

15th European Cytogenomics Conference Leuven, June 29-July 1, 2025

Rooms The rooms of plenary and concurrent sessions (GA0 and GA1) are on the same floor as the reception area, posters, and company booths. Due to the building's underground levels, this is considered the 4th floor. Consequently, rooms ALO 05.xxx, and ALO 7.xxx are located one, and three floors above the GA0/GA1 rooms, respectively.

	TIME	SPEAKERS	PRESENTATIONS	** ROOMS **		
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	9:30-11:00	Hands-on workshops / 1st Slots				
The first position reconstruction controllers produced (CAN), About KERNY Sept. SECURITY Se		Analysis of clinical and haemotologic	al samples, in group of three (the computer connects directly to the Bionano US server in US), Dana JABER	ALO 05.100		
		Bridging cytogenetics workflows: Hai	nds-on analysis of arrays to NGS, Kyle CUTLER, Marco RUSSMAN	ALO 05.200		
		The use of online resources to annote	ate/map clinical CNVs, Robert KUHN	ALO 07.100		
Institution In		Nanopore based sequencing for struc	tural variant detection, from sample to report, "WET LAB", Erwin REILING, Erika SOUCHE	Meet. Point:		
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145-15-15-16 Second or IAMNUIZ2 Confirmed Interference Interfere	14:35-14:45	Andreas HOUBEN	Does chromoanagenesis play a role in the origin of B chromosomes?			
Sept	14:45-14:55	Alla KRASIKOVA	Retrotransposable elements drive transcription of tandem repeats			
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143-16-183 PMC Coordinators: Harald RIEDER, Paola CARIA 143-1435 Coordinators: Welcome and forward by PMC Coordinators 143-15-1435 Tadoux AGUIXVSMI Coordinators 143-15-1435 Tadoux AGUIXVSMI Coordinators 143-15-15-150 Mane-Bérengée RIOADEC What is wrong with the dietion of the romosome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome region 5g in myelodyciplastic syndrome? Identification of a novel actor of the sensitivity to benalidomide of MOS with deficion of the vinescome syndrome? Identification of a novel actor of the vinescome region 5g in myelodyciplastic syndrome? Identification of syndrome? Identification from the vinescome region 5g in myelodyciplastic syndrome? Identification from the vinescome region 5g in myelodyciplastic syndrome Mosphing and promote of promote synd						
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ALO 07.100 Second Historium GA1	14:45-14:55	Marija DENCIC FEKETE	Distribution of gene aberrations in chronic lymphocytic leukemia by NGS testing in a Serbian patient cohort			
15:05-15:15 Ulana PKRIOVA Seyond (12:21): unveiling the hidden layers in all laryotypes Seyond (12:21): unveiling the hidden layers in all laryotypes Seyond (12:21): unveiling the hidden layers in all laryotypes Seyond (12:21): unveiling the hidden layers in all laryotypes Seyond (12:21): unveiling the hidden layers in all laryotypes Seyond (12:21): unveiling the hidden layers in all laryotypes Seyond (12:21): unveiling the Affection of measurable residual disease using fluorescence in situ hybridization compared with multiparametric flow cytometry in patients with B. ymphobilastic leukemia (15:51-15:51) Seon Y KIM	14:55-15:05	Marie-Bérengère TROADEC				
Detection of measurable residual disease using fluorescence in situ hybridication compared with multiparametric flow cytometry in patients with B- yrmphoblastic leukemia September Property Property Property Property	15:05-15:15	Uliana LYKHOVA	Beyond t(12;21): unveiling the hidden layers in all karyotypes	ALO 07.100		
