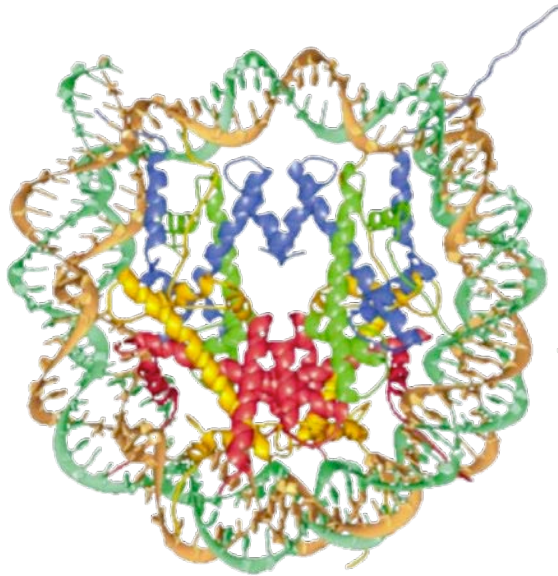


The Topic

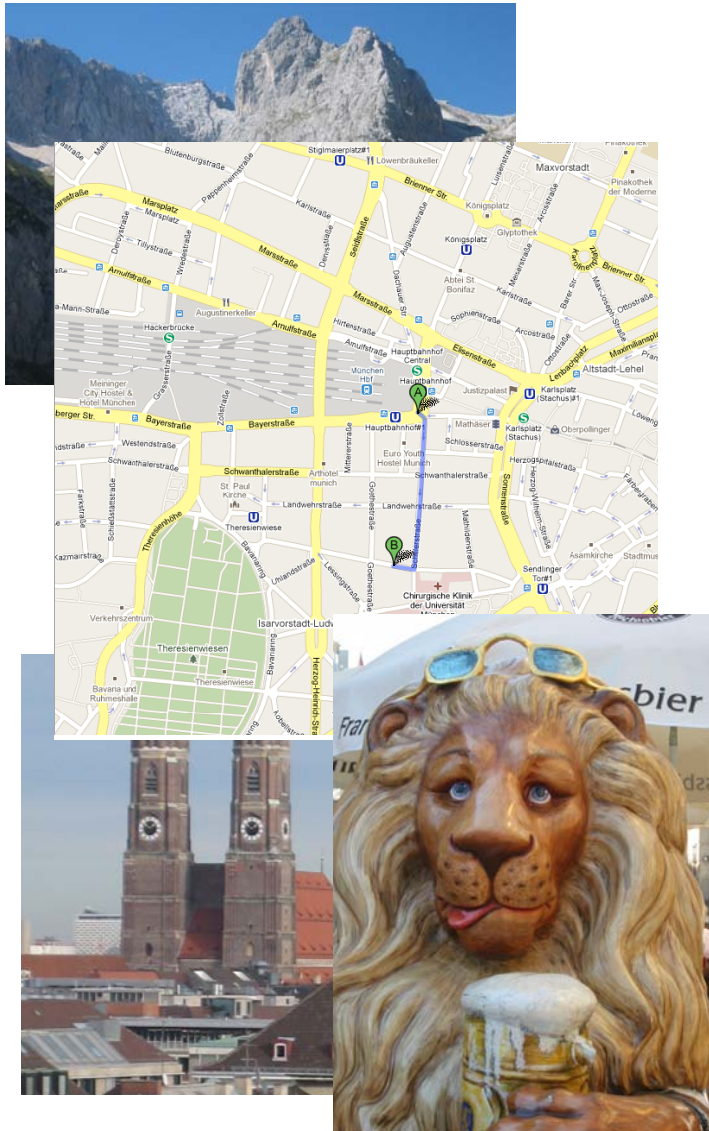
The large diversity of cell types and associated functions in multicellular organisms arises through complex molecular, biochemical and cellular processes in cellular differentiation. Whereas genetic information is stored in a linear fashion in DNA sequence, its utilisation occurs within a “three dimensional” context of chromatin, chromosomes and the nucleus, all of which contribute to the multiple layers of gene regulation. Thus, regulation of gene activity involves transcription factors and DNA regulatory elements, chromatin structure and modification, genome organisation and nuclear compartmentalisation of gene activity and interactions. It is a challenge to determine the identity, the quantity and the dynamic changes of the many proteins that regulate the epigenetic utilisation of the DNA sequence within its chromatin environment. This workshop brings together leading experts in the field of chromatin proteomics



The Location

The workshop will take place in the center of Munich within walking distance of Munich Central Station (“Kleiner Hörsaal, Pettenkofenstr. 12, 80336 Munich, GERMANY, see map below).

