

GENETICS

# SINGLE CELL GENOMICS UPDATE

16.11.2013

Friday, November 15, 2013 – 16:15 h

Venue: Raum H030, Fakultät für Physik, Schellingstraße 4,  
80799 München

Leica Scientific Forum **Munich** & CeNS Colloquium

**Advances in Life Science**  
**Stephen Quake**  
Lee Otterson Professor, Applied Physics and Bioengineering  
Stanford University and Howard Hughes Medical Institute

**"Single Cell Genomics"**

**16:15** Welcome Coffee  
**16:30** Introduction by Prof. Hermann Gaub  
Keynote lecture  
In his talk, Stephen Quake will present his research on single-cell genomic analysis by the use of microfluidic tools for:

- Gene expression analysis and genome sequencing from single cells
- "Reverse tissue engineering" by dissecting complex tissues into their component cell populations
- Analysis of rare cells such as circulating tumor cells or minor population within a tissue
- Single-cell genomic sequencing

**17:30** Discussion & Post Lecture Reception – Meet the Speaker

**Scientific Advisory Board:** Berlin: Prof. Michael Brecht (HUB), Prof. Stephan Sigrist (FUB) / Heidelberg: Prof. Winfried Denk (MPI), Prof. Roland Eils (DKFZ), Prof. Stefan Hell (DKFZ and MPI Göttingen), Dr. Rainer Pepperkok (EMBL) / Munich: Prof. Ulrike Gaul (LMU), Prof. Hermann Gaub (LMU), Prof. Arthur Konnerth (TUM) / Dr. Thomas Zapf (Leica Microsystems)

I have been attending yesterday an interesting talk of [Stephen Quake](#).

Yes, this was a Leica sponsored event, but not about photography, it was about single cell genomics. I was always interested in that field and quite impressed by the Quake approach. These biology-baptized mathematicians and physicists can easily compete with whole research centers and a 100fold head count.

The commercial spin-off is [fluidigm.com](http://fluidigm.com) while his main research is not only sequencing of the fastest moving bacterium but also an estimate of mutations in his own haploid (sperm) genomes, single cell expression along with single cell methylation patterns.

One of the really exciting questions is the mismatch of single cell RNA and protein content where I need to go for some papers that I wasn't aware of. Another excellent idea is the clustering of single cell expression profiles. This is already leading to new classes of cells and a probably much more valid approach than using random? surface markers as [immunologists](#) usually do, yea, yea.

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