stimulation in mouse embryonic fibroblasts. We identified how the sensitivity the system changes with TNF concentration and indicate the essential features of the nuclear NF-kB temporal profile that are most sensitive to TNF changes. Our method provides essential methodological advancement needed to gain understanding how temporal activity profiles encode information about a given stimulus.

Keywords: Information Processing, Sensitivity Analysis, Signal Transduction.

WED-030
How do peptidic tree-like molecules fold?

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Peptide dendrimers are tree-like molecules formed by alternating functional amino acids with branching diamino acids such as lysine [1]. Dendrimers of this kind have already rendered several models for different applications, such as vitamin B12 transporters, antimicrobial agents and catalytic systems.

Unfortunately these molecules have not yet yield to experimental structural characterization, hampering the possibility of constructing truly tailor-made peptide dendrimers and improve the existing ones. Computational methods seem to be an adequate tool to address these issues.

Herein we present a comprehensive set of computational studies using molecular dynamics simulation methods, including stochastic titration constant-pH simulations, to explore the conformational behavior of these molecules and the key determinants to such behavior [2,3].

Moreover, we unravel the first hints on the influence of pH in the folding of these molecules, and the role played by dendrimer-substrate interactions during dendrimer-catalyzed ester hydrolysis.

We used several conformational analysis procedures (clustering, energy landscapes and multivariate analysis) to analyze conformational changes that can be correlated with particular structural trends.

Our results show that peptide dendrimers exhibit a remarkable structural plasticity which is crucial for their activities.

This work provides new insights into the atomic-level structures of these systems and might, in a near future, contribute to the development of novel knowledge-based dendritic systems with enhanced functionalities.

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Keywords: Molecular Dynamics simulations, Peptide dendrimers.

WED-031
IKKα regulates hair follicle morphogenesis and hair growth cycle

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The IKKα protein is mainly known by its essential function in epithelial physiology. It is also recognized by its role in non-melanoma skin cancer (NMSC) tumor development. To gain insight into IKKα function in adult skin as well as in skin appendages such as hair follicles- considered the place of origin of NMSC-, we have generated IKKα-siRNA transgenic mice. Here, we compare the skin of these mice with that of IKKa+/- mice expressing reduced levels of IKKα.

Both types of transgenic mice show similar external phenotypic features consisting in scarce and ruffled hair. This hair coat phenotype was observed in the first hair growth cycle. After depilation, hair regrowth was delayed in IKKa-siRNA transgenic mice and