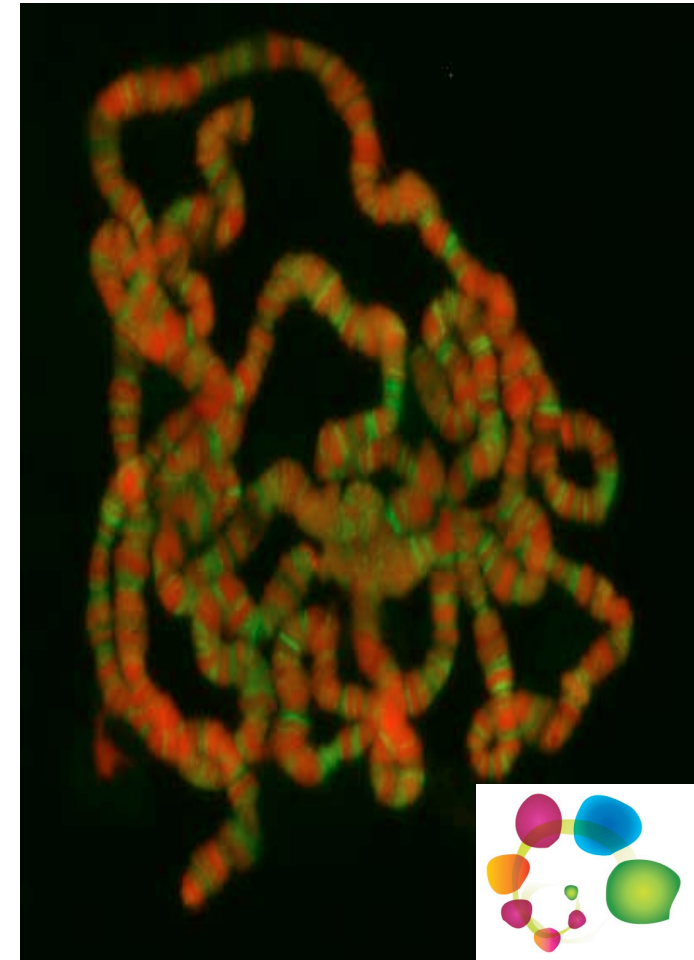
Attendance is free but registration is required. For a detailed program and registration details, please go to <http://www.integer-itn.org/i1/index.php>. In order to apply for a travel grant, please send a short description of your scientific interests and a letter of support by your supervisor to integer@fleming.gr. Registration deadline: February 26, 2010



1st Workshop in Chromatin Proteomics

23/24 March 2010

Ludwig Maximilians University of Munich



Program

March 23

10.30 Registration, Lunch
12:30 Welcome

12:45-14:00

The Nuclear Proteome

Francois-Michel Boivert

A quantitative proteomic approach for measuring the subcellular distribution of the proteins.

Jeroen Krijgsveld

The yeast nuclear proteome: closing in on chromatin

14:00-14:30 Coffee Break

14:30-15:45

Chromosomal Proteomics

Youri Rappsilber

The protein composition of mitotic chromosomes determined using multidimensional proteomics

Achim Grisenbeck

Isolation and biochemical analysis of specific chromosomal domains

15:45-16:30 Coffee Break

March 23

16:30-17:45

Histone Modifications

Ole N. Jensen

Advancing epigenetic research by mapping and quantification of histone modifications by mass spectrometry

Tiziana Bonaldi

Histone methylation turnover assessed quantitatively by heavy methyl SILAC strategy



March 24

9:00-10:15

Histone Methylation

Wolfgang Fischle

Molecular dissection of H3K9me3 readout

Michiel Veermeulen

The histone methyl-lysine interactome

10:15-10:45 Coffee Break

10:45-12:00

Functional Chromatinomics

Axel Imhof

Chromatin dynamics during assembly

John Strouboulis

Isolation and characterization of transcription factor complexes by biotinylation tagging

