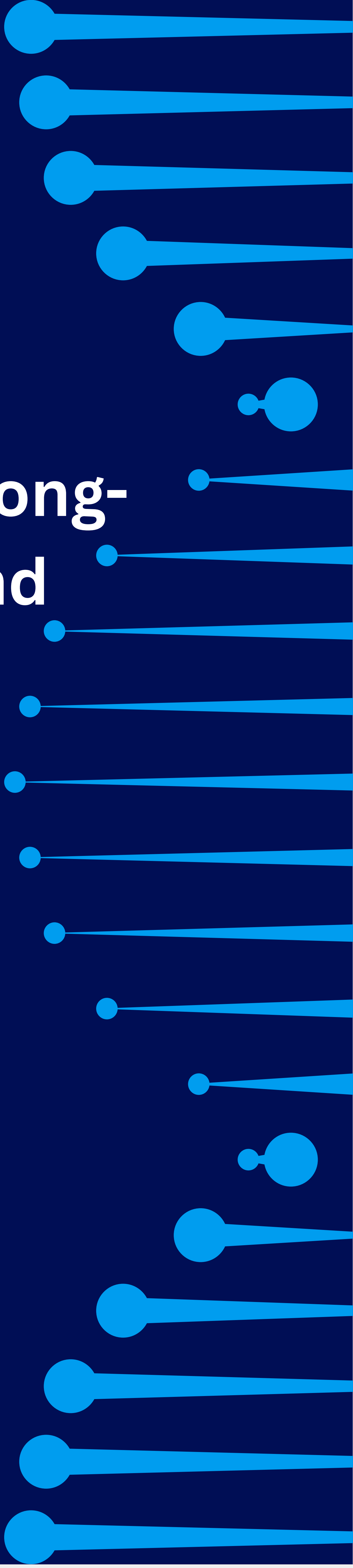
Advanced course on long-read sequencing and medical genomics

AGENDA



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EASIGEN-DS
Designing a Research Infrastructure on Advanced Genomics Technologies

EASIGEN-DS is funded by the European Union

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WELCOME

08:30–08:50 - Registration

08:50–09:00 – Welcome and course objectives
Joris Vermeesch, KU Leuven
Head of Laboratory for Cytogenetics and Genome Research

BLOCK 1 – TECHNOLOGIES AND DATA ANALYSIS

09:00–9:40 - Long-read sequencing: Technology update and applications
Wouter Bossuyt, KU Leuven
Manager of the Genomics Core Leuven, Center for Human Genetics

09:40–10:20 - Getting the most out of nanopore sequencing: From sample to library prep
Mojca Strazisar, University of Antwerp
Head of the Neuromics Support Facility, Center for Molecular Neurology, VIB

10:20–11:00 - Processing, QC and analysis of long-read RNA-seq data
Kristin Köhler, Charité
Bioinformatician and PhD Student at the Intelligent Imaging Group, Berlin Institute of Health

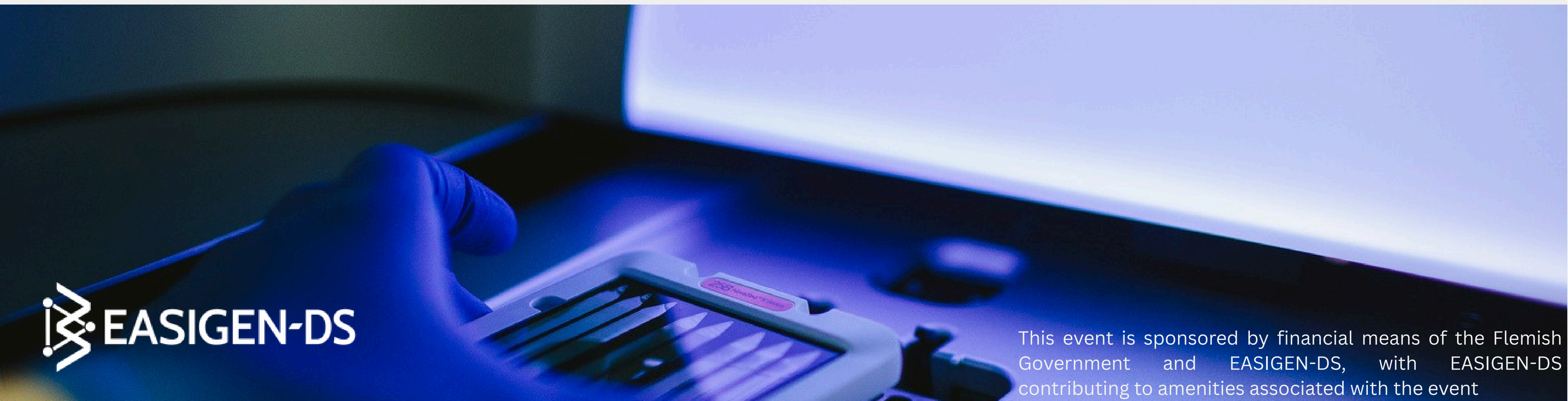
11:00–11:20 - Coffee break I (20 min)

11:20–12:00 - Handling and sharing long-read data
Teresa D'Altri, CRG
Scientific project manager and coordinator, EGA Team, Centre for Genomic Regulation

BLOCK 2 – APPLICATIONS IN MEDICAL GENOMICS

12:00–12:40 - Long-read sequencing for rare kidney disease
Janine Altmüller, BIH & MDC
Head of Genomics Platform at BIH & MDC Berlin

12:40–13:30 - Lunch break (50 min)



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13:30–14:10 - Long-read sequencing in neuromuscular disorders (African population)
Pedro Rodríguez Cruz, CNAG
La Caixa Junior Leader Fellow, Centro Nacional de Análisis Genómico

14:10–14:50 - Nanopore long-read whole-genome sequencing in developmental disorders
Joris Vermeesch, KU Leuven
Head of Laboratory for Cytogenetics and Genome Research

14:50–15:00 – FLASH TALK: CiFi long-read chromatin contact mapping to decode multi-way 3D genome interactions
Nelson Martins, UGent
PhD Student, Department of Biomolecular Medicine, Ghent University, Ghent & Center for Medical Genetics, Ghent University Hospital, Ghent, Belgium

15:00–15:15 - Coffee break II (15 min)

15:15–15:55 - From cytogenetics to cytogenomics: Can we replace traditional cytogenetics with HiFi long-read sequencing?
Robert Månsson Welinder, KTH
Associate professor, Department of Laboratory medicine, Karolinska Institutet and Head of Unit, National Genomics Infrastructure (NGI), KTH Royal Institute of Technology

15:55–16:35 - Multiomic long-reads for clinical genomics in hematologic cancer: pilot using Fiber-Seq
Laurens Lambrechts, VIB-KU Leuven
Postdoctoral fellow at Laboratory of Integrative Cancer Genomics, VIB - KU Leuven

16:35–17:15 - Analysis of leukemia fusion gene expression at single-cell level
Henrik Gezelius, SciLifeLab
Researcher, National Genomics Infrastructure - Single Cell Sequencing, SciLifeLab & Uppsala University

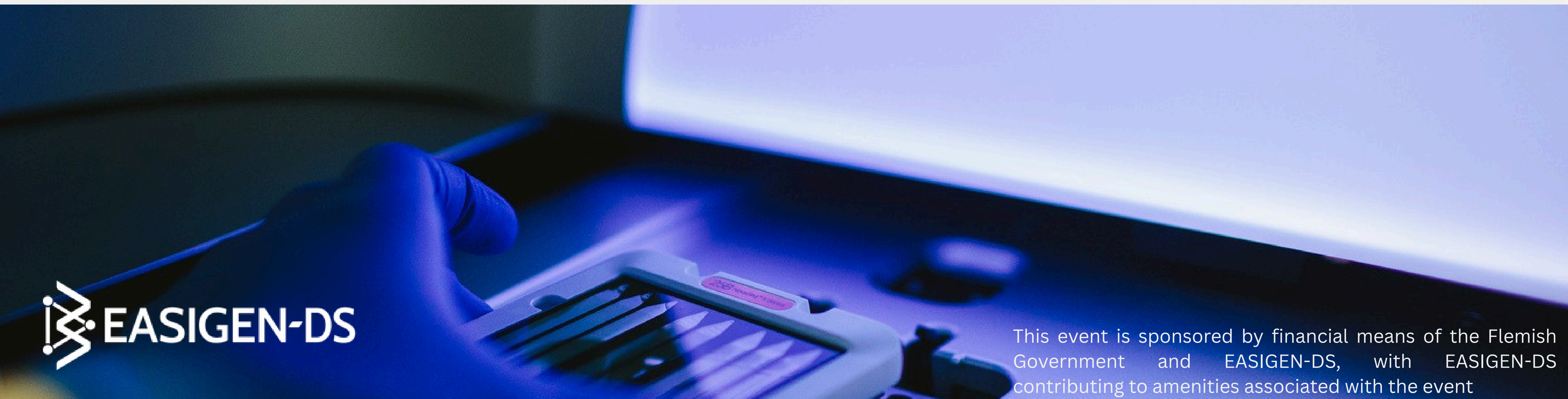
17:15–17:25 – FLASH TALK: Isoseq analysis of 22q11.2DS family trios
Marta Sousa Santos, KU Leuven
PhD student, Laboratory for Cytogenetics and Genome Research, KU Leuven

BLOCK 3 – ASK THE EXPERTS: YOUR QUESTIONS ON MEDICAL GENOMICS

17:25–17:55 - Panel Q&A – “Everything you wanted to ask about long-read sequencing”
All Speakers

CLOSING REMARKS

17:55–18:00 - Closing Remarks and next steps
Organising Committee



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