

6th Polish Illumina SymposiumThursday 20th & Friday 21st October 2016

Adam Mickiewicz University, Faculty of Biology
 ul. Umultowska 89
 61-614 Poznań
 Venue: Aula
 Event location: Collegium Biologicum

Thursday 20th October**SEMINAR SCHEDULE**

9:30	Registration	
10:00	Welcome and introduction	
10:05	Updates and new developments	Florian Graedler, Illumina
10:50	Global distribution of histone variant H2A.Z and its correlation with transcriptional response to stress in Arabidopsis thaliana	Weronika Sura, Department of Biotechnology, Faculty of Biology AMU, Poznan
11:20	Characterization of Pi-responsive microRNAs in barley roots and shoots	Andrzej Pacak, Department of Gene Expression, Faculty of Biology AMU Poznan
11:50	Coffee break	
12:10	Beyond GWAS - the application of SNP chips in genomic selection	Joanna Szyda, Department of Genetics, Wrocław University of Environmental and Life Sciences
12:40	Next generation sequencing of ancient DNA samples – practical aspects	Ireneusz Stolarek, Luiza Handschuh, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan
13:10	Next generation sequencing as a new dimension of genetic studies of the Neolithic communities	Arkadiusz Marciniak, Department of History and Methodology of Prehistory, Institute of Prehistory, AMU Poznan
13:50	Targeted deep sequencing of cancer related genes in human neoplasms	Maciej Giefing, Department of Cancer Genetics, Institute of Human Genetics, Polish Academy of Sciences, Poznan
14:20	Lunch	
14:50	Search for forensically useful age prediction markers based on genome wide DNA methylation analysis	Rafał Płoski, Department of Medical Genetics, Medical University of Warsaw
15:20	Practical use of next generation sequencing in forensic	Michał Boroń, Department of Biology, Central Forensic Laboratory of the Police, Warsaw
15:50	Coffee break	
16:15	Massively Parallel Sequencing and its application in Human Identification from skeletal remains.	Maria Wróbel, Forensic Genetics Section, Institute of Forensic Research in Cracow
16:45	Utility of massively parallel sequencing within a specialist forensic casework laboratory	David Ballard, Department of Analytical & Environmental Sciences King's College, London
17:45	Departure for a dinner	

Friday 21st October
SEMINAR SCHEDULE

09:15	Organizational issues	
09:30	Genotyping the extreme MHC class I diversity in passerine birds with Illumina platform	Sebastian Alvaro, Evolutionary Biology Group, AMU Poznan
10:00	The type I IFN-induced transcriptome and chromatin interactions mediated by phosphorylated and un-phosphorylated ISGF3 components	Johannes Bluysen, Department of Human Molecular Genetics, Faculty of Biology AMU Poznan
10:45	Coffee break	
11:00	Revealing genomic diversity by complete, robust assemblies of complex genomes	NR Gene
11:45	Workshop Part 1: Analysis of forensic mtDNA data using the Variant Processor and Variant Analyzer BaseSpace Apps	Nicola Oldroyd Clark, Illumina
12:30	Lunch	
13:15-15:00	Workshop Part 2: Analysis of forensic SNP/STR data using the ForenSeq Universal Analysis Software	Nicola Oldroyd Clark, Illumina