Location

University of Konstanz
Department of Chemistry
Laboratory of Analytical Chemistry
and Biopolymer Structure Analysis
Universitätsstr. 10
78457 Konstanz

Accommodation

Since Konstanz is a major tourist attraction, accommodation limitations are always possible, therefore we recommend booking in advance. For extensive information on accommodation in Konstanz please visit: http://www.konstanz-tourismus.de/. Major hotels located downtown, in walking distance from the train station, are listed below.

1) Viva Sky Hotel KN
Sigismundstr. 19, 78462 KN
Tel. 07531 - 692362 - 0
welcome@hotel-viva-sky.de
http://www.hotel-viva-sky.de/
ab 80.- EUR

2) Hotel Arcadia Halm KN
Bahnhofplatz 6
78462 KN
Tel. 00 800 - 97 33 42 26
http://arcadia-halm-konstanz.hotel-rez.com/index_de.html
ab 69 EUR

3) City Hotel KN
Bahnhofstr. 10
78462 KN
Tel. 07531 - 1331-0
info@city-hotel-konstanz.de
http://www.city-hotel-konstanz.de/
EZ ab EUR 65.- inkl. Frühstück

4) Gästehaus Centro KN
Bahnhofstr. 4
78462 Konstanz
07531 - 457 181 8
info@gaestehauscentro.de
http://www.gaestehauscentro.de/
EZ ab EUR 55.- inkl. Frühstücksbuffet

5) Hotel Bayrischer Hof KN
Rosgartenstr. 30
78462 KN
Tel. 07531 - 1304-0
info@bayrischer-hof-konstanz.de
http://www.bayrischer-hof-konstanz.de/
EZ ab EUR 68.- inkl. Frühstück .

Fees and registration

Fee: 350 Euro

Bioaffinity-Mass Spectrometry

Methods & Applications in immunology, proteomics and biomedicine

Prof. Dr. Michael O. Glocker
Prof. Dr. Michael Przybylski

- Molecular recognition structures in protein-ligand interactions
- Determination of antibody – epitope structures
- Online bioaffinity – MS for identification & quantification of affinity-interactions

August 8 – 10, 2012 · Konstanz

DGMS
Deutsche Gesellschaft für Massenspektrometrie

Universität Konstanz

Objectives

Affinity-based separation methods can be used to increase the selectivity and sensitivity of a mass spectrometric analysis of biopolymers and small molecules, respectively. However, beyond this highly appreciated analytical feature, targetet molecule interactions also reveal information on functionalities of biomacromolecules that, once precisely analyzed, help to understand biological processes. Examples are identification of epitope – paratope interactions in antigen – antibody complexes, studies on protein inhibitor selectivity, and transcriptional regulation by studying repressor interacting proteins. Hence, bioaffinity mass spectrometry opens the door to powerful new applications in biochemistry, immunology and biomedicine. Participants shall learn about state-of-the-art bioaffinity methods and highly sophisticated mass spectrometric analysis methods and cutting-edge combination possibilities therefrom.

Highlights

- ESI-MS and MALDI-MS on-line and off-line coupling methods to LC separation tools
- Online SAW-Bioaffinity-MS coupling for affinity-interaction and quantification
- MALDI-MS target preparation methods for bioaffinity investigations
- Scope and limitations of affinity enrichment methods for phosphopeptides
- Scope and limitations of affinity enrichment of epitope – paratope interaction studies
- Mass spectrometric epitope determination

Target groups

Industrial and academic scientists working in the biochemical / bioanalytical / biomedical field.

Prior knowledge

Basic knowledge beginner level with mass spectrometric analysis of peptides and proteins by MALDI-MS and/or ESI-MS

Training / Teaching / Instruction

lectures, seminars, practical courses and demonstrations at instruments

Participants

max. 16 participants

Programme

Wednesday, August 8, 2012
9.00 Welcome and Introduction
9.30 Lecture (I)
10.15 Lecture (II)
11.00 Coffee break
11.30 Lecture (III)
12.15 Lecture (IV)
13.00 Lunch break
14.00 Practicals / Demonstrations (I)
15.45 Seminar and coffee (I)
16.30 Practicals / Demonstrations (II)
17.45 Discussion, Questions from Participants (I)
18.30 End of first day

20.00 Casual evening program / dinner

Thursday, August 9, 2012
9.30 Lecture (V)
10.15 Lecture (VI)
11.00 Coffee break
11.30 Lecture (VII)
12.15 Lecture (VIII)
13.00 Lunch break
14.00 Practicals / Demonstrations (III)
15.45 Seminar and coffee (II)
16.30 Practicals / Demonstrations (IV)
17.30 Discussion, Questions from Participants (II):
18.15 End of second day

Friday, August 10, 2012
10.00 Lecture (IX)
11.45 Lecture (X)
12.30 Final Remarks / Conclusion
13.00 Lunch

14:00 Special topic – lecture and demonstration
New proteomics methods based on stainfree-geleletrophoresis - mass spectrometry

Organisers

Prof. Dr. Michael O. Glocker
Universität Rostock
Institut für Immunologie Abteilung für Proteomforschung

Chemistry and Biology studies, Promotion (Konstanz); Post-Doc (Oregon State Univ., USA); Habilitation in Analytical Chemistry (Konstanz); Director of the Proteome Center Rostock and Dept. for Proteome research (Rostock); Guest professor at Shanghai Center for Bioinformation Technology; Head of the Special Interest group „Affinity-MS“.
Research areas: Clinical Proteome Analysis, Mass spectrometric protein structure- / function characterization, Immunoanalytical methods and diagnostic assays in polygenic diseases.

Prof. Dr. Michael Przybylski
Universität Konstanz; Laboratory of Analytical Chemistry & Biopolymer Structure Analysis; Director, Steinbeis Research Center for Biopolymer Structure Analysis & Biomolecular Mass Spektrometry

Chemistry & Pharmacology studies, Dissertation, University of Mainz; Visiting Scientist, NIH/Bethesda, USA; Habilitation, Organic Chemistry (Univ. Mainz); since 1989, Professor & Head, Analytical Chemistry & Biopolymer Structure Analysis, University of Konstanz. Since 2004, Director, Steinbeis Research Center Biopolymer Structure Analysis; guest professorships, Univ. Budapest, Odense, Chinese Academy of Sciences, Changchun; since 2011, Adjunct professor of Chemistry, Indiana University. Head, Special Interest group „Affinity-MS“.
Research areas: Mass spectrometry and peptide biochemistry of neurodegenerative proteins; pathophysiological protein modification; vaccine chemistry; structure and epitope analysis of therapeutic antibodies; affinity-mass spectrometry;
pathways and structures of “misfolding” – aggregating proteins in neurodegenerative diseases.