

SEMINAR ÜBER NEUERE ORGANISCH-CHEMISCHE ARBEITEN

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ORT: Hörsaal C, Zentralgebäude Chemie

REFERENT: Prof. Dr. Andreas Marx
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THEMA: *“Deciphering the Information Layer beyond the
Genome Sequence”*

http://www.uni-konstanz.de/chemie/~agmarx/group_hauptseite.htm

Die Dozenten für Organische Chemie

Abstract

Deciphering the Information Layer beyond the Genome Sequence

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The human genome consists of approximately 20,000 genes, which is only about five times the genome of the bacterium *E. coli* and significantly less compared to the genome of a potato or cabbage. This astonishingly low number of genes in the human genome was already discussed in the landmark C. Venter et al. *Science* paper from 2001 that reports on the human genome sequence stating the following: “The modest number of human genes means that we must look elsewhere for the mechanisms that generate the complexities inherent in human development and the sophisticated signaling systems that maintain homeostasis. There are a large number of ways in which the functions of individual genes and gene products are regulated.” Over the years, mechanisms have been elucidated that indeed show that proteins and nucleic acids are often chemically modified during their “life span” and that this is involved in regulating their action.

These processes include posttranslational modifications of proteins which represent an information level that is beyond the genetic code and varies with time and cellular location to allow cells to adjust protein activities to changes in intra- and extracellular conditions. Here, the protein-based modification *ubiquitin* and nucleic acid-reminiscent modification *poly(ADP-ribose)* are of particular interest to us. I will report about our recent results in studies on these biopolymers using synthetic tools.

Moreover, recent studies have highlighted the paramount importance of “non-standard” Watson-Crick nucleobases in DNA and RNA. I will report on our recent results in the aim to develop DNA polymerase-based systems that allow tracing of these rare nucleobases.