General information

Scientific committee

R. Giegerich (Bielefeld University, D)

A. Pühler (Bielefeld University, D/Chair)

S. Schreiber (UKSH, D)

S. Schuster (PSU, USA)

Ch. Sensen (University of Calgary, CA)

J. Stoye (Bielefeld University, D)

B. Weisshaar (Bielefeld University, D)

Information

W. Selbitschka Bielefeld University Chair of Genetics P.O. Box 100131 D-33501 Bielefeld

Tel. +49 521 106 5604 Fax +49 521 106 5626

Werner.Selbitschka@Genetik.Uni-Bielefeld.DE

Registration

For details regarding registration please see http://www.genetik.uni-bielefeld.de/genomikplus/

Location

Center for Interdisciplinary Research (ZiF), Wellenberg 1, 33615 Bielefeld (http://www.uni-bielefeld.de/ZiF)

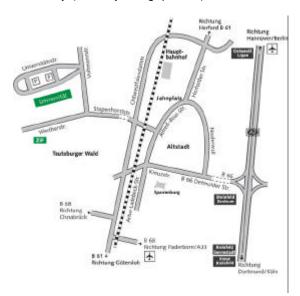
Arrival

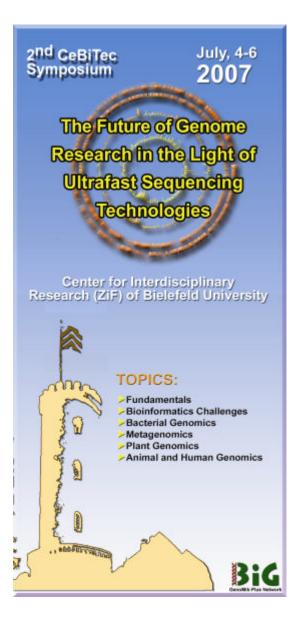
By car, you can take the A 2 Dortmund - Hanover, exit at "Bielefeld-Zentrum", follow the street signs

General information

towards the center ("Zentrum"), and from there follow the signs to "Werther". From the "Wertherstrasse", the ZiF is on the left side on the slope of the hill. The entrance is signposted.

Bielefeld can be reached from any major town by trains running on an hourly schedule (Eurocity train system: marked EC, IC, or ICE on the train schedule). From Bielefeld's main station you can either take a taxi to the ZiF (approx. EUR 10,-) or take the underground tram line 4 (destination "Universität" or "Lohmannshof"). From the tram stop "Universität" you can reach the ZiF by walking up the hill behind the main building of the university (the way is signposted).





Invitation

The Center for Biotechnology (CeBiTec) of Bielefeld University together with the German Genome Research Network "Functional Genome Research on Bacteria Relevant for Agriculture, Environment and Biotechnology" funded by the Federal Ministry of Education and Research (BMBF) under the GenoMik-Plus guideline cordially invites you to attend the international symposium "The Future of **Genome Research in the Light of Ultrafast** Sequencing Technologies" which will be held at the Center for Interdisciplinary Research (ZiF) of Bielefeld University from July 4th to 6th, 2007. The major objective of the symposium is to present a survey of next generation sequencing technologies as well as the application of these novel technologies in the various fields of genome research. The major topics to be addressed are:

- Next Generation Technologies
- Bioinformatics Challenges
- Bacterial Genomics
- Metagenomics
- Plant Genomics
- Animal and Human Genomics

Looking forward to welcome you in Bielefeld to an exciting meeting!

A. Pühler (Chair of the Scientific Committee)

July 4", 2007

Stephan Schuster, Pennsylvania State University, US

Mammoth Genomics (Opening Lecture)

Susan Hardin, VisiGen Inc., Huston, US The VisiGen® sequencing system for singlemolecule genetic analysis

Further speakers:

Stefan Schreiber, Universitätsklinikum Schleswig-Holstein, Kiel, D

Marcus Dröge, Roche Diagnostics, Penzberg, D

July 5", 2007

Richard Reinhardt, Max-Planck Institute of Molecular Genetics, Berlin, D

How projects benefit from the integration of ultrashort to long reads

Heinz Himmelbauer, Max-Planck Institute of Molecular Genetics, Berlin, D

Assembly and annotation of short-read datasets

Daniel Huson, Tübingen University, DAlgorithms and tools for analyzing metagenomic data

Andreas Tauch, Bielefeld University, D

Ultrafast *de novo* sequencing of the human pathogen *Corynebacterium urealyticum* with the Genome Sequencer 20 System

Andreas Schlüter, Bielefeld University, D Access to the plasmid mobilome of wastewater treatment plant bacteria by applying the ultra-fast 454-sequencing technology

Riccardo Velasco, San Michele all'Adige, IT Vitis vinfera cv. Pinot Noir: dealing with heterozygous genomes by merging Sanger and pyrosequencing methods

Andreas Weber, Michigan State University, US Profiling plant transcriptomes by massivelyparallel pyrosequencing

Further speakers:

Darren Platt, Joint Genome Institute, US
Paul Richardson, Joint Genome Institute, US
Jens Stoye, Bielefeld University, D
Dirk Evers, Bielefeld University, International
Graduate School, D

July 6", 2007

Edwin Cuppen, Hubrecht Institute, NL

Mutation discovery using SOLiD sequencing for the identification of gene knockouts in model organisms

Johannes Krause, Max-Planck Institute for Evolutionary Anthropology, Leipzig, D Neanderthal Genomics

Further Speakers:

Roman Thomas, MPI for Neurological Research, Cologne, D

Chia-Lin Wei, Genome Institute of Singapore, SG