Sequencing Simplified

Illumina sequencing is fuelling groundbreaking discoveries across a wide range of research areas. By enabling the broadest range of applications including whole-genome resequencing, de novo sequencing, targeted resequencing, transcriptome and epigenetic analysis, researchers are publishing at amazing rates.

This seminar series will showcase presentations from scientists using Illumina technology to power their next-generation sequencing studies. We invite you to join us, learn about their research, and receive an update on new sequencing products from Illumina.

THURSDAY, SEPTEMBER 9, 2010

ELLINGTON HOTEL BERLIN
NURNBERGER STR 50-55
10789 BERLIN, GERMANY
HALL SENATOR ROOM

SEMINAR SCHEDULE		
9:00	Registration	
9:30	Introduction	Illumina
9:35	The Expanded Illumina Sequencing Portfolio, New Sample Prep Solutions and Workflow	Marcus Hausch, Ph.D., Illumina
10:00	The Compendium of Genomic DNA Sequencing Applications	Abizar Lakdawalla, Ph.D., Illumina
10:30	Studying Modern Human Origins from Neanderthal DNA	Martin Kircher, Ph.D., Max Planck Institute
11:00	Identity-by-Descent Filtering of Exome Sequence Data identifies PIGV Mutations in Hyperphosphatasia Mental Retardation Syndrome (HPMR).	Peter Krawitz, Ph.D., Institute for Medical Genetics
11:30	LUNCH	
12:30	Transcriptome Sequencing: The Switch from Arrays to Sequencing	Shawn Baker, Ph.D., Illumina
1:00	Large-Scale Mutation Screening by Combining Genome Partitioning and Illumina Sequencing	Wei Chen, Ph.D., The Max Delbrück Centre for Molecular Medicine
1:30	Talk title to be confirmed	Speaker
2:00	Illumina NGS Sequencing Analysis Process: Turning Data Into Biology	Lukas Smink, Illumina
2:30	Closing Remarks	Illumina

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