Auditorium GA1	15:15-15:25	Laura YISSEL RENGIFO	Dynamic Follow Up Of Tumor Burden In Multiple Myeloma Through Analysis Of Ccfdna Markers			
Souraya MAUGOU-ZERELII (pending)	15:25-15:35	Seon Y KIM				
15:55-16:30 Coordinators General discussion and conclusive remarks by PWG Coordinators	15:35-15:45	Hila LEDERMAN NACHMIAS (pending)	New Insights Affecting Classification, Prognosis and Treatment of Multiple Myeloma Using Optical Genome Mapping			
Clinical and molecular approaches to cytogenetic syndromes & cytogenomics PWG Coordinators: Joris VERMEESCH, Anna LINDSTRAND, Damien SANLAVILLE 15:30-15:35 Coordinators Welcome and foreword by PWG Coordinators 15:35-15:45 Paola EVANGELIDOU Arare and complex case of a male patient with DiGeorge – like phenotype, carrying three different mosaic copy number variants on chromosome 22 15:45-15:55 Caroline SCHIUTH-BOLARD FGF14 disruption by constitutional chromoanagenesis as a cause of spinocerebellar ataxia 15:55-16:05 Lesile KULIKOWSKI Resolving the Unresolved: Epigenomic Profiling as a Diagnostic Tool for Copy Number Variants of Uncertain Significance Martine DOCO-FENZY Involuged Or Duptry Rearrangements Revisited Using Array-CGH and Optical Genome Mapping 16:15-16:25 Lusine NAZARYAN-PETERSEN Detection Of Structural Variants By Short Read Whole Genome Sequencing And Interpretation For Genetic Diagnosis 16:25-16:35 Marlene EK Long Read Genome Sequencing Enhances Diagnosis Of Pediatric Neurological Disorders 16:35-16:45 Igor LEBEDEV X Chromosome Cru Reclassification Integrating X Inactivation Status For Improved Pathogenicity Assessment 16:35-16:35 Isome TEN BERK DE BOER Investigating X Chromosome Invalidation Patterns in X Autosome Translocations Using Long Read Sequencing And The T2t Genome Assembly 16:30-17:30 Coordinators Chromosomes' integrity, stability, and dynamics PWG Coordinators: Losé M. GARCIA-SAGREDO, Emanuela VOLPI Exploring new chromosomal poradigms for precision medicine and early disease detection 16:30-16:40 Coordinators 16:40-16:50 Ulrike MAU-HOLZMANN Multiple Variable Chromosomal Aberrations in Primary Fibroblasts: Further Hints to Chromosomal Instability as a Long-Term Effect Even Years After Irradiation 16:50-17:00 Claudia OLIVERA The DEE SE Beyond Fancon anaemia: A new look into chromosome instability 17:10-17:20 Radhia M'KACHER Telomero Dysfunction, DNA Breaks, Chromosomal Aberration Formation and the Dark Side of the Centromere	15:45-15:55	Soumaya MAUGOU-ZERELLI (pending)				
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17:20 Coordinators Conclusive remarks and new initiative announcement by PWG Coordinators	17:10-17:20	Radhia M'KACHER	Telomere Dysfunction, DNA Breaks, Chromosomal Aberration Formation and the Dark Side of the Centromere			
	17:20	Coordinators	Conclusive remarks and new initiative announcement by PWG Coordinators			

16:30-17:30	~	Prenatal diagnosis PWG Coordinators: Rosário Carvalho PINTO LEITE, Jean-Michel DUPONT				
16:30 -16:35	Rosário Carvalho PINTO LEITE	Introduction				
16:35 -16:45	A.VARDANYAN	Retrospective analysis of cytogenetic findings in pregnant women at risk following first-trimester screening: insights from NIPT in Armenia	_			
16:45 - 16:55	M.A.CARO MIRO	Circuit of prenatal screening with free circulating fetal DNA in the balearic islands	ALO 07.100			
16:55 - 17:10	Rosário Carvalho PINTO LEITE	NIPT in Europe, Result of the PWG survey				
17:10 - 17:20	K.CASSINARI	First Prenatal Case of Jumping-like Translocations: Unraveling Complex Chromosomal Rearrangements				
17:20 - 17:30	N.CHATRON	Comparative Efficacy of cfDNA and aCGH in Detecting Chromosomal Aberrations Post-Miscarriage				
18:00-19:00	Opening Lecture Evan E. EICHLER "Complete chromosomes and complex genomes" Chaired by Mariano ROCCHI, Joris VERMEESCH					
19:00-20:30	ECA 2025 Kick-off party		Exhibition Area			
Monday,	June 30					
8:30-10:15	Plenary session 1 Structural variation in health and disease Chaired by: Joris VERMEESCH, Anna LINDSTRAND					
8:30-9:00	Alexandre REYMOND	The pleiotropic spectrum of proximal 16p11.2 CNVs	GA0			
9:00-9:30	David PORUBSKY	Structural variation of 22q11.2 region in normal and diseased human population				
9:30-10:00	Tobias MARSCHALL	Mapping structural variation in the pangenome				
10:00-10:15	Nivin MOUSTAFA-HAWASH	Optical genome mapping in the clinic reveals germline and somatic findings that may influence the treatment approach				
10:15-10:45		COFFEE BREAK	Exhibition Area			
10:45-12:15	Plenary session 2 Complexity of cancer genomes Chaired by Roberta VANNI, Barbara DEWAELE					
10:45-11:15	Jonas DEMEULEMEESTER	Multiomic long-read sequencing to improve diagnosis and care of genomically complex sarcomas	GA0			
11:15-11:45	Stefano SANTAGUIDA	Mechanistic insights into the consequences of chromosome segregation errors on cell physiology				
11:45-12:00	Amber VERHASSELT	Optical genome mapping is a powerful diagnostic tool in non Hodgkin lymphoma				
12:00-12:15	Şule ALTINER	Cytogenetic profile of hematological malignancies with complex karyotype a single center study from Turkey				
12:15-14:30		POSTER SESSION	Poster Area			
12:30-14:30	Sponsored Workshop: Next-ger	n cytogenetics: Applications of AI and digital FISH in diagnostics	ALO 05.100			
12.00 100	Speakers: Jana BUKOLSKÀ, Yarir	n HADID, Lee KAPLAN	ALO 03.100			
14:30-15:30	Concurrent Session 1 Meiosis and Mitosis Chaired by Jean-Michel DUPONT, Elisabeth SYK LUNDBERG					
14:30-15:00	Marta DE RUIJTER VILLANI	Meiosis/mitosis transition	GA0			
15:00-15:30	Carolina VILLARROYA-BELTRI	Mosaic variegated aneuploidy in development, ageing and cancer				
14:30-15:30	Concurrent Session 2 Automation and AI in Clinical Genetics Chaired by Barbara DEWAEKE, Franck PELLESTOR					
14:30-15:00	Claudia HAFERLACH	Application of AI in hematological diagnostics				
15:00-15:30	Robert KUHN	Online resources at UCSC				
15:30-15:45		COFFEE BREAK	Exhibition Area			
15:45-17:30	Plenary Session 3 Clinical Cytogenomics Chaired by Damien SANLAVILLE	, Orsetta ZUFFARDI				
15:45-16:15	Thomas BOURGERON	The genetic architecture of autism: from medicine to neurodiversity	GA0			
16:15-16:45	Jesper EISFELDT	Long read genome sequencing in clinical cytogenomics	JAU			
16:45-17:15	Andrea CIOLFI	DNA methylation profiling as a diagnostic tool				
17:15-17:30	Dominik REZNY	Precision approaches in clinical cytogenomics the role of optical genome mapping and long read sequencing in structural variant detection				
17:30-20:00		POSTER SESSION	Poster Area			
18:00-19:00	ECA General Assembly		GA0			

Tuesday,	July 1		
8:30-10:30	Plenary Session 4 Animal, Plant and Comparative Cytogenomics Chaired by Pat HESLOP-HARRISON, Mariano ROCCHI		
8:30-9:00	Aurora RUIZ-HERRERA	Evolution and function of 3D chromatin folding	
