



Swiss Institute of
Bioinformatics

Mini-Symposium

Clinical research in the era of deep sequencing

Thursday, March 28, 2013

Jéquier-Doge Auditorium, CHUV

- 09:10 Welcome
- 09:15 **Ioannis Xenarios**, SIB/Vital-IT/Swiss-Prot, Lausanne
Coordinating efforts in exome/genome sequencing, annotation and interpretation: challenges and opportunities
- 09:30 **Amélie Piton**, Department of Translational Medicine and Neurogenetics, IGBMC, Illkirch, France
Targeted high-throughput sequencing of 220 genes identifies a high proportion of causative mutations in patients with undiagnosed intellectual disability
- 10:15 **Andrea Superti-Furga**, Department of Pediatrics, CHUV, Lausanne
Exoming in research and diagnosis of genetic disorders
- 11:00 *Coffee break*
- 11:30 **Kalliope Panoutsopoulou**, Wellcome Trust Sanger Institute, Hinxton, UK
Next generation association studies: in search of low frequency and rare variants affecting complex traits
- 12:15 **Mauno Vihinen**, Department of Experimental Medical Science, Lund University, Sweden
Prediction of variation pathogenicity
- 13:00 *Lunch break*
- 14:00 **Jacques Fellay**, Global Health Institute, EPFL School of Life Sciences, Lausanne
Host genomic analysis in infectious diseases
- 14:45 **Daniel Wegmann**, Department of Biology, University of Fribourg
Common variants are dead - or maybe not
- 15:30 **Manolis Dermitzakis**, Department of Genetic Medicine and Development University of Geneva Medical School
Population and personalized genomics: all for one, one for all
- 16:15 Final remarks and farewell

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Open to all - no registration required