

MMGC
2012

MÜNSTER
MEDICAL
GENOMICS
CONFERENCE
MARCH 8/9 2012

Date: March 8/9, 2012

Venue

Factory Hotel

Event Hall "Cloud"
An der Germania Brauerei 5
481 59 Münster, Germany
www.factoryhotel.de



Parking at the conference venue is free, please exchange your parking ticket for a validated ticket at the registration desk.

Participation fee and meals

The conference fee amounts to 250 euros per participant. Fee includes refreshments, lunch and evening meal at the get-together.

Conference organization

Alexander Mellmann | University Münster, Germany
Dag Harmsen | University Münster, Germany

Scientific committee

Sebastian Suerbaum | Hannover Medical School, Germany
Martin Beer | Friedrich-Loeffler-Institut, Riems, Germany
Andreas Nitsche | Robert Koch Institute, Berlin, Germany

In co-operation with

National
Research Platform
for Zoonoses

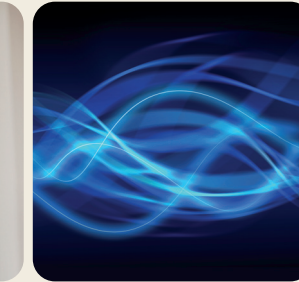


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MARKERS
European Society of Clinical Microbiology and Infectious Diseases

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**Rapid Next-Generation-
Sequencing Conference
for Public Health &
Clinical Microbiology
March 8/9, 2012**

Rapid Next-Generation-Sequencing Conference for Public Health & Clinical Microbiology

It is our great pleasure to welcome you to the *Rapid Next-Generation-Sequencing Conference for Public Health and Clinical Microbiology* in Münster.

Next-Generation-Sequencing (NGS) technology has developed rapidly during the last years. Innovative benchtop NGS platforms broaden application opportunities, especially for diagnostic use.

We are very pleased to welcome renowned experts from the United States and Europe who will give new insights into NGS technology and future applications. Thereby the meeting offers a unique chance to discuss novel aspects of NGS in an international setting.

The program highlights opportunities and challenges posed by this technology for public health and clinical microbiology. The conference has been designed to boost knowledge exchange as well as ample discussions with your colleagues from all over the world.

We are happy to welcome you in Münster – looking forward to an exciting and stimulating conference. Enjoy your stay!

Sincerely yours
Alexander Mellmann & Dag Harmsen

Conference program

Thursday, March 8, 2012

10:00 a.m.: **Registration**

Opening keynote*

12:00 a.m.: **Putting the genes into genomics: from MLST to BIGSdb**

Martin Maiden; University Oxford, United Kingdom

1:00-02:00 p.m.: **Lunch break**

Proof of principle: rapid NGS application for public health

2:00 p.m.: **German EHEC 2011 outbreak NGS analysis**

Alexander Mellmann; University Münster, Germany

2:30 p.m.: **Haiti Cholera 2010 outbreak NGS analysis**

Rene S. Hendriksen; Technical University Denmark, Lyngby, Denmark

Rapid genomics platforms

3:00 p.m.: **Assembling the biome of emerging pathogens; a public health perspective**

Saheer Gharbia; Health Protection Agency, Colindale, United Kingdom

3:30 p.m.: **Filling in the gaps: using the PacBio RS in microbial whole genome sequencing projects**

Thomas Connor; Wellcome Trust Sanger Institute, Cambridge, United Kingdom

4:00 p.m.: **The MiSeq system and applications to human disease**

Geoff Smith; Illumina, Chesterford Research Park, United Kingdom

4:30-05:00 p.m.: **Coffee break**

5:00 p.m.: **Using MiSeq to investigate typhoid fever**

John Wain; Health Protection Agency, Colindale, United Kingdom

5:30 p.m.: **Ion Torrent Semiconductor sequencing - an overview and outlook**

Simone Guenther; Life Technologies, Darmstadt, Germany

6:00 p.m.: **Whole genome mapping for de-novo assembly and typing**

Richard Moore; OpGen, Gaithersburg, Maryland, USA

Rapid bioinformatics for genomics

6:30 p.m.: **Comparison of NGS platform error rates**

Arndt von Haeseler; University Vienna, Austria

7:00 p.m.: **Bioinformatics software tools for analyzing and comparing microbial genomes**

Alexander Goesmann; University Bielefeld, Germany

7:30 p.m.: **Bioinformatics for rapid single read based analysis of diagnostic metagenome datasets**

Dirk Höper; Friedrich-Loeffler-Institut, Riems, Germany

8:00 p.m.: **Get-together**

Friday, March 9, 2012

Rapid genomics for diagnostics & therapeutics

8:30 a.m.: **Microbe hunting: ultra deep sequencing to discover microbes in human tissue**

Thomas Brieze; Columbia University, New York, USA

9:00 a.m.: **Design of pathogen-based diagnostic assays for the German EHEC and Dutch Klebsiella OXA-48 outbreaks 2011**

Craig A. Cummings; Life Technologies, Foster City, California, USA

9:30 a.m.: **Genomic reverse vaccinology**

Michele Barocchi; Novartis Vaccines and Diagnostics, Siena, Italy

10:00 a.m.: **Evaluating vaccine preventability by bacterial whole genome sequencing**

Ulrich Vogel; University Würzburg, Germany

10:30-11:00 a.m.: **Coffee break**

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11:00 a.m.: **The use of NGS for MRSA hospital surveillance**

Ulrich Nübel; Robert Koch Institute, Wernigerode, Germany

11:30 a.m.: **The use of NGS on the taxonomy of prokaryotes**

Ramon Rosselló-Móra; Institut Mediterrani d'Estudis Avanc, Esporles, Spain

12:00 a.m.-1:00 p.m.: **Lunch break**

Outlook and implementation of rapid NGS for public health

1:00 p.m.: **Real-time genomic surveillance of infectious disease**

Dag Harmsen; University Münster, Germany

1:30 p.m.: **EU Patho-NGen-Trace project**

Stefan Niemann; FZB, Borstel, Germany

1:45 p.m.: **Microbial typing ontology**

João A. Carriço; Faculdade de Medicina de Lisboa, Portugal

2:00 p.m.: **Danish global, real-time microbiological genomic identification system project**

Frank M. Aarestrup; Technical University Denmark, Lyngby, Denmark

2:15 p.m.: **European perspective of NGS for public health**

Marc J. Struelens; ECDC, Stockholm, Sweden

Closing keynote

2:30 p.m.: **The sunset of culture techniques and the dawning of genomics for the diagnosis and investigation of infectious disease outbreaks**

Peter Gerner-Smidt; CDC, Atlanta, Georgia, USA

* We apologize, but due to unforeseen circumstances Jonathan Rothberg had to cancel his participation on short notice!

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