9:00-9:30	Julie SARDOS	Diversity and diversification in banana: how in silico chromosome painting opens new perspectives for the conservation and use of an iconic fruit	GA0
9:30-10:00	Pat HESLOP-HARRISON	What cytogenomics has done, and is doing, for agriculture in our world	
10:00-10:15	Simon MALLET	Interstitial telomeric sequences and accumulation of dna damage hallmarks of genomic instability in cancer resistant wild vertebrates	
10:15-10:30	Fengtang YANG	Genomic complexity and evolutionary plasticity in dugesia japonica revealed by multi ploidy chromosome level assemblies	
10:30-11:00		COFFEE BREAK	Exhibition Area
11:00-12:15	Concurrent Session 3 Nuclear organisation and disease Chaired by Emanuela VOLPI, Pat HESLOP-HARRISON		
11:00-11:30	Martin MENSAH	Nucleolar dysfunction in rare genetic diseases	GA1
11:30-12:00	Cristina CARDOSO	Epigenetic reprogramming and disease	
12:00-12:15	Lusine NAZARYAN-PETERSEN	Detection of structural variants by short read whole genome sequencing and interpretation for genetic diagnosis	
11:00-12:15	Concurrent Session 4 Clonal correction of constitutional chromosome imbalances Chaired by Damien SANLAVILLE, Orsetta ZUFFARDI		
11:00-11:30	Diane VAN OPSTAL	Placental cytogenetic studies provide a glimpse into the black box of early embryogenesis	GA0
11:30-12:00	Alfredo BRUSCO	Somatic recombination and the removal of the structural variant: any phenotypic outcome?	
12:00-12:15	Anikó UJFALUSI	Evaluation of X-inactivation pattern in carriers of X chromosome aberrations and DMD gene mutations	
12:15-14:00		POSTER SESSION	Poster Area
12:30-13:15	Sponsored Session:		
12:30-12:45	Drew ELLERSHAW	Introduction	641
12:45-13:05	Inga NAGEL	Addressing clinical challenges in rare diseases through long-range insights by a novel genome sequencing technology	GA1
13:05-13:15		Q&A	
14:00-15:45	Concurrent Session 5 Accreditation and workshop on ISCN Chaired by Franck PELLESTOR, Harald RIEDER		
14:00-14:30	Konstantin MILLER	ISO15189 and cytogenetic laboratories	
14:30-15:45	Jean-Michel DUPONT	Workshop on ISCN 2024	
14:00-15:15	Concurrent Session 6 Applied Cytogenotoxicity Chaired by José GARCIA SAGREDO, Joan BLANCO		
14:00-14:30	Alba HERNADEZ BONILLA	Genotoxicity and carcinogenicity of long-term micro- & nano-plastics exposure: current understanding and future directions	GA1
14:30-15:00	Ans BAEYENS	Chromosomal radiosensitivity testing for inborn errors of immunity	
15:00-15:15	Marlene EK	Long-read genome sequencing enhances diagnosis of pediatric neurological disorders	
15:45-16:15		COFFEE BREAK	Exhibition Area
16:15-17:30	Plenary Session 5 Prenatal Diagnosis and Preimplantation Chaired by Elisabeth SYK LUNDBERG, Rosario PINTO LEITE		
16:15-16:45	Alan HANDYSIDE	PGT, with a focus on aneuploidies	GA0
16:45-17:15	Nathalie JANEL	Prenatal treatment of chromosomal anomalies	
17:15-17:30	Charlotte TARDY	Transforming prenatal cytogenetics rapid chromosomal rearrangement characterization with Nanopore sequencing	
17:30-18:30	Closing Keynote Joris VERMEESCH "Cytogenomics, where we are and where we are heading" Chaired by Mariano ROCCHI, Jean-Michel DUPONT		

Rooms The rooms of plenary and concurrent sessions (GA0 and GA1) are on the same floor as the reception area, posters, and company booths. Due to the building's underground levels, this is considered the 4th floor. Consequently, rooms ALO 05.xxx, and ALO 7.xxx are located one, and three floors above the GA0/GA1 rooms, respectively.