

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)
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Information

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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

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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).



2nd CeBiTec Symposium July, 4-6 2007

The Future of Genome Research in the Light of Ultrafast Sequencing Technologies

Center for Interdisciplinary Research (ZiF) of Bielefeld University

TOPICS:

- Fundamentals
- Bioinformatics Challenges
- Bacterial Genomics
- Metagenomics
- Plant Genomics
- Animal and Human Genomics

3iG
Genomics Plus Network

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 4th, 2007

Stephan Schuster, Pennsylvania State University, US

Mammoth Genomics (**Opening Lecture**)

Susan Hardin, VisiGen Inc., Huston, US

The VisiGen® sequencing system for single-molecule genetic analysis

Further speakers:

Stefan Schreiber, Universitätsklinikum Schleswig-Holstein, Kiel, D

Marcus Dröge, Roche Diagnostics, Penzberg, D

July 5th, 2007

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

How projects benefit from the integration of ultra-short to long reads

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

Assembly and annotation of short-read datasets

Daniel Huson, Tübingen University, D

Algorithms 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 vinifera cv. Pinot Noir: dealing with heterozygous genomes by merging Sanger and pyrosequencing methods

Andreas Weber, Michigan State University, US

Profiling plant transcriptomes by massively-parallel 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 6th, 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