

# High Content Screening: Instrumentation, Assay Development, Screening, Image and Data Analysis

## Course Description

High-content screening is a powerful technology platform for implementing functional cell-based assays that allow truly multi-parametric analysis in the physiological context of intact cells. This course provides a state-of-the-art overview of the components of HCS (instrumentation, reagents, HC assay development, automated image analysis and multi-parametric data analysis, and data standards) together with some showcases of small molecule and RNAi high-content screens in industry and academia.

During the image and data analysis modules, a demonstration will be given using the open source software CellProfiler how to analyze early endosomes in HeLa cells. Nuclei, cytosol and endosomes will be segmented and quantified. The resulting data will then be analyzed using the open source software KNIME. Parameters will be tested for normality, normalized and assembled into multi-parametric profiles. The profiles will be quantified to estimate phenotypic strength and clustered to determine phenotypes. Both the slides describing the analysis and the pipelines will be made available to course participants to allow them to recreate the workflow in their own laboratories.

## Who Should Attend

- Individuals who plan to develop or apply HCS technologies
- Individuals who look to implement HCS capacity at a screening center
- Individuals familiar with HCS but want to get a systematic overview and particularly how to manage and analyze data
- Individuals who are applying HCS on a regular basis, and want to optimize the screening pipeline including data management and analysis, and the development of standards

## How You'll Benefit from This Course

The course will provide:

- an introduction to all aspects of HCS including data analysis
- a thorough overview on available HCS instrumentation
- guidance to assay selection and systematic optimization
- demonstration of image analysis with CellProfiler (open source software)
- demonstration of multi parametric data analysis with KNIME (open source software)
- demonstration how HCS/HCA can uncover novel biology
- clustering multi parametric data with various distance metrics and clustering approaches
- dimensionality reduction
- on demand, a discussion on hit verification and target deconvolution strategies

## Course Topics

- Introduction to High-Content Analysis and Screening (HCA / HCS)
- HCS instrumentation
- Assay development
- Image analysis
- Data analysis

## Instructors:



**Eberhard Krausz**, ChemBioCon, is employed by a major research organisation. Since 2008, he has been supporting scientists during various positions in industry and academia in technology selection, target identification & validation, assay development and screening. In 2003-2008, he was heading the central high-content screening labs at the Max Planck Institute in Dresden, Germany. Before, he held responsible positions in biotech industry at Cenix BioScience (Germany) and Cyclacel (Scotland, UK) dealing with RNA interference (RNAi) and drug discovery, respectively. Before joining a medical research centre in Munich running a gene therapy project in restenosis, he earned his Ph.D. at the LMU München (Munich) studying gene regulation in eye lens development. By training he is a microbiologist.

Eberhard Krausz was for many years member of the Academic Outreach Committee (AOC) of the Society of Biomolecular Screening. He was re-elected recently to serve the Steering Committee of the Joint Working Group Chemical Biology of Dechema, GBM, GDCh and DPhG in Germany.



**Marc Bickle** heads the Technology Development Studio (TDS) of the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden, Germany. The TDS is an open access screening facility specialised in high content screening of RNAi and chemical libraries. The TDS uses open source software to allow its clients to recreate the analytical workflows in their own laboratories. There is therefore a strong need for its client to learn how to use these powerful analytical tools and hands on courses are consequently offered. Marc Bickle obtained his PhD at the Biozentrum in Basel, Switzerland, studying the immunosuppressive drug Rapamycin helping elucidate its mode of action. He then went to the LMB in Cambridge, UK, to study the genetics of behavior in *C. elegans*. He then participated in the creation of Aptanomics, a drug discovery Biotech in Lyon, France, where he set up several yeast two hybrid screening